

**Figure S1 (Figure 1 continued). ECT2 Deregulation Contributes to Breast Carcinogenesis.** (A) Box plots of ECT2 transcript levels in normal human mammary tissues and distinct histological breast carcinoma samples based on six independent analyses from Oncomine. (B) Box plots of ECT2 transcript levels in breast carcinoma samples with distinct molecular traits based on four independent datasets from GEO. *P* value was determined by one-way analysis of variance (ANOVA). (C) Immunohistochemistry analysis of the expression levels of ECT2 in different histologic types of invasive ductal breast tumors and adjacent normal mammary tissues. Representative images (200 × and 400 × magnification as indicated) from these samples are shown (left panel). Scale bar, 200 µm. Scores of the stained sections were determined by evaluating the nuclear intensity of immunopositivity by Image-pro Plus software and are presented with box plots (right panel). *P* values were determined by one-way ANOVA. (D) Kaplan-Meier survival analysis for the relationship between survival time of breast cancer patients and the mRNA expression level of ECT2 with survival packages from K-M plotter database. Sample size is shown as indicated. OS, overall survival; RFS, relapse free survival; DMFS, distant metastasis free survival; and PPS, post progression survival. (E) Colony formation assays were conducted with ZR-75-1 cells stably expressing the indicated shRNAs or genes. Representative images from biological triplicate experiments are shown. The expression of ECT2 was examined by Western blotting. (F) Colony formation assays were conducted with DA-MB-468 cells stably expressing the indicated shRNAs or genes. Representative image experiments are shown. The expression of ECT2 was examined by Western blotting.



**Figure S2 (Figure 3 continued). ECT2 Prevents USP7 Degradation through Opposing Its Polyubiquitination.** (A) ZR-75-1 cells were transfected with control siRNA or different sets of ECT2 siRNAs. Cellular extracts and total RNA were prepared and analyzed by Western blotting and qRT-PCR, respectively. Each bar represents the mean  $\pm$  S.D. for biological triplicate experiments. \*\**P* < 0.01, one-way ANOVA (B) Experiments analogous to (A) were performed with MDA-MB-468 cells. Each bar represents the mean  $\pm$  S.D. for biological triplicate experiments. \*\**P* < 0.01, one-way ANOVA. (C) MCF-7 cells were transfected with control siRNA, CDC42 siRNA, RAC1 siRNA, or CDC42 and RAC1 siRNA in combination. Cellular extracts were collected and analyzed by Western blotting with antibodies against the indicated proteins. (D) MCF-7 cells transfected with control siRNA or ECT2 siRNA were treated with 50 µg/mL cycloheximide (CHX) and harvested at the indicated time followed by Western blotting analysis. (E) Quantitation and statistical analysis of ubiquitinated USP7 from experiments in Figure 3F. Each bar represents the mean  $\pm$  S.D. for biological triplicate experiments. \*\**P* < 0.01, one-way ANOVA. (F) Quantitation and statistical analysis of ubiquitinated USP7 from experiments in Figure 3G. Each bar represents the mean  $\pm$  S.D. for biological triplicate experiments. \*\**P* < 0.01, one-way ANOVA. (G) Quantitation and statistical analysis of ubiquitinated USP7 from experiments in Figure 3H. Each bar represents the mean  $\pm$  S.D. for biological triplicate experiments. \*\**P* < 0.01, one-way ANOVA. (G) Quantitation and statistical analysis of ubiquitinated USP7 from experiments in Figure 3H. Each bar represents the mean  $\pm$  S.D. for biological triplicate experiments. \*\**P* < 0.01, one-way ANOVA.



Figure S3 (Figure 4 continued). ECT2 Facilitates USP7 Intermolecular Self-association, -Deubiquitination and -Stabilization. (A) MCF-7 cells were transfected with control siRNA or siRNAs targeting USP11, UHRF1, RAD18, MDM2 or RNF168. Cellular extracts were prepared and analyzed by Western blotting. (B) MCF-7 cells allowing Dox-inducible expression of stably integrated GFP-USP7/C223S were cultured in the presence of increasing amounts of doxycycline. Cellular extracts were prepared and analyzed by Western blotting. For USP7 bands, the higher one with larger molecular weight represents GFP-tagged USP7/C223S, while the lower one indicates endogenous USP7. The quantitation of endogenous USP7 was shown. Each bar represents the mean  $\pm$  S.D. for biological triplicate experiments. P value was determined by one-way ANOVA. (C) MCF-7 cells allowing Dox-inducible expression of stably integrated GFP-USP7/C223S were cultured in the absence or presence of USP7 inhibitor GNE-6640 for 24 h. Cellular extracts were prepared and analyzed by Western blotting. For USP7 bands, the higher one with larger molecular weight represents GFP-tagged USP7/C223S, while the lower one indicates endogenous USP7. The quantitation of endogenous USP7 was shown. Each bar represents the mean ± S.D. for biological triplicate experiments. \*P < 0.05, \*\*P < 0.01, one-way ANOVA. (D) Cellular extracts from HeLa cells expressing USP7/wt or USP7/C223S and His-Ub/wt were prepared for affinity-based precipitation assays via Ni-NTA agarose beads. The quantitation of ubiquitinated USP7 was shown. Each bar represents the mean  $\pm$  S.D. for biological triplicate experiments. \*\*P < 0.01, one-way ANOVA. (E) The quantitation of ubiquitinated USP7 in experiments from Figure 4E was shown. Each bar represents the mean ± S.D. for biological triplicate experiments. \*\*P < 0.01, one-way ANOVA. (F) Transfer energy between EYFP-USP7 and Rluc-USP7 in the absence or presence of ECT2 was examined by BRET assay. Control cells or HEK293T cells stably expressing FLAG-ECT2 were co-transfected with a constant amount of Rluc-USP7 plasmid and increasing amounts of EYFP-USP7. Then, fresh coelenterazine h (5 µM) was added to cells and Bioluminescence emission profiles were measured. Each bar represents the mean  $\pm$  S.D. for biological triplicate experiments. \*\*P < 0.01, two-way ANOVA. (G) The quantitation of ubiquitinated USP7 in experiments from Figure 4H was shown. Each bar represents the mean ± S.D. for biological triplicate experiments. \*\*P < 0.01, one-way ANOVA. (H) The quantitation of GFP and endogenous USP7 in experiments from Figure 4I was shown. Each bar represents the mean ± S.D. for biological triplicate experiments. P value was determined by one-way ANOVA. \*P < 0.05, \*\*P < 0.01. (I) Experiments analogous to Figure 4I were performed with USP7 antibody from Sigma (05-1946).



Figure S4 (Figure 5 continued). USP7 Promotes ECT2 Stabilization and Deubiquitination. (A) The quantitation of ubiquitinated ECT2 in experiments from Figure 5H was shown. Each bar represents the mean  $\pm$  S.D. for biological triplicate experiments. \*\**P* < 0.01, one-way ANOVA. (B) The quantitation of ubiquitinated ECT2 in experiments from Figure 5I was shown. Each bar represents the mean  $\pm$  S.D. for biological triplicate experiments. \*\**P* < 0.01, one-way ANOVA. (C) The quantitation of ubiquitinated ECT2 in experiments from Figure 5J was shown. Each bar represents the mean  $\pm$  S.D. for biological triplicate experiments from Figure 5J was shown. Each bar represents the mean  $\pm$  S.D. for biological triplicate experiments from Figure 5K was shown. Each bar represents the mean  $\pm$  S.D. for biological triplicate experiments. \*\**P* < 0.01, one-way ANOVA. (E) The quantitation of ubiquitinated ECT2 in experiments. \*\**P* < 0.01, one-way ANOVA. (E) The quantitation of ubiquitinated ECT2 in experiments. \*\**P* < 0.01, one-way ANOVA. (E) The quantitation of ubiquitinated ECT2 in experiments. \*\**P* < 0.01, one-way ANOVA. (E) The quantitation of ubiquitinated ECT2 in experiments from Figure 5L was shown. Each bar represents the mean  $\pm$  S.D. for biological triplicate experiments. \*\**P* < 0.01, one-way ANOVA. (E) The quantitation of ubiquitinated ECT2 in experiments from Figure 5L was shown. Each bar represents the mean  $\pm$  S.D. for biological triplicate experiments. \*\**P* < 0.01, one-way ANOVA. (E) The quantitation of ubiquitinated ECT2 in experiments from Figure 5L was shown. Each bar represents the mean  $\pm$  S.D. for biological triplicate experiments. \*\**P* < 0.01, one-way ANOVA. (E) The quantitation of ubiquitinated ECT2 in experiments from Figure 5L was shown. Each bar represents the mean  $\pm$  S.D. for biological triplicate experiments. \*\**P* < 0.01, one-way ANOVA.



Figure S5 (Figure 6 continued). ECT2/USP7 Circuit Is Implicated in Breast Carcinogenesis through Controlling MDM2. (A) Cellular extracts were collected from MCF-7 cells expressing the indicated siRNAs and examined by Western blotting. (B) Cellular extracts were collected from MCF-7 cells stably expressing the indicated shRNAs or/and genes and examined by Western blotting. Colony numbers from Figure 6E were counted and statistically analysed. \*\*P < 0.01, one-way ANOVA. (C) Cellular extracts were collected from MCF-7 cells (p53 null) stably expressing the indicated shRNAs or/and genes and examined by Western blotting. Colony numbers from Figure 6F were counted and statistically analysed. \*\*P < 0.01, one-way ANOVA. (D) Colony formation assays with MCF-7 cells stably expressing the indicated shRNAs or/and genes. Representative images from biological triplicate experiments are shown. Cellular extracts were collected and examined by Western blotting. Colony numbers were counted and statistically analyzed. \*\*P < 0.01, one-way ANOVA. (E) Colony formation assays with p53 null MCF-7 cells stably expressing the indicated shRNAs or/and genes. Representative images from biological triplicate experiments are shown. Cellular extracts were collected and examined by Western blotting. Colony numbers were counted and statistically analyzed.  $**P \le 0.01$ , one-way ANOVA. (F) Scores of the stained sections from Figure 6H were determined by evaluating the nuclear intensity of immunopositivity by Image-pro Plus software and are presented with box plots. P values were determined by two-tailed unpaired Student's t-test. (G) The correlation plot, coefficient and P values were analyzed as indicated. (H) Working model. ECT2 coordinates with USP7, in a GEF activity-independent manner, to form a feedforward circuit and promote breast cancer cell survival. In ECT2-deficient cells, monomeric USP7 is susceptible to be ubiquitinated and degraded by proteasome, accompanying by low abundance of MDM2, while in ECT2-proficient cells, ECT2 acts as a scaffolding protein to facilitate USP7 intermolecular self-association, deubiquitination, and -stabilization, and, in turn, USP7 deubiquitinates and stabilizes ECT2 as well as MDM2. In this manner, ECT2 promotes breast cancer cell survival regardless of the expression status of p53.

Figure S6. Uncropped Blots Related to Figures 1-6 and Supplemental Figures 1-5.

