Supporting Table 2A. List of Proteins Detected in Negative Controls from HeLa and HEK293 Cells.

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Supporting Table 2B. Detailed List of Proteins and Peptides Detected in the Combined Negative Control Dataset.

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Supporting Table 2A. List of Proteins Detected in Negative Controls from HeLa and HEK293 Cells.

The number of peptides (column header ends with _P), number of spectra (_S), sequence coverage (_SC), and normalized spectral abundance factor (_NSAF) are specified for each run (i.e. each run is represented by 4 columns of numbers).
Proteins are grouped by: "proteins detected in *n* runs", proteins detected in (*n*-1) runs, and proteins unique to each run.

Contrast_Rank	Locus	Description	ALL_P	ALL_S	ALL_SC	ALL_NSAF	HsHeLa_FLAG-IP_Ti_1_P	HsHeLa_FLAG-IP_Ti_1_S	HsHeLa_FLAG-IP_Ti_1_SC	HsHeLa_FLAG-IP_Ti_1_NSAF	HsHeLa_FLAG-IP_Ti_2_P	HsHeLa_FLAG-IP_Ti_2_S	HsHeLa_FLAG-IP_Ti_2_SC	HsHeLa_FLAG-IP_Ti_2_NSAF	HsHeLa_FLAG-IP_Ti_3_P	HsHeLa_FLAG-IP_Ti_3_S	HsHeLa_FLAG-IP_Ti_3_SC	HsHeLa_FLAG-IP_Ti_3_NSAF
1	gi|4501885	beta actin [Homo sap	44	365	62.7	0.013	1	2	4.3	0.005	3	9	11.7	0.264	5	6	19.2	0.009
3	gi|5701327	tubulin, alpha, ubiquit	45	852	63.6	0.026	6	11	22.4	0.021	x	x	x	x	8	14	27.3	0.018
4	gi|4885431	heat shock 70kDa pro	119	605	63.5	0.013	1	2	1.9	0.003	x	x	x	x	8	11	16.2	0.01
5	gi|1438930	tubulin alpha 6 [Homo	41	800	54.3	0.024	5	10	19.6	0.019	x	x	x	x	8	13	27.6	0.017
6	gi|1798628	tubulin, alpha 3 [Hom	39	745	64.1	0.022	5	10	19.5	0.019	x	x	x	x	7	10	24.4	0.013
7	gi|5059299	tubulin, beta, 4 [Homo	38	352	29.6	0.011	1	4	3.1	0.008	x	x	x	x	6	16	12.9	0.021
8	gi|1367685	heat shock 70kDa pro	16	212	15.5	0.004	1	1	2.7	0.001	x	x	x	x	2	3	4.5	0.003
9	gi|5729877	heat shock 70kDa pro	94	552	56.7	0.012	1	1	2.6	0.001	x	x	x	x	6	8	13.3	0.007
10	gi|6005814	serine/threonine kinas	204	1626	68.4	0.047	35	96	61.7	0.18	4	5	7.3	0.118	13	45	36.8	0.056
11	gi|1792198	tubulin, alpha 1 [Hom	33	503	53.8	0.015	4	7	14.7	0.014	x	x	x	x	4	8	15.4	0.01
12	gi|9507215	tubulin, alpha 8 [Hom	20	418	31	0.013	3	6	11.8	0.012	x	x	x	x	4	7	15.6	0.009
13	gi|3441963	heat shock 70kDa pro	33	234	20.2	0.005	1	2	1.9	0.003	x	x	x	x	2	3	4.5	0.003
16	gi|1416543	heterogeneous nuclea	57	489	57.9	0.014	5	7	15.1	0.013	1	1	3.7	0.024	2	4	6.5	0.005
17	gi|2978878	tubulin, beta polypept	98	648	70.7	0.02	2	6	6.5	0.012	x	x	x	x	13	27	33.1	0.035
18	gi|2978876	tubulin, beta polypept	77	422	63.1	0.013	1	4	3.1	0.008	x	x	x	x	11	23	27.2	0.03
19	gi|5174735	tubulin, beta, 2 [Homo	87	532	66.7	0.016	1	4	3.1	0.008	x	x	x	x	11	23	25.8	0.03
20	gi|2743692	heat shock 70kDa pro	21	251	21.2	0.005	x	x	x	x	x	x	x	x	3	4	6.4	0.004
21	gi|2007022	SKB1 homolog [Homo	178	1423	64.1	0.03	10	25	17.6	0.034	2	4	3.1	0.069	13	30	33	0.027
22	gi|4503471	eukaryotic translation	57	295	48.5	0.009	x	x	x	x	x	x	x	x	2	5	10.6	0.006
23	gi|1650723	heat shock 70kDa pro	23	196	43.1	0.004	1	2	2.6	0.003	x	x	x	x	4	7	10.7	0.006
24	gi|1369982	kinesin family membe	236	1845	67.1	0.024	23	45	26.4	0.037	5	8	6.4	0.083	33	83	36	0.046
25	gi|2430797	serine/threonine kinas	69	330	49.8	0.01	13	23	23.7	0.043	1	1	2.4	0.024	4	13	8.2	0.016
28	gi|3245526	peroxiredoxin 1 [Hom	43	144	74.4	0.01	2	2	14.1	0.009	x	x	x	x	2	4	16.1	0.012
30	gi|4501881	alpha 1 actin precurs	20	161	32.6	0.006	1	2	4.2	0.005	1	3	4.2	0.087	3	3	5.6	0.005
31	gi|4503475	eukaryotic translation	36	156	26.1	0.005	x	x	x	x	x	x	x	x	1	2	2.4	0.003
32	gi|5031753	heterogeneous nuclea	30	337	52.6	0.01	1	4	3.8	0.008	x	x	x	x	3	5	13.4	0.006

394	gi|450779	ubiquitin-conjugating	8	22	32.2	0.002
395	gi|199231	karyopherin beta 1 [H	9	40	14.8	6E-04
396	gi|383275	Ras-GTPase-activatin	3	12	11.6	3E-04
398	gi|244321	p30 DBC protein [Hor	9	19	16.8	3E-04
400	gi|503012	glutathione reductase	3	5	10.7	1E-04
404	gi|134353	damage-specific DNA	3	8	4.3	1E-04
406	gi|450342	dUTP pyrophosphatas	2	6	19.5	5E-04
408	gi|175052	nucleolar and spindle	8	15	24.1	5E-04
409	gi|450663	ribosomal protein L30	3	6	24.3	7E-04
411	gi|559569	heterogeneous nucle	7	15	23.5	6E-04
412	gi|506590	DEAD (Asp-Glu-Ala-A	6	9	10.3	2E-04
413	gi|890340	PREDICTED: similar	3	4	8.3	7E-05
416	gi|450600	protein phosphatase	7	11	30.9	5E-04
417	gi|136998	methylenetetrahydrof	4	4	8.3	6E-05
435	gi|450661	ribosomal protein L17	4	15	22.3	0.001
436	gi|488553	protein-L-isoaspartate	2	8	14.5	5E-04
438	gi|140430	heterogeneous nucle	9	18	40.2	7E-04
439	gi|241192	tropomyosin 3 isoform	3	7	16.5	4E-04
440	gi|450403	guanine monophosph	3	6	8.8	1E-04
442	gi|300899	actin-like 6A isoform	6	15	26.4	5E-04
444	gi|572984	glyoxalase I [Homo sa	1	6	10.9	4E-04
445	gi|450633	6-pyruvoyltetrahydrop	1	7	6.2	7E-04
447	gi|890471	PREDICTED: myosin	48	155	31.3	0.001
449	gi|154313	ribosomal protein L8	6	12	16.3	6E-04
450	gi|321893	ATP synthase, H+ tra	4	4	10.2	1E-04
451	gi|450676	S100 calcium-binding	4	6	42.6	8E-04
452	gi|213617	TIP120 protein [Homo	8	20	8.5	2E-04
