

Supporting Information File S1 for
Ran GTPase-activating protein 1 is a therapeutic target in diffuse
large B-cell lymphoma

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1 **Supporting Materials and Methods**

2 *Culture of DLBCL and B-lymphoblastoid cell lines*

3 The cells (HT, SU-DHL-5 and EBV-transformed B-lymphoblastoid cell line
4 [LCL]) were cultured at 37°C and 7% CO₂ in RPMI 1640 medium (Gibco/BRL,
5 Grand Island, NY, USA) supplemented with 10% heat-inactivated FCS, 4 mM of
6 glutamine, 75 units/ml of streptomycin, and 100 units/ml of penicillin. Before the
7 analysis, the DLBCL and LCL lines were washed three times with PBS to minimize
8 contamination from serum. Cell viability was determined using the trypan blue
9 exclusion test. Samples from whole cell lysate were normalized based on protein
10 concentration and labeled for comparative proteomics analysis.

11 *Proteomic analysis*

12 *Protein separation and in-gel digestion*

13 Each 5×10^5 cells were lysed by boiling and each 30 µg of extracted protein was
14 applied to 10% polyacrylamide gel electrophoresis. The gel was subsequently
15 visualized through Coomassie blue-staining. Gel lanes were divided into 18 sections
16 and all slices were cut into small gel pieces ($< 1 \text{ mm}^3$), followed by in-gel digestion.
17 All in-gel digestions of proteins were done manually in a laminar flow hood to reduce
18 the amount of keratin contamination. The gel pieces were destained with 50%
19 acetonitrile (ACN) and 25 mM of ammonium bicarbonate. Then, the gel pieces were
20 placed in 10 mM of dithiothreitol for 45 min at 56°C to reduce disulfide bonds. An
21 alkylation reaction was performed using freshly prepared iodoacetamide (55 mM) for
22 45 min at room temperature in the dark. Sequencing grade trypsin (final concentration:
23 4 ng/µl) was used to digest protein at 37°C for 16-18 h. Tryptic peptides were
24 extracted using a 60% ACN/1% trifluoroacetic acid solution. After the peptides had
25 been dried to remove the solvent, the re-dissolved tryptic peptides were subjected to

1 LC LTQ-FT ICR MS analysis.

2 *LC LTQ-FT ICR MS analysis*

3 MS/MS experiments were performed with an LTQ-FT ICR MS (Thermo
4 Electron, San Jose, CA, USA) equipped with a nano-electrospray ion source (New
5 Objective, Woburn, MA, USA), a binary HPLC pump (1100 Series; Agilent
6 Technologies, Santa Clara, CA, USA) and an autosampler (Famos 900 / 920 LC
7 Packings, Sunnyvale, CA, USA). Tryptic peptide mixtures were injected at a 10
8 $\mu\text{L}/\text{min}$ flow rate into a self-packed pre-column in line with a reverse phase C_{18}
9 nano-column ($75 \mu\text{m}$ I.D. \times 200 mm) that used resin (particle size, $5 \mu\text{m}$; pore size,
10 200 \AA) (Magic C_{18}AQ ; Michrom Bioresources, Auburn, CA, USA). The analytic
11 program was set at a linear gradient from 5% to 50% ACN with a 60-min running
12 cycle and a split flow rate of $300 \text{ nl}/\text{min}$. The full-scan survey MS experiment (m/z
13 320-2,000) was executed in FT ICR MS with a mass resolution of 100,000 at m/z 400.
14 The top ten most abundant multiply charged ions were sequentially isolated for
15 MS/MS by LTQ. Singly charged ions were rejected for MS/MS sequencing.

16 *Mascot search and label-free quantitative analysis*

17 The *.raw files of spectra were converted to *.mgf files (Mascot Daemon 2.2;
18 Matrix Science Ltd., London, UK) and merged into a single file for searching using
19 Mascot Daemon software based on the IPI human database (v 3.66). The following
20 Mascot Daemon parameter settings were used: the peptide tolerance was 15 ppm with
21 2^+ and 3^+ peptide charges and the MS/MS tolerance was 0.6 Da. Two missed
22 cleavages by trypsin were allowed; carbamidomethyl (C) was used as a fixed
23 modification; and oxidation (M) and deamidated (NQ) were used as variable
24 modifications. The significance threshold for the identification was set as $p < 0.01$,
25 and at least two peptides were matched. Label-free quantitative analysis was done

1 using quantitative proteomics software (MaxQuant; Max Planck Institute of
2 Biochemistry, Munich, Germany. Available at: <http://www.maxquant.org/>) [22].

3 ***Enzyme-linked immunosorbent assay (ELISA) for RanGAP1***

4 Polystyrene 96 well ELISA plates (eBioscience, San Diego, CA, USA) were
5 incubated overnight at 4°C with 100 µl of coating buffer (0.1 M NaHCO₃ [pH = 9.6])
6 containing 0.2 µg/ml of purified capture monoclonal antibody (mAb, RanGAP1, C-5;
7 Santa Cruz). The wells were blocked with 100 µl of PBS with 10% FBS for 1 h at
8 room temperature (RT), and triplicates of 100 µl of serially diluted standard
9 (RanGAP1 full-length recombinant protein, Novus Biologicals, Littleton, CO, USA)
10 or test samples at various dilutions were added and incubated for 2 h at 37°C. Control
11 and samples as well as subsequent detection reagents were diluted in PBS with 0.05%
12 Tween 20. The fluid from the wells was aspirated and the plates were washed and
13 then incubated for 1 h at RT with 100 µl of detection polyclonal Ab (RanGAP1, N-19,
14 sc-1862; Santa Cruz) at 0.8 µg/ml. Subsequently, the wells were washed and then
15 incubated with 100 µl of goat IgG-HRP conjugate (1:2500, Dako) for 1 h at RT.
16 Between incubations, the plates were washed with PBS containing 0.05% Tween 20.
17 Finally, 100 µl of tetramethylbenzidine (TMB, ES001-500ML; Millipore, Billerica,
18 MA, USA) buffer was added to each well and incubated in the dark for 30 min. After
19 adding stop solution (2N H₂SO₄), the optical density (OD) was measured with a
20 spectrophotometer (µQuant, BIO-TEK instruments, Inc., Winooski, VT, USA) at 450
21 nm.

22 ***Transfecting RANGAP1-specific shRNA into cell lines***

23 The sequences for the RANGAP1 shRNA were as follows:

24 5'-GATCCCCCAAGAGTGAAGACAAGGTCAATTCAAGAGATTGACCTTGTCT
25 TCACTCTTGTTTTTGGAAA-3' (forward), and

1 5'-AGCTTTTCCAAAAACAAGAGTGAAGACAAGGTCAATCTCTTGAATTGAC
2 CTTGTCTTCACTCTTGGGG-3' (reverse). shRNAs were controlled for sequence
3 specificity using a BLAST search and did not show homology to other known human
4 genes. All shRNAs were purchased from Purigo Biotech (Taipei, Taiwan). The
5 plasmids expressing gene-specific shRNA were constructed using synthetic
6 oligonucleotides cloned into the *Bg*III/*Hind*III cloning sites of the pSUPER-EGFP
7 vector (pSUPER RNAi System; OligoEngine, Seattle, WA, USA). Each of the
8 shRNA expression plasmids had a 21 nucleotide gene-specific target in both sense and
9 antisense orientation, separated by a 9 nucleotide spacer sequence. The 5' end
10 corresponded to the *Bg*III site, while the 3' end contained the five-thymidine sequence
11 and *Hind*III-corresponding nucleotides. In all siRNA (small interfering RNA)
12 experiments, a control sample treated with empty vector was included. Other two sets
13 of siRNA sequences were as follows: siRNA1,
14 5'-GATCCCCGAACTTGTCAATTCTGTGAAATTTCAAGAGAATTCACAGAATG
15 ACAAGTTCTTTTTGGAAA-3' (forward), and
16 5'-AGCTTTTCCAAAAAGAACTTGTCAATTCTGTGAAATTCTCTTGAAATTTCA
17 CAGAATGACAAGTTCGGG-3' (reverse); siRNA2,
18 5'-GATCCCCCTGCCTTCCTAAAGGTGTCATTTCAAGAGAATGACACCTTTAG
19 GAAGGCAGTTTTTGGAAA-3' (forward), and
20 5'-AGCTTTTCCAAAAACTGCCTTCCTAAAGGTGTCATTCTCTTGAAATGACA
21 CCTTTAGGAAGGCAG GGG-3' (reverse).