# Full unedited gel for Figure 1A



### Full unedited gel for Figure 1B





### Full unedited gel for Figure 1D





Full unedited gel for Figure 1F



### Full unedited gel for Figure 2A



**Right panel** 

### Full unedited gel for Figure 2B

MCF-7

Left panel



# HeLa

### Left panel



Shorter exposure

**Right panel** 



### upper panel

lower panel







#### Full unedited gel for Figure 2G







































# Full unedited gel for Figure 4C















MCF-7



MDA-MB-468




















# Left panel





#### Left panel













Full unedited gel for Figure S1F







MDA-MB-468







#### Full unedited gel for Figure S3A







Full unedited gel for Figure S3C







Left panel















lower panel





#### Supplementary File 1

Mass Spectrometry Analysis of ECT2-containing Protein Complex

E3 ubiquitin-protein ligase TRIP12 OS=Homo sapiens GN=TRIP12	Score	Coverage	# Proteins	# Unique Peptides	# Peptides	# PSMs	# AAs	MW [kDa]	calc. pI				
	317.9541893	27.9	10	1	47	115	2025	223.7604282	8.396972656			-	
	Sequence	# PSMs	# Proteins	Modifications	ΔCn	q-Value	PEP	XCorr	Charge	MH+ [Da]	ΔM [ppm]	RT [min]	# Missed Cleavages
	KPNPLANSNTSGYSESK IIEAAHOVGEDEISLSTLGR	2	4 2		0.0000	0	0.001063 5.39E-09	5.26 5.23	3	1793.86448 2138.11284	-1.12	12.84 28.08	0
	HLAESESLLTSPPK	4	4		0.0000	0	0.000004566	4.81	2	1508.79387	-1.12	19.76	0
	LVDNFQHEENLLQQVASK	2	4		0.0000	0	0.000001033	4.58	3	2112.07322	0.53	30.08	0
	GLPPHLFGPLGPR	5	4		0.0000	0	0.0000353	4.36	3	1357.77326	-0.54	27.41	0
	NHAVSSHIASMLSSQDLK	1 .	4		0.0000	0	0.0001226	4.29	3	1924.95224	-1.23	22.67	0
	QAESVMQDLGSSR	1	4		0.0000	0	0.00004503	4.23	2	1931.89116 1407.64763	-4.06	20.73 21.78	0
	QETSLTSHDLFDIDPVVAR	1	5		0.0000	0	0.00008031	3.99	3	2143.06583	-0.40	30.84	0
	QAESVmQDLGSSR	2	4	M6(Oxidation)	0.0000	0	0.000261	3.90	2	1423.64470	-3.53	29.44 15.09	0
	SSAVVVDAIPVFLEK	2	4		0.0000	0	0.001619	3.67	2	1573.87798	-3.62	33.09	0
	mADPESNQEAVNSSAAR AOI mKEDPELAK	2	6 4	MI(Oxidation) Md(Oxidation)	0.0000	0	0.000005125	3.55	2	1792.77410 1388 70525	-1.47	12.64	0
	VEPVGNAPLLALVHK	4	4		0.0000	0	0.00003521	3.42	2	1556.91265	-2.14	28.48	0
	IDPLALVQAIER LETOENENNITRAD	5	4		0.0000	0	0.0000567	3.25	2	1337.77617	-1.97	36.51	0
	KPNPLANSNTSGYSESKK	1	4		0.0000	0	0.01366	3.11	3	1921.95407	-3.84	10.65	1
	EGIFAVDTmLK	2	4	M9(Oxidation)	0.0000	0	0.00648	2.97	2	1239.62798	-0.85	27.91	0
	QALLEAR	1	4	N-Term(Acetyl)	0.0000	0	0.01071	2.95	2	955.55419	-3.11	27.90	0
	LVDLPLGLPFYK	2	5		0.0000	0	0.0003355	2.92	2	1374.79900	-3.06	35.05	0
	LPDYSSIEIMR	1	4		0.0000	0	0.0001731	2.85	2	1323.65862	-2.08	29.92	0
	SVESTcLcFAR	1	4	C6(Carbamidomethyl); C	0.0000	0	0.0005841	2.79	2	1329.59111	-1.15	22.66	0
	TCPFFFPFDTR EIIPTSEFINSK	3	4	C2(Carbamidomethyl)	0.0000	0	0.004412 0.0004296	2.79	2	1434.64543 1377.72368	-3.98 -1.74	34.98 27.50	0
	LQALLEAR	3	4		0.0000	0	0.006551	2.72	2	913.54570	-0.97	20.00	0
	EGIFAVDTMLK AI TYmmFAI PR	1 .	4	M5(Oxidation): M6(Oxid	0.0000	0	0.007084	2.69	2	1223.63188	-1.82	31.40	0
Bloom syndrome protein OS=Homo sapiens GN=BLM	221.1557527	33.31	6	38	38	74	1417	158.900716	7.488769531				
	Sequence DCI AAI A VHACI SDSARDEVOOK	# PSMs	# Proteins	Modifications	ΔCn	q-Value	PEP	XCorr 6.74	Charge 2	MH+ [Da]	ΔM [ppm]	RT [min]	# Missed Cleavages
	DGEISHALLFYTYHDVTR	1	2	C7(Carbamidomethyl)	0.0000	0	1.744E-09	6.29	3	2226.02579	-1.21	30.00	0
	SSSIIGSSSASHTSQATSGANSK	3	2		0.0000	0	0.00001953	5.87	3	2152.00504	-2.92	11.17	0
	QKFPSVPVMALTATANPR	3	2		0.0000	0	0.0003488	5.38	3	1687.82939 1928.03299	-0.23	27.93 28.26	1
	ELNFSHLPSNSVSPGDeLLTTTLGK	2	2	C17(Carbamidomethyl)	0.0000	0	0.000005394	5.23	3	2687.32614	-3.15	31.96	0
	VRPDSLDGPMEGDScPTGNSMK	1	2	C15(Carbamidomethvl)	0.0000	0	0.00002305	4.64	3	2413.99948	-2.59 -2.63	29.07	0
	TSSDNNVSVTNVSVAK	1	3		0.0000	0	0.0001626	4.09	2	1621.79802	-2.97	17.75	0
	NLFERPLENTHLQK	1	2		0.0000	0	0.0002898	3.78 3.65	2	1206.67351 1756.94731	0.50 -1.18	25.57 24.54	0
	YRPDSLDGPmEGDScPTGNSMK	1	2	M10(Oxidation); C15(Cr	0.0000	0	0.00008263	3.60	3	2429.99924	-0.63	19.03	0
	DLDTSDRKEDVLSTSK REcDTMADTLOR	3	3	C3(Carbamidomathu <sup>h</sup>	0.0000	0	0.0002317	3.51 3.38	2	1808.88469	-1.45	16.03 15.88	2
	LLDcGNELLQQR	2	2	C4(Carbamidomethyl)	0.0000	0	0.0002694	3.37	2	1458.73406	-2.02	24.91	0
	SLLPDFLQTPK mSm0ELNPETSTD:DAR	2	3	M1(Oxidation): M2(O-1	0.0000	0	0.003379	3.27 2.94	2	1258.70342 2016.78972	-0.64	32.39 17.35	0
	LIDTIPDDKLK	3	2	(Constitution); M3(OXB	0.0000	0	0.001392	2.92	2	1270.72319	-1.71	20.37	1
	SVEGYYQESGR	2	2		0.0000	0	0.00142	2.91	2	1274.56255	-1.77	17.28	0
	H LASINDLER LISTLENLYER	4 3	2		0.0000	0	0.01173 0.0002124	2.88 2.75	2	1155.57659 1350.72551	-0.66	14.42 29.03	0
	EVVcTTQNTPTVK	3	3	C4(Carbamidomethyl)	0.0000	0	0.0001385	2.61	2	1476.73186	-3.02	15.33	0
	AQLYTINTVK NI FFAFI HSTEK	2	3		0.0000	0	0.003047	2.60	2	1138.60869	-1.41	14.38	0
	LLTEVDFNK	2	2		0.0000	0	0.004363	2.54	2	1078.57781	-0.12	23.75	0
Ubiquitin carboxyl-terminal hydrolase 7 OS=Homo sapiens GN=USP7	244.1806576	33.15 # PSMc	9 # Proteins	36 Modifications	36 ACn	103 a Value	1086 PEP	126.1885602 XCorr	5.706542969 Charge	MIL: (Da)	AM [nom]	PT (min)	# Mircad Clammar
	LSEVLQAVTDHDIPQQLVER	3	4	Model California	0.0000	0	6.737E-09	5.65	3	2290.20096	-1.26	30.24	0
	HQYINEDEYEVNLK FDKDHDVMLFLK	1	3		0.0000	0	5.012E-08 0.0000395	5.03	2	1793.83000	-2.29	23.45	0
	IQSLLDIQEKEFEK	2	3		0.0000	0	0.0000627	4.25	3	1719.91349	-1.71	27.61	1
	VFYELQHSDKPVGTK INTDPmILOFEK	2	5	M6(Oridation)	0.0000	0	0.0001171	4.00	3	1747.89786	-2.04	16.73	0
	IGVHQEDELLEcLSPATSR	2	+ 4	C13(Carbamidomethyl)	0.0000	0	0.0005371	3.47	3	2267.12473	-3.97	30.21	0
	RPAMLDNEADGNK	3	4		0.0000	0	0.0002683	3.46	2	1430.66728	-1.44	11.72	0
	TIPNDPGFVVTLSNR	5	4		0.0000	0	0.00004238	3.43	2	1629.86040	0.51	28.86	0
	KLYYQQLK	3	4		0.0000	0	0.00488	2.84	2	1083.61833	-1.28	14.91	1
	FDDDVVSR DLLQFFKPR	3	4		0.0000	0	0.01051 0.005438	2.79	2	952.43511 1163.65361	-2.09 -3.09	16.85 31.25	0
	LSESVLSPPcFVR	4	7	C10(Carbamidomethyl)	0.0000	0	0.004489	2.78	2	1490.76421	-2.04	28.89	0
	MNYFQVAK IODYDVSLDK	4	4		0.0000	0	0.007779	2.78	2	1000.49199	-0.11	22.23	0
	VDVIFcDK	5	4	C6(Carbamidomethyl)	0.0000	0	0.008613	2.72	2	995.48442	-2.28	22.72	0
	FMYDPQTDQNIK	1	5		0.0000	0	0.0005958	2.68	2	1499.67912	-2.96	23.28	0
	INYRDDEK	2	9		0.0000	0	0.001534	2.60	2	1028.56890 1165.58196	-2.46	10.03	1
	AVYMMPTEGDDSSK	1	5		0.0000	0	0.0004965	2.52	2	1530.63994	-3.40	22.37	0
	VILDNVENK DDPENDNSELPTAK	1	5 4		0.0000	0	0.004559 0.003594	2.49	2	1043.57195 1544.66533	-1.20 -3.77	17.77	0
	LLEIVSYK	4	4		0.0000	0	0.01301	2.48	2	964.56993	-1.51	25.14	0
	ION I DIODU	2	د	7	0.0000	0	747	2.41 81.62996464	4.665527344	1186.66582	-1.70	25.58	0
NAD-dependent protein deacetylase sirtuin-1 OS-Homo sapiens GN-SIRT1	IQSLLDIQEK 33.09188819	10.71	4	<i>i</i>	7	14	DCD.	XCorr	Charge				
NAD-dependent protein deacetylase sittuin-1 OS=Homo sapiens GN=SIRT1	IQSLLDIQEK 33.09188819 Sequence	10.71 # PSMs	4 # Proteins	Modifications	7 ΔCn	q-Value	PEP 0.000000012	4.14		MH+ [Da]	ΔM [ppm]	RT [min]	# Missed Cleavages
NAD-dependent protein deacetylase simuin-1 OS-Homo supiens GN-SIRT1	IQSLIDQEK 350918819 Sequence NYTQNIDLQVAGIQR LSEITEKPR	10.71 # PSMs 1 2	4 # Proteins 4 3	Modifications	7 ΔCn 0.0000 0.0000	q-Value 0 0	0.000004943 0.001248	4.15 2.85	2	MH+ [Da] 1962.98711 1169.65141	ΔM [ppm] -0.46 -0.95	RT [min] 32.21 12.90	# Missed Cleavages 0 0
NAD-dependent postein deacetylase situin i 0.8-Homo sapiens GN-SIRTI Protein ECT2 OS-Homo saviens GN-ECT2	IQSLEDQGK 350918819 Sopenne NYTQNIDTEQVAGQR LSEFTEKPPR PALSDKECK 71227402	10.71 # PSMs 1 2 3 68.29	4 # Proteins 4 3 4 19	79	7 ΔCn 0.0000 0.0000 0.0000 79	q-Value 0 0 0 2486	PEP 0.000004943 0.001248 0.007814 883	4.15 2.85 2.54 99.98727694	2 2 2 7.488769531	MH+ [Da] 1962.98711 1169.65141 1107.60466	ΔM [ppm] -0.46 -0.95 0.14	RT [min] 32.21 12.90 14.16	# Missed Clearvages 0 0 1
NAD dependent protein descriptae silmais 108-Homo supiens GN-SIRT1 Protein ECT2 08-Homo supiens GN-ECT2	IQSLEDGRK         33098883           Sappase         NYTQNID1LQVACIQK           LSETTERMPM         PALASDREGOK           7712.734362         Sogenation	10.71 ************************************	4 # Proteins 4 3 4 19 # Proteins	79 Modifications	7 ΔCn 0.0000 0.0000 0.0000 79 ΔCn 0.0000	q-Value 0 0 2486 q-Value	PEP 0.000004943 0.001248 0.007814 883 PEP	4.15 2.85 2.54 99.98727694 XCorr	2 2 7.488769531 Charge	MH+ [Da] 1962.98711 1169.65141 1107.60466 MH+ [Da]	ΔM [ppm] -0.46 -0.95 0.14 ΔM [ppm]	RT [min] 32.21 12.90 14.16 RT [min]	# Missed Cleavages 0 0 1 # Missed Cleavages
NAD-dependent protein deacetylane siteain 1 OS-Homo sapiera GN-SIRT1 Protein ECT2 OS-Homo sapiera GN-ECT2	IQSLED/GRK           30078883 (9)           Sequence           VITV[NITTLED/VAG0/R           LSETEKRPR           PLASDREGK           711273021           Sequence           KRPA-REN.SIGNELDINTPENSINYGOTPK           REDGEPT-AVDEPENSERK	10.71 # PSMs 1 2 3 68.29 # PSMs 14 53	4 # Proteins 4 3 4 19 # Proteins 5 5	79 Modifications	7 ΔCn 0.0000 0.0000 0.0000 79 ΔCn 0.0000 0.0000	q-Value 0 0 0 2486 q-Value 0 0	PEP 0.000004943 0.001248 0.007814 883 PEP 8.437E-11 6.083E-11	4.15 2.85 2.54 99.98727694 XCorr 10.09 8.79	2 2 7.488769531 Charge 3 3	MH+ [Da] 1962.98711 1169.65141 1107.60466 MH+ [Da] 3413.72092 2264.03281	ΔM [ppm] -0.46 -0.95 0.14 ΔM [ppm] 0.72 -1.75	RT [min] 32.21 12.90 14.16 RT [min] 32.02 31.78	# Missed Cleavages 0 1 # Missed Cleavages 1 2
NAD-dependent protein descriptuse similis 1 08-Homo supiens GN-SIRTI Protein ECT2 08-Homo supiens GN-ECT2	IQULLD(REK           3009188319           Sequence           VYTONDTLD(VAG)OR           LSETERKIPPR           PLASDREGK           Sequence           KRPSARESLSICSLIDENTPESSIN/GDTPK           KRSQDFYAAVDERNERK           KRQUPYAAVDERNERK	10.71 # PSMs 1 2 3 68.29 # PSMs 14 53 11	4 # Proteins 4 3 4 19 # Proteins 5 5 5	79 Modifications N-Term(Acetyl)	7 ΔCn 0.0000 0.0000 79 ΔCn 0.0000 0.0000 0.0000 0.0000	14 q-Value 0 0 0 2486 q-Value 0 0 0 0 0 0 0	PEP 0.000004943 0.001248 0.007814 883 PEP 8.437E-11 6.083E-11 4.647E-10 0.025	4.15 2.85 2.54 <u>99.98727694</u> XCorr 10.09 8.79 8.56	2 2 2 7.488769531 Charge 3 3 3	MH+ [Da] 1962.98711 1169.65141 1107.60466 MH+ [Da] 3413.72092 2264.03281 2306.0489 2000.0489	ΔM [ppm] -0.46 -0.95 0.14 ΔM [ppm] 0.72 -1.75 -1.05	RT [min] 32.21 12.90 14.16 RT [min] 32.02 31.78 36.40	# Missed Cleavages 0 0 1 # Missed Cleavages 1 2 2 0
NAD-dependent protein descriptare sitmin-108-Homo supiens GN-SIRT1 Potein ECT2 08-Homo supiens GN-ECT2	IQSLEDGEK JUDISBASH Sequence INTYRNIDTLEV/VACIOR LSETTRATIVE PLASDAGGO TILIJABAS Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence	10.71 # PSMs 1 2 3 68.29 # PSMs 14 53 11 1 4	4 # Proteins 4 3 4 4 19 # Proteins 5 5 5 5 5 5	Modifications 79 Modifications N-Term(Acetyl) C?(Carbamklomethvh)	7 ΔCn 0.0000 0.0000 0.0000 79 ΔCn 0.0000 0.0000 0.0000 0.0000 0.0000	14           q-Value           0           0           0           0           2486           q-Value           0           0           0           0           0           0           0           0           0           0           0           0           0           0           0	PEP 0.000004943 0.001248 0.007814 883 PEP 8.437E-11 6.083E-11 4.647E-10 3.31E-08 4.524E-08	4.15 2.85 2.54 99.98727694 XCorr 10.09 8.79 8.56 7.57 7.29	2 2 2 7.488769531 Charge 3 3 3 4 4 4	MH+ [Da] 1962-98711 1169.65141 1107.60466 MH+ [Da] 3413.72092 2264.03281 2306.04489 3285.60561 3694.63759	ΔM [ppm] -0.46 -0.95 0.14 ΔM [ppm] 0.72 -1.75 -1.06 -5.44 -1.24	RT [min] 32.21 12.90 14.16 RT [min] 32.02 31.78 36.40 33.81 44.10	# Missed Cleavages 0 0 1 # Missed Cleavages 1 2 2 0 1