453	gi|450645	reticulocalbin 2, EF-h	9	34	28.7	0.001
454	gi|889539	PREDICTED: hypothe	7	13	7	8E-05
457	gi|890315	PREDICTED: similar	3	4	16.1	2E-04
458	gi|475850	hydroxyacyl-Coenzym	4	15	33	8E-04
459	gi|405563	cytokine-like nuclear	2	6	6	1E-04
462	gi|450735	transgelin 2 [Homo sa	1	5	9	3E-04
463	gi|590203	periodic tryptophan p	4	9	11	2E-04
464	gi|450541	NAD(P)H dehydrogen	4	27	36.4	0.002
465	gi|113216	phosphofructokinase,	4	7	9.4	1E-04
466	gi|450718	sepiapterin reductase	2	8	15.3	4E-04
468	gi|503205	ribosomal protein S14	5	10	24.5	9E-04
470	gi|450660	ribosomal protein L19	2	5	13.3	3E-04
471	gi|889532	PREDICTED: hypothe	1	5	0.5	4E-05
473	gi|183793	RNA-binding protein	1	7	4.9	3E-04
475	gi|450418	glutathione transferas	6	14	26.2	9E-04
476	gi|462494	latent transforming gr	13	41	15.5	4E-04
478	gi|167519	dermcidin precursor [	5	16	22.7	0.002
479	gi|414060	myosin, heavy polype	2	6	1.8	4E-05
480	gi|345946	HCCA2 protein [Hom	5	8	19.4	5E-04
481	gi|546070	GCN1 general contro	8	16	5.9	8E-05
482	gi|450554	vesicle docking prote	3	6	5.2	8E-05
483	gi|450340	desmoglein 1 preprop	4	18	6.8	2E-04
484	gi|110560	pyrophosphatase (ino	2	7	12.8	3E-04
485	gi|181050	carbamoylphosphate	1	6	1.7	4E-05
487	gi|450804	zyxin [Homo sapiens]	4	6	9.3	1E-04
488	gi|450658	replication protein A3	3	8	14	9E-04
489	gi|503217	tripartite motif-contain	5	15	11.1	2E-04
490	gi|450384	ATP-dependent DNA	5	9	13.3	2E-04
491	gi|450374	filamin B, beta (actin	7	16	4.7	8E-05
492	gi|770633	coatomer protein com	5	8	42.4	6E-04
493	gi|231110	sorting nexin 12 [Hom	3	7	25.3	6E-04
494	gi|321893	nucleoporin 43kDa [H	4	13	8.2	5E-04
497	gi|488522	Ewing sarcoma break	2	7	5	1E-04
498	gi|450765	translocated promote	8	10	5.9	6E-05
499	gi|450195	poly (ADP-ribose) pol	6	13	8.4	2E-04
500	gi|624606	RNA-binding motif pro	4	10	5.8	1E-04
501	gi|455766	immunoglobulin bindi	2	6	8.8	2E-04
502	gi|545359	adenylyl cyclase-asso	6	13	18.5	4E-04
503	gi|450451	DnaJ (Hsp40) homolo	1	4	3.3	1E-04
504	gi|632529	gelsolin-like capping	2	6	7.2	2E-04
506	gi|600574	DEAD (Asp-Glu-Ala-A	1	4	3.1	1E-04
509	gi|545362	dynactin 2 [Homo sap	3	14	11.8	5E-04
510	gi|333509	dynein, cytoplasmic,	11	23	3.6	7E-05
511	gi|892360	nuclear protein locali	2	7	5.3	2E-04
513	gi|567883	phosphatidylinositol-b	12	28	27.5	6E-04
514	gi|515991	chromodomain helica	6	12	5.3	9E-05
515	gi|638207	RAN binding protein 2	5	12	2.9	5E-05
516	gi|172986	fuse-binding protein-i	5	10	15.9	2E-04
518	gi|407892	splicing factor, argini	2	7	2.8	8E-05
520	gi|663466	SERPINE1 mRNA bi	5	6	20.3	2E-04
521	gi|450664	ribosomal protein L38	2	8	32.9	0.002
522	gi|766201	PHD finger protein 3	2	3	1.9	2E-05
523	gi|475196	microtubule-associate	3	3	4.4	4E-05
525	gi|298376	DNA polymerase delt	3	3	13.5	1E-04
526	gi|450486	KH-type splicing regu	14	28	20.3	5E-04
528	gi|354939	ubiquitin-conjugating	4	6	8.2	5E-04
531	gi|427162	high density lipoprote	5	5	6.7	5E-05
533	gi|154312	ribosomal protein L10	3	6	17.1	4E-04
534	gi|622410	glutamyl-prolyl tRNA	3	4	2.8	4E-05
535	gi|450442	high-mobility group bo	3	6	18.6	4E-04
536	gi|450672	ribosomal protein S4,	3	7	13.7	4E-04
537	gi|425441	splicing factor 1 isofo	4	7	10.9	2E-04
540	gi|691247	karyopherin alpha 6 [	3	9	9.9	2E-04
541	gi|450209	solute carrier family 2	7	23	15.4	0.001
542	gi|503187	lamin B1 [Homo sapie	6	15	15	3E-04
544	gi|450577	solute carrier family 2	3	7	13	3E-04
545	gi|557496	hypothetical protein L	3	5	5.6	8E-05
546	gi|517444	guanine nucleotide bi	3	5	11.7	2E-04
547	gi|454393	aspartyl-tRNA synthet	2	5	5.8	1E-04
548	gi|257776	proteasome 26S non-	3	3	5.8	5E-05
549	gi|150555	ribosomal protein S2	2	4	10.6	2E-04
550	gi|450518	macrophage migratio	1	6	7.8	7E-04
552	gi|742753	S-adenosylmethionine	3	4	18	2E-04
553	gi|334699	minichromosome mai	3	3	7.6	8E-05
555	gi|450675	TATA binding protein	5	7	12.5	2E-04
556	gi|243081	DnaJ (Hsp40) homolo	4	8	8.1	1E-04
557	gi|450249	complement compone	2	12	17.7	6E-04
558	gi|590192	cleavage and polyade	6	10	28.2	6E-04
559	gi|425423	serine/arginine repetit	5	9	9.3	1E-04
562	gi|315633	integrin beta 4 binding	3	6	17.1	3E-04
563	gi|200701	prolyl 4-hydroxylase,	5	10	17.1	3E-04
566	gi|450288	CDC-like kinase 3 iso	2	5	4.1	1E-04
567	gi|131288	histone deacetylase 6	2	12	3.8	1E-04
568	gi|611752	hypothetical protein L	2	4	14.3	2E-04
569	gi|766212	zinc finger and BTB d	2	6	4.4	1E-04
570	gi|151494	arginyl-tRNA syntheta	3	7	8.2	1E-04
572	gi|546071	lactotransferrin [Hom	2	10	4.6	2E-04
573	gi|215362	brain creatine kinase	3	7	13.6	2E-04
574	gi|450764	triosephosphate isom	3	5	17.3	3E-04
575	gi|482689	profilin 1 [Homo sapie	6	11	47.9	0.001
577	gi|141104	heterogeneous nucle	3	3	10.9	1E-04
579	gi|120564	junction plakoglobin [	5	19	7	3E-04
580	gi|134890	SAPS domain family,	1	6	2.6	1E-04
581	gi|449559	E2F transcription fact	4	5	5.4	7E-05
584	gi|450765	tropomyosin 4 [Homo	3	5	19.4	3E-04
587	gi|154312	ribosomal protein L15	9	20	36.3	0.001
601	gi|181049	ribosomal protein L21	1	6	9.4	5E-04