22 An shRANGAP1 expression construct was transfected using an electroporation
23 machine (Microporator; Digital Bio Technology, Suwon, Korea) with 6-8 µg of DNA
24 at 1100-1300 V for 20-30 ms [23]. Transfection efficiency was determined by flow
25 cytometric analysis on fluorescent cells with a flow cytometer (FACSCalibur with

1 CellQuest Pro 4.0.2; Becton Dickinson, Franklin Lakes, NJ, USA) [27].

2 ***Quantitative real-time polymerase chain reaction (Q-PCR)***

3 Primers used for Q-PCR were described as followed: *Aurora-A* forward,

4 5'-AATGCCCTGTCTTACTGTCATTC-3' and reverse,

5 5'-TCCAGAGATCCACCTTCTCATC-3'; *Aurora-B* forward, 5'-

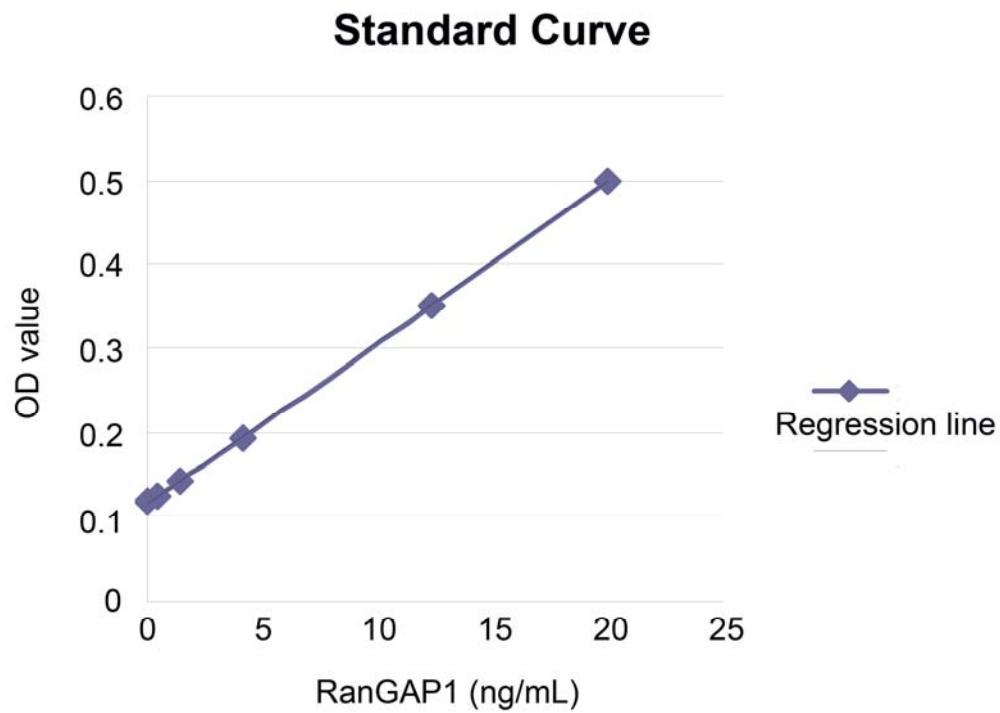
6 CATGGAGGAGTTGGCAGATGC-3' and reverse 5'-

7 TTAGGTCCACCTTGACGATGC-3'; *actin* forward,

8 5'-CTGGACTTCGAGCAAGAGATG-3' and reverse

9 5'-TGATGGAGTTGAAGGTAGTTTCG-3'.

1 **Supporting Figure S1**



2

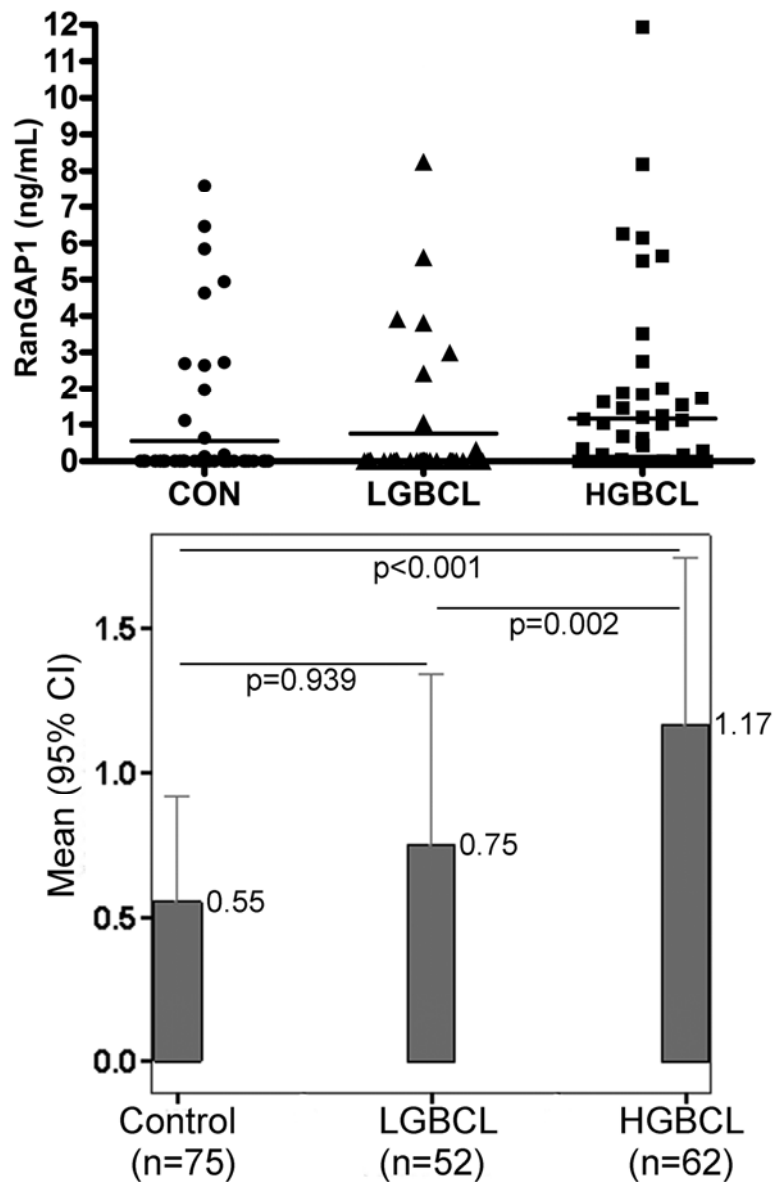
3 **Supporting Figure S1. The standard curve of RanGAP1 serum level.**

4 The colorimetric noncompetitive (immunometric sandwich assay) ELISA has been
5 developed and the standard curve was established by testing triplicates of serially
6 diluted standard. The detection range was 0-20 ng/mL (OD: 0.11-0.5). The regression
7 line formula is: $y=0.0191x+0.116$, $R^2=0.9998$.

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1 Supporting Figure S2.



2

3 **Supporting Figure S2. Higher serum level of RanGAP1 in patients with**

4 **high-grade BCL than in low-grade BCL and healthy controls.** Serum levels of

5 RanGAP1 were higher in patients with high-grade BCL (1.71 ± 2.28 ng/mL, $n = 62$)

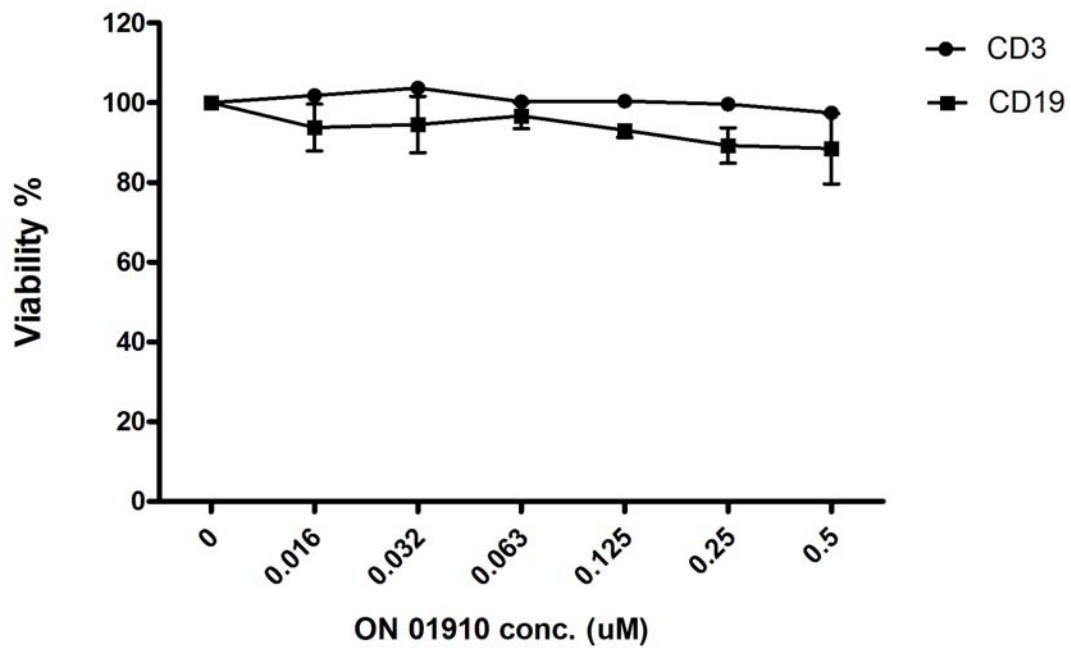
6 than in low-grade BCL (0.75 ± 2.12 ng/mL, $n = 52$) and healthy controls (0.55 ± 1.58

7 ng/mL, $n = 75$) (high-grade BCL vs. low-grade BCL, $p = 0.002$; high-grade BCL vs.