NAD-dependent protein descriptare siteain 1 05-Homo sapiera GN-SIRT1 Protein ECT2 05-Homo sapiera GN-ECT2	IQSLEDGRK StopBass Sapense NYCNDITLEVVACUQR LSETEKTMPR PALSDREGK XRIPAGESLSIGNELDENTFESSINYGDTPK KRIPAGESLSIGNELDENTFESSINYGDTPK NEQDPYAAVDDRENETK NEQDPYAAVDDRENETK NEQDPYAAVDDRENETK NEQDPYAAVDDRENETK NEQDPYAAVDDRENETK NEQDPYAAVDDRENETK NEQDPYAAVDDRENETK NEQDPYAAVDDRENETK NEQDPYAAVDDRENETK NEQDPYAAVDDRENETK NEQDPYAAVDDRENETK NEQDPYAAVDDRENETK NEQDPYAAVDDRENETK NEQDPYAAVDDRENETK NEQDPYAAVDDRENETK NEQDPYAAVDDRENETK NEQDPYAAVDDRENETK NEQDPYAAVDDRENETK NEQDPYAAVDDRENETK NEQDPYAAVDDRENETK NEQDPYAAVDDRENETK NEQDPYAAVDDRENETK NEQDPYAAVDDRENETK NEQDPYAAVDDRENETK NEQDPYAAVDDRENETK NEQDPYAAVDDRENETK NEQDPYAAVDDRENETK NEQDPYAAVDDRENETK NEQDPYAAVDDRENETK NEQDPYAAVDDRENETK NEQDPYAAVDDRENETK NEQDPYAAVDDRENETK NEQDPYAAVDDRENETK NEQDPYAAVDDRENETK NEQDPYAAVDDRENETK NEQDPYAAVDDRENETK NEQDPYAAVDDRENETK NEQDPYAAVDDRENETK NEQDPYAAVDDRENETK NEQDPYAAVDDRENETK NEQDPYAAVDDRENETK NEQDPYAAVDDRENETK NEQDPYAAVDDRENETK NEQDPYAAVDDRENETK NEQDPYAAVDDRENETK NEQDPYAAVDDRENETK NEQDPYAAVDRENETK NEQDPYAAVDDRENETK NEQDPYAAVDDRENETK NEQDPYAAVDDRENETK NEQDPYAAVDDRENETK NEQDPYAAVDDRENETK NEQDPYAAVDDRENETK NEQDPYAAVDDRENETK NEQDPYAAVDDRENETK NEQDPYAAVDDRENETK NEQDPYAAVDDRENETK NEQDPYAAVDDRENETK NEQDPYAAVDDRENETK NEQDPYAAVDDRENETK NEQDPYAAVDDRENETK NEQDPYAAVDDRENETK NEQDPYAAVDDRENETK NEQDPYAAVDDRENETK NEQDPYAAVDDRENETK NEQDPYAAVDDRENETK NEQDPYAAVDDRENETK NEQDPYAAVDDRENETK NEQDPYAAVDDRENETK NEQDPYAAVDDRENETK NEQDPYAAVDDRENETK NEQDPYAAVDDRENETK NEQDPYAAVDDRENETK NEQDPYAAVDRENETK NEQDPYAAVDRENETK NEQDPYAAVDRENETK NEQDPYAAVDRENETK NEQDPYAAVDRENETK NEQDPYAAVDRENETK NEQDPYAAVDRENETK NEQDPYAAVDRENETK NEQDPYAAVDRENETK NEQDPYAAVDRENETK NEQDPYAAVDRENETK NEQDPYAAVDRENETK NEQDPYAAVDRENETK NEQDPYAAVDRENETK NEQDPYAAVDRENETK NEQDPYAAVDRENETK NEQDPYAAVDRENETK NEQDPYAAVDRENETK NEQDPYAAVDRENETK NEQDPYAAVDRENETK NEQDPYAAVDRENETK NEQDPYAAVDRENETK NEQDPYAAVDRENETK NEQDPYAAVDRENETK NEQDPYAAVDRENETK NEQDPYAAVDRENETK NEQDPYAAVDRENETK NEQDPYAAVDRENETK NEQDPYAAVDRENETK N	10.71 # PSMs 1 2 3 68.29 # PSMs 14 53 11 1 1 4 2	4 # Proteins 4 3 4 4 # Proteins 5 5 5 5 5 5 5 5	79 Modifications N-Term(Acetyl) C?(Carbamidomethyl) C1(Carbamidomethyl)	7  ΔCn  0.0000  0.0000  0.0000  0.0000  ΔCn  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000 0.0000  0.0000  0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0	q-Value         0           0         0           2486         q-Value           0         0           0         0           0         0           0         0           0         0           0         0           0         0           0         0           0         0	PEP 0.000004943 0.001248 0.007814 883 PEP 8.437E-11 6.083E-11 4.647E-10 3.31E-08 4.524E-08 5.464E-07	4.15 2.85 2.54 99.98727694 XCorr 10.09 8.79 8.56 7.57 7.29 7.17	2 2 7.488769531 Charge 3 3 4 4 4 3	MH+[Da] 1962.98711 1169.65141 1107.60466 MH+[Da] 3413.72092 2264.03281 2306.04489 3285.60561 3694.63759 2354.19980	ΔM [ppm] -0.46 -0.95 0.14 ΔM [ppm] 0.72 -1.75 -1.06 -5.44 -1.24 -2.70	RT [min] 32.21 12.90 14.16 RT [min] 32.02 31.78 36.40 33.81 44.10 32.02	# Missed Clearages 0 0 1  # 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NAD-dependent protein deacetylane sitrain 1 OS-Homo supiems GN-SIRT1 Protein ECT2 OS-Homo supiem GN-ECT2	IQSLEDGEK JOJEBASH Separe NYTQINITLEVOVAGUR LSETEKMPR PLASDREGK KURSAELSIGSLEDNITTESSINYGDTK KURSAELSIGSLEDNITTESSINYGDTK KURSAELSIGSLEDNITTESSINYGDTK NEGOPTAVADORENEK REGOPTAVADORENEK REGOPTAVADORENEK REGOPTAVADORENEK REGOPTAVADORENEK REGOPTAVADORENEK REGOPTAVADORENEK REGOPTAVADORENEK REGOPTAVADORENEK UPADOLENJCAGEREKTMELETELEGOGK	10.71 # PSMs 1 2 3 68.29 # PSMs 14 53 11 1 1 4 2 4 6	4 # Proteins 4 4 3 4 19 19 # Proteins 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	79 Modifications N-Term(Acetyl) C1(Carbamidomethyl) C1(Carbamidomethyl) C1(Carbamidomethyl)	7           ΔCn           0.0000           0.0000           0.0000           0.0000           0.0000           0.0000           0.0000           0.0000           0.0000           0.0000           0.0000           0.0000           0.0000           0.0000           0.0000           0.0000           0.0000           0.0000	q-Value           Q-Value           Q           Q           Q           Q           Q           Q           Q           Q           Q           Q           Q           Q           Q           Q           Q           Q           Q           Q           Q           Q           Q           Q           Q           Q           Q           Q           Q           Q           Q           Q           Q           Q           Q           Q           Q           Q           Q           Q           Q           Q           Q           Q           Q           Q           Q           Q           Q           Q           Q           Q           Q           <	PEP 0.000004943 0.001248 0.001784 883 PEP 8.437E-11 6.083E-11 4.647E-10 3.31E-08 4.524E-08 5.464E-07 5.411E-10 4.006E-08	4.15 2.85 2.54 99.98727694 XCorr 10.09 8.79 8.56 7.57 7.57 7.29 7.17 6.92 6.87	2 2 7.488769531 Charge 3 3 3 4 4 4 3 3 4 4 4 3 3 4	MH+[Da] 1962;98711 1169;65141 1107;00466 MH+[Da] 3413;72092 2264;03281 2306;04489 3285;60561 3694;63759 2354;19980 2482;29544 3710;62788	ΔM [ppm] -0.46 -0.95 0.14 ΔM [ppm] 0.72 -1.75 -1.06 -5.44 -1.24 -2.70 -2.29 -2.56	RT [min] 32.21 12.90 14.16 RT [min] 32.02 31.78 36.40 33.81 44.10 32.02 30.37 43.44	# Missed Clearages 0 0 1  # Missed Clearages 1  2 2 0 1 1 2 1 1 1 1 1 1 1 1 1 1 1 1
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N-Term(Acetyl) C2(Carbamidomethyl); C12(Carbamidomethyl); C12(Carbamidomethyl); C12(Carbamidomethyl); C7(Carbamidomethyl)	γ           ΔCn           0.0000           0.0000           0.0000           0.0000           0.0000           0.0000           0.0000           0.0000           0.0000           0.0000           0.0000           0.0000           0.0000           0.0000           0.0000           0.0000           0.0000           0.0000           0.0000           0.0000           0.0000           0.0000           0.0000           0.0000           0.0000           0.0000           0.0000           0.0000           0.0000           0.0000	2440 0 0 2486 2486 0 0 0 0 0 0 0 0 0 0 0 0 0	PEP 0000004943 0001248 0007814 883 PEP 8437E-11 4647E-10 4647E-10 4524E-08 5.464E-07 5.41E-10 4.006E-08 5.464E-07 5.41E-10 4.006E-08 5.464E-07 0.000000451 1.536E-07 0.000004451	4.15 999727694 2.54 099727694 10.07 8.56 8.56 7.57 7.59 7.57 7.59 7.57 7.59 6.63 6.63 6.63 6.64 6.64 6.64 6.64 6.64	2 2 7,488769531 Charge 3 3 4 4 4 3 3 3 3 3 3 3 3 3 3 3 3 3 3	MH+ [Da] 10962.98711 1109.85144 1107.850466 MH+ [Da] 3413.72092 2246.03281 2246.03281 2246.03281 2246.03281 2246.03281 2246.03281 2246.03281 2246.03281 2452.9590 2467.952890 2107.92890 2107.92890 2107.92890 2107.92890 2107.92890 2107.92890 2107.92890 2107.92890 2107.92890 2107.92890 2107.92890 2107.92890 2107.92890 2107.92890 2107.92890 2107.92890 2107.92890 2107.92890 2107.92890 2107.92890 2107.92890 2107.92890 2107.92890 2107.92890 2107.92890 2107.92890 2107.92890 2107.92890 2107.92890 2107.92890 2107.92890 2107.92890 2107.92890 2107.92890 2107.92890 2107.92890 2107.92890 2107.92890 2107.92890 2107.92890 2107.92890 2107.92890 2107.92890 2107.92890 2107.92890 2107.92890 2107.92890 2107.92890 2107.92890 2107.92890 2107.92890 2107.92890 2107.92890 2107.92890 2107.92890 2107.92890 2107.92890 2107.92890 2107.92890 2107.92890 2107.92890 2107.92890 2107.92890 2107.92890 2107.92890 2107.92890 2107.92890 2107.92890 2107.92890 2107.92890 2107.9280 2107.92800 2107.92800 2107.92800 2107.92800 2107.92800 2107.92800 2107.92800 2107.92800 2107.92800 2107.92800 2107.92800 2107.92800 2107.92800 2107.92800 2107.92800 2107.92800 2107.92800 2107.92800 2107.92800 2107.92800 2107.92800 2107.92800 2107.92800 2107.92800 2107.92800 2107.92800 2107.92800 2107.92800 2107.92800 2107.92800 2107.92800 2107.92800 2107.92800 2107.92800 2107.92800 2107.92800 2107.92800 2107.92800 2107.92800 2107.92800 2107.92800 2107.92800 2107.92800 2107.92800 2107.92800 2107.92800 2107.92800 2107.92800 2107.92800 2107.92800 2107.92800 2107.92800 2107.92800 2107.92800 2107.92800 2107.92800 2107.92800 2107.92800 2107.92800 2107.92800 2107.92800 2107.92800 2107.92800 2107.92800 2107.92800 2107.92800 2107.92800 2107.92800 2107.92800 2107.92800 2107.92800 2107.92800 2107.92800 2107.92800 2107.92800 2107.92800 2107.92800 2107.92800 2107.92800 2107.92800 2107.92800 2107.92800 2107.92800 2107.9280	AM (ppm) -0.46 -0.95 0.14 AM (ppm) 0.72 -1.75 -1.06 -5.44 -2.70 -2.26 -1.51 -0.97 -2.73 1.91 -0.97 -2.73 -1.03 -2.46 -0.97 -2.73 -1.03 -2.46 -0.97 -2.73 -1.03 -2.46 -0.97 -2.73 -1.03 -2.46 -1.03 -2.46 -1.03 -2.45 -1.03 -2.46 -1.03 -2.46 -1.03 -2.46 -1.03 -2.46 -1.03 -2.46 -1.03 -2.46 -1.03 -2.46 -1.03 -2.46 -1.03 -2.46 -1.03 -2.46 -1.03 -2.46 -1.03 -2.46 -1.03 -2.46 -1.03 -2.46 -1.03 -2.46 -1.03 -2.46 -1.03 -2.46 -1.03 -2.46 -1.03 -2.46 -1.03 -2.46 -1.03 -2.46 -1.03 -2.46 -1.03 -2.46 -1.03 -2.46 -1.03 -2.46 -1.03 -2.46 -1.03 -2.46 -1.03 -2.46 -1.03 -2.46 -1.03 -2.46 -1.03 -2.46 -1.03 -2.46 -1.03 -2.46 -1.03 -2.46 -1.03 -2.46 -1.03 -2.46 -1.03 -2.46 -1.03 -2.46 -1.03 -2.46 -1.03 -2.46 -1.03 -2.46 -1.03 -2.46 -1.03 -2.46 -1.03 -2.46 -1.03 -2.46 -1.03 -2.46 -1.03 -1.03 -2.46 -1.03 -1.03 -1.03 -1.03 -1.03 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08 -1.08	RT [min] 32.21 12.90 14.16 RT [min] 32.02 31.78 36.40 33.81 44.10 32.02 30.37 30.37 33.81 44.10 32.02 30.37 30.37 37.30 37.30 37.30 37.30 37.30 37.30 37.47 25.84 37.64 45.25	# Missel Cleanges 0 0 4 Missel Cleanges 1  # Missel Cleanges 1  4 Missel Cleanges 1  2  1  1  1  1  1  1  2  0  0  0  0  0  0  0  0  0  0  0  0
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ACn	q-Value           Q           Q           Q           Q           Q           Q           Q           Q           Q           Q           Q           Q           Q           Q           Q           Q           Q           Q           Q           Q           Q           Q           Q           Q           Q           Q           Q           Q           Q           Q           Q           Q           Q           Q           Q           Q           Q           Q           Q           Q           Q           Q           Q           Q           Q           Q           Q           Q           Q           Q           Q           Q           Q </td <td>PEP 0000004943 0001248 00007814 883 PEP 8.437E-11 6.058E-11 4.457E-10 3.31E-08 4.528E-08 5.44EE-07 0.00000253 1.3546E-07 0.00000025 1.358E-08 0.000000137 2.818E-08 4.557E-10 0.0000004 2.838E-08 0.0000004 2.838E-08 0.0000004 2.838E-08 0.0000004 2.838E-08 0.0000004 2.838E-08 0.000004 2.338E-08 0.000009 3.83E-08 0.000009 3.83E-08 0.000009 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         -0.17           -0.17</td> <td>RT (min) 32.21 12.90 14.16 22.02 33.78 36.40 33.81 33.81 33.81 33.81 33.81 33.81 33.81 33.81 33.83 33.81 33.83 33.73 33.73 33.73 33.73 33.73 33.73 33.73 33.73 33.73 33.73 33.73 33.73 33.73 33.73 33.73 33.73 33.73 33.73 33.73 33.73 33.73 33.73 33.73 33.73 33.73 33.73 33.73 33.73 33.73 33.73 33.73 33.73 33.73 33.73 33.73 33.73 33.73 33.73 33.73 33.73 33.73 33.73 33.73 33.73 33.73 33.73 33.73 33.73 33.74 33.74 33.75 33.75 33.75 33.75 33.75 33.75 33.75 33.75 33.75 33.75 33.75 33.75 33.75 33.75 33.75 33.75 33.75 33.75 33.75 33.75 33.75 33.75 33.75 33.75 33.75 33.75 33.75 33.75 33.75 33.75 33.75 33.75 33.75 33.75 33.75 33.75 33.75 33.75 33.75 33.75 33.75 33.75 33.75 33.75 33.75 33.75 33.75 33.75 33.75 33.75 33.75 33.75 33.75 33.75 33.75 33.75 33.75 33.75 33.75 33.75 33.75 33.75 33.75 33.75 33.75 33.75 33.75 33.75 33.75 33.75 33.75 33.75 33.75 33.75 33.75 33.75 33.75 33.75 33.75 33.75 33.75 33.75 33.75 33.75 33.75 33.75 33.75 33.75 33.75 33.75 33.75 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35.75 35.75 35.75 35.75 35.75 35.75 35.75 35.75 35.75 35.75 35.75 35.75 35.75 35.75 35.75 35.