608	gi|450659	ribosomal protein L12	3	8	24.2	7E-04
611	gi|201495	serine/threonine kinas	2	4	10	2E-04
617	gi|450220	ADP-ribosylation fact	2	4	17.1	3E-04
618	gi|590207	splicing factor, argini	4	6	15.7	3E-04
619	gi|545355	ras-related nuclear pr	5	9	15.7	6E-04
620	gi|450576	phosphoglycerate kin	8	16	26.1	5E-04
621	gi|450326	dihydrolipoamide bra	4	6	16.2	2E-04
622	gi|213613	carbamoyl-phosphate	17	36	20.2	3E-04
623	gi|285577	zinc binding alcohol d	3	5	13.5	2E-04
624	gi|475917	splicing factor, argini	4	6	5.5	7E-05
631	gi|233976	copine I [Homo sapie	1	4	3.7	1E-04
634	gi|158090	myosin regulatory ligh	3	4	23.3	3E-04
635	gi|335989	LIM domain only 7 [H	9	12	13	1E-04
636	gi|450641	Ran GTPase activati	10	16	27.3	4E-04
637	gi|118631	archain [Homo sapie	7	10	19	3E-04
639	gi|455784	regulatory factor X, 5	2	6	5.4	1E-04
640	gi|557708	catenin, alpha 1 [Hom	2	4	5.1	6E-05
641	gi|557417	RNA binding motif pro	3	5	3.8	8E-05
642	gi|545406	RNA binding motif pro	6	11	13.9	2E-04
643	gi|691228	AHA1, activator of he	4	5	16.6	2E-04
644	gi|475776	Rho GTPase activati	8	15	21.9	5E-04
645	gi|765764	tropomodulin 3 (ubiqu	3	12	15.1	5E-04
647	gi|573002	RuvB-like 2 [Homo sa	4	8	9.7	2E-04
650	gi|590192	CDC37 homolog [Ho	1	3	5.6	1E-04
656	gi|413229	plectin 1 isoform 3 [H	3	5	1	2E-05
659	gi|304107	proteasome activator	3	10	16.1	5E-04
661	gi|766174	basic leucine zipper a	2	11	9.8	4E-04
662	gi|343351	SEC13-like 1 isoform	2	4	12.4	2E-04
664	gi|244967	leucyl-tRNA syntheta	2	4	3.1	5E-05
665	gi|243078	dynein, cytoplasmic, i	1	5	3.3	1E-04
666	gi|450353	eukaryotic translation	2	3	5.1	5E-05
667	gi|455749	cleavage stimulation	4	9	12	2E-04
668	gi|450714	sorting nexin 3 isofor	3	8	33.3	7E-04
669	gi|141411	metastasis-associate	3	7	7.3	1E-04
670	gi|890300	PREDICTED: far ups	8	16	23.9	5E-04
674	gi|242347	interleukin enhancer	7	17	21.3	6E-04
675	gi|468771	upstream stimulatory	2	7	11.6	4E-04
677	gi|260512	nucleoporin 54kDa [H	4	6	11.4	2E-04
678	gi|503157	A-kinase anchor prote	1	3	2.9	6E-05
679	gi|770632	chromosome 14 open	3	6	18.4	3E-04
681	gi|571649	colonic and hepatic tu	4	5	4.2	3E-05
682	gi|450259	carbonyl reductase 1	13	28	51.3	0.001
684	gi|335194	thioredoxin reductase	1	5	7.2	1E-04
687	gi|450668	ribosomal protein S13	2	4	18.5	4E-04
689	gi|244301	nucleoporin 155kDa i	1	3	1.6	3E-05
690	gi|131289	hypothetical protein M	3	3	17	2E-04
691	gi|450676	S100 calcium-binding	2	2	19.6	3E-04
692	gi|108352	advanced glycosylatio	1	2	3.7	7E-05
693	gi|220276	adaptor-related prote	3	3	5.7	4E-05
695	gi|199134	DNA topoisomerase I	2	3	2.2	3E-05
696	gi|201275	TPX2, microtubule-as	1	3	2.8	5E-05
697	gi|517444	lanthionine synthetas	4	9	17.8	3E-04
698	gi|580311	EBNA1 binding prote	2	5	11.1	2E-04
699	gi|167532	ribosomal protein L14	2	3	11.1	2E-04
702	gi|230655	glutathione S-transfe	12	34	39.6	0.002
703	gi|475851	hepatoma-derived gr	2	3	14.6	2E-04
706	gi|307943	polybromo 1 isoform	2	2	2.5	2E-05
707	gi|450664	ribosomal protein L37	3	7	18.5	0.001
708	gi|450674	ribosomal protein S8	2	6	12	4E-04
709	gi|450510	microtubule-associate	2	2	6.1	4E-05
710	gi|113861	cytidine deaminase [H	4	6	41.1	6E-04
712	gi|203575	cortactin isoform a [H	1	3	2.7	7E-05
713	gi|482686	nucleoside-diphospha	2	2	15.5	1E-04
715	gi|462768	elongin B isoform b [H	4	6	23	5E-04
716	gi|503216	elongin C [Homo sapi	5	14	50	0.002
717	gi|450490	karyopherin alpha 4 [	2	3	8.8	8E-05
718	gi|450640	RAN binding protein 1	2	4	22.4	3E-04
719	gi|537591	importin 8 [Homo sap	2	2	3.4	3E-05
720	gi|538293	potassium channel te	7	23	38.4	0.001
721	gi|235104	minichromosome mai	3	11	5	2E-04
722	gi|450455	isoleucine-tRNA synth	5	6	6.2	6E-05
724	gi|243080	hypothetical protein L	3	6	9.7	2E-04
725	gi|397256	la related protein isof	3	5	3.7	7E-05
729	gi|765758	solute carrier family 2	2	2	5.2	4E-05
731	gi|154208	neuralized [Mus musc	2	2	4.7	5E-05
732	gi|411468	PREDICTED: hypothe	2	4	5.7	9E-05
733	gi|344820	adaptor-related prote	2	3	3	4E-05
735	gi|514758	PREDICTED: dpy-19-	3	6	4.6	1E-04
746	gi|450669	ribosomal protein S16	1	6	7.5	6E-04
756	gi|889428	PREDICTED: similar	2	3	7.8	1E-04
760	gi|575277	odorant response abr	3	8	8.8	2E-04
763	gi|455931	guanine nucleotide bi	2	2	6.4	5E-05
764	gi|765701	hypothetical protein L	3	4	7.7	1E-04
765	gi|495745	hypothetical protein L	2	4	32.1	5E-04
766	gi|450284	cold inducible RNA bi	1	5	12.2	4E-04
767	gi|475916	small nuclear ribonuc	1	2	16.7	2E-04
768	gi|425602	peptidyl-prolyl isomer	2	4	3.4	7E-05
769	gi|450448	hypoxanthine phosph	1	2	13.8	1E-04
770	gi|545409	serine/threonine kinas	2	3	6	8E-05
772	gi|455749	C-terminal binding pro	2	3	9.8	9E-05
777	gi|213615	ribonuclease/angioge	2	3	7.2	9E-05
781	gi|487629	liver phosphofructoki	2	3	6.2	5E-05
783	gi|580303	heterogeneous nucle	2	3	11.8	1E-04
788	gi|108001	H2B histone family, m	3	9	19.8	1E-03
798	gi|450726	statherin isoform a [H	1	3	48.4	7E-04
799	gi|600580	proline rich 4 (lacrima	1	3	10.4	3E-04
800	gi|375957	lamin B receptor [Hor	2	5	6.5	1E-04