8 control, $p < 0.001$, Mann-Whitney U test). However, the RanGAP1 serum level was

9 not so sensitive since half ($n = 31$) cases of high-grade BCL were not elevated.

1 **Supporting Figure S3**



2

3 **Supporting Figure S3. No cytotoxic effect on B or T cells from healthy donors at**

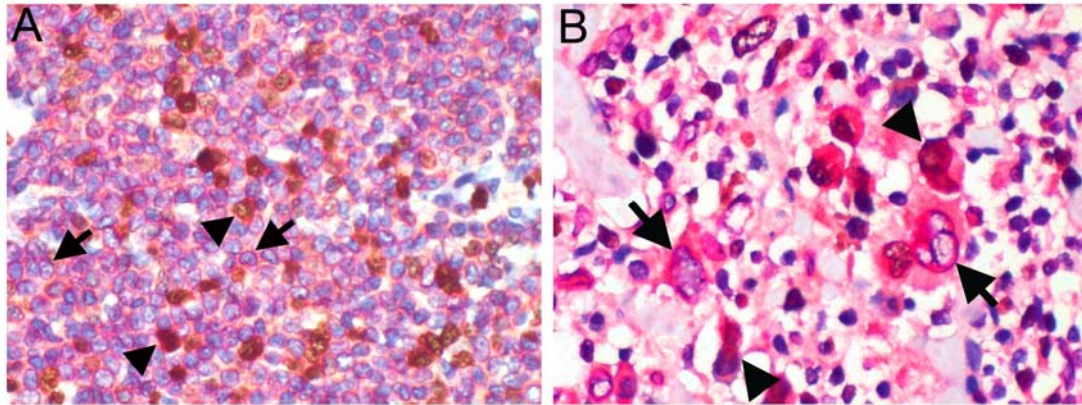
4 **48 hours.** Peripheral blood mononuclear cells of healthy donors were treated with ON

5 01910.Na at increasing doses for 48 hours. Then, cell viability was assessed by flow

6 cytometry by gating CD3⁺ T cells and CD19⁺ B cells. The percentage of viable cells

7 normalized to the untreated control is shown.

1 **Supporting Figure S4**



2

3 **Supporting Figure S4. Double staining of RanGAP1 (red in cytoplasm) and**
4 **Ki-67 (a proliferation marker, brown in nuclei) in mantle cell lymphoma (A) and**
5 **Hodgkin lymphoma (B).** Many RanGAP1-positive tumor cells were negative for
6 Ki-67 staining in mantle cell (A, ×400) and Hodgkin lymphomas (B, ×400) (arrow:
7 RanGAP1⁺/Ki-67⁻; arrowhead: RanGAP1⁺/Ki-67⁺).

Supporting Table S1. Protein identification data expressed according to Paris guidelines

Uniprot		Error			Sequence	Score
Acc#	Protein Name	m/z	z	(ppm)		
P23526	Adenosylhomocysteinase	780.3815	2	-0.5853	ALDIAENEMPGLMR	93
P23526	Adenosylhomocysteinase	550.2774	3	0.1819	GISEETTTGVHNLYK	100
P23526	Adenosylhomocysteinase	944.9854	4	-1.1118	GISEETTTGVHNLYKMMANGILKVPAINVNSVTK	41
P23526	Adenosylhomocysteinase	573.9517	3	-0.5940	KALDIAENEMPGLMR	119
P23526	Adenosylhomocysteinase	460.9209	3	-0.2246	KLDEAVAE AHLGK	137
P23526	Adenosylhomocysteinase	612.3510	3	-0.1584	KLDEAVAE AHLGKLNVK	74
P23526	Adenosylhomocysteinase	705.7149	3	1.2895	MMANGILKVPAINVNSVTK	100
P23526	Adenosylhomocysteinase	668.0301	3	-0.1086	SDKLPYKVADIGLAAWGR	123
P23526	Adenosylhomocysteinase	420.5328	3	0.1559	SKFDNLYGCR	60
P23526	Adenosylhomocysteinase	419.5752	3	-0.1964	VADIGLAAWGRK	107
P23526	Adenosylhomocysteinase	631.0000	3	-0.2310	VAVVAGYGDVGKGCAQALR	97
P23526	Adenosylhomocysteinase	793.7499	3	0.6960	VAVVAGYGDVGKGCAQALRGFGAR	59
P23526	Adenosylhomocysteinase	356.8769	3	-0.0880	VNIKPVDR	85
P23526	Adenosylhomocysteinase	463.2650	3	-0.2040	VNIKPVDRYR	60
P23526	Adenosylhomocysteinase	393.2278	3	-0.0462	YSASKPLKGR	81
P27707	Deoxycytidine kinase	450.9066	3	-0.3478	DAEKPV LFFER	110
P27707	Deoxycytidine kinase	481.2961	3	-0.2589	IKKISIEG NIAAGK	74
P27707	Deoxycytidine kinase	531.2996	3	-0.0249	LKDAEKPV LFFER	109
P27707	Deoxycytidine kinase	686.7935	2	0.2152	SCPSFSASSEGTR	64
P27707	Deoxycytidine kinase	792.6755	3	0.8743	WCNVQSTQDEFEE LTMSQK	178

P52701	DNA mismatch repair protein Msh6	881.4405	3	-0.0823	AAAAPGASPSPPGGDAAWSEAGPGRPLAR	78
P52701	DNA mismatch repair protein Msh6	889.7889	3	0.8626	GGDGPMCRPVILLPEDTPPFLELK	58
P52701	DNA mismatch repair protein Msh6	369.4505	4	-0.4559	GGHFYSAKPEILR	51
P52701	DNA mismatch repair protein Msh6	401.7283	4	0.1167	LANLPEEVIQKGHR	108
P52701	DNA mismatch repair protein Msh6	433.7521	4	-0.1229	LANLPEEVIQKGHRK	61
P52701	DNA mismatch repair protein Msh6	336.2026	3	0.4997	LLKPYTGSK	103
P52701	DNA mismatch repair protein Msh6	594.3041	3	-0.6350	NRYQLEIPENFTTR	71
P52701	DNA mismatch repair protein Msh6	512.6056	3	0.2851	QATSISSETKNTLR	97
P52701	DNA mismatch repair protein Msh6	429.8932	3	0.0529	SPALSDANKASAR	88
P52701	DNA mismatch repair protein Msh6	923.1288	3	-0.0671	SSLSCSLQEGLIPGSQFWDASKTLR	47
P52701	DNA mismatch repair protein Msh6	660.7174	3	0.0670	STVDAAEAVHKLLTLIKEL	61
P52701	DNA mismatch repair protein Msh6	617.3067	4	0.3812	TLFSTHYHSLVEDYSQNVAVR	118
P52701	DNA mismatch repair protein Msh6	486.2488	3	0.2446	TLLEEEYFREK	101
P49736	DNA replication licensing factor MCM2	633.9549	3	-0.1862	AESSESFTMASSPAQRR	70
P49736	DNA replication licensing factor MCM2	1021.4823	3	-0.1481	AIPELDAYEAEGLALDDEDVEELTASQR	63
P49736	DNA replication licensing factor MCM2	773.3478	4	0.4157	ATEDGEEDEEMIESIENLEDLKGHSVR	69
P49736	DNA replication licensing factor MCM2	883.1533	3	-0.1071	DNNELLLFILKQLVAEQVTYQR	123
P49736	DNA replication licensing factor MCM2	362.8636	3	-0.0792	DREAGRGLGR	60
P49736	DNA replication licensing factor MCM2	744.8536	2	0.7520	DTVDPVQDEMLAR	120
P49736	DNA replication licensing factor MCM2	831.0822	3	0.4679	FDILCVVRDTVDPVQDEMLAR	54
P49736	DNA replication licensing factor MCM2	678.0126	3	-0.6861	FGAQQDTIEVPEKDLVDK	43
P49736	DNA replication licensing factor MCM2	565.5459	4	-0.1379	FGAQQDTIEVPEKDLVDKAR	124
P49736	DNA replication licensing factor MCM2	586.8373	2	0.5195	GLALALFGGEPK	97