</td> <td># Mused Changes 0 1 4 Mused Changes 1 2 4 Mused Changes 1 2 2 0 1 1 2 1 1 1 2 1 1 1 1 1 1 1 2 0 1 1 2 0 1 1 2 0 1 1 2 1 1 2 1 1 2 1 1 2 1 1 2 1 1 2 1 1 2 1 1 2 1 1 2 1 1 2 1 1 2 1 1 1 2 1 1 1 2 1 1 1 2 1 1 1 1 1 1 1 1 1 1 1 1 1</td>	PEP 0000004943 0001248 00007814 883 PEP 8.437E-11 6.058E-11 4.457E-10 3.31E-08 4.528E-08 5.44EE-07 0.00000253 1.3546E-07 0.00000025 1.358E-08 0.000000137 2.818E-08 4.557E-10 0.0000004 2.838E-08 0.0000004 2.838E-08 0.0000004 2.838E-08 0.0000004 2.838E-08 0.0000004 2.838E-08 0.000004 2.338E-08 0.000009 3.83E-08 0.000009 3.83E-08 0.000009 3.83E-08 0.000009 3.83E-08 0.000009 3.83E-08 0.000009 3.83E-08 0.000009 3.83E-08 0.000009 3.83E-08 0.000009 3.83E-08 0.000009 3.83E-08 0.000009 3.83E-08 0.000009 3.83E-08 0.000009 3.83E-08 0.000009 3.83E-08 0.000009 3.83E-08 0.000009 3.83E-08 0.000009 3.83E-08 0.000009 3.83E-08 0.000009 3.83E-08 0.000009 3.83E-08 0.000009 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2483.0447 2483.0447 2483.0447 2483.0	AM (ppm)           -0.46           -0.95           -0.91           -0.91           -0.92           -0.93           -0.14           -0.92           -0.93           -0.16           -5.44           -1.24           -2.26           -2.56           -0.97           -1.91           -1.03           -2.73           1.91           -1.03           -2.46           -4.03           -2.45           -2.53           -2.54           -1.08           -1.08           -1.08           -1.09           -0.51           -0.97           -0.97           -0.97           -0.97           -0.97           -0.17           -0.17           -0.17	RT (min) 32.21 12.90 14.16 22.02 33.78 36.40 33.81 33.81 33.81 33.81 33.81 33.81 33.81 33.81 33.83 33.81 33.83 33.73 33.73 33.73 33.73 33.73 33.73 33.73 33.73 33.73 33.73 33.73 33.73 33.73 33.73 33.73 33.73 33.73 33.73 33.73 33.73 33.73 33.73 33.73 33.73 33.73 33.73 33.73 33.73 33.73 33.73 33.73 33.73 33.73 33.73 33.73 33.73 33.73 33.73 33.73 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NAD-dependent protein deacrylae simin 108-Hono supers GN-SIRT1 Prinein ECT2 08-Hono supers GN-ECT2	IQUILIDGEK JOHRSHY JOHRSHY JOHRSHY HASDAGK JUSTBARMPK HASDAGK HASDAGK HASDAGK HASDAGK HASDAGK HASDAGK HASDAGK HASDAGK HASDAGK HASDAGK HASDAGK HASDAGK HASDAGK HASDAGK HASDAGK HASDAGK HASDAGK HASDAGK HASDAGK HASDAGK HASDAGK HASDAGK HASDAGK HASDAGK HASDAGK HASDAGK HASDAGK HASDAGK HASDAGK HASDAGK HASDAGK HASDAGK HASDAGK HASDAGK HASDAGK HASDAGK HASDAGK HASDAGK HASDAGK HASDAGK HASDAGK HASDAGK HASDAGK HASDAGK HASDAGK HASDAGK HASDAGK HASDAGK HASDAGK HASDAGK HASDAGK HASDAGK HASDAGK HASDAGK HASDAGK HASDAGK HASDAGK HASDAGK HASDAGK HASDAGK HASDAGK HASDAGK HASDAGK HASDAGK HASDAGK HASDAGK HASDAGK HASDAGK HASDAGK HASDAGK HASDAGK HASDAGK HASDAGK HASDAGK HASDAGK HASDAGK HASDAGK HASDAGK HASDAGK HASDAGK HASDAGK HASDAGK HASDAGK HASDAGK HASDAGK HASDAGK HASDAGK HASDAGK HASDAGK HASDAGK HASDAGK HASDAGK HASDAGK HASDAGK HASDAGK HASDAGK HASDAGK HASDAGK HASDAGK HASDAGK HASDAGK HASDAGK HASDAGK HASDAGK HASDAGK HASDAGK 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883 PEP 8.437E-11 6.058E-11 4.647E-10 3.31E-08 4.524E-08 5.441E-10 4.000E-08 5.441E-10 4.000E-08 0.000000253 1.536E-07 0.000000451 2.538E-08 0.000000451 2.538E-08 0.000000451 2.538E-08 0.000000451 2.538E-08 0.000000451 2.538E-08 0.000000451 2.538E-08 0.00000451 2.538E-08 0.00000451 2.538E-08 0.00000451 2.538E-08 0.00000451 2.538E-08 0.00000451 2.538E-08 0.00000451 2.538E-08 0.00000451 2.538E-08 0.00000451 2.538E-08 0.00000228 3.5376E-08</td> <td>4.15 2.54 2.54 2.54 2.54 2.54 2.54 2.55 2.57 7.29 2.57 7.29 2.57 7.29 2.57 7.29 2.57 7.29 2.57 2.59 2.57 2.59 2.59 2.59 2.59 2.59 2.59 2.50 2.50 2.50 2.50 2.50 2.50 2.50 2.50</td> <td>2 2 2 2 2 2 2 3 3 3 3 4 4 4 3 3 3 4 4 3 3 3 3</td> <td>MHI-[Da] 1062.9711 1169.85141 1169.85141 1169.85141 1167.85142 2266.01281 2266.01281 2266.01281 2266.01281 2266.01281 2266.01281 2266.01281 2266.01281 2266.01281 2266.01281 2266.01281 2266.01281 2267.01285 2278.01295 2278.0578 2278.0578 2278.0579 2278.0579 2278.0579 2278.0579 2278.0579 2288.017949 2288.017949 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11.05 11.05 11.05 11.05 11.05 11.05 11.05 11.05 11.05 11.05 11.05 11.05 11.05 11.05 11.05 11.05 11.</td> <td># Mused Cleanges 0 0 1   # Mused Cleanges 1</td>	PEP 0000004943 0001248 00007814 0007814 883 PEP 8.437E-11 6.058E-11 4.647E-10 3.31E-08 4.524E-08 5.441E-10 4.000E-08 5.441E-10 4.000E-08 0.000000253 1.536E-07 0.000000451 2.538E-08 0.000000451 2.538E-08 0.000000451 2.538E-08 0.000000451 2.538E-08 0.000000451 2.538E-08 0.000000451 2.538E-08 0.00000451 2.538E-08 0.00000451 2.538E-08 0.00000451 2.538E-08 0.00000451 2.538E-08 0.00000451 2.538E-08 0.00000451 2.538E-08 0.00000451 2.538E-08 0.00000451 2.538E-08 0.00000228 3.5376E-08	4.15 2.54 2.54 2.54 2.54 2.54 2.54 2.55 2.57 7.29 2.57 7.29 2.57 7.29 2.57 7.29 2.57 7.29 2.57 2.59 2.57 2.59 2.59 2.59 2.59 2.59 2.59 2.50 2.50 2.50 2.50 2.50 2.50 2.50 2.50	2 2 2 2 2 2 2 3 3 3 3 4 4 4 3 3 3 4 4 3 3 3 3	MHI-[Da] 1062.9711 1169.85141 1169.85141 1169.85141 1167.85142 2266.01281 2266.01281 2266.01281 2266.01281 2266.01281 2266.01281 2266.01281 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544EE-08 544EE-08 544EE-08 544EE-08 544EE-08 544EE-08 544EE-08 544EE-08 544EE-08 544EE-08 544EE-08 544EE-08 544EE-08 544EE-08 544EE-08 544EE-08 544EE-08 544EE-08 544EE-08 544EE-08 544EE-08 544EE-08 544EE-08 544EE-08 544EE-08 544EE-08 544EE-08 544EE-08 544EE-08 544EE-08 544EE-08 544EE-08 544EE-08 544EE-08 544EE-08 544EE-08 544EE-08 544EE-08 544EE-08 544EE-08 544EE-08 544EE-08 544EE-08 544EE-08 544EE-08 544EE-08 544EE-08 544EE-08 544EE-08 544EE-08 544EE-08 544EE-08 544EE-08 544EE-08 544EE-08 544EE-08 544EE-08 544EE-08 544EE-08 544EE-08 544EE-08 544EE-08 544EE-08 544EE-08 544EE-08 544EE-08 544EE-08 544EE-08 544EE-08 544EE-08 544EE-08 544EE-08 544EE-08 544EE-08 544EE-08 544EE-08 544EE-08 544EE-08 544EE-08 544EE-08 544EE-08 544EE-08 544EE-08 544EE-08 544EE-08 544EE-08 544EE-08 544EE-08 544EE-08 544EE-08 544EE-08 544EE-08 544EE-08 544EE-08 544EE-08 544EE-08 544EE-08 544EE-08 544EE-08 544EE-08 544EE-08 544EE-08 544EE-08 544EE-08 544EE-08 544EE-08 544EE-08 544EE-08 544EE-08 544EE-08 544EE-08 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          30.33           30.34           30.32           30.32           77.30           30.42           77.30           30.42           77.38           30.45           30.36           77.38           30.45           30.45           30.45           30.45           30.45           30.45           30.45           30.45           30.45           30.45           30.45           30.45           30.45           30.45           30.45           30.45           30.45           30.45           30.46           30.47           30.41           30.41           30.41           30.42           30.43           30.44           3	# Missel Changes 0 1 # Missel Changes 1 2 2 3 4 4 5 5 5 6 6 7 7 7 7 7 7 7 7 7 7 7 7 7
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       2.65           2.64	Filment           32.21           12.00           12.10           12.10           12.20           14.10           ATEMAN           30.27           30.26           30.31           44.00           30.27           30.38           44.00           30.27           20.26           30.37           7.38           30.4           10.6           30.7           25.4           30.7           30.7           30.7           25.4           30.7           30.7           30.7           30.7           30.7           30.7           30.7           30.7           30.7           30.7           30.7           30.7           30.7           30.7           30.7           30.7           30.7           30.7           30.7           30.7           30.7           30.7	# Mussi Canages 0 0 1  # Mussi Canages 1 2 4 4 4 5 5 6 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7
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  13.30           33.31           4.40           30.20           30.31           4.40           30.32           30.33           4.40           30.32           30.33           30.34           4.53           30.7           23.81           30.7           23.81           30.7           23.81           30.7           30.7           30.8           20.91           30.8           20.91           30.4           13.24           13.24           13.24           13.24           13.24           13.24           13.24           13.24           13.24           13.24           23.64           23.75           33.61           23.27           33.28           23.29           33.20           23.20           33.21 </td <td># Mased Clanages 0 0 4 9 9 9 1 9 9 9 1 1 2 2 0 1 1 2 1 1 2 1 1 1 1 1 1 1 1 1</td>	# Mased Clanages 0 0 4 9 9 9 1 9 9 9 1 1 2 2 0 1 1 2 1 1 2 1 1 1 1 1 1 1 1 1
NAD-dependent protein dearrylae simis 108-Hono supers GN-SIRT	igoLLDQKK JOPISKIY Sequese VTVRNIFLIQVAGQK LSGTBATMP MUTVRNIFLIQVAGQK LSGTBATMP MUTVRNIFLIQVAGQK LSGTBATMP KREQPFXAVDDFRNIFK REAGEDSCLIDSVTHFSSNVGDTK REAGEDSCLIDSVTHFSSNVGDTK REAGEDSCLIDSVTHFSSNVGDTK REAGEDSCLIDSVTHFSSNVGDTK REAGEDSCLIDSVTHFSSNVGDTK REAGEDSCLIDSVTHFSSNVGDTK REAGEDSCLIDSVTHFSSNVGDTK REAGEDSCLIDSVTHFSSNVGDTK REAGEDSCLIDSVTHFSSNVGDTK REAGEDSCLIDSVTHFSSNVGDTK REAGEDSCLIDSVTHFSSNVGDTK REAGEDSCLIDSVTHSSNVGDTK REAGEDSCLIDSVTHFSSNVGDTK REAGEDSCLIDSVTHFSSNVGDTK REAGEDSCLIDSVTHFSSNVGDTK REAGEDSCLIDSVTHSSNVGDTK REAGEDSCLIDSVTHSSNVGDTK REAGEDSCLIDSVTHSSNVGDTK REAGEDSCLIDSVTHSSNVGDTK REAGEDSCLIDSVTHSSNVGDTK REAGEDSCLIDSVTHSSNVGDTK REAGEDSCLIDSVTHSSNG REAGEDSCLIDSVTHSSN REAGENSTVHEIMOUTR REAGENSTVHEIMOUTR REAGENSTVHEIMOUTR REAGENSTVHEIMOUTS REAGENSTVHEIMOUTS REAGENSTVHEIMOUTS REAGENSTVHEIMOUTS REAGENSTVHEIMOUTS REAGENSTVHEIMOUTS REAGENSTVHEIMOUTS REAGENSTVHEIMOUTS REAGENSTVHEIMOUTS REAGENSTVHEIMOUTS REAGENSTVHEIMOUTS 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REAGENST REAGENST REAGENST REAGENST REAGENST REAGENST REAGENST REAGENST REAGENST REAGENST REAGENST REAGENST REAGENST	1007 1007 1 2 3 3 1 1 2 2 3 3 1 1 1 2 2 3 3 1 1 1 2 3 3 1 1 1 4 4 2 4 4 4 4 4 4 4 4 4 4 4 4 4	4 9 Protectines 4 9 Protectines 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	Nodification           79           Mindification           N:Tem(Acryl)           CliCabanidosterly()           M2(Nikidos)           M2(Nikidos)           NTem(Acryl)	7 7 7 7 7 7 7 7 7 7 7 7 7 7	Notace         Notace           0         0         0         0           2486         0         0         0         0         0         0         0         0         0         0         0         0         0         0         0         0         0         0         0         0         0         0         0         0         0         0         0         0         0         0         0         0         0         0         0         0         0         0         0         0         0         0         0         0     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       4.02           4.03           4.04           4.05           4.06           6.07           4.08           4.09           4.01           4.02           4.03           4.04           4.05           4.06           4.07           4.08           4.09           4.04           4.05           4.06	RT (mm)           22.21           12.30           12.30           14.36           30.76           30.76           30.71           30.73           30.73           30.73           30.73           30.73           30.73           30.73           30.73           30.73           30.76           30.76           30.76           30.76           30.76           30.76           30.76           30.76           30.76           30.76           30.76           30.76           30.76           30.76           30.76           30.76           30.76           30.77           30.76           30.76           30.77           30.76           30.77           30.78           30.71           30.72           30.73           30.74           30.75           30.76           30.77           30.78	# Missel Changes 0 # Missel Changes 1 2 3 4 4 5 4 5 5 5 5 5 5 5 5 5 5 5 5 5