803	gi|154313	ribosomal protein L9 [	3	7	15.6	5E-04
804	gi|770648	TNF receptor-associa	2	2	3.3	4E-05
805	gi|503209	solute carrier family 1	1	2	3.7	5E-05
806	gi|557495	splicing factor 3B sub	2	2	1.8	3E-05
809	gi|450238	barrier to autointegrat	1	2	15.7	3E-04
810	gi|624606	importin 4 [Homo sap	3	5	5.2	6E-05
811	gi|163064	cell division cycle 2 p	2	2	16.7	1E-04
813	gi|475909	splicing factor, argini	1	2	5.6	9E-05
816	gi|450601	protein phosphatase	1	2	3.6	9E-05
818	gi|450669	ribosomal protein S17	1	3	16.3	3E-04
820	gi|677823	corneodesmosin prec	4	6	23.8	2E-04
821	gi|685635	hypothetical protein L	2	4	7.8	9E-05
822	gi|621229	filaggrin 2 [Homo sap	3	5	2.2	3E-05
823	gi|600979	filaggrin [Homo sapie	4	14	1.2	5E-05
824	gi|450582	prolactin-induced prot	2	3	18.5	3E-04
825	gi|450233	alpha-2-glycoprotein	1	2	7	9E-05
826	gi|397776	transglutaminase 3 pr	1	2	2.3	4E-05
827	gi|141411	ribosomal protein S9	2	4	10.3	3E-04
829	gi|890522	PREDICTED: hypothe	3	4	6.7	4E-05
830	gi|119680	5-azacytidine induced	2	4	8.2	1E-04
831	gi|450658	replication protein A2	3	4	16.3	2E-04
832	gi|545415	valyl-tRNA synthetase	2	2	4.4	2E-05
833	gi|475841	fragile X mental retar	3	6	4.9	1E-04
834	gi|413277	aldo-keto reductase f	3	3	15.3	1E-04
835	gi|233085	unactive progesteron	2	3	18.8	3E-04
842	gi|130276	small nuclear ribonuc	2	2	8.8	1E-04
843	gi|375447	PREDICTED: similar	1	3	9.9	4E-04
848	gi|154313	ribosomal protein L7 [	6	11	23.4	6E-04
849	gi|380161	RNA binding motif pro	3	5	12.9	2E-04
850	gi|559567	nucleolin [Homo sapie	5	9	6.2	2E-04
853	gi|345771	aldolase A [Homo sap	9	18	31.6	7E-04
855	gi|547920	small ubiquitin-like mo	2	3	23.2	4E-04
859	gi|334699	minichromosome mai	3	3	4.9	5E-05
860	gi|450525	moesin [Homo sapien	2	5	4.7	1E-04
861	gi|182019	glucose phosphate is	4	7	9.9	2E-04
863	gi|618351	fragile X mental retar	3	4	6.3	9E-05
865	gi|210403	SON DNA-binding pro	3	4	2	2E-05
870	gi|398123	RAN binding protein 9	2	2	4.4	4E-05
871	gi|285701	NADP-dependent leu	3	4	15.8	2E-04
872	gi|113454	hypothetical protein L	1	2	1.8	4E-05
873	gi|503197	pre-B-cell colony enh	2	3	10.2	8E-05
877	gi|199134	major vault protein [H	2	3	5.5	5E-05
878	gi|482668	DEAD (Asp-Glu-Ala-A	6	14	10.4	3E-04

879	gi|5453597	F-actin capping protei	2	5	11.5	2E-04	286	32923	5.7	N
880	gi|6850992	DEAH (Asp-Glu-Ala-H	2	3	4.9	5E-05	795	90933	7.5	N
881	gi|1083523	metallothionein 1G [H	1	3	19.7	7E-04	61	6070	8	N
886	gi|2855770	phosphoribosyl pyrop	2	5	9.4	2E-04	318	34839	6.4	N
888	gi|4506749	ribonucleoside-diphos	2	2	3.7	3E-05	792	90070	7.1	N
889	gi|4506765	S100 calcium-binding	2	9	10.9	0.001	101	11728	6.1	N
892	gi|4826860	NHP2 non-histone ch	2	4	30.5	4E-04	128	14174	8.5	N
893	gi|5149263	PREDICTED: U2-ass	2	2	3.1	3E-05	1085	124025	8.6	N
895	gi|5654911	dynamin 2 isoform 3 [	5	6	9.9	9E-05	866	97652	7.6	N
897	gi|3345733	RAVER1 [Homo sapie	9	13	24.3	3E-04	606	63877	8.5	N
898	gi|1740290	far upstream element	7	10	17.5	2E-04	644	67560	7.6	N
899	gi|4504809	jun B proto-oncogene	2	3	15.3	1E-04	347	35879	9.2	N
900	gi|4503251	disabled homolog 2 [H	2	3	4.8	5E-05	770	82588	5.7	N
901	gi|1086388	squamous cell carcin	2	3	2.9	5E-05	800	90255	6.1	N
903	gi|3857008	CUG triplet repeat, R	2	2	11.2	6E-05	483	51617	8.5	N
905	gi|6117525	hypothetical protein L	1	3	10.4	3E-04	125	14116	8.3	N
907	gi|4134945	proline arginine-rich e	1	3	4.5	1E-04	382	43810	9.4	N
909	gi|2136180	RNA binding motif pro	1	3	3.6	1E-04	390	42142	9.9	N
911	gi|2978900	pleckstrin homology d	1	3	2.8	6E-05	680	77861	6.7	N
912	gi|4506715	ribosomal protein S28	1	3	17.4	6E-04	69	7841	10.7	N
920	gi|1870232	dynein, cytoplasmic, I	1	4	12.5	6E-04	96	10855	7.5	N
921	gi|5729953	nuclear distribution ge	1	6	4.5	2E-04	331	38243	5.4	N
922	gi|8923114	OTU domain, ubiquiti	1	2	5.5	1E-04	271	31312	4.9	N
923	gi|4507877	vinculin isoform VCL [	2	2	3.3	3E-05	1066	116722	6.1	N
925	gi|2136165	importin 9 [Homo sap	2	6	3.5	8E-05	1041	115963	4.8	N
926	gi|1132160	thyroid hormone rece	2	2	5.8	6E-05	432	48551	6.1	N
927	gi|3804428	gelsolin isoform b [Ho	3	6	7.8	1E-04	731	80641	5.8	N
929	gi|4885417	huntingtin interacting	2	2	14.5	1E-04	200	22407	5.4	N
930	gi|8894884	PREDICTED: hypothe	2	6	19.6	8E-04	107	11186	9.1	N
931	gi|5453990	proteasome activator	7	13	32.5	7E-04	249	28723	6	N
932	gi|2430820	leucine rich repeat co	2	3	5	7E-05	583	63473	8.3	N
933	gi|3820161	eukaryotic translation	2	2	2.6	2E-05	1403	154804	5.2	N
934	gi|2479708	RAN binding protein 5	6	12	9.1	1E-04	1115	125545	4.9	N
939	gi|2888204	replication factor C 2 (	3	5	16.6	2E-04	320	35244	5.5	N
941	gi|4507791	ubiquitin-conjugating (	2	4	25.7	3E-04	183	20900	7.7	N
942	gi|4132773	calponin 2 isoform b [	1	5	6.3	3E-04	270	29500	7	N
945	gi|5031677	dynamin 1-like protein	3	5	8.3	1E-04	699	78061	6.7	N
947	gi|3394632	nucleoporin 214kDa [	2	3	1.9	2E-05	2090	213618	7.5	N
948	gi|5730041	suppressor of G2 alle	1	2	6.9	8E-05	333	37805	5.2	N
949	gi|2443016	proteasome 26S ATP	2	3	7.5	1E-04	389	44173	7.5	N