P49736	DNA replication licensing factor MCM2	542.6385	3	0.1122	GLALALFGGEPKNPGGK	96
P49736	DNA replication licensing factor MCM2	631.9536	3	0.1116	GLLYDSDEEDEERPAR	46
P49736	DNA replication licensing factor MCM2	480.0112	4	-0.1332	IFASIAPSIYGHEDIKR	74
P49736	DNA replication licensing factor MCM2	522.7690	4	-0.6374	IHLRDYVIEDDVNMAIR	61
P49736	DNA replication licensing factor MCM2	343.2013	3	0.0162	IRIQESPGK	124
P49736	DNA replication licensing factor MCM2	435.9224	3	-0.1752	ISHLPLVEELR	100
P49736	DNA replication licensing factor MCM2	556.3310	5	-0.3008	ISHLPLVEELRSLRQLHLNQLIR	50
P49736	DNA replication licensing factor MCM2	330.5262	3	-0.0166	ITNHIHVR	56
P49736	DNA replication licensing factor MCM2	435.8871	3	-0.1826	LNQMDQDKVAK	81
P49736	DNA replication licensing factor MCM2	576.2973	4	-0.5071	NRFGAQQDTIEVPEKDLVDK	51
P49736	DNA replication licensing factor MCM2	378.8963	3	-0.3042	QLHLNQLIR	99
P49736	DNA replication licensing factor MCM2	497.6353	3	0.5051	SLRQLHLNQLIR	103
P49736	DNA replication licensing factor MCM2	554.9414	3	-0.0827	THVDSHGHNVFKER	92
P49736	DNA replication licensing factor MCM2	660.6762	3	-1.7177	TSGVVTSTCTGVLPQLSMVK	69
P49736	DNA replication licensing factor MCM2	327.8503	3	-0.0673	YIEKVSSR	52
P25205	DNA replication licensing factor MCM3	878.1106	3	-0.6099	AIPTTGRGSSGVGLTAAVTTDQETGER	120
P25205	DNA replication licensing factor MCM3	538.2909	3	0.0764	ALKDFVASIDATYAK	83
P25205	DNA replication licensing factor MCM3	669.0253	3	-0.1994	ANRLLNNAFEELVAFQR	110
P25205	DNA replication licensing factor MCM3	692.3387	3	0.2754	CSVLAAANPVYGRYDQYK	54
P25205	DNA replication licensing factor MCM3	771.0775	3	-0.1079	IIKPVLTKESATYIAEEYSR	101
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P25205	DNA replication licensing factor MCM3	404.5788	3	0.2523	LIVNVNDLRR	87
P25205	DNA replication licensing factor MCM3	555.2983	3	-0.4969	LLNNAFEELVAFQR	161

P25205	DNA replication licensing factor MCM3	485.2282	3	0.4832	LRSQDSMSSDTAR	62
P25205	DNA replication licensing factor MCM3	388.8802	3	0.1901	SKDIFDQLAK	118
P25205	DNA replication licensing factor MCM3	397.5377	3	-0.5910	SVHYCPATKK	54
P25205	DNA replication licensing factor MCM3	718.0170	3	0.3516	TADSQETKESQKVELSESR	65
P25205	DNA replication licensing factor MCM3	513.3069	3	-0.4061	TLETLIRLATAHAK	106
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P33991	DNA replication licensing factor MCM4	469.2527	3	-0.2505	ELSRKPDIIYER	80
P33991	DNA replication licensing factor MCM4	940.8090	3	-0.5629	FIDPLAKEEENVGIDITEPLYMQR	136
P33991	DNA replication licensing factor MCM4	877.1032	3	-1.1575	GLQVDLQSDGAAAEDIVASEQSLGQK	94
P33991	DNA replication licensing factor MCM4	633.3157	3	-0.3575	GSSAVGLTAYVMKDPETR	55
P33991	DNA replication licensing factor MCM4	765.7316	3	-0.5290	LGEINVIGEPFLNVNCEHIK	127
P33991	DNA replication licensing factor MCM4	468.9889	4	0.2407	LHGLDEEAEQKLFSEK	78
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P33991	DNA replication licensing factor MCM4	508.0142	4	-0.2248	RLHGLDEEAEQKLFSEK	81
P33991	DNA replication licensing factor MCM4	414.9225	3	0.3475	RVELLKELSR	71
P33991	DNA replication licensing factor MCM4	348.1821	3	0.0499	SFDKNLYR	106

P33991	DNA replication licensing factor MCM4	408.4730	4	0.1329	SVYKTHIDVIHYR	75
P33991	DNA replication licensing factor MCM4	440.4967	4	-0.0311	SVYKTHIDVIHYRK	58
P33991	DNA replication licensing factor MCM4	911.9826	2	1.4597	TGIVDISILTTGMSATSR	54
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P33991	DNA replication licensing factor MCM4	461.2613	2	-0.1477	VNVTGIYR	76
P33992	DNA replication licensing factor MCM5	582.8133	2	1.0803	AIACLLFGGSR	88
P33992	DNA replication licensing factor MCM5	595.2787	3	-0.9109	CPLDPYFIMPDKCK	102
P33992	DNA replication licensing factor MCM5	714.3708	4	0.3975	EVADEVTRPRPSGEEVLQDIQVMLK	84
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Q14566	DNA replication licensing factor MCM6	598.3003	3	0.7555	ESEDFIVEQYKHLR	49
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Q14566	DNA replication licensing factor MCM6	339.4543	4	0.0920	HVKEAFRLLNK	54
Q14566	DNA replication licensing factor MCM6	565.6443	3	0.3425	IQETQAELPRGSIPR	74
Q14566	DNA replication licensing factor MCM6	531.0298	4	0.6264	ISKESEDFIVEQYKHLR	69
Q14566	DNA replication licensing factor MCM6	521.2617	3	1.3634	KVEEEEDDESALKR	164
Q14566	DNA replication licensing factor MCM6	884.7572	3	-0.5284	MDLAAAEPGAGSQHLEVRDEVAEK	113
Q14566	DNA replication licensing factor MCM6	562.6250	3	0.3377	TSILAAANPISGHYDR	121
Q14566	DNA replication licensing factor MCM6	480.6037	3	0.1131	VRIQETQAELPR	119
Q14566	DNA replication licensing factor MCM6	569.9602	3	-0.2810	VSGVDGYETEGIRGLR	114
P33993	DNA replication licensing factor MCM7	450.5819	3	0.2258	ALKDYALEKEK	125
P33993	DNA replication licensing factor MCM7	662.8347	4	0.5299	EVVNKDVLVDVYIEHRLMMEQR	79
P33993	DNA replication licensing factor MCM7	640.6790	3	0.5216	LFADAVQELLPQYKER	127
P33993	DNA replication licensing factor MCM7	418.2314	3	0.1677	QFKYGNQLVR	65
P33993	DNA replication licensing factor MCM7	609.3163	3	-0.0064	RFELYFQGPSSNKPR	126
P33993	DNA replication licensing factor MCM7	571.3099	4	-0.1619	YAKLFADAVQELLPQYKER	118
P33993	DNA replication licensing factor MCM7	382.2277	3	0.1045	ADSVGKLVTVR	96
P33993	DNA replication licensing factor MCM7	515.3062	2	0.3469	AGILTTLNAR	55
P33993	DNA replication licensing factor MCM7	517.6470	3	-0.3478	ALLLLLGGVDQSPR	135
P33993	DNA replication licensing factor MCM7	420.8896	3	-0.1551	DSLLGDKGQTAR	84
P33993	DNA replication licensing factor MCM7	510.2984	3	0.0843	EVRADSVGKLVTVR	106
P33993	DNA replication licensing factor MCM7	698.3480	4	-0.8026	FIKFQEMKMQEHSDQVPVGNIPR	59
P33993	DNA replication licensing factor MCM7	456.8823	3	-0.2028	FSEAEQRCVSR	54
P33993	DNA replication licensing factor MCM7	995.1455	3	0.6224	GFTPAQFQAALDEYEELNVWQVNASR	131