	TIFGSIPDIFDVHTK	37	6	MR(Onidation)	0.0000	0	0.000009481	4.09	2	1689.88298	-1.03	37.07	0
	TSLADSSIFDSK	62	10	M8(Oxidation)	0.0000	0	0.0006022	4.08	2	1447.81789	-0.33	27.86	0
	RALMTSHGSVEGR	10	6		0.0000	0	0.0001842	4.07	3	1400.70600	-0.27	12.11	1
	cTHLVVEENIVKDLPFEPSKK	1	5	N-Term(Acetyl)	0.0000	0	2.856E-08	4.04	2	2467.27837	-4.81	33.23	2
	VSMLSLNTPNSNR VTHLVAN/TOGEK	20	6	N-Term(Acetyl): C8(C)	0.0000	0	0.00004773	3.98	2	1519.75347	-1.42	23.81	0
	HIHLMPLSQIKK	5	6	M5(Oxidation)	0.0000	0	0.001305	3.90	4	1460.83791	-1.89	16.18	1
	sVSMLSLNTPNSNR	5	6	N-Term(Acetyl)	0.0000	0	0.00003582	3.89	2	1561.76177	-1.40	30.87	0
	VETISLGEHPcDR	8	6	N-Term(Acetyl); C11(0	2a 0.0000	0	0.00004534	3.82	2	1554.71782	-2.53	22.27	0
	aGETMVI VEK	22	6	N-Term(Acetyl); M5(O N-Term(Acetyl)	0.0000	0	0.003626	3.77	3	13/4./5428	-1.45	22.37	0
	EVMTHINEDKR	14	5	(A-Team(Access))	0.0000	0	0.0001818	3.74	2	1371.66728	-0.95	12.28	1
	TNMEEMTEMQGGK	11	5		0.0000	0	0.00003197	3.71	2	1485.59831	-2.43	20.46	0
	KSVSmLSLNTPNSNR	7	6	M5(Oxidation)	0.0000	0	0.000003351	3.71	2	1663.84099	-1.37	15.83	1
	LVTLVHHmGGVIRK TNMEEMTEmOGGK	9	6	M8(Oxidation) M8(Oxidation)	0.0000	0	0.002784	3.68	4	1575.91433	-0.59	12.76	1
	ALMTSHGSVEGR	27	6	M)(()(Manifold)	0.0000	0	0.0002534	3.57	3	1244.60538	0.10	10.41	0
	aLMTSHGSVEGR	18	6	N-Term(Acetyl)	0.0000	0	0.0001481	3.57	2	1286.61589	0.05	13.90	0
	vIGPPVVLNcSQK	12	7	N-Term(Acetyl); C10(C	a 0.0000	0	0.00127	3.56	2	1452.78459	-2.33	30.15	0
	HIHLMPLSQIKK	7	6		0.0000	0	0.0007603	3.54	4	1444.84499	-0.53	19.07	1
	LKETLAQLSR	40	6		0.0000	0	0.009676	3.53	3	1158.68222	-0.97	16.82	1
	TYPPFVNFFEMSK	80	6		0.0000	0	0.0001392	3.50	2	1606.75505	-3.76	39.98	0
	al.mTSHGSVEGR	17	6	N-Term(Acetyl); M3(O	xi 0.0000	0	0.0001129	3.49	3	1302.60688	-2.97	10.68	0
	SVSmLSLNTPNSNRK	11	6	M4(Oxidation)	0.0000	0	0.000203	3.49	3	1663.84165	-0.97	19.05	1
	SVSmLSLNTPNSNR	31	6	M3(Oxidation) M4(Oxidation)	0.0000	0	0.0007889	3.45	2	1260.59809	-1.66	10.74	0
	eTDVSPFPPR	51	5	N-Term(Acetyl)	0.0000	0	0.001715	3.41	2	1186.57219	-1.47	30.55	0
	ETDVSPFPPR	82	5		0.0000	0	0.0009315	3.39	2	1144.56389	0.45	20.00	0
	AGETMYLYEK	23	6		0.0000	0	0.001105	3.37	2	1204.55205	-2.86	21.69	0
	KETLAQLSR N/T VIIII-COVID	10	6	N-Term(Acetyl)	0.0000	0	0.0019	3.34	2	1200.69438	-0.28	22.21	1
	SIGDIFLKYSK	3	6	re-reality accession and the	0.0000	0	0.001023	3.31	2	1270.70415	-0.05	29.21	1
	tYPPFVNFFEMSK	8	6	N-Term(Acetyl)	0.0000	0	0.0001373	3.29	2	1648.77629	2.81	42.90	0
	sVSmLSLNTPNSNR	6	6	N-Term(Acetyl); M4(O	xi 0.0000	0	0.002336	3.27	2	1577.75920	0.22	22.34	0
	dFGSIPDIFDVHTK	2	6	N-Term(Acetyl)	0.0000	0	0.0001788	3.26	2	1731.89958	2.48	39.23	0
	aSLVELLIRPVOR	40	5	N-Term(Acetyl)	0.0000	0	0.001444	3.16	3	1592,94669	-2.33	32.48	0
	ETDVSPFPPRK	7	5		0.0000	0	0.001184	3.14	2	1272.65740	-0.74	14.79	1
	cTHLVVEENIVK	2	5	N-Term(Acetyl)	0.0000	0	0.001507	3.13	2	1425.73296	-5.42	24.73	0
	TNmEEmTEmQGGK	4	5	M3(Oxidation); M6(Ox	ic 0.0000	0	0.000619	3.04	2	1533.58269	-2.59	13.75	0
	EVMTHINEDK	9	5	.s-remi(Acetyl); C8(Ci	0.0000	0	0.0008405	3.03	2	1214.59220 1215.56548	-2.05	12.89	0
	EVMTHINEDKRK	4	5		0.0000	0	0.0009712	3.02	4	1499.76162	-1.30	10.57	2
	aGETm YLYEK	11	6	N-Term(Acetyl); M5(O	si 0.0000	0	0.002713	3.02	2	1262.55730	-2.91	20.45	0
	DLVKTYPPFVNFFEmSK AIGSLKEVAPTUINEDK	1	6	M15(Oxidation)	0.0000	0	0.001084	3.01	3	2078.03391	1.68	34.39	1
	sGPILAPEEIK	8	6	N-Temp(Acetob	0.0000	0	0.001388	2.99	2	1/64.91776	-1.95	24.07	0
	EVmTHINEDK	6	5	M3(Oxidation)	0.0000	0	0.0002602	2.98	2	1231.56206	-0.27	10.29	0
	GGPILAPEEIK	30	6		0.0000	0	0.007524	2.97	2	1123.63432	-1.33	22.08	0
	QEWFWGSIQMDAR	1	6		0.0000	0	0.00004909	2.93	2	1653.75163	2.25	44.53	0
	QEWFWGSIQmDAR eNLLIGSTSYVEEEmPOIET®	3	8	M10(Oxidation)	0.0000	0	0.01817	2.93 2.90	2	2496 17148	-0.58	32.53 33.13	0
	TYPPFVNFFEmSK	51	6	M11(Oxidation)	0.0000	0	0.0006005	2.89	2	1622.75005	-3.67	36.60	0
	ALKDIKVGFVK	1	6		0.0000	0	0.002802	2.89	2	1217.75920	-2.04	19.49	2
	AGETmYLYEK	19	6	M5(Oxidation)	0.0000	0	0.01303	2.74	2	1220.54766	-2.25	18.15	0
	eVMTHINEDKRK	2	5	N-Term(Acetyl)	0.0000	0	0.009522	2.63	3	1541.77073	-2.21	10.16	2
	dMDSTLSR	5	6	N-Term(Acetyl)	0.0000	0	0.01822	2.55	2	917.50316 966.41802	-2.13	16.54	0
	EVmTHINEDKR	5	5	M3(Oxidation)	0.0000	0	0.02088	2.43	2	1387.66203	-1.06	12.24	1
	eTLAQLSR	7	6	N-Term(Acetyl)	0.0000	0	0.02042	2.40	2	959.51384	-1.91	21.75	0
	hVANTICK	4	6	N-Term(Acetyl); C7(C	url 0.0000	0	0.005384	2.32	2	984.48906	-4.16	10.85	0
	TNMEEmTEmQGGK vII VOFAGK	5	5	M6(Oxidation); M9(Ox N-Term(Acetyl)	0.0000	0	0.0003859	2.28	2	1517.59416 998 58476	-3.37	25.03	0
	VILVQEAGK	28	10		0.0000	0	0.009837	2.21	2	956.57622	-1.40	16.05	0
	SPHGQTRPPASLK	7	6		0.0000	0	0.004593	2.09	2	1375.74272	-1.02	7.76	0
	AFSFSKTPK	4	6		0.0000	0	0.01422	2.04	2	1012.54503	-1.21	13.49	1
	eVmTHINEDKR	6 24	5	N-Term(Acetyl); M3(O	0.0000	0	0.004246	2.01	3	1429.67118	-2.02	10.86	1
	tYPPFVNFFEmSK	2	6	N-Term(Acetyl); M11(	D: 0.0000	0	0.002092	1.99	2	1664.76103	-3.33	34.93	0
	sIGDIFLK	5	6	N-Term(Acetyl)	0.0000	0	0.008099	1.95	2	934.52410	-0.39	30.11	0
	YLPLGDER	25	5		0.0000	0	0.02069	1.94	2	962.49260	-1.67	24.99	0
Nucleolin OS=Homo saniens GN=NCI	qEWFWGSIQMDAR 200.4449061	2 25.21	2	N-Term(Acetyl)	0.0000	0	0.004424	1.82	2 4 703613281	1695.75432	-2.46	37.61	0
	Sequence	# PSMs	# Proteins	Modifications	ΔCn	q-Value	PEP	XCorr	Charge	MH+ [Da]	ΔM [ppm]	RT [min]	# Missed Cleavages
	GLSEDTTEETLKESFDGSVR	4	2		0.0000	0	0.000009844	5.92	3	2200.02298	-1.04	31.27	1
			-		0.0000								
	TLVLSNLSYSATEETLQEVFEK	3	2		0.0000	0	0.00001404	5.81	3	2501.26810	0.91	41.49	0
	TI. VLSNLSYSATEETI.QEVFEK VTQDELKEVFEDAAEIR VEGTEPTTAPNLFVGNLNFNK	3 5 2	2 2 1		0.0000	0	0.00001404 0.00000017 0.000002352	5.81 5.50 5.05	3 2 2	2501.26810 1991.99236 2312.15386	0.91 0.11 -0.86	41.49 36.52 40.17	0 1 0
	TLVLSNLSYSATEETLQEVFEK VTODELKEVFEDAAEIR VEGTEPTTAFNLFVGNLNFNK KFGVVDFESAEDLEK	3 5 2 1	2 2 1 1		0.0000 0.0000 0.0000 0.0000	0 0 0	0.00001404 0.00000017 0.000002352 4.036E-08	5.81 5.50 5.05 4.20	3 2 2 2	2501.26810 1991.99236 2312.15386 1776.82573	0.91 0.11 -0.86 -3.95	41.49 36.52 40.17 28.72	0 1 0 1
	TLVLSNLSYSATEETLQEVFEK VTODELKEVFEDAAEIR VEGTEPTTAFNLFVGNLNFNK KFGYVDFESAEDLEK GFGFVDFNSEEDLEK	3 5 2 1 6	2 2 1 1 2		0.0000 0.0000 0.0000 0.0000 0.0000	0 0 0 0	0.00001404 0.00000017 0.000002352 4.036E-08 0.00005361	5.81 5.50 5.05 4.20 3.99	3 2 2 2 2	2501.26810 1991.99236 2312.15386 1776.82573 1561.67668	0.91 0.11 -0.86 -3.95 -2.52	41.49 36.52 40.17 28.72 30.67	0 1 0 1 0
	TLVLSN SYSTERT OFVFEK VTQDELKEVFEDAAER VTQDELKEVFEDAAER VGTUPTTARILVOLLNNK KGVVPFESAEDLEK GGGVUPNSEEDAK TEADAEKFFEEK	3 5 2 1 6 6	2 2 1 1 2 2 2 1 1 2 2 2 2 2 2 2 2 2 2 2		0.0000 0.0000 0.0000 0.0000 0.0000 0.0000	0 0 0 0 0	0.00001404 0.00000017 0.000002352 4.036E-08 0.00005361 0.00002404	5.81 5.50 5.05 4.20 3.99 3.86	3 2 2 2 2 2 2	2501.26810 1991.99236 2312.15386 1776.82573 1561.67668 1397.64055	0.91 0.11 -0.86 -3.95 -2.52 -1.86	41.49 36.52 40.17 28.72 30.67 13.63	0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1
	TU VISNU SINN TEETL GAVVER VIOEL EKYPENAAR VEETETT JUNI FVOLUSION KIKVI VIOEL EKYPENA GREVITIONSEEDUK GREVITIONSEEDUK TAJADAKTEEK FVYVTERSAEDLEK	3 5 2 1 6 2 6	2 2 1 1 2 2 1 1 1 2 1 1 1 1 1 1 1 1 1 1		0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0		0.00001404 0.00000017 0.0000002352 4.036E-08 0.00005361 0.0002404 0.0002411 0.000241	5.81 5.50 5.08 4.20 3.99 3.86 3.45 3.27	3 2 2 2 2 2 2 2 2 2 2 2 2	2501.26810 1991.99236 2312.15386 1776.82573 1561.67668 1397.64055 1648.73491 1000 \$4020	0.91 0.11 -0.86 -3.95 -2.52 -1.86 -1.74 -1.54	41.49 36.52 40.17 28.72 30.67 13.63 34.55 25.18	0 1 0 1 0 1 0
	TLVISNYSATEETLQVYEEK YUDDE KEYPENAAR VEGTEPTTAINLFVON NYNK KGVYDPESADLLK GGVDNSEEDLK TEADAERTHEEK FGYVDESAELEK NULAYVDVR NULAYDVR	3 5 1 6 2 6 5	2 2 1 1 2 2 2 1 1 1 1		0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000	0 0 0 0 0 0 0 0	0.00001404 0.00000017 0.0000002352 4.036E-08 0.00005361 0.0002404 0.0002404 0.0002411 0.0002296 0.004657	5.81 5.50 5.05 4.20 3.99 3.86 3.45 3.32 3.00	3 2 2 2 2 2 2 2 2 2 2 2 2 2	2501.26810 1991.99236 2312.15386 1776.82573 1561.67668 1397.64055 1648.73491 1000.54070 937.49816	0.91 0.11 -0.86 -3.95 -2.52 -1.86 -1.74 -1.54 -0.87	41.49 36.52 40.17 28.72 30.67 13.63 34.55 25.18 23.85	0 1 0 1 0 1 0 0 0
	TU VI.SNA SVANEET.LQVYEK VTOOLEKSYPKAARR VEGTEPTTANILYVOLININI KIGVYDEFASDLAE GGUVINISEEDAK LGADAEKTEEK FGYVDEFASDLAE KILAVIDVR TGISDYFAK GASDTTEET.K	3 5 2 1 6 6 2 6 5 1	2 2 1 1 2 2 1 1 1 1 2 2 1 1 1 2 2 2 1 1 1 2 2 2 1 1 1 2 2 2 1 1 1 1 2 2 2 1 1 1 1 2 2 2 1 1 1 1 1 2 2 2 1 1 1 1 1 1 1 1 1 2 2 2 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.00	0 0 0 0 0 0 0 0	0.00001404 0.00000017 0.000002352 4.036E-08 0.0002404 0.0002404 0.0002401 0.0002401 0.00024057 0.004657 0.001547	5.81 5.50 5.08 4.20 3.99 3.86 3.45 3.32 3.00 2.73	3 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	2501.26810 1991.99236 2312.15386 1776.82573 1561.67668 1397.64055 1648.73491 1000.54070 937.49816 1322.62883	0.91 0.11 -0.86 -3.95 -2.52 -1.86 -1.74 -1.54 -0.87 -2.58	41.49 36.52 40.17 28.72 30.67 13.63 34.55 25.18 23.85 17.88	0 1 0 1 0 0 0 0 0
	TUVISNYSNTEELQEVEE VTOOE KEVFORAAR VEGIETTUNIFVORISNIK KFOVYDFREADLEK GFOVYDNSEEDLK GFOVYDNSEEDLK TEODAKTEEK NELAVITUR TEODAKTEEK GISUTTAK GISUTTEELK ESTELAAR	3 5 2 1 6 6 5 5 1 3	2 2 1 1 2 2 1 1 1 1 2 2 1 1 1 2 2 2 1		0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0.00001404 0.00000017 0.000002352 4.036E-08 0.00005361 0.0002404 0.0002404 0.0002404 0.0002411 0.000296 0.004657 0.001547 0.000547	5.81 5.50 5.05 4.20 3.99 3.86 3.45 3.45 3.32 3.00 2.73 2.27	3 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	2501.26810 1991.59236 2312.15386 1776.82573 1561.67668 1397.64055 1648.73491 1000.54070 937.49816 1322.62883 1178.56743	0.91 0.11 -0.86 -3.95 -2.52 -1.86 -1.74 -1.54 -0.87 -2.58 -1.21	41.49 36.52 40.17 28.72 30.67 13.63 34.55 25.18 23.85 17.88 23.20	0 1 0 1 0 0 0 0 0
Tubuln ajala: 14 chair OS-Hamo sapient GN-TUBA1A	TU VI.SNA STATEET. QVVEK VTOELEKVPSAAER VIGTEFTANLFVOLINNK KIGVVDFSAEDLEK GRUPVINSEEDLK GRUPVINSEEDLK ROVVERSAEDLEK GRUPVER GRUPVINK GRUPVER GRUPVER USADAR ZOUST/16	3 5 2 1 6 6 5 2 6 5 1 3 3 56.01	2 2 1 1 2 2 1 1 1 1 2 2 2 2 2 2 2 2 2 2	1 Modifications	0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0.00001404 0.00000017 0.000002352 4.036E-08 0.000025361 0.0002404 0.0002411 0.0002411 0.0002411 0.0002413 0.001547 0.001547 0.001547 0.001547 0.0003873 416 BED	5.81 5.50 4.20 3.99 3.86 3.45 3.32 3.00 2.73 2.27 46.26784264 WCorr	3 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	2501.26810 1991.99236 2312.15386 1776.82573 1561.67668 1397.64055 1648.73491 1000.54070 937.49816 1322.62883 1178.56743	0.91 0.11 -0.86 -3.95 -2.52 -1.86 -1.74 -1.74 -1.54 -0.87 -2.58 -1.21	41.49 36.52 40.17 28.72 30.67 13.63 34.55 25.18 23.85 17.88 23.20 PT [min]	0 1 0 1 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0
Tubuin apha-1A chan OS-Homo sapiens GN-TUBA1A	TU VISNI SYSNEEDL GVYEK VTOOR KAYPBAARR VEGTEPT TANLFYCULININ KGYVDFSAEDLAK GREVPONSEEDLA TADAKTEEK RYYDFSAEDLEK NOLAVDOV GSLOTVERK GSLOTVERK GSLOTVERK GSLOTVERK GSLOTVERK GSLOTVERK GSLOTSFELK EVFEDAARR Soguest (GFLOFGLOTGEDAANNYAR	3 5 2 1 6 6 2 6 5 1 3 5 5 0 1 3 5 6 0 1 3 4	2 2 1 1 2 2 2 1 1 1 1 2 2 2 21 # Proteins 23	1 Modifications	0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 18 ΔCn 0.0000	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0.00001404 0.00000017 0.000002352 4.036E-08 0.000025361 0.0002404 0.0002411 0.0002411 0.0002411 0.0002413 0.001547 0.001547 0.001547 0.001547 1.626E-09	5.81 5.50 5.05 4.20 3.99 3.86 3.45 3.32 2.03 2.03 2.27 42.26784264 XCorr 7.24	3 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	2501.26810 1991.99236 2312.15386 1776.82573 1561.67668 1397.64055 1648.73491 1000.54070 937.49816 1322.62883 1178.56743 MH+ [Da] 2415.19974	0.91 0.11 -0.86 -3.95 -2.52 -1.86 -1.74 -1.74 -0.87 -2.58 -1.21 ΔM [ppm] -2.28	41.49 36.52 40.17 28.72 30.67 13.63 34.55 25.18 23.85 17.88 23.20 RT [min] 29.09	0 1 1 0 1 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0
Tubulin apha-1A chain OS-Homo sapiens GN-TUBA1A	TU VI.SN SYNTEELQGVYEK VTOOELSGVYEALAR VIGUETTUNILYVOLINSIK KIGVYDFASEDALAR GIGVYDFASEDAL GIGVYDFASEDAL KADAGXTHEK FGYYEFINAELEK GIGVTUNSEEDAK GIGVTUNSEEDAK GIGVTUNSEETIK FYETAADAR SOURSYTEETIK Soursyte Soursyte Soursyte	3 5 2 1 6 6 2 6 5 1 3 5 6 01 3 7 5 6 01 4 1	2 2 2 1 1 2 2 1 1 1 1 2 2 2 1 <i>#</i> Proteins 23 9	1 Modifications C15(Carbanidomethyl	0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 18 ΔCn 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.00	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 54 4 0 0 0 0	0.00001404 0.00000017 0.0000002352 4.036E-08 0.00005361 0.0002404 0.0002404 0.0002404 0.0002411 0.000236 0.0004657 0.001547 0.001547 0.0003573 416 PEP 1.626E-09 0.000005865	5.81 5.50 5.05 4.20 3.99 3.86 3.45 3.32 3.00 2.73 2.27 46.26784264 XCorr 7.24 6.78	3 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	2501.26810 1991.99236 2312.15386 1776.82573 1561.67668 1397.64055 1648.73491 1000.54070 937.49816 1322.62883 1178.56743 MH+ [Da] 2415.19974 2750.27634	0.91 0.11 -0.86 -3.95 -2.52 -1.86 -1.74 -1.54 -0.87 -2.58 -1.21 -2.28 -5.47	41.49 36.52 40.17 28.72 30.67 13.63 34.55 25.18 23.85 17.88 23.20 <b>RT [min]</b> 29.09 32.54	0 1 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0
Tabulin apha-1A chain OS-Homo suprem GN-TUBA1A	TU VI.SN SYNTEEL QVYEK VTOOLE KEYPENAAR VEGTEPT TANLFVOLINNK KGYVTPESABDLAK GGUVTONSEEDAK TADAEKTEEK GGUVTONSEEDAK TADAEKTEEK GGUSTTEELK EVFEDAAR SQURES GGUSTTEELK EVFEDAAR SQURES GQUITELK EVFEDAAR SQURES GQUITELK	3 5 2 1 6 6 5 2 6 5 7 3 3 56.01 # PSMs 4 1 1	2 2 1 1 2 2 1 1 1 1 2 2 2 2 21 # Proteins 23 9 15	1 Modifications C15(Carbamidomethyl	0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 18 4 4 Cn 0.0000 0.0000 0.0000 0.0000	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 54 54 0 0 0	0.00001404 0.0000017 0.000000352 4.036E-08 0.00005361 0.0002411 0.0002411 0.0002411 0.0002411 0.0003873 0.001547 0.001547 0.001547 4.165 PEP 1.636E-09 0.000008885 4.302E-08	5.81 5.05 4.20 3.96 3.386 3.35 3.32 2.00 2.73 2.27 462.67584264 XCorr 7.24 6.267	3 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	2501.26810 1991.99236 2312.15386 1776.82573 1561.67668 1397.64055 1397.64055 1397.64055 1397.64055 1397.64055 1322.62883 1178.56743 MH+ [Da] 2415.19974 2415.19974 2409.20195	0.91 0.11 -0.86 -3.95 -2.52 -1.86 -1.74 -1.54 -0.87 -2.58 -1.21 -2.28 -5.47 -2.28 -5.47 -2.76	41.49 36.52 40.17 28.72 30.67 13.63 34.55 25.18 23.85 17.88 23.20 <b>RT (min)</b> 29.09 32.54 40.43	0 1 0 1 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0