951	gi|1992339	Ras-GTPase activatin	1	2	3.5	6E-05	482	54121	5.6	N
953	gi|5109386	hypothetical protein L	4	7	9.4	1E-04	746	84138	6.2	N
954	gi|7740439	staphylococcal nuclea	1	2	2.3	3E-05	910	101997	7.2	N
955	gi|2351037	transportin 1 [Homo s	3	7	5.6	1E-04	890	101310	5	N
957	gi|4128152	chromosome condens	1	3	1.4	3E-05	1401	157168	6.6	N
960	gi|3867996	acetyl-Coenzyme A c	2	3	1.4	2E-05	2383	269997	6.5	N
961	gi|2846699	tau tubulin kinase 2 [H	2	2	0.5	2E-05	1649	182466	7	N
962	gi|1837934	vesicle amine transpo	3	5	11.7	2E-04	393	41920	6.3	N
963	gi|3837290	jumonji domain conta	2	4	2.8	3E-05	1761	191610	7.2	N
964	gi|2146410	tyrosine 3-monooxyge	3	4	15.4	2E-04	247	28303	4.9	N
965	gi|1675320	ubiquilin 2 [Homo sap	1	3	2.6	7E-05	624	65696	5.2	N
966	gi|3041072	Sec3 isoform 1 [Hom	1	3	2.5	5E-05	894	101982	6.6	N
968	gi|5453998	importin 7 [Homo sap	2	4	2.8	5E-05	1038	119516	4.8	N
969	gi|4502565	calpain, small subunit	5	14	26.1	7E-04	268	28316	5.2	N
971	gi|4503519	eukaryotic translation	3	9	10.1	3E-04	357	37564	5.4	N
973	gi|2173559	programmed cell deat	2	4	4.7	1E-04	469	51735	5.2	N
974	gi|4557495	cleavage stimulation f	2	4	5.7	8E-05	717	82922	8.1	N
977	gi|1837932	WW domain-containin	3	3	6.5	6E-05	647	70724	9.5	N
978	gi|8922673	parvin, alpha [Homo s	1	5	3.8	2E-04	372	42244	5.9	N
979	gi|2821227	hypothetical protein L	2	2	7.7	4E-05	636	69438	7.3	N
980	gi|4506445	RNA binding motif pro	1	3	4.4	1E-04	366	40940	8.2	N
981	gi|1432789	cyclin B1 [Homo sapie	1	4	3.9	1E-04	433	48337	7.5	N
983	gi|8903002	PREDICTED: far upst	5	7	24.1	4E-04	261	28492	7.9	N
984	gi|2339742	synaptotagmin bindin	5	6	14.9	1E-04	623	69633	8.6	N
985	gi|5031755	heterogeneous nucle	4	6	11.4	1E-04	633	70943	8.1	N
986	gi|4247616	POU domain, class 2,	4	7	10.5	1E-04	743	76472	6.8	N
987	gi|7661892	REST corepressor 1 [	1	3	3.3	8E-05	482	53028	7	N
988	gi|3999506	hypothetical protein L	1	3	2.7	4E-05	1042	118013	5.8	N
989	gi|4885399	chondroitin sulfate pro	2	2	3.3	2E-05	1217	141541	7.2	N
991	gi|1508225	chromobox homolog 3	2	3	14.2	2E-04	183	20811	5.3	N
993	gi|3252830	replication factor C la	2	4	3.1	5E-05	1147	128183	9.4	N
995	gi|2007026	cofactor of BRCA1 [H	2	2	7.4	5E-05	580	65697	6.1	N
996	gi|3058113	SMC1 structural main	2	2	2.4	2E-05	1233	143233	7.6	N
998	gi|2123780	SWI/SNF-related mat	9	14	10.1	2E-04	1214	132879	5.7	N
999	gi|3165224	CCAAT displacement	4	5	5.1	5E-05	1505	164312	6	N
1000	gi|4488882	hypothetical protein L	4	4	4.4	4E-05	1424	152587	7.3	N
1001	gi|5454004	D4, zinc and double P	1	2	5.6	7E-05	391	44156	6.3	N
1002	gi|4759100	splicing factor p54 [H	3	4	6.4	1E-04	484	53542	10.5	N
1004	gi|2773502	MOB1, Mps One Bind	2	3	5.6	2E-04	216	25091	6.7	N
1007	gi|4502549	calmodulin 2 [Homo s	2	24	22.8	0.002	149	16838	4.2	N
1008	gi|8906156	PREDICTED: similar	6	14	24.5	5E-04	367	39994	8.4	N
1009	gi|8906214	PREDICTED: similar	5	9	17.2	3E-04	430	47445	6.1	N
1010	gi|6224400	modulator of estrogen	2	2	3	3E-05	1016	115409	8.1	N
1014	gi|1083505	cysteinyl-tRNA synthe	5	7	11.1	1E-04	748	85473	6.7	N
1016	gi|7177408	myc proto-oncogene	1	3	3.7	9E-05	454	50565	5.4	N
1017	gi|7706254	nucleolar protein NOP	1	3	3.2	8E-05	529	59578	8.9	N
1018	gi|1275149	hypothetical protein L	1	2	14.4	1E-04	229	24992	10	N
1019	gi|2136206	hypothetical protein L	1	2	10.2	2E-04	147	15015	7.8	N
1020	gi|7570920	glutathione peroxidas	1	2	6.6	1E-04	197	22025	8.4	N
1021	gi|3165710	WD repeat domain 23	2	2	6.2	5E-05	520	58846	6.1	N
1023	gi|8922358	PRP38 pre-mRNA pro	1	2	4.6	5E-05	546	64441	10.5	N
1025	gi|4757880	BUB3 budding uninhib	2	2	14.6	8E-05	328	37155	6.8	N
1026	gi|5005387	ribosomal protein L7-l	2	2	10.2	1E-04	246	28661	10.5	N
1027	gi|1694597	PC4 and SFRS1 inter	1	2	6.9	8E-05	333	37653	9.2	N
1029	gi|1132160	TNF receptor-associa	2	2	3.6	5E-05	557	64406	7.4	N
1032	gi|4507389	elongin A [Homo sapi	26	137	26.4	0.002	772	87230	9.6	N
1033	gi|3448572	karyopherin alpha 3 [	2	3	6.1	8E-05	521	57811	4.9	N
1034	gi|5174529	methionine adenosylt	2	3	7.6	1E-04	395	43661	6.5	N
1035	gi|8922491	transmembrane prote	1	2	4.9	1E-04	247	27951	9.7	N
1036	gi|4827050	ubiquitin specific prot	1	2	2.6	6E-05	494	56069	5.3	N
1037	gi|7706377	ankyrin repeat and S0	2	3	6.6	1E-04	335	37014	8.2	N
1038	gi|4502563	calpain 2, large subun	1	2	5	4E-05	700	80007	5	N
1039	gi|2887579	hypothetical protein L	2	3	14.5	2E-04	248	26397	12.2	N
1040	gi|1348909	potassium channel te	4	14	31	7E-04	290	32494	4.8	N
1041	gi|2136111	solute carrier family 2	1	3	5.1	1E-04	314	34062	9.9	N
1043	gi|1474193	PREDICTED: small n	1	2	12	3E-04	92	10678	8.1	N
1045	gi|4852650	translocase of inner m	1	2	3.5	6E-05	456	50465	9.4	N
1046	gi|4557365	Bloom syndrome prot	12	31	14	3E-04	1417	159000	7.5	N
1048	gi|4247628	voltage-dependent an	2	3	13.3	1E-04	294	31566	7.6	N
1050	gi|6005854	prohibitin 2 [Homo sa	2	3	10.7	1E-04	299	33296	9.8	N
1051	gi|2014959	solute carrier family 2	1	2	8.4	9E-05	287	31282	9.5	N
1052	gi|4504795	inositol 1,4,5-triphosp	1	2	0.9	1E-05	2671	304115	6.5	N