P33993	DNA replication licensing factor MCM7	438.2698	3	0.0261	GIVTRVSEVKPK	63
P33993	DNA replication licensing factor MCM7	678.3896	3	-0.2999	IAQPGDHVSVTGIFLPILR	138
P33993	DNA replication licensing factor MCM7	499.7514	4	-0.1521	LMEMSKDSSLGDKGQTAR	67
P33993	DNA replication licensing factor MCM7	756.0133	3	-0.2404	MNKSEDESAGELTREELR	74
P33993	DNA replication licensing factor MCM7	569.6141	3	0.2587	MQEHSQVPVGNIPR	50
P33993	DNA replication licensing factor MCM7	631.6205	3	-0.4835	SEDESAGELTREELR	92
P33993	DNA replication licensing factor MCM7	384.2158	3	0.0889	SGGRLYLQTR	138
P33993	DNA replication licensing factor MCM7	826.9701	2	0.0413	SLEQNIQLPAALLSR	110
P33993	DNA replication licensing factor MCM7	511.2912	3	-0.0429	SQLLSYIDRLAPR	101
P33993	DNA replication licensing factor MCM7	403.5388	3	-0.2140	SVRFSEAEQR	116
P33993	DNA replication licensing factor MCM7	768.7414	3	1.0386	TGFRQVVQGLLSETYLEAHR	118
P33993	DNA replication licensing factor MCM7	529.6972	5	-0.3452	TGFRQVVQGLLSETYLEAHRIVK	94
P33993	DNA replication licensing factor MCM7	491.9439	3	-0.2180	TQRPADVIFATVR	102
P33993	DNA replication licensing factor MCM7	543.8026	4	0.0384	TQRPADVIFATVRELVSGGR	107
C9J4C3	DNA topoisomerase 2	969.4456	3	1.0212	AGEMELKPFNGEDYTCITFQPDLSK	45
C9J4C3	DNA topoisomerase 2	423.2225	3	-0.0892	AYDIAGSTKDVK	80
C9J4C3	DNA topoisomerase 2	365.5380	3	-0.5069	DKYGVFPLR	65
C9J4C3	DNA topoisomerase 2	427.2434	3	-0.1949	DKYGVFPLRGK	112
C9J4C3	DNA topoisomerase 2	541.9494	3	0.2375	DPALNSGVSQKPDPAK	100
C9J4C3	DNA topoisomerase 2	468.5590	3	0.5509	EAKYFADMKR	51
C9J4C3	DNA topoisomerase 2	543.6435	3	-1.0781	HRFLEEFITPIVK	151
C9J4C3	DNA topoisomerase 2	681.0491	3	-0.0277	HVDYVADQIVTKLVDVVK	162
C9J4C3	DNA topoisomerase 2	582.6442	3	-0.1266	IFDEILVNAADNKQR	123

C9J4C3	DNA topoisomerase 2	696.0358	3	-0.4381	IFDEILVNAADNKQRDPK	55
C9J4C3	DNA topoisomerase 2	389.5595	3	-0.0822	ILNVREASHK	55
C9J4C3	DNA topoisomerase 2	566.9810	3	-0.5322	IPNFDVREIVNNIR	72
C9J4C3	DNA topoisomerase 2	464.5129	4	-0.0750	IPNFDVREIVNNIRR	53
C9J4C3	DNA topoisomerase 2	469.5902	3	0.1319	ITIEMKAEAEKK	60
C9J4C3	DNA topoisomerase 2	425.5992	3	0.2726	KQTTLAFKPIK	84
C9J4C3	DNA topoisomerase 2	564.5063	4	-0.7549	KSKGESDDFHMDFDSAVAPR	52
C9J4C3	DNA topoisomerase 2	458.2466	3	0.4294	KTQMAEVLPSPR	43
C9J4C3	DNA topoisomerase 2	908.4190	3	-0.2327	LDDANDAGGRNSTECTLILTEGDSAK	120
C9J4C3	DNA topoisomerase 2	375.5318	3	0.3545	LHGGKDSASPR	78
C9J4C3	DNA topoisomerase 2	475.2696	3	-0.3213	LLFPPKDDHTLK	50
C9J4C3	DNA topoisomerase 2	395.5714	3	-0.0518	LSNKELKPQK	79
C9J4C3	DNA topoisomerase 2	800.7469	3	-0.5023	MEVSPLQPVNENMQVNKIKK	41
C9J4C3	DNA topoisomerase 2	845.7368	3	-0.7346	MYVPALIFGQLLTSSNYDDDEK	105
C9J4C3	DNA topoisomerase 2	883.1035	3	-0.3986	MYVPALIFGQLLTSSNYDDDEKK	61
C9J4C3	DNA topoisomerase 2	784.1432	4	-0.6536	MYVPALIFGQLLTSSNYDDDEKKVTGGR	142
C9J4C3	DNA topoisomerase 2	494.9072	3	0.4303	NYEDEDLTKTLR	76
C9J4C3	DNA topoisomerase 2	475.2562	3	0.3585	RAYDIAGSTKDVK	111
C9J4C3	DNA topoisomerase 2	593.9831	3	0.1333	RDPALNSGVSQKPDPAK	66
C9J4C3	DNA topoisomerase 2	636.6462	3	-1.0086	RLMDGEEPLPMLPSYK	50
C9J4C3	DNA topoisomerase 2	500.9328	3	0.3133	SIPSMVDGLKPGQR	48
C9J4C3	DNA topoisomerase 2	709.6410	3	-0.2953	SKGESDDFHMDFDSAVAPR	76
C9J4C3	DNA topoisomerase 2	991.2443	4	0.0981	SVVSDLEADDVKGSVPLSSPPATHFPDETEITNPVPK	44

C9J4C3	DNA topoisomerase 2	614.8214	2	0.8599	TQMAEVLPSPR	101
C9J4C3	DNA topoisomerase 2	804.7299	3	0.3575	TWTQTYKEQVLEPMLNGTEK	62
C9J4C3	DNA topoisomerase 2	397.9885	4	-0.1083	VFLNGNKLPVKGFR	88
C9J4C3	DNA topoisomerase 2	659.3472	2	0.3943	YIFTMLSSLAR	79
Q02880	DNA topoisomerase 2-beta	359.8732	3	-0.8253	FKAQTQLNK	52
Q02880	DNA topoisomerase 2-beta	414.2347	3	0.5676	GKPSSDTVPKPK	81
Q02880	DNA topoisomerase 2-beta	362.8720	3	0.7570	GREVNDLKR	70
Q02880	DNA topoisomerase 2-beta	510.6169	3	-0.3885	HGFLEEFITPIVK	174
Q02880	DNA topoisomerase 2-beta	671.3344	4	-0.7738	HLTYNDFINKELILFSNSDNER	134
Q02880	DNA topoisomerase 2-beta	680.3894	3	-0.2464	HVDYVVDQVVGKLIEVVK	91
Q02880	DNA topoisomerase 2-beta	582.6442	3	-0.1266	IFDEILVNAADNKQR	123
Q02880	DNA topoisomerase 2-beta	389.5595	3	-0.0822	ILNVREASHK	55
Q02880	DNA topoisomerase 2-beta	979.7978	3	-1.0993	KTSFDQSDVDIFPSDFPTEPPSLPR	90
Q02880	DNA topoisomerase 2-beta	760.8743	2	0.0562	LQLEETMPSPYGR	66
Q02880	DNA topoisomerase 2-beta	500.9438	3	0.2491	SIPSLVDGFKPGQR	62
Q02880	DNA topoisomerase 2-beta	466.5684	3	-0.3526	SYDDAESLKTLR	53
Q02880	DNA topoisomerase 2-beta	829.7478	3	-0.8241	VYVPALIFGQLLTSSNYDDDEK	48
Q02880	DNA topoisomerase 2-beta	872.4462	3	-0.7687	VYVPALIFGQLLTSSNYDDDEKK	66
Q02880	DNA topoisomerase 2-beta	772.1515	4	0.2253	VYVPALIFGQLLTSSNYDDDEKKVTGGR	94
P62807	Histone H2B type 1-C/E/F/G/I	592.6079	3	0.0268	AMGIMNSFVNDIFER	189
P62807	Histone H2B type 1-C/E/F/G/I	820.7264	3	0.9082	AMGIMNSFVNDIFERIAGEASR	96
P62807	Histone H2B type 1-C/E/F/G/I	328.8502	3	0.2151	AVTKYTSSK	75
P62807	Histone H2B type 1-C/E/F/G/I	584.3524	3	-0.4233	EIQTAVRLLLLPGELAK	159