Tubulin ajaha 1A chain OS-Homo sapiens GN-TUBA1A	TU VI.SN SYNTEEL QEVYEK VTOOEL SEVYENAAER VIGTEET TANILYVOLLSINK KIGYVDFISALDLIK GIGVIDISSEEDAK TADMATTEEK FOLUTISSEEDAK TADMATTEEK GIGUIYAK GISDIYTAK GISDIYTAK GISDIYTAK GISDIYTAK GISDIYTAK GISDIYTAK GISDIYTAK GISDIYTAK GISDIYTAK GISDIYTAK GISDIYTAK GISDIYTAK HURDINGUTUSELSANNYAK HURDINGUTUSELSANNYAK HURDINGUTUSELSANNYAK HURDINGUTUSELSANNYAK	3 5 2 1 6 6 5 5 5 6 5 5 5 6 0 1 3 3 5 5 601 4 1 1 7 7 6	2 2 1 1 2 2 1 1 1 2 2 1 1 2 2 2 1 <i>#</i> 1 2 2 2 1 <i>#</i> 1 2 2 1 1 1 2 2 1 1 1 2 2 1 1 1 2 2 1 1 1 2 2 1 1 1 2 2 1 1 1 2 2 1 1 1 2 2 1 1 1 2 2 1 1 2 2 1 1 1 2 2 1 1 2 2 1 1 2 2 1 1 2 2 1 1 2 2 1 1 2 2 1 1 2 2 1 1 2 2 1 1 2 2 1 1 2 2 1 1 2 2 1 1 2 2 1 1 2 2 1 1 2 2 1 1 2 2 1 1 2 2 1 1 2 2 2 1 1 2 2 2 1 1 2 2 2 1 1 2 2 2 1 2 2 2 1 2 2 2 2 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	1 Modifications C15(Carbamidomethyl	0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 18 MCn 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.00000 0.00000 0.000000	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0.00001404 0.00000017 0.00000017 0.000002352 0.00005361 0.0002404 0.0002404 0.0002404 0.0002411 0.000236 0.0003873 416 PEP 1.626E-09 0.000005845 4.302E-08 0.000005845	5.81 5.00 4.20 3.99 3.386 3.45 3.32 2.73 2.27 46.26784264 XCorr 7.24 6.78 5.40 4.73	3 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	2501.26810 1991.99236 2312.15386 1776.82573 1561.67668 1397.64055 1648.73491 1000.54070 937.49816 1322.62883 1178.56743 MH+ [Da] 2415.19974 250.27634 2340.27634 2340.27634	0.91 0.11 -0.86 -3.95 -2.52 -1.86 -1.74 -1.54 -0.87 -2.58 -1.21 ΔM [ppm] -2.28 -5.47 -2.76 -0.87 -2.76 -0.87 -2.76	41,49 36,52 40,17 28,72 30,67 13,63 34,55 23,85 17,88 23,30 RT [min] 29,09 32,54 40,43 32,09 32,67 32,67 32,07 32,07 32,07 32,07 32,07 32,07 32,07 32,07 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,55 34,555 34,555 34,555 34,555 34,555 34,555 34,555 34,555 34,555 34,555 34,555 34,555 34,555 34,555 34,555 34,555 34,555 35,555 35,555 35,555 35,555 35,555 35,555 35,555 35,555 35,555 35,555 35,555 35,555 35,555 35,555 35,555 35,555 35,555 35,555 35,555 35,555 35,555 35,555 35,555 35,555 35,555 35,555 35,555 35,555 35,555 35,555 35,555 35,555 35,555 35,555 35,555 35,555 35,555 35,555 35,555 35,555 35,555 35,555 35,555 35,555 35,555 35,555 35,555 35,555 35,555 35,555 35,555 35,555 35,555 35,555 35,555 35,555 35,555 35,555 35,555 35,555 35,555 35,555 35,555 35,555 35,555 35,555 35,555 35,555 35,555 35,555 35,555 35,555 35,555 35,555 35,555 35,555 35,555 35,555 35,555 35,555 35,555 35,555 35,555 35,555 35,555 35,555 35,555 35,555 35,555 35,555 35,555 35,555 35,555 35,555 35,555 35,555 35,555 35,555 35,555 35,555 35,555 35,555 35,555 35,5555 35,5555 35,555 35,555 35,5555 35,5555 35,5555 35,5555	0 1 1 1 0 1 1 0 1 0 1 0 0 1 8 Missed Charages 1 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
Tubuln abba-1A cluir OS-Homo sapien GN-TUBATA	TU VI.SN SYNTEEL QVYREK VTOOEL SKYPBAARR VGCHET TANILYKON.NNN KGYVDFFASDELK GGUYDNSEEDAK GGUYDNSEEDAK GGUYDNSEEDAK SADAEXTPEK GGUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK GUSDTEELK	3 5 2 1 1 6 6 2 6 5 5 1 3 3 5 6 01 # <b>PSM5</b> 4 1 7 6 4	2 2 2 1 1 2 2 1 1 1 2 2 2 2 2 2 2 2 2 9 9 15 12 2 17	1 Modifications C15(Carbamidomethyl	0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0.00001404 0.0000017 0.000000352 4.036E-08 0.00005361 0.0002411 0.0002411 0.0002411 0.0002411 0.0002413 0.0003467 0.0003473 416 PEP 1.626E-09 0.000005848 0.000005848 0.000005848	5.81 5.00 4.20 3.96 3.46 3.45 3.32 3.00 2.73 2.27 46.26784264 X.Corr 7.24 6.78 5.40 5.43 4.58	3 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	2201.2840 1991.99236 2312.15386 1776.82573 1561.67668 1397.49055 1648.73491 1000.54709 937.49816 1000.54709 937.49816 1322.62883 1178.56743 2415.19974 2215.127634 2415.19974 2750.27634 2419.21957 1756.96177 1701.03366	0.91 0.11 -0.86 -3.95 -2.52 -1.86 -1.74 -1.54 -0.87 -2.28 -1.21	41,49 40,17 28,72 30,67 13,83 34,85 23,85 17,88 23,20 23,20 23,20 20,09 32,54 40,43 32,09 36,07 34,99	0 1 1 1 1 1 0 1 1 0 1 0 0 0 0 0  # Missed Cherrages 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
Tabuin abha-1A chait OS-Homo sapiens GN-TUBALA	TU VISN SYSNEEDL GEVYEK VTOOLE KEVYENALAER VIGTERT TANLI YVOLN SYSN GEG TU SYNSEEDLA GEG VIDNSEEDLA GEG VIDNSEEDLA GEG VIDNSEEDLA GEG VIDNE GEG VIDNE VIDNE GEG VIDNE GEG VIDNE	3 5 2 1 6 6 5 5 5 5 1 3 3 5 6 01 4 1 7 6 6 4 2	2 2 2 1 1 2 2 2 1 1 1 2 2 2 2 2 2 2 2 2	1 Modifications C15(Carbanidomethyl C3(Carbanidomethyl)	0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 18 ACn 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0.00001404 0.0000017 0.00000172 4.036E-08 0.00002351 0.000244 0.0000241 0.000244 0.0002457 0.001547 0.001547 4.16 PEP 0.000005865 4.302E-08 0.000005865 0.00000549 0.00000549	5.81 5.50 5.05 4.20 3.99 3.86 3.32 2.73 2.27 46.26784264 46.26784264 46.26784264 4.80 4.83 4.49	3 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	2201.28810 1991.99236 2312.15386 1776.82573 1561.67668 1997.64055 1648.73491 1000.54070 937.49816 1322.62883 11778.65743 MH+ [Da] 2415.19974 2415.19974 2415.19974 2415.19974 2415.19974 1756.96177 1701.90386 2007.86628 1864.89250	0.91 0.11 -0.86 -3.95 -2.52 -1.86 -1.74 -1.54 -0.87 -2.58 -1.21 -2.28 -5.47 -2.28 -5.47 -1.18 -3.42 -6.44	41,49 41,49 40,17 28,72 13,63 34,55 25,18 23,30 23,30 <b>RT</b> [min] 23,00 32,54 40,43 22,909 32,24 40,43 32,09 36,07 34,99 36,18	0 1 1 1 1 1 0 1 0 1 1 0 0 0 0 1 # Missed Cherroges 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
Tabulin aplas IA chais OS-Homo sapiens GN-TUBAIA	TU VI.SN SYNTEELQUYVEK VTOOELSUYVEALAER VIGUPTAUNLYVOLINNIK KIGYVDFSALDLAE GIGUYDINSEEDAK GIGUYDINSEEDAK TADAGKTEEK KOVDERAULE NULAVUTAU TUSSVYAK GISTUELE SUBSYIG SUBSYIG SUBSYIG SUBSYIG SUBSYIG SUBSYIG SUBSYIG SUBSYIG SUBSYIG SUBSYIG SUBSYIG SUBSYIG SUBSYIG SUBSYIG SUBSYIG SUBSYIG SUBSYIG SUBSYIG SUBSYIG SUBSYIG SUBSYIG SUBSYIG SUBSYIG SUBSYIG SUBSYIG SUBSYIG SUBSYIG SUBSYIG SUBSYIG SUBSYIG SUBSYIG SUBSYIC SUBSYIG SUBSYIG SUBSYIC SUBSYIC SUBSYIC SUBSYIC SUBSYIC SUBSYIC SUBSYIC SUBSYIC SUBSYIC SUBSYIC SUBSYIC SUBSYIC SUBSYIC SUBSYIC SUBSYIC SUBSYIC SUBSYIC SUBSYIC SUBSYIC SUBSYIC SUBSYIC SUBSYIC SUBSYIC SUBSYIC SUBSYIC SUBSYIC SUBSYIC SUBSYIC SUBSYIC SUBSYIC SUBSYIC SUBSYIC SUBSYIC SUBSYIC SUBSYIC SUBSYIC SUBSYIC SUBSYIC SUBSYIC SUBSYIC SUBSYIC SUBSYIC SUBSYIC SUBSYIC SUBSYIC SUBSYIC SUBSYIC SUBSYIC SUBSYIC SUBSYIC SUBSYIC SUBSYIC SUBSYIC SUBSYIC SUBSYIC SUBSYIC SUBSYIC SUBSYIC SUBSYIC SUBSYIC SUBSYIC SUBSYIC SUBSYIC SUBSYIC SUBSYIC 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SUBSYIC SUBSYIC SUBSYIC SUBSYIC SUBSYIC SUBSYIC SUBSYIC SUBSYIC SUBSYIC SUBSYIC SUBSYIC SUBSYIC SUB	3 5 2 1 6 6 6 5 1 3 3 5 6 0 1 3 3 7 6 4 1 1 7 6 4 2 1	2 2 2 1 1 2 2 2 1 1 1 2 2 2 1 1 2 2 2 2	1 Modifications C15(Carbamidomethyl C3(Carbamidomethyl) N-Terne(Acetyl)	0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 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0.00000548 0.00000545 0.00000545 0.00000545	5.81 5.50 5.05 4.20 3.89 3.84 3.45 3.45 2.77 2.27 46.26794264 XCorr 7.24 4.58 5.40 4.73 5.40 4.73 4.49 4.27	3 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	2201.28810 1991.99236 2312.15386 1776.82573 1551.67668 1397.64055 1688.73491 1605.54070 937.49816 1358.74055 1688.73491 MH+ [Da] 2415.19974 2415.19974 2499.20195 1756.66177 1750.15038 2007.388628 1864.89250	0.91 0.11 -0.86 -3.95 -2.52 -1.86 -1.74 -1.54 -1.74 -1.54 -1.74 -1.54 -2.28 -1.21 -2.28 -1.21 -2.28 -1.21 -2.28 -1.21 -2.28 -1.21 -2.28 -1.21 -2.26 -1.21 -2.26 -1.21 -2.25 -1.21 -2.25 -1.21 -2.25 -1.25 -1.25 -1.25 -1.25 -1.25 -1.25 -1.25 -1.25 -1.25 -1.25 -1.25 -1.25 -1.25 -1.25 -1.25 -1.25 -1.25 -1.25 -1.25 -1.25 -1.25 -1.25 -1.25 -1.25 -1.25 -1.25 -1.25 -1.25 -1.25 -1.25 -1.25 -1.25 -1.25 -1.25 -1.25 -1.25 -1.25 -1.26 -1.74 -1.24 -1.25 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.24 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 -1.21 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Tabulin apha-1A chain OS-Homo sapieni GN-TUBA1A	TU VI.SN SYNTEEL QVYEK VTOOLE KEYPENAAER VEGTEPT TANLFVOLINNK KGYUTPESABDLAK GGUTVINSEEDAK TADAEKTEEK GGUTVINSEEDAK TADAEKTEEK GGUTVINSEEDAK TGISDYTELK GGUTVINSEEDAK GGUSTTELK EVFEDAAR ZOUESTIG GGUTVINSEEDANNYAR QGUFFUGUTGEDAANNYAR QGUFFUGUTGEDAANNYAR AVHEQKVAETINAFEPANQWVK HOGALNVDLAFEDAAQMVK HOGALNVDLAFEDAAQMVK HOGALNVDLAFEDAAQMVK HOGALNVDLAFEDAAQMVK BURGALNVLAFEDAAQMVK BURGALNVLAFEDAAQMVK BURGALNVLAFEDAAQMVK BURGALNVLAFEDAAQMVK BURGALNVLAFEDAAQMVK BURGALNVLAFEDAAQMVK BURGALNVLAFEDAAQMVK BURGALNVLAFEDAAQMVK BURGALNVLAFEDAAQMVK BURGALNVLAFEDAAQMVK BURGALNVLAFEDAAQMVK BURGALNVLAFEDAAQMVK BURGALNVLAFEDAAQMVK BURGALNVLAFEDAAQMVK BURGALNVLAFEDAAQMVK BURGALNVLAFEDAAQMVK BURGALNVLAFEDAAQMVK BURGALNVLAFEDAAQMVK BURGALNVLAFEDAAQMVK BURGALNVLAFEDAAQMVK BURGALNVLAFEDAAQMVK BURGALNVLAFEDAAQMVK BURGALNVLAFEDAAQMVK BURGALNVLAFEDAAQMVK BURGALNVLAFEDAAQMVK BURGALNVLAFEDAAQMVK BURGALNVLAFEDAAQMVK BURGALNVLAFEDAAQMVK BURGALNVLAFEDAAQMVK BURGALNVLAFEDAAQMVK BURGALNVLAFEDAAQMVK BURGALNVLAFEDAAQMVK BURGALNVLAFEDAAQMVK BURGALNVLAFEDAAQMVK BURGALNVLAFEDAAQMVK BURGALNVLAFEDAAQMVK BURGALNVLAFEDAAQMVK BURGALNVLAFEDAAQMVK BURGALNVLAFEDAAQMVK BURGALNVLAFEDAAQMVK BURGALNVLAFEDAAQMVK BURGALNVLAFEDAAQMVK BURGALNVLAFEDAAQMVK BURGALNVLAFEDAAQMVK BURGALNVLAFEDAAQMVK BURGALNVLAFEDAAQMVK BURGALNVLAFEDAAQMVK BURGALNVLAFEDAAQMVK BURGALNVLAFEDAAQMVK BURGALNVLAFEDAAQMVK BURGALNVLAFEDAAQMVK BURGALNVLAFEDAAQMVK BURGALNVLAFEDAAQMVK BURGALNVLAFEDAAQMVK BURGALNVLAFEDAAQMVK BURGALNVLAFEDAAQMVK BURGALNVLAFEDAAQMVK BURGALNVLAFEDAAQMVK BURGALNVLAFEDAAQMVK BURGALNVLAFEDAAQMVK BURGALNVLAFEDAAQMVK BURGALNVLAFEDAAQMVK BURGALNVLAFEDAAQMVK BURGALNVLAFEDAAQMVK BURGALNVLAFEDAAQMVK BURGALNVLAFEDAAQMVK BURGALNVLAFEDAAQMVK BURGALNVLAFEDAAQMVK BURGALNVLAFEDAAQMVK BURGALNVLAFEDAAQMVK BURGALNVLAFEDAAQMVK BURGALNVLAFEDAAQMVK BURGALNVLAFEDAAQMVK BURGALNVLAFEDAAQMVK BURGALNVLAFEDAAQMVK BURGALNVLAFEDAAQMVK BURGALNVLAFEDAAQMVK BURGALNVLAFEDAAQMVK BURGALNVLAFEDAAQMVK 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Tabula aplas-1A. chain OS-Homo supiers GN-TUBA1A         Nackophomini OS-Homo supiers GN-NPM1         Strike implaine etch spliking factor 5 OS-Homo supiers GN-SRSH5	T.V.I.S.V.S.N.TET.LQVYEK VIGUELSKYERALER VIGUELSKYERALER GRUYNDESEDALER GRUYNDESEDAL GRUYNDESEDAL GRUYNDESEDAL GRUYNDESEDAL GRUYNDESEDAL ALLADALTTER VIGUELSKYERA GRUYNDESEDAL ALLADALTTER VIELSKYERA GRUYNDESEDAL ALLADALTR GRUYNDESEDAL GRUYNDESEDAL GRUYNDESEDAL GRUYNDESEDAL GRUYNDESEDAL GRUYNDESEDAL GRUYNDESEDAL GRUYNDESEDAL GRUYNDESEDAL GRUYNDESEDAL GRUYNDESE GRUYNDESE GRUYNDESE GRUYNDESE GRUYNDESE GRUYNDESE GRUYNDESE GRUYNDESE GRUYNDESE GRUYNDESE GRUYNDESE GRUYNDESE GRUYNDESE GRUYNDESE GRUYNDESE GRUYNDESE GRUYNDESE GRUYNDESE GRUYNDESE GRUYNDESE GRUYNDESE GRUYNDESE GRUYNDESE GRUYNDESE GRUYNDESE GRUYNDESE GRUYNDESE GRUYNDESE GRUYNDESE GRUYNDESE GRUYNDESE GRUYNDESE GRUYNDESE GRUYNDESE GRUYNDESE GRUYNDESE GRUYNDESE GRUYNDESE GRUYNDESE GRUYNDESE GRUYNDESE GRUYNDESE GRUYNDESE GRUYNDESE GRUYNDESE GRUYNDESE GRUYNDESE GRUYNDESE 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VLATVTKPVGGDKNGGTR	3	6		0.0000	0	0.000005866	5.10	3	1769.98368	-1.83	10.62	1
HQEGEIFDTEKEK	27	1		0.0000	0	0.0006259	4.89	3	1589.74161	-1.67	13.44	1
HQEGEIFDTEK	17	1		0.0000	0	0.00001201	4.88	2	1332.60222	-3.35	15.69	0
eKVLATVTKPVGGDK	7	6	N-Term(Acetyl)	0.0000	0	0.00006081	4.76	3	1583.90128	0.56	18.14	1
EKVLATVTKPVGGDK	8	6		0.0000	0	0.00003067	4.41	3	1541.88810	-1.12	13.77	1
sVFALTNGIYPHK	3	1	N-Term(Acetyl)	0.0000	0	0.00001775	4.33	2	1488.78520	0.41	28.42	0
QLASGLLLVTGPLVLNRVPLR	1	1		0.0000	0	0.0005082	4.28	3	2229.37772	-1.31	34.26	1
VLATVTKPVGGDK	89	6		0.0000	0	0.0005606	4.20	2	1284.75066	-1.24	12.95	0
hQEGEIFDTEKEK	12	1	N-Term(Acetyl)	0.0000	0	0.0004805	4.18	3	1631.75571	0.54	16.63	1
SVFALTNGIYPHKLVF	3	1		0.0000	0	0.0000901	4.11	2	1805.99285	-1.15	32.59	1
SVFALTNGIYPHK	8	1		0.0000	0	0.00009149	3.98	2	1446.77104	-2.06	25.87	0
hQEGEIFDTEK	11	1	N-Term(Acetyl)	0.0000	0	0.00001705	3.96	2	1374.61809	0.61	19.61	0
ASITPGTILIILTGR	79	4		0.0000	0	0.0005484	3.94	3	1525.92890	-1.56	38.67	0
HLTDAYFKK	14	1		0.0000	0	0.0008581	3.86	2	1122.59184	-2.14	12.25	1
KIDQKAVDSQILPK	1	1		0.0000	0	0.0003542	3.83	2	1582.91313	-2.04	16.48	2
IDISNVKIPK	2	1		0.0000	0	0.0009151	3.73	2	1126.68169	-1.25	22.21	1
aSITPGTILIILTGR	15	4	N-Term(Acetyl)	0.0000	0	0.00004455	3.72	2	1567.93987	-1.26	41.64	0
IKAIPQLQGYLR	4	1		0.0000	0	0.001207	3.43	3	1399.84101	-0.75	25.26	1
hLTDAYFK	20	1	N-Term(Acetyl)	0.0000	0	0.0009781	3.40	2	1036.50847	-1.33	23.14	0
vLATVTKPVGGDK	4	6	N-Term(Acetyl)	0.0000	0	0.0001064	3.34	2	1326.76177	-0.79	20.91	0
THQKFVIATSTK	2	1		0.0000	0	0.0001925	3.32	2	1360.75517	-2.35	10.11	1
HLTDAYFK	72	1		0.0000	0	0.00203	3.25	2	994.49858	-0.70	16.01	0
IPKHLTDAYFK	1	1		0.0000	0	0.0004346	2.83	2	1332.72905	-1.53	18.58	1
hLTDAYFKK	4	1	N-Term(Acetyl)	0.0000	0	0.002547	2.81	2	1164.60491	0.08	18.34	1
KGKPHcSRNPVLVR	2	6	C6(Carbamidomethyl)	0.0000	0	0.004736	2.76	4	1647.92287	0.25	9.13	2
aVDSQILPK	43	1	N-Term(Acetyl)	0.0000	0	0.0007101	2.70	2	1012.56737	-0.02	21.14	0
EKYEITEQR	8	1		0.0000	0	0.01104	2.67	2	1195.59221	-2.65	12.08	1
YYPTEDVPRK	9	4		0.0000	0	0.0009458	2.51	3	1267.62979	-1.55	14.35	1
eKYEITEQR	5	1	N-Term(Acetyl)	0.0000	0	0.009544	2.47	2	1237.60344	-2.02	15.92	1