1053	gi|5763453	nucleoporin 205kDa [	1	2	0.7	1E-05	2012	227918	6.2	N
1054	gi|1459190	ribosomal protein L5 [	6	12	18.9	5E-04	297	34363	9.7	N
1056	gi|4506649	ribosomal protein L3 i	6	11	10.2	4E-04	403	46109	10.2	N
1057	gi|4503765	fragile X mental retard	5	10	9.2	2E-04	632	71175	7.4	N
1059	gi|5174449	H1 histone family, me	4	6	17.8	4E-04	213	22487	10.8	N
1076	gi|4114914	PREDICTED: similar	3	6	9.4	4E-04	203	23619	10.9	N
1079	gi|7615062	nucleolar protein 1, 12	3	5	3.7	8E-05	808	88973	9.2	N
1080	gi|4506633	ribosomal protein L31	4	4	20.8	4E-04	125	14463	10.5	N
1084	gi|4506621	ribosomal protein L26	3	4	15.9	4E-04	145	17258	10.6	N
1085	gi|4758950	peptidylprolyl isomera	2	4	12	3E-04	216	23743	9.4	N
1086	gi|4507149	superoxide dismutase	1	4	9.1	4E-04	154	15936	6.1	N
1087	gi|1611779	ribosomal protein L35	2	3	14.5	4E-04	110	12538	11.1	N
1088	gi|4506607	ribosomal protein L18	2	3	12.8	2E-04	188	21634	11.7	N
1089	gi|4506623	ribosomal protein L27	2	3	6.6	3E-04	136	15798	10.6	N
1090	gi|5577090	BRIX [Homo sapiens]	2	3	6.5	1E-04	353	41401	9.9	N
1091	gi|7348665	aspartate aminotrans	2	3	6	9E-05	430	47518	9	N
1092	gi|4505587	platelet-activating fac	1	3	3.9	2E-04	231	25734	6.8	N
1095	gi|1611778	ribosomal protein L34	1	2	8.5	2E-04	117	13293	11.5	N
1097	gi|4505621	prostatic binding prote	1	2	8	1E-04	187	21057	7.5	N
1098	gi|4265727	PREDICTED: similar	1	2	7.3	2E-04	124	13614	10.1	N
1101	gi|1571868	ribosomal protein S3 [	2	2	7	1E-04	243	26688	9.7	N
1102	gi|1427770	ribosomal protein S12	1	2	6.1	2E-04	132	14515	7.2	N
1108	gi|8894236	PREDICTED: similar	1	2	4	8E-05	328	34023	10.8	N
1109	gi|4503729	FK506-binding protein	1	2	3.1	6E-05	459	51805	5.4	N
1110	gi|4557032	lactate dehydrogenas	1	2	3	8E-05	334	36639	6.1	N
1111	gi|4507521	transketolase [Homo s	1	2	2.9	4E-05	623	67878	7.7	N
1112	gi|8922388	RNA binding motif pro	1	2	1.7	4E-05	759	85766	9.2	N
1113	gi|5065806	centrosomal protein 7	3	5	6	1E-04	597	69752	5.7	N
1114	gi|6912618	glutaminyl-peptide cy	1	4	3.9	2E-04	361	40877	6.6	N
1115	gi|4557809	ornithine aminotransfe	1	2	3.6	6E-05	439	48535	7	N
1116	gi|5089785	Hook-related protein 1	1	2	0.9	2E-05	1843	212619	6	N
1117	gi|2743695	ALMS1 [Homo sapien	2	2	0.5	6E-06	4167	460996	6.3	N
1118	gi|6242088	dipeptidyl peptidase 7	8	22	24.8	6E-04	492	54341	6.3	N
1119	gi|5453543	aldo-keto reductase fa	7	17	27.2	7E-04	323	36788	7.9	N
1121	gi|4503285	aldo-keto reductase fa	7	17	24.5	7E-04	323	36735	7.5	N
1122	gi|5574315	WD repeat domain 26	6	10	15.6	3E-04	514	58604	6.2	N
1123	gi|6693301	inosine monophospha	5	9	15.2	2E-04	514	55805	6.9	N
1124	gi|2449758	aldo-keto reductase fa	5	6	24.5	3E-04	323	36853	7.9	N
1125	gi|8923557	chromosome 20 open	3	5	13.2	3E-04	228	26749	5	N
1126	gi|4053873	RAN binding protein 1	3	5	10.3	1E-04	620	67257	6.8	N
1127	gi|3245474	serine (or cysteine) pr	2	4	6.7	1E-04	418	46441	8.7	N
1133	gi|6174447	solute carrier family 3	2	4	4.7	8E-05	661	71123	5	N
1136	gi|6850895	carboxylesterase 1 is	2	3	10.2	7E-05	566	62393	6.6	N
1137	gi|1414962	ubiquitin specific prot	2	3	5.4	4E-05	952	109297	5.2	N
1140	gi|2139648	protease, serine, 15 [	1	2	3.6	3E-05	959	106489	6.4	N
1141	gi|2161452	glucose-6-phosphate	2	2	3.1	5E-05	515	59258	6.7	N
1142	gi|3252689	armadillo repeat conta	1	2	2.9	4E-05	659	73994	6.7	N
1143	gi|5170222	hypothetical protein L	1	2	1.5	4E-05	685	75599	9.8	N
1144	gi|2743696	potassium voltage-ga	4	6	14.7	2E-04	353	39287	8.6	N
1146	gi|4502945	alpha 1 type I collage	3	6	1.5	6E-05	1464	138912	5.9	N
1147	gi|4876293	alpha 2 type I collage	1	5	1	5E-05	1366	129314	9	N
1148	gi|4506133	phosphoribosyl pyrop	2	4	8.9	1E-04	369	40926	7.4	N
1149	gi|2447584	influenza virus NS1A	3	4	6.9	8E-05	642	71729	5.5	N
1150	gi|4643064	myosin IC [Homo sap	2	2	2.9	3E-05	1028	117949	9.4	N
1151	gi|4080616	thyroid hormone rece	3	4	10.6	1E-04	461	52788	7.1	N
1152	gi|4507955	YY1 transcription fact	2	3	6.8	1E-04	414	44713	6.3	N
1153	gi|1971873	bromodomain-contain	2	3	1.5	3E-05	1362	152218	9.2	N
1155	gi|1274659	C-terminal binding pro	2	2	3.2	3E-05	985	106208	8	N
1156	gi|1701799	FtsJ homolog 3 [Hom	1	3	2.2	5E-05	847	96576	8.2	N
1157	gi|1415014	syndesmos [Homo sa	1	2	8.1	1E-04	211	23338	8.9	N
1158	gi|4827071	zinc finger protein 9 [H	4	11	30.5	8E-04	177	19463	7.7	N
1159	gi|1555921	RE1-silencing transcr	4	5	5.8	6E-05	1097	121888	6.7	N
1160	gi|5453593	adenylyl cyclase-asso	1	2	3.1	6E-05	477	52824	6.4	N
1161	gi|4758012	clathrin heavy chain 1	4	7	4.4	6E-05	1675	191613	5.7	N
1162	gi|2202753	programmed cell deat	3	6	7.7	9E-05	868	96023	6.5	N
1163	gi|5579478	mitogen-activated pro	2	4	12	1E-04	393	43439	6.6	N
1164	gi|4028829	chloride intracellular c	2	3	14.4	2E-04	236	26648	6.4	N
1165	gi|3174253	diaphanous 1 [Homo	2	3	2.6	3E-05	1248	138907	5.4	N
1166	gi|6167618	HECT, UBA and WW	3	3	1.6	9E-06	4374	481896	5.2	N
1167	gi|2007013	basic transcription fac	1	2	13.6	2E-04	162	17699	7.5	N
1168	gi|3802791	COP9 signalosome s	1	2	13.1	2E-04	160	17909	7.3	N