P62807	Histone H2B type 1-C/E/F/G/I	414.7141	2	-0.0110	HAVSEGTK	104
P62807	Histone H2B type 1-C/E/F/G/I	409.8946	3	-0.1258	HAVSEGTKAVTK	175
P62807	Histone H2B type 1-C/E/F/G/I	598.6513	3	-0.1595	HAVSEGTKAVTKYTSSK	182
P62807	Histone H2B type 1-C/E/F/G/I	529.2901	3	0.1882	IAGEASRLAHYNKR	115
P62807	Histone H2B type 1-C/E/F/G/I	422.5519	3	0.0435	KESYSVYVYK	89
P62807	Histone H2B type 1-C/E/F/G/I	535.9677	3	0.0880	KESYSVYVYKVLK	167
P62807	Histone H2B type 1-C/E/F/G/I	477.3051	2	-0.0812	LLLPGELAK	71
P62807	Histone H2B type 1-C/E/F/G/I	441.5070	4	-0.1314	LLLPGELAKHAVSEGTK	76
P62807	Histone H2B type 1-C/E/F/G/I	364.8731	3	-0.4260	PEPAKSAPAPK	136
P62807	Histone H2B type 1-C/E/F/G/I	390.2034	3	-0.0487	QVHPDTGISSK	90
P62807	Histone H2B type 1-C/E/F/G/I	539.9726	3	1.2034	RSTITSREIQTAVR	104
P62807	Histone H2B type 1-C/E/F/G/I	503.5963	3	-0.3514	SRKESYSVYVYK	199
P62807	Histone H2B type 1-C/E/F/G/I	487.9388	3	0.1818	STITSREIQTAVR	122
P62807	Histone H2B type 1-C/E/F/G/I	599.8522	4	-0.7458	STITSREIQTAVRLLLPGELAK	77
P62807	Histone H2B type 1-C/E/F/G/I	503.6192	3	0.0631	VLKQVHPDTGISSK	121
P36776	Lon protease homolog, mitochondrial	397.8728	3	-0.0751	ALCGLDESKAK	100
P36776	Lon protease homolog, mitochondrial	356.8577	3	0.1272	ALNREYFR	66
P36776	Lon protease homolog, mitochondrial	1291.6337	3	0.0568	GYQGDPSALLELLDPEQANFLDHYLDVPVDLSK	78
P36776	Lon protease homolog, mitochondrial	775.6318	4	0.7393	HVMDVVDEELSKLGLLDNHSSEFNVTR	66
P36776	Lon protease homolog, mitochondrial	351.8937	3	-0.0234	ILPVGGIKEK	80
P36776	Lon protease homolog, mitochondrial	1059.2101	3	0.4965	IVSGEAEVETPENLQDFVGKPVFTVER	105
P36776	Lon protease homolog, mitochondrial	500.6279	3	-0.4744	LAIAERYLVPQAR	88
P36776	Lon protease homolog, mitochondrial	464.2784	3	-0.4114	LAQPYVGVFLKR	98

P36776	Lon protease homolog, mitochondrial	603.6695	3	-0.6243	LSSDVLTLLIKQYCR	116
P36776	Lon protease homolog, mitochondrial	796.9090	2	0.5307	NYLDWLTSIPWGK	78
P36776	Lon protease homolog, mitochondrial	923.4608	3	0.3294	NYLDWLTSIPWGKYSNENLDLAR	113
P36776	Lon protease homolog, mitochondrial	540.5236	4	-0.3397	QLEVEPEEPEAENKHKPR	74
P36776	Lon protease homolog, mitochondrial	833.3910	5	0.8011	RDDSNESDVVESLDEIYHTGTFAQIHEMQDLGDKLR	52
P36776	Lon protease homolog, mitochondrial	906.9663	4	0.3790	SAYKIVSGEAEVVEVTPENLQDFVGKPVFTVER	54
P36776	Lon protease homolog, mitochondrial	609.0070	3	-0.5357	TENPLILIDEVDKIGR	118
P36776	Lon protease homolog, mitochondrial	737.8916	4	-1.0571	TIRDIIALNPLYRESVLQMMQAGQR	101
P36776	Lon protease homolog, mitochondrial	685.3879	3	0.0298	TKTENPLILIDEVDKIGR	139
P36776	Lon protease homolog, mitochondrial	1228.9365	3	0.5697	VVDNPIYLSDMGAALTGAESHELQDVLEETNIPK	117
P36776	Lon protease homolog, mitochondrial	849.8335	5	0.0203	VVDNPIYLSDMGAALTGAESHELQDVLEETNIPKRLYK	48
P36776	Lon protease homolog, mitochondrial	597.7911	2	0.3798	YSNENLDLAR	77
Q14676	Mediator of DNA damage checkpoint protein 1	980.8607	3	0.4982	AAESLTAIPEPASPQLLETPIHASQIQK	36
Q14676	Mediator of DNA damage checkpoint protein 1	888.2282	4	-0.1156	AAESLTAIPEPASPQLLETPIHASQIQKVEPAGR	39
Q14676	Mediator of DNA damage checkpoint protein 1	600.3101	4	-0.5916	AAGNPGSLAAPIDHKPCSAPLEPK	42
Q14676	Mediator of DNA damage checkpoint protein 1	514.2499	3	0.0060	DQAEEEPNRIPSR	88
Q14676	Mediator of DNA damage checkpoint protein 1	748.0326	3	0.3126	LEPSTSTDQPVTPEPTSQATR	52
Q14676	Mediator of DNA damage checkpoint protein 1	852.1740	4	-0.7820	MTPFPATSAAPEPHSTSTAQPVTPKPTSQATR	38
Q14676	Mediator of DNA damage checkpoint protein 1	934.7285	4	0.2094	SSGKTPETLVPTAPKLEPSTSTDQPVTPEPTSQATR	88
Q14676	Mediator of DNA damage checkpoint protein 1	756.8936	4	-0.1103	SSVKTPEPVVPTAPEPHPTTSTDQPVTPK	50
Q14676	Mediator of DNA damage checkpoint protein 1	1145.2493	3	0.1649	SSVKTPEVVVPAPELQPSTSTDQPVTPEPTSR	75
Q14676	Mediator of DNA damage checkpoint protein 1	950.2405	4	-0.1154	SSVKTPEVVVPTALELQPSTSTDRPVTSEPTSQATR	82
Q14676	Mediator of DNA damage checkpoint protein 1	1133.2372	3	0.0006	SSVKTPEVVVPTAPELQASASTDQPVTSEPTSR	82

Q14676	Mediator of DNA damage checkpoint protein 1	1126.2300	3	-0.3539	TPEPVVPTAPELQPSTSTDQPVTSEPTSQVTR	79
Q14676	Mediator of DNA damage checkpoint protein 1	875.1132	3	-0.0843	TPEPVVPTAPEPHPTTSTDQPVTPK	105
Q14676	Mediator of DNA damage checkpoint protein 1	1011.5068	3	-0.9907	TPETVVVPAPELQPSTSTDQPVTPEPTSR	62
Q14676	Mediator of DNA damage checkpoint protein 1	999.4947	3	0.0003	TPETVVVPTAPELQASASTDQPVTSEPTSR	86
Q14676	Mediator of DNA damage checkpoint protein 1	1026.5382	3	-0.0080	TPETVVVPTAPELQISTSTDQPVTPKPTSR	104
Q14676	Mediator of DNA damage checkpoint protein 1	1165.2493	3	-0.1516	TPKPVVEPAASDLEPFTPTDQSVTPEAIAQGGQSK	74
P19338	Nucleolin, isoform 1	348.1929	3	0.1356	AGKNQGDPPK	133
P19338	Nucleolin, isoform 1	384.8998	3	-0.2113	AIRLELQGPR	138
P19338	Nucleolin, isoform 1	578.9956	3	0.6816	AIRLELQGRGSPNAR	104
P19338	Nucleolin, isoform 1	544.6504	3	-0.2532	ALELTGLKVFGEIK	166
P19338	Nucleolin, isoform 1	498.3118	3	-0.1267	ALVATPGKKGAAPAK	47
P19338	Nucleolin, isoform 1	482.2684	3	0.1004	ATFIKVPQNQNGK	80
P19338	Nucleolin, isoform 1	438.2576	3	-0.2129	AVTTPGKKGATPGK	73
P19338	Nucleolin, isoform 1	782.7143	3	0.6047	EAMEDGEIDGNKVTLDWAKPK	111
P19338	Nucleolin, isoform 1	816.1696	4	-0.1778	FGYVDFESAEDLEKALELTGLKVFGEIK	41
P19338	Nucleolin, isoform 1	465.9488	3	0.2718	GATPGKALVATPGKK	82
P19338	Nucleolin, isoform 1	781.3439	2	0.2731	GFGFVDFNSEEDAK	130
P19338	Nucleolin, isoform 1	611.2881	3	-0.1322	GFGFVDFNSEEDAKAAK	87
P19338	Nucleolin, isoform 1	734.0132	3	0.5886	GLSEDTTEETLKESFDGSVR	158
P19338	Nucleolin, isoform 1	809.7260	3	0.8582	GLSEDTTEETLKESFDGSVRAR	95
P19338	Nucleolin, isoform 1	700.3228	3	0.0594	GQNQDYRGGKNSTWSGESK	60
P19338	Nucleolin, isoform 1	667.5682	4	-0.2765	GYAFIEFASFEDAKEALNSCNKR	95
P19338	Nucleolin, isoform 1	912.4314	3	-0.2406	IVTDRETGSSKGFVDFNSEEDAK	143