# **Supplementary File 2**

#### siRNA sequences

siRNAs	Sequences
USP7-1	GACGUUUCGAAUAGAGGAA
USP7-2	GCACUAAUGCUUACAUGUU
USP7-3	GACUUUGAGAACAGGCGAA
USP7 5'UTR-1	CUCACCUCGUCAGCCACUA
ECT2-1	GCACUCACCUUGUAGUUGA
ECT2-2	CAGAGGAGAUUAAGACUAU
ECT2 5'UTR-1	GGUGGAACUCCUAGGGCUU
ECT2 5'UTR-2	CCGGCGAGGAAUGGCGGUA
USP11-1	AATGAGAATCAGATCGAGTCC
USP11-2	AAGGCAGCCTATGTCCTCTTC
UHRF1-1	GCCAUACCCUCUUCGACUATT
UHRF1-2	AGGUGGUCAUGCUCAACUACA
RAD18-1	GAGCAUGGAUUAUCUAUUCAA
RAD18-2	UUAUAAAUGCCCAAGGAAAUU
MDM2-1	GCCAGTATATTATGACTAA
MDM2-2	AAUGGUUGCAUUGUCCAUGGC
RNF168-1	GACACUUUCUCCACAGAUA
RNF168-2	GGCGAAGAGCGAUGGAAGA

### Lentiviral shRNA sequences

shRNAs	Sequences
Control	CCGGGATATGGGCTGAATACAAACTCGAGTTTGTATTCAGCCCATATCTTTTTG
ECT2-1	CCGGGCCCGTTGTATTGTACAAGTACTCGAGTACTTGTACAATACAACGGGCTTTTTG
ECT2-2	CCGGCGGAATGAACAGGATTTCTATCTCGAGATAGAAATCCTGTTCATTCCGTTTTTG
ECT2-3	CCGGCCAGCAATGATAAGCATGTAACTCGAGTTACATGCTTATCATTGCTGGTTTTTG

Note: Red color indicates the targeting sequence against the corresponding genes.

# qRT-PCR primers

Genes	Sequences
GAPDH	F: GAAGGTGAAGGTCGGAGTC
	R: GAAGATGGTGATGGGATTTC
USP7	F: ATTCCTAACATTGCCACCAG
	R: ATTTACACCATTTGCCATCC
USP7 (5'UTR)	F: TCCAAGCTGGTGTGTTCAAG
	R: CAGCGAATCCTCTTGCTGAA
ECT2	F: TGTAGTCACGGACTTTCAGGA
	R: GTACAATACAACGGGCGACAT
MDM2	F: GAATCATCGGACTCAGGTACATC
	R: TCTGTCTCACTAATTGCTCTCCT
PHF8	F: AGGACAAGGAAAGCGTCCCAA
	R: ACACAGGAGGGCTCACAGAA
RNF168	F: TCAACGTGGAACTGTGGACG
	R: CAGGTTTACTGAGCAGACGAAC
TP53	F: CAGCACATGACGGAGGTTGT
	R: TCATCCAAATACTCCACACGC
p21	F: CTTGTGGAGCCGGAGCT
	R: TGGTGTCTCGGTGACAAAGT
PUMA	F: GACCTCAACGCACAGTACGAG
	R: AGGAGTCCCATGATGAGATTGT
TP53INP1	F: TTCCTCCAACCAAGAACCAGA
	R: GCTCAGTAGGTGACTCTTCACT
TP53INP2	F: GCTGGTTTGTTACCCCTCCC
	R: GGTGACGTAAACGGACATGCT
GDF15	F: ACCTGCACCTGCGTATCTCT
	R: CGGACGAAGATTCTGCCAG
IGFBP3	F: AGACACACTGAATCACCTGAAGT
	R: AGGGCGACACTGCTTTTTCTT

# Supplementary File 3

#### RNA-seq Analysis of Co-regulated Genes by ECT2 and USP7

Gene	log2Ratio(Control_siRNA-VS-ECT2_siRNA)	log2Ratio(Control_siRNA-VS-USP7_siRNA)	Symbol
9635	2.998578	2.783536	CLCA2
3486	2.918072	2.814632	IGFBP3
9518	2.895453	2.552165	GDF15
100506696	2.711829	2.228975	KDM5B-AS1
1026	2.70063	2.877388	CDKN1A
55065	2.663808	3.810116	SLC52A1
8537	2.590283	1.404705	BCAS1
3635	2.457357	2.937028	INPP5D
3488	2.35554	1.108654	IGFBP5
51566	2.315407	1.867743	ARMCX3
7832	2.310668	3.678548	BTG2
6662	2.306474	2.208475	SOX9
3909	2.294314	1.588172	LAMA3
5655	2.189877	1.890735	KLK10
8835	2.107414	3.834778	SOCS2
1056	2.070578	2.537098	CEL
2872	2.027905	1.927106	MKNK2
2934	2.007105	2.449209	GSN
638	1.998578	2.372467	BIK
90427	1.997231	2.209523	BMF
2066	1.945951	1.785485	ERBB4
624	1.921771	1.901916	BDKRB2
8000	1.887314	2.250477	PSCA
5337	1.875562	1.826604	PLD1
11259	1.867948	1.896994	FILIP1L
80352	1.866406	1.902747	RNF39
94241	1.86241	1.859026	TP53INP1
4322	1.827306	1.191601	MMP13
27113	1.827306	2.086785	BBC3
2329	1.827306	2.367173	FMO4
55384	1.791327	1.223437	MEG3
401320	1.772024	1.432128	LOC401320
58476	1.751271	1.645622	TP53INP2
1649	1.747426	1.230851	DDIT3
80726	1.698023	4.259564	KIAA1683
8609	1.686907	1.423026	KLF7
23105	1.686214	2.998429	FSTL4
55062	1.67678	1.324368	WIPI1
9901	1.669765	1.223437	SRGAP3
7139	1.66765	2.865424	TNNT2
55911	1.657381	2.079891	APOBR
360	1.650495	1.70821	AQP3
8228	1.638861	2.12206	PNPLA4
1647	1.604914	1.330647	GADD45A
79603	1.604914	2.037711	CERS4
144811	1.585549	1.182/48	LACCI
59	1.579379	3.188024	ACTA2
1850	1.559373	1.620239	DUSP8
1326/1	1.556004	2.10/741	SPATAI8
5/198	1.550/89	2.058226	ATP8B2
27076	1.543/4/	1.28475	LYPD3
/045	1.522021	1.203528	IGFBI
10150505087	1.516325	1.38980	FAM84A
100505687	1.505378	2.039398	LUC100505687
22J0 20256	1.400,000	1.233791 2.019067	FUF15 EAM214D
00230	1.403077 1.491095	J.U10907 1 214651	
220 54103	1.461062	-1.314031 1 302708	ALDHIA3
J410J 720001	1.400324	1.372700	USAP LOC720001
101642	1.474440	1.002110	EOU / 50091
253100	1.7++++2 1.4/2185	1.753020	SERUI 2
153222	1 /3/080	1.0+0127	CREBPE
7042	1 426577	-1 666775	TGFR?
400073	1 425944	1 537098	C12orf76
10/2	1 423774	1.01/1500	EEN A 1
1774	1.743//7	1.014377	L1 11/11