1169	gi|4826774	interferon, alpha-indu	1	2	12.1	2E-04	165	17887	7.5	N
1170	gi|4504011	glutamate-cysteine lig	1	2	11.3	1E-04	274	30727	6	N
1172	gi|2136174	hypothetical protein L	1	2	6.5	9E-05	307	33879	6.3	N
1176	gi|5487362	CDA02 protein [Homo	2	2	5.3	5E-05	585	64990	8.9	N
1177	gi|1337621	ubiquitin-activating en	1	2	5.2	7E-05	404	44863	4.8	N
1179	gi|2161833	signal transducer and	2	2	5.2	4E-05	769	87981	6.3	N
1180	gi|4506013	protein phosphatase 1	1	2	5	8E-05	360	41564	4.9	N
1183	gi|4504341	histone acetyltransfer	1	2	4.3	6E-05	419	49513	5.7	N
1184	gi|5730104	thioredoxin-like [Hom	1	2	3.9	8E-05	335	37490	5.3	N
1185	gi|4507835	uridine monophospha	1	2	3.5	6E-05	480	52222	7.2	N
1186	gi|4502111	annexin VII isoform 1	1	2	3.4	6E-05	466	50316	6.6	N
1188	gi|2311103	sorting nexin 1 isofor	1	2	3.1	6E-05	457	51813	5.6	N
1190	gi|2311103	sorting nexin 2 [Homo	1	2	2.7	5E-05	519	58471	5.1	N
1195	gi|8903007	PREDICTED: inositol	1	2	2.3	3E-05	828	89468	5.5	N
1204	gi|1155992	coatomer protein com	1	2	2.1	3E-05	874	97718	5.5	N
1207	gi|2274893	exportin 5 [Homo sap	1	2	1.7	2E-05	1204	136311	5.8	N
1213	gi|2220263	prefoldin 5 isoform alp	1	2	9.7	2E-04	154	17328	6.3	N
1214	gi|2982633	eukaryotic translation	1	2	4.5	8E-05	333	38388	5.8	N
1215	gi|4053880	hypothetical protein L	1	2	3.3	5E-05	510	55216	6.1	N
1216	gi|3856946	ROD1 regulator of dif	1	2	2.2	5E-05	552	59690	9	N
1217	gi|3993035	superkiller viralicidic a	1	2	1.3	3E-05	1042	117761	6.7	N
1218	gi|4759196	symplekin [Homo sap	3	5	7.2	6E-05	1142	126500	6.4	N
1223	gi|3457706	ras suppressor protein	2	3	18.8	2E-04	224	25545	8.7	N
1229	gi|1690551	FUS interacting prote	1	3	6.1	2E-04	262	31301	11.3	N
1231	gi|8393116	chromatin accessibility	1	2	13.7	2E-04	131	14711	5.1	N
1234	gi|1641838	mediator of RNA poly	1	2	9	1E-04	212	22741	9.7	N
1243	gi|3837290	Sp1 transcription facto	1	2	3.6	3E-05	785	80693	7.3	N
1244	gi|1343537	glucocorticoid modula	1	2	3.4	5E-05	563	61327	4.8	N
1246	gi|4758032	coatomer protein com	1	2	2.1	3E-05	906	102487	5.3	N
1247	gi|3179553	replication factor C 3 (	1	2	6.9	1E-04	202	22710	9	N
1249	gi|1354058	hypothetical protein L	1	2	4.8	5E-05	518	57341	5.2	N
1251	gi|5595691	myosin IE [Homo sap	4	5	5.9	6E-05	1108	127062	8.9	N
1253	gi|1343536	desmocollin 1 isoform	2	4	4.1	6E-05	894	99987	5.4	N
1254	gi|1799855	serine (or cysteine) pr	3	3	12.3	1E-04	405	46276	5.5	N
1255	gi|1312901	hypothetical protein L	1	2	12.2	1E-04	188	21008	5.1	N
1256	gi|6813155	ankyrin repeat domain	2	2	3.9	3E-05	1053	112966	6.3	N
1257	gi|1411041	heterogeneous nucle	11	23	31.7	0.001	306	32835	8.2	N
1259	gi|2736348	E74-like factor 1 (ets d	9	17	25	4E-04	619	67498	5.2	N
1263	gi|4582770	quaking homolog, KH	7	15	27.3	6E-04	341	37671	8.5	N
1264	gi|8903789	PREDICTED: similar	8	12	14.7	3E-04	600	64322	7.4	N
1265	gi|3079523	brain abundant, mem	6	10	39.2	6E-04	227	22693	4.6	N
1266	gi|1555312	hexokinase 2 [Homo s	5	10	7.4	1E-04	917	102380	6.1	N
1267	gi|3410128	zinc finger RNA bindi	4	10	5.5	1E-04	1074	117012	9	N
1268	gi|5611912	chromodomain helica	7	10	4.3	6E-05	2302	262345	6.7	N
1270	gi|4254417	E74-like factor 2 (ets d	7	9	21.9	2E-04	581	62711	6.7	N
1271	gi|5876154	amine oxidase (flavin	6	9	12.4	1E-04	852	92903	6.5	N
1274	gi|1514946	caldesmon 1 isoform	5	9	10.9	2E-04	558	64256	7	N
1277	gi|2123780	SWI/SNF-related mat	6	8	8.3	1E-04	1105	122721	5.8	N
1278	gi|3414754	hypothetical protein L	4	7	30	7E-04	140	14564	8.5	N
1279	gi|5574167	hypothetical protein L	7	7	10.1	9E-05	1083	121837	6.5	N
1280	gi|8659574	transcription factor bi	4	7	9.2	2E-04	575	61521	5.6	N
1282	gi|2547088	DAZ associated prote	4	6	11.5	2E-04	407	43383	8.6	N
1283	gi|2443201	pre-mRNA cleavage f	2	6	7.9	2E-04	471	52050	8	N
1284	gi|5032057	S100 calcium binding	2	5	25.7	6E-04	105	11740	7.2	N
1286	gi|4504983	galectin 3 [Homo sapi	3	5	16	3E-04	250	26188	8.5	N
1288	gi|2754532	SWI/SNF related, mat	4	5	13.8	2E-04	385	44141	6.2	N
1290	gi|5031857	lactate dehydrogenas	3	5	12	2E-04	332	36689	8.3	N
1291	gi|3814610	hypothetical protein L	3	5	11.3	2E-04	434	50560	11.3	N
1293	gi|5803137	RNA binding motif pro	2	4	31.8	3E-04	157	17170	8.9	N
1294	gi|2773470	hypothetical protein L	4	4	20	2E-04	330	37221	6.3	N
1295	gi|1378612	Cdc42 effector protein	2	4	13.5	2E-04	356	37980	5.2	N
1296	gi|5174751	Yes-associated prote	3	4	12.1	1E-04	454	48755	5.1	N
1297	gi|9506671	hypothetical protein L	3	4	11.3	1E-04	524	56876	6.3	N
1298	gi|5576953	PRKC, apoptosis, WT	2	4	10.9	2E-04	340	36568	5.4	N
1300	gi|5667633	HP1-BP74 [Homo sap	3	4	9.6	1E-04	553	61207	9.7	N
1301	gi|4885063	fructose-bisphosphate	2	4	8.2	1E-04	364	39456	6.9	N
1302	gi|6183750	sine oculis homeobox	3	4	7.9	7E-05	781	82893	5.6	N
1303	gi|4507847	upstream stimulatory	2	4	7.8	2E-04	346	36955	5.1	N
1305	gi|4503735	forkhead box C1 [Hor	3	4	7.4	1E-04	553	56788	8.6	N
1306	gi|3499648	hypothetical protein L	3	4	5.9	7E-05	749	79423	9	N
1308	gi|2107105	SWI/SNF-related mat	4	4	5.9	5E-05	1009	113928	8.6	N