P19338	Nucleolin, isoform 1	592.9491	3	0.9760	KFGYVDFESAEDLEK	119
P19338	Nucleolin, isoform 1	651.3376	4	-0.7448	KFGYVDFESAEDLEKALELTGLK	105
P19338	Nucleolin, isoform 1	337.8818	3	0.2470	KGAAIPAKGAK	103
P19338	Nucleolin, isoform 1	899.4729	3	0.5416	KQKVEGTEPTTAFNLFVGNLNFNK	140
P19338	Nucleolin, isoform 1	338.2220	3	-0.5283	KVAVATPAKK	111
P19338	Nucleolin, isoform 1	329.2183	3	-0.6655	KVVVSPTKK	109
P19338	Nucleolin, isoform 1	1024.4361	4	-0.8873	MAPPPKEVEEDSEDEEMSEDEEDDSSGEEVVIPQKK	73
P19338	Nucleolin, isoform 1	869.7815	3	0.1240	NLPYKVTQDELKEVFEDAAEIR	135
P19338	Nucleolin, isoform 1	1159.9018	3	0.0594	NSTWSGESKTLVLSNLSYSATEETLQEVFEK	159
P19338	Nucleolin, isoform 1	673.0006	3	-0.3923	QGTEIDGRSISLYYTGEK	40
P19338	Nucleolin, isoform 1	856.7746	3	-0.2439	QKVEGTEPTTAFNLFVGNLNFNK	101
P19338	Nucleolin, isoform 1	799.1687	4	-0.4634	QKVEGTEPTTAFNLFVGNLNFNKSAPELK	41
P19338	Nucleolin, isoform 1	848.7938	3	0.7305	SAPELKTGISDVFAKNDLAVVDVR	157
P19338	Nucleolin, isoform 1	674.6570	3	-0.3313	SISLYYTGEKGQNQDYR	136
P19338	Nucleolin, isoform 1	755.3696	3	-0.2550	SISLYYTGEKGQNQDYRGGK	125
P19338	Nucleolin, isoform 1	378.8888	3	-0.0213	SQPSKTLFVK	71
P19338	Nucleolin, isoform 1	503.9108	3	-0.2130	TFEEKQGTEIDGR	124
P19338	Nucleolin, isoform 1	640.3459	3	0.4741	TGISDVFAKNDLAVVDVR	146
P19338	Nucleolin, isoform 1	826.4442	3	0.2521	TGISDVFAKNDLAVVDVRIGMTR	50
P19338	Nucleolin, isoform 1	930.1344	3	-0.1070	TLFVKGLSEDTEETLKESFDGSVR	136
P19338	Nucleolin, isoform 1	834.4268	3	-0.3273	TLVLSNLSYSATEETLQEVFEK	232
P19338	Nucleolin, isoform 1	1021.2042	3	-0.2678	TLVLSNLSYSATEETLQEVFEKATFIK	80
P19338	Nucleolin, isoform 1	982.5151	4	-0.8613	TLVLSNLSYSATEETLQEVFEKATFIKVPQNQNGK	61

P19338	Nucleolin, isoform 1	771.3901	3	0.5138	VEGTEPTTAFNLFVGNLNFNK	259
P19338	Nucleolin, isoform 1	979.8379	3	-0.5022	VEGTEPTTAFNLFVGNLNFNKSAPELK	78
P19338	Nucleolin, isoform 1	351.2080	4	0.2442	VFGNEIKLEKPK	72
P19338	Nucleolin, isoform 1	664.6689	3	0.2744	VTQDELKEVFEDAAEIR	148
P19338	Nucleolin, isoform 1	807.0954	3	0.9731	VTQDELKEVFEDAAEIRLVSK	129
P13010	Protein X-ray repair cross-complementing 5	321.8468	3	-0.3177	AFREEAIK	53
P13010	Protein X-ray repair cross-complementing 5	807.6841	4	0.2029	ALHPREPLPPIQQHIWNMLNPPAEVTTK	76
P13010	Protein X-ray repair cross-complementing 5	1106.1871	3	0.6769	ASFEEASNQLINHIEQFLDTNETPYFMK	154
P13010	Protein X-ray repair cross-complementing 5	780.1238	4	0.6511	CDISLQFFLPSLKGEDGSGDRGDGPFR	36
P13010	Protein X-ray repair cross-complementing 5	913.8005	3	-0.7129	DDEAAAVALSSLIHALDDLDMVAIVR	107
P13010	Protein X-ray repair cross-complementing 5	842.3794	3	-0.0605	DKPSGDTAAVFEEGGDVDDLDMI	88
P13010	Protein X-ray repair cross-complementing 5	748.3452	3	-0.3412	DQVTAQEIFQDNHEDGPTAK	82
P13010	Protein X-ray repair cross-complementing 5	885.1317	3	0.5489	EPLPPIQQHIWNMLNPPAEVTTK	55
P13010	Protein X-ray repair cross-complementing 5	967.7868	3	0.2773	ETVYCLNDDDETEVLKEDIHQGFR	58
P13010	Protein X-ray repair cross-complementing 5	1027.8251	3	-0.1540	FLAPKDKPSGDTAAVFEEGGDVDDLDMI	100
P13010	Protein X-ray repair cross-complementing 5	506.6101	3	0.0296	FQRLFQCLLHR	192
P13010	Protein X-ray repair cross-complementing 5	524.6262	3	-0.1383	GITEQQKEGLEIVK	49
P13010	Protein X-ray repair cross-complementing 5	560.6299	3	-0.1422	HIEIFTDLSSRFSK	80
P13010	Protein X-ray repair cross-complementing 5	644.3204	3	0.0887	HLMLPDFDLLEDIESK	180
P13010	Protein X-ray repair cross-complementing 5	431.2505	3	-0.0060	IAAYKSILQER	122
P13010	Protein X-ray repair cross-complementing 5	424.9357	3	-0.3596	IKTLFPLIEAK	135
P13010	Protein X-ray repair cross-complementing 5	865.9146	4	-0.2009	KASFEEASNQLINHIEQFLDTNETPYFMK	56
P13010	Protein X-ray repair cross-complementing 5	627.6544	3	0.1370	KDEKTDLTLEDLFPTTK	121

P13010	Protein X-ray repair cross-complementing 5	833.7419	3	-0.1027	KKDQVTAQEIFQDNHEDGPTAK	189
P13010	Protein X-ray repair cross-complementing 5	873.4445	4	0.7922	KLKTEQGGAHFSVSSLAEGSVTSVGSVNPAENFR	52
P13010	Protein X-ray repair cross-complementing 5	822.4246	3	-0.1309	KYAPTEAQLNAVDALIDSMSLAK	134
P13010	Protein X-ray repair cross-complementing 5	362.8674	3	-0.0958	LFQCLLHR	115
P13010	Protein X-ray repair cross-complementing 5	370.5416	3	0.1109	LGGHGPSFPLK	106
P13010	Protein X-ray repair cross-complementing 5	888.1569	3	-0.1796	LGGHGPSFPLKGITEQQKEGLEIVK	99
P13010	Protein X-ray repair cross-complementing 5	841.4207	4	-0.2742	LKTEQGGAHFSVSSLAEGSVTSVGSVNPAENFR	55
P13010	Protein X-ray repair cross-complementing 5	1016.2514	4	-0.6479	QVFAENKDEIALVLFGTDTNPLSGGDQYQNITVHR	139
P13010	Protein X-ray repair cross-complementing 5	338.5500	3	-0.3166	SQIPLSKIK	51
P13010	Protein X-ray repair cross-complementing 5	653.3458	3	-0.0569	TDTLEDLFPTTKIPNPR	132
P13010	Protein X-ray repair cross-complementing 5	368.2204	3	-0.7047	TLKKEDIQK	116
P13010	Protein X-ray repair cross-complementing 5	817.6815	4	0.0599	VFAARDDEAAVALSSLIHALDDLDMVAIVR	127
P13010	Protein X-ray repair cross-complementing 5	505.2786	2	0.1154	VITMFVQR	96
P13010	Protein X-ray repair cross-complementing 5	779.7263	3	0.2345	YAPTEAQLNAVDALIDSMSLAK	223
P13010	Protein X-ray repair cross-complementing 5	657.9838	3	0.0965	YGSDIVPFSKVDDEEQMK	104
P46060	Ran GTPase-activating protein 1	878.7784	3	-0.9728	AIANLYGPLMALNHMVQQDYFPK	53
P46060	Ran GTPase-activating protein 1	859.4684	3	0.1677	ALAPLLLAFFVTKPNSALESCSFAR	121
P46060	Ran GTPase-activating protein 1	601.3506	2	0.2345	HSLLTLYKV	66
P46060	Ran GTPase-activating protein 1	1097.5659	3	1.1537	ILDPTGEPAPVLSSPPPADVSTFLAFPSPEK	105
P46060	Ran GTPase-activating protein 1	1224.9890	3	0.6336	ILDPTGEPAPVLSSPPPADVSTFLAFPSPEKLLR	68
P46060	Ran GTPase-activating protein 1	541.9895	3	0.0794	SKGAVAIADAIRGGLPK	80
P46060	Ran GTPase-activating protein 1	821.7708	3	-0.1952	SSVLIAQQTDTSDPEKVVSAFLK	102
P46060	Ran GTPase-activating protein 1	440.9139	3	0.2841	TQVAGGQLSFKGK	44