64063	1.421314	1.350059	PRSS22
387264	1.42105	1.174528	KRTAP5-1
10133	1.406975	1.632517	OPTN
134111	1 401318	1 436677	UBE20L1
5264	1 30102	1 522884	PHVH
1842	1.30122	1.322004	DUSDI
51126	1.39032	1.300799	DUSFI
51136	1.3/3388	1.259024	KNFII
10396	1.360027	1.023394	ATP8A1
9935	1.350597	2.935647	MAFB
84952	1.34188	1.551173	CGNL1
79720	1.34188	1.050437	VPS37B
9149	1.335453	2.515565	DYRK1B
54850	1.32928	1.405853	FBXL12
10457	1 315407	2 077666	GPNMB
51646	1 31/237	1 667884	VPEL 5
10608	1.202526	1.007884	MYD4
110008	1.502520	1.870755	MAD4
112483	1.296283	1.727069	SAT2
2627	1.29297	1.274063	GATA6
2034	1.284585	1.588193	EPAS1
150962	1.282986	1.21517	PUS10
148523	1.263065	1.741112	Clorf51
54800	1.259527	1.024739	KLHL24
9536	1 258111	1 0/1773	PTGES
120202	1.254417	1.420457	TMEM150A
129303	1.234417	1.429437	CODOL
/464	1.23568	1.319867	CORO2A
94121	1.234964	1.571045	SYTL4
6253	1.234964	2.344453	RTN2
10043	1.234395	1.236589	TOM1
84532	1.223485	2.004268	ACSS1
23542	1 217891	3 222224	MAPK8IP2
10628	1 212026	1 556884	TYNID
(202	1.212020	1.550084	
0303	1.205964	1.455414	SATT
51092	1.200524	1.754903	SID12
23135	1.195477	1.119863	KDM6B
8418	1.193719	1.047047	CMAHP
57037	1.189877	1.352066	ANKMY2
1408	1.180416	1.137691	CRY2
6560	1 177493	1 631074	SLC12A4
9764	1 176021	1 12206	KIA A0513
570 <del>4</del>	1.170/21	2.046772	ED A2D
60401	1.159676	2.046772	EDA2K
1513	1.150348	1.415107	CTSK
8974	1.142808	1.070077	P4HA2
5652	1.131885	1.067821	PRSS8
4758	1.127592	1.101596	NEU1
25946	1.122665	1.620308	ZNF385A
57491	1 119487	1 612386	AHRR
28/7/9	1 100441	1 278786	LINC00494
204749	1.075447	2 228077	TEE
7008	1.073447	2.228077	
1318	1.0/3063	1.51285	SLC31A2
901	1.058426	1.239868	CCNG2
355	1.056477	1.876186	FAS
3155	1.056293	1.195406	HMGCL
53349	1.050602	1.717149	ZFYVE1
55902	1.035511	1.162058	ACSS2
283219	1 031356	1 104138	KCTD21
81700	1.03084	1.037024	DNE170
01790	1.03084	1.037024	KNF170
1851	1.026662	1.442119	ISC22D3
154091	1.019952	2.138325	SLC2A12
83667	1.016496	1.666841	SESN2
80271	1.012496	1.197713	ITPKC
5376	1.009225	1.035191	PMP22
6004	1.001573	1.493845	RGS16
55260	1.001336	1.561551	TMEM143
1781	1.00111	2 249499	NEIV
+/04	-1.00111	-2.247477	NEIA
1/19	-1.003333	-1.151088	DHFK
55159	-1.007972	-1.061759	RFWD3
84930	-1.010422	-1.856723	MASTL
4796	-1.010866	-1.324767	TONSL
55573	-1.013733	-1.184171	CDV3
3397	-1.015799	-1.202111	ID1
55055	-1 019577	-1 244494	
55055	1.01/3//	1.2777/7	LUILLU

79075	-1.020206	-1.632827	DSCC1
85439	-1.02069	-1.335147	STON2
81930	-1.023117	-1.434888	KIF18A
109	-1.023117	-1.238087	ADCY3
90411	-1.023483	-1.691035	MCFD2
7023	-1.025852	-1.103006	TFAP4
29127	-1.028121	-1.04149	RACGAP1
5984	-1.028547	-1.121238	RFC4
9908	-1.031032	-1.06196	G3BP2
24137	-1.035791	-1.330378	KIF4A
79723	-1.037499	-1.026364	SUV39H2
128239	-1.037534	-1.1775	IQGAP3
4751	-1.038263	-1.157918	NEK2
5985	-1.039605	-1.520618	RFC5
81624	-1.041449	-1.443003	DIAPH3
6790	-1.042924	-1.644172	AURKA
9055	-1.047728	-1.245605	PRC1
7019	-1.060968	-1.22796	TFAM
4605	-1.063177	-1.131768	MYBL2
9401	-1.063366	-1.349183	RECOL4
54821	-1.064113	-1.731391	ERCC6L
9129	-1.068478	-1.295792	PRPF3
81610	-1.068533	-1.665899	FAM83D
64105	-1.068706	-2.964341	CENPK
3227	-1.069053	-1.13687	HOXC11
2305	-1.069536	-1.341262	FOXM1
1058	-1.070814	-1.405417	CENPA
5347	-1.071298	-1.31556	PLK1
79915	-1.072698	-1.897243	ATAD5
79066	-1.074078	-1.303745	METTL16
90417	-1.077785	-1.132181	KNSTRN
55143	-1.078677	-1.223362	CDCA8
55013	-1.081135	-1.375227	CCDC109B
6891	-1.083999	-1.290978	TAP2
84515	-1.084637	-1.715883	MCM8
5983	-1.089538	-1.284904	RFC3
7112	-1.090444	-1.672704	TMPO
55165	-1.091839	-1.886401	CEP55
25939	-1.092523	-1.047865	SAMHD1
1033	-1.097315	-1.815546	CDKN3
10615	-1.103521	-1.333739	SPAG5
201725	-1.103623	-1.386033	C4orf46
5422	-1.10412	-1.144191	POLA1
9787	-1.106581	-1.321067	DLGAP5
78995	-1.106806	-1.174622	C17orf53
54556	-1.10716	-1.065352	ING3
167227	-1.107866	-1.379882	DCP2
147015	-1.111293	-1.134021	DHRS13
993	-1.122737	-1.600837	CDC25A
699	-1.123379	-1.54813	BUB1
3619	-1.12689	-1.102885	INCENP
2237	-1.128258	-1.800873	FEN1
332	-1.129386	-2.197203	BIRC5
79071	-1.141687	-1.878679	ELOVL6
3978	-1.144632	-1.081065	LIG1
26227	-1.144902	-1.497172	PHGDH
254102	-1.148836	-1.31181	EHBP1L1
90381	-1.150957	-1.923645	TICRR
4288	-1.15236	-1.893526	MKI67
991	-1.161245	-1.550989	CDC20
11113	-1.174525	-1.040198	CIT
63967	-1.178137	-1.578098	CLSPN
10024	-1.180393	-1.483837	TROAP
1111	-1.185597	-2.05178	CHEK1
54069	-1.191553	-1.185368	MIS18A
337873	-1.195438	-1.560934	HIST2H2BC
1848	-1.195777	-1.173396	DUSP6
8877	-1.198229	-1.116989	SPHK1
81704	-1.199362	1.683541	DOCK8
51527			
51557	-1.202441	-1.167164	MTFP1

55215	-1.213108	-1.746811	FANCI
11004	-1.213539	-1.735921	KIF2C
5557	-1.216707	-1.790164	PRIM1
145508	-1 217088	-1 391819	CEP128
259266	_1 222258	-2 125263	ASPM
01452	1 224671	1 202070	ACPD5
91432	-1.224071	-1.302979	ACBDJ
10555	-1.225525	-1.236382	RNASEH2A
9521	-1.227976	-1.447795	EEF1E1
4176	-1.229667	-1.65454	MCM7
22995	-1.230592	-1.111995	CEP152
6671	-1.239435	-1.397449	SP4
8318	-1.239916	-2.333267	CDC45
3835	-1.242544	-1.201367	KIF22
890	-1 253255	-3 359692	CCNA2
0212	1.253255	1 388235	AUDER
9212	-1.234430	-1.300233	AUKKB
55055	-1.201030	-1./31384	DEPDCI
11169	-1.262331	-1.110021	WDHD1
7298	-1.264175	-1.428421	TYMS
11247	-1.271511	-1.276134	NXPH4
675	-1.272958	-1.600066	BRCA2
9194	-1.275504	-1.077859	SLC16A7
150468	-1.275939	-2.286269	CKAP2L
4173	-1 278143	-1 546779	MCM4
2130	1.270145	1 24051	EVA2
2137	1 282825	-1.24051	ETA2 TTV
1212	-1.282825	-1.098565	
9700	-1.285629	-1.415729	ESPLI
3833	-1.285969	-1.657177	KIFC1
3070	-1.292433	-1.564263	HELLS
701	-1.292537	-1.861547	BUB1B
6566	-1.292931	-2.60586	SLC16A1
10293	-1.293709	-1.446414	TRAIP
26271	-1 295736	-1 416404	FBXO5
3832	-1 295791	_1 31/312	KIE11
2197	1 201077	1 822205	EANCE
2187	-1.301977	-1.822505	FAINCB
55247	-1.301977	-1./8483	NEIL3
55723	-1.302794	-1.403682	ASF1B
4172	-1.304453	-1.593777	MCM3
10036	-1.304948	-1.668896	CHAF1A
8208	-1.310694	-1.030587	CHAF1B
23649	-1.311701	-1.680687	POLA2
3837	-1 317059	-1.067386	KPNB1
11065	1 317586	1.076816	LIBE2C
112120	1 210225	2.052775	CDCA5
115150	-1.319233	-2.032773	CDCAS
10/21	-1.320592	-1.574822	POLQ
51512	-1.320808	-1.420567	GTSE1
116832	-1.322441	-1.469691	RPL39L
4174	-1.3231	-1.586604	MCM5
254263	-1.324003	-1.092259	CNIH2
29028	-1.3304	-1.765389	ATAD2
54619	-1 332034	-2.003921	CCNI
1860	_1 332259	-1.46719	F2F1
57092	1.22529	1.94006	
294402	-1.33330	-1.04000	UADUS WIDDCO
284403	-1.33627	-1.506812	WDR62
51203	-1.336368	-1.621906	NUSAP1
161742	-1.336742	-1.440182	SPRED1
5424	-1.344963	-1.020796	POLD1
51514	-1.351559	-2.389422	DTL
1063	-1.351945	-1.488087	CENPF
5888	-1.352466	-1.727464	RAD51
11130	-1 355498	-1 59182	ZWINT
221150	-1 365642	1 068207	
0000	-1.3030+2	-1.700277	
7000	-1.30/0/2	-1./98293	PKMY11
195828	-1.3/116	-3.142583	ZNF367
7153	-1.377918	-1.267234	TOP2A
2491	-1.378598	-1.905846	CENPI
9833	-1.386674	-1.686983	MELK
10403	-1.393124	-1.680722	NDC80
672	-1.393607	-2.252609	BRCA1
1958	-1 408892	-2 592185	FGR1
083	-1 /1/731	1 671209	CDV1
703	-1.414/31	-1.0/1208	
/083	-1.423051	-1.959958	TKI

146909	-1.424987	-1.610801	KIF18B
23279	-1.425573	-1.906012	NUP160
83540	-1.4355	-1.570431	NUF2
83990	-1 442962	-1 905194	BRIP1
83879	-1 44433	-2 38/30	CDCA7
0770	1 444717	1 111005	PASSE2
9770	-1.444/17	-1.111993	KASSF2
21//	-1.450857	-1./48304	FANCD2
80150	-1.454651	-1.128553	ASRGL1
10733	-1.456951	-1.601118	PLK4
7516	-1.468709	-2.306599	XRCC2
56992	-1.474813	-1.505635	KIF15
54892	-1 474873	-1 648747	NCAPG2
3014	-1 48962	-1.001456	H2AFX
10502	1.48006	1 544541	SMC2
10392	-1.48996	-1.544541	SMC2
51361	-1.491122	-1.52/506	HOOKI
5427	-1.492697	-1.397014	POLE2
55872	-1.49382	-2.246134	PBK
1870	-1.507678	-1.449963	E2F2
9493	-1.512781	-1.411385	KIF23
10460	-1 514448	-1 550671	TACC3
4171	1 515280	1 540462	MCM2
4171	-1.515289	-1.549402	MCM2
9150	-1.515/16	-2.550365	EXUI
79019	-1.517705	-1.895862	CENPM
29893	-1.522576	-1.654522	PSMC3IP
55355	-1.536011	-2.156847	HJURP
374393	-1.54378	-3.190823	FAM111B
4085	-1 545329	-1 522236	MAD2L1
64046	1.554285	1.136674	CENPH
4602	-1.554285	-1.1500/4	CENTII MVDL 1
4603	-1.556906	-1.508313	MYBLI
5933	-1.559536	-1.532195	RBL1
9824	-1.56007	-1.657788	ARHGAP11A
6941	-1.567923	-1.946779	TCF19
990	-1.578686	-2.483003	CDC6
220042	-1.587911	-2.840152	C11orf82
9133	-1 5935	-1 264894	CCNB2
22207	1.600218	1.204074	NCADU
25597	-1.000518	-1.970697	INCAPH CD122
51659	-1.608681	-1.844505	GINS2
29128	-1.611404	-2.094258	UHRF1
10635	-1.616541	-1.632827	RAD51AP1
79682	-1.620675	-2.375552	MLF1IP
22974	-1.621634	-1.43693	TPX2
157313	-1 623017	-1 484382	CDCA2
54478	-1 639558	-1 674953	FAM64A
100129101	1.635330	2 220700	
100128191	-1.040311	-2.530799	TMPO-AST
145773	-1.652474	-3.398362	FAM81A
157570	-1.665615	-2.055359	ESCO2
1138	-1.673387	-1.187268	CHRNA5
4940	-1.675194	-1.135328	OAS3
163786	-1.682505	-1.381933	SASS6
55388	-1 712261	-2 341504	MCM10
2118	_1 71/758	-2.460646	FTV4
55790	1 722157	2.251554	
33789	-1.722137	-2.231334	DEPDCIB
115207	-1.723273	-2.992723	KCID12
8438	-1.730476	-2.193431	RAD54L
79733	-1.732611	-2.323989	E2F8
83461	-1.763655	-2.078111	CDCA3
100131211	-1.787403	-1.340646	TMEM194B
147841	-1 787403	-1 78483	SPC24
/008	_1 906709	1 025032	0001
+770	-1.000/98	-1.703030	UKCI
9319	-1.810921	-1.590392	1 KIP13
347240	-1.819112	-1.471891	KIF24
9837	-1.819584	-1.520618	GINS1
55270	-1.882122	-3.227472	NUDT15
145270	-1.886939	-2.177148	PRIMA1
203547	-1.891873	-1.876593	VMA21
162681	-1 908965	-2 429294	C180rf54
641	1.02/320	2.50260	DI M
041	-1.924339	-2.039209	
80178	-1.931139	-2.098491	C16orf59
83903	-1.967558	-2.369793	GSG2
9134	-1.973096	-2.419424	CCNE2
64151	-1.980048	-1.972314	NCAPG

79801	-1.994216	-1.651748	SHCBP1
2119	-2.024836	-1.799606	ETV5
55329	-2.099788	-1.65859	MNS1
79968	-2.114978	-2.15478	WDR76
26150	-2.149973	-2.310899	RIBC2
2583	-2.196366	-1.786861	B4GALNT1
4900	-2.198472	-2.6448	NRGN
6023	-2.243083	-2.825472	RMRP
3674	-2.395086	-2.462902	ITGA2B
7161	-2.43948	-2.507296	TP73
6241	-2.464507	-2.559674	RRM2
126567	-2.680488	-1.748304	C2CD4C
8626	-2.702515	-5.092259	TP63
9768	-3.354684	-1.325203	KIAA0101
3008	-3.838029	-2.905846	HIST1H1E
348738	-8.206569	-8.206569	C2orf48