P46060	Ran GTPase-activating protein 1	446.5735	3	-0.0226	VSSVFKDEATVR	55
P43487	Ran-specific GTPase-activating protein	984.1847	4	-0.2676	DTHEDHDTSTENTDESNHDPQFEPIVSLPEQEIK	93
P43487	Ran-specific GTPase-activating protein	540.9266	3	-0.1036	FASENDLPEWKER	168
P43487	Ran-specific GTPase-activating protein	726.6869	3	-0.1946	FASENDLPEWKERGTGDVK	80
P43487	Ran-specific GTPase-activating protein	437.2348	3	0.3173	FLNAENAQKFK	83
P43487	Ran-specific GTPase-activating protein	613.2870	4	-0.0831	ICANHYYITPMMELKPNAGSDR	49
P43487	Ran-specific GTPase-activating protein	510.0102	4	-0.2324	LFRFASENDLPEWKER	107
P43487	Ran-specific GTPase-activating protein	691.3221	2	0.2915	TLEEDDEELFK	101
P43487	Ran-specific GTPase-activating protein	556.9310	3	0.3946	TLEEDDEELFKMR	139
P23246	Splicing factor, proline- and glutamine-rich	426.2032	3	0.2319	AELDDTPMRGR	55
P23246	Splicing factor, proline- and glutamine-rich	426.2032	3	0.1462	AELDDTPMRGR	55
P23246	Splicing factor, proline- and glutamine-rich	581.9697	3	-0.3033	ALAEIAKAELDDTPMR	150
P23246	Splicing factor, proline- and glutamine-rich	658.3422	3	-0.2152	ALAEIAKAELDDTPMRGR	91
P23246	Splicing factor, proline- and glutamine-rich	491.6108	3	-0.3333	AVVIVDDRGRSTGK	61
P23246	Splicing factor, proline- and glutamine-rich	760.7196	3	-0.4043	CRLFVGNLPADITEDEFKR	103
P23246	Splicing factor, proline- and glutamine-rich	1199.6062	3	0.4770	CSEGVFLLTTTPRPVIVEPLEQLDDEDGLPEK	154
P23246	Splicing factor, proline- and glutamine-rich	1010.0251	4	-0.5049	CSEGVFLLTTTPRPVIVEPLEQLDDEDGLPEKLAQK	69
P23246	Splicing factor, proline- and glutamine-rich	588.2655	3	-0.0092	FAQHGTFEYEYSQR	121
P23246	Splicing factor, proline- and glutamine-rich	519.9945	4	0.0294	FAQHGTFEYEYSQRWK	84
P23246	Splicing factor, proline- and glutamine-rich	381.8805	3	3.1809	FATHAAALSVR	80
P23246	Splicing factor, proline- and glutamine-rich	941.7324	4	0.4736	FATHAAALSVRNLSPLYVSNELLEAFSQFGPIER	62
P23246	Splicing factor, proline- and glutamine-rich	671.3366	2	0.0895	FGQGGAGPVGGQGPR	74
P23246	Splicing factor, proline- and glutamine-rich	820.3926	3	-0.9705	FGQGGAGPVGGQGPRGMGPOTPAGYGR	86

P23246	Splicing factor, proline- and glutamine-rich	385.2170	3	-0.5874	GFGFIKLESR	96
P23246	Splicing factor, proline- and glutamine-rich	535.4616	5	-0.3647	GGRQHHPYHQHHQGGPPGPGGR	79
P23246	Splicing factor, proline- and glutamine-rich	415.9032	3	-0.0279	GIVEFASKPAAR	82
P23246	Splicing factor, proline- and glutamine-rich	415.9032	3	-0.0675	GIVEFASKPAAR	82
P23246	Splicing factor, proline- and glutamine-rich	458.6015	3	-0.3023	GIVEFASKPAARK	56
P23246	Splicing factor, proline- and glutamine-rich	335.4437	4	-0.1112	GKGFIFIKLESR	71
P23246	Splicing factor, proline- and glutamine-rich	550.6334	3	0.2175	ISDSEGFKANLSLLR	161
P23246	Splicing factor, proline- and glutamine-rich	412.8850	3	-0.1042	LAQKNPMYQK	70
P23246	Splicing factor, proline- and glutamine-rich	655.3423	3	-0.2395	LFVGNLPADITEDEFKR	94
P23246	Splicing factor, proline- and glutamine-rich	606.5797	4	-0.0481	LFVGNLPADITEDEFKRLFAK	100
P23246	Splicing factor, proline- and glutamine-rich	593.3117	4	-0.7630	MPGGPKPGGGPGLSTPGGHPKPPHR	73
P23246	Splicing factor, proline- and glutamine-rich	880.4378	3	-0.1505	NLSPYVSNELLEAFSQFGPIER	199
P23246	Splicing factor, proline- and glutamine-rich	601.5392	4	-0.2203	QHHPYHQHHQGGPPGPGGR	53
P23246	Splicing factor, proline- and glutamine-rich	412.5546	3	-0.8042	RPGEKTYTQR	126
P23246	Splicing factor, proline- and glutamine-rich	531.5299	4	-0.7422	SEEKISDSEGFKANLSLLR	97
P23246	Splicing factor, proline- and glutamine-rich	626.3072	3	0.1167	SLDEMEKQQREQVEK	76
P23246	Splicing factor, proline- and glutamine-rich	405.4782	4	0.2990	STGKGIVEFASKPAAR	121
P23246	Splicing factor, proline- and glutamine-rich	576.6239	3	0.1482	TERFGQGGAGPVGGQGPR	105
P23246	Splicing factor, proline- and glutamine-rich	466.9370	3	0.3792	VRFATHAAALSVR	86
P23246	Splicing factor, proline- and glutamine-rich	479.9173	3	-0.6885	YGEPGEVFINKGK	128
Q13428	Treacle protein	558.3003	3	-0.3191	ISDGKKQEGPATQVSK	124
Q13428	Treacle protein	867.7716	3	-1.3755	TQPSSGVDSAVGTLPATSPQSTSVQAK	154
Q13428	Treacle protein	769.0910	3	-0.0804	AAISNKITSCIFQLLQEAGIK	131

Q13428	Treacle protein	645.3738	3	0.1560	AASVPVKGSLGQGTAPVLP GK	84
Q13428	Treacle protein	688.8092	2	-0.7972	GMGTVEGGDQSNPK	76
Q13428	Treacle protein	634.6411	3	-0.8727	GSLGSQGAKDEPEEELQK	40
Q13428	Treacle protein	523.9702	3	0.0532	GTISAPGKVV TAAAQAK	114
Q13428	Treacle protein	434.5735	3	0.1224	KAEEDAALQAKK	103
Q13428	Treacle protein	679.0174	3	1.3368	LASTNSSVLGADLPSSMKEK	66
Q13428	Treacle protein	573.2919	3	-0.2487	SPQVKPASTMGMGPLGK	105
Q13428	Treacle protein	465.7664	2	0.8273	TGPTVTQVK	68
Q13428	Treacle protein	441.8994	3	-0.1997	TNVVTMPTAHPR	105
Q13428	Treacle protein	519.6058	3	-1.0026	TSQVGAASAPAKESPR	48