1309	gi|3165709	anillin, actin binding p	3	4	3.9	5E-05	1124	124199	8.1	N
1310	gi|8906156	PREDICTED: similar	1	4	3.7	1E-04	377	41540	8.3	N
1312	gi|8903751	PREDICTED: AHNAK	3	4	2.2	2E-05	2779	295336	5.2	N
1313	gi|1312909	hypothetical protein L	2	3	12.9	2E-04	232	25858	9.7	N
1314	gi|4758556	PRP3 pre-mRNA proc	2	3	7.5	6E-05	683	77529	9.5	N
1317	gi|3978058	hypothetical protein L	3	3	6.3	5E-05	804	91810	7.4	N
1319	gi|4544674	DEAD box polypeptid	2	3	5.8	4E-05	938	102975	7	N
1321	gi|2476222	homeobox protein Me	2	3	5.5	1E-04	381	41542	6.3	N
1329	gi|2027021	tankyrase 1-binding p	3	3	2.7	2E-05	1729	181804	4.9	N
1330	gi|2107105	SWI/SNF-related mat	3	3	2.6	3E-05	1647	184644	7.9	N

1331	gi|2430803	formin binding protein	1	3	2	4E-05	x	x	x	x	x	x	x	x	x	x	x	x	1	3	2	7E-04	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	1015	110064	4.7	N
1332	gi|4503337	dyskerin [Homo sapie	1	3	1.9	8E-05	x	x	x	x	x	x	x	x	x	x	x	x	1	3	1.9	0.001	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	514	57674	9.4	N
1333	gi|5411240	chromodomain helica	1	3	0.4	1E-05	x	x	x	x	x	x	x	x	x	x	x	x	1	3	0.4	3E-04	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	2997	335928	6.3	N
1334	gi|1132159	high-mobility group bo	2	2	12	1E-04	x	x	x	x	x	x	x	x	x	x	x	x	2	2	12	0.002	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	209	24034	7.8	N
1336	gi|1837550	APEX nuclease [Hom	2	2	11	9E-05	x	x	x	x	x	x	x	x	x	x	x	x	2	2	11	0.002	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	318	35554	8.1	N
1338	gi|2350329	casein kinase 2, beta	1	2	10.7	1E-04	x	x	x	x	x	x	x	x	x	x	x	x	1	2	10.7	0.002	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	215	24942	5.6	N
1339	gi|4550514	nuclear factor I/C isof	2	2	10.3	6E-05	x	x	x	x	x	x	x	x	x	x	x	x	2	2	10.3	0.001	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	428	47629	8.2	N
1340	gi|4885073	activating transcriptio	1	2	9.6	1E-04	x	x	x	x	x	x	x	x	x	x	x	x	1	2	9.6	0.002	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	271	29233	8.4	N
1341	gi|4505117	methyl-CpG binding d	1	2	9.5	7E-05	x	x	x	x	x	x	x	x	x	x	x	x	1	2	9.5	0.001	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	411	43255	10	N
1342	gi|2750144	density-regulated prot	1	2	9.1	1E-04	x	x	x	x	x	x	x	x	x	x	x	x	1	2	9.1	0.003	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	198	22092	5.3	N
1344	gi|4502801	regulator of chromoso	2	2	8.1	6E-05	x	x	x	x	x	x	x	x	x	x	x	x	2	2	8.1	0.001	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	421	44969	7.5	N
1345	gi|1312888	histone deacetylase 1	2	2	7.3	6E-05	x	x	x	x	x	x	x	x	x	x	x	x	2	2	7.3	0.001	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	482	55103	5.5	N
1346	gi|4641116	muscleblind-like 1 iso	2	2	7	7E-05	x	x	x	x	x	x	x	x	x	x	x	x	2	2	7	0.001	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	388	41817	8.9	N
1347	gi|1425121	Kruppel-like factor 5 [	2	2	6.6	6E-05	x	x	x	x	x	x	x	x	x	x	x	x	2	2	6.6	0.001	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	457	50792	8.6	N
1348	gi|4505623	pre-B-cell leukemia tr	2	2	6.5	6E-05	x	x	x	x	x	x	x	x	x	x	x	x	2	2	6.5	0.001	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	430	46626	7	N
1349	gi|4557641	histone deacetylase 2	2	2	6.4	6E-05	x	x	x	x	x	x	x	x	x	x	x	x	2	2	6.4	0.001	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	488	55325	5.8	N
1350	gi|1238306	likely ortholog of kine	2	2	6.3	4E-05	x	x	x	x	x	x	x	x	x	x	x	x	2	2	6.3	8E-04	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	622	68935	7.2	N
1353	gi|1740290	homolog of yeast mR	1	2	5.9	1E-04	x	x	x	x	x	x	x	x	x	x	x	x	1	2	5.9	0.002	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	272	28235	6.3	N
1354	gi|2814491	hypothetical protein L	1	2	5.3	1E-04	x	x	x	x	x	x	x	x	x	x	x	x	1	2	5.3	0.002	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	246	28383	8.7	N
1355	gi|2887279	CCAAT/enhancer bin	1	2	5.2	8E-05	x	x	x	x	x	x	x	x	x	x	x	x	1	2	5.2	0.001	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	345	36106	8.3	N
1356	gi|3366702	interferon regulatory f	1	2	4.8	5E-05	x	x	x	x	x	x	x	x	x	x	x	x	1	2	4.8	9E-04	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	587	61099	8.8	N
1357	gi|2037317	musashi 2 isoform a [	2	2	4.6	8E-05	x	x	x	x	x	x	x	x	x	x	x	x	2	2	4.6	0.002	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	328	35197	8.5	N
1358	gi|8922328	RNA binding motif pro	1	2	4.5	6E-05	x	x	x	x	x	x	x	x	x	x	x	x	1	2	4.5	0.001	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	420	46896	8.5	N
1360	gi|4825588	protein kinase C subs	1	2	4	5E-05	x	x	x	x	x	x	x	x	x	x	x	x	1	2	4	9E-04	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	528	59425	4.4	N
1361	gi|4506567	RNA (guanine-7-) me	1	2	4	6E-05	x	x	x	x	x	x	x	x	x	x	x	x	1	2	4	0.001	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	476	54844	6.6	N
1363	gi|2957079	casein kinase II alpha	1	2	3.8	7E-05	x	x	x	x	x	x	x	x	x	x	x	x	1	2	3.8	0.001	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	391	45144	7.7	N
1365	gi|4251991	forkhead box O3A [Ho	1	2	3.7	4E-05	x	x	x	x	x	x	x	x	x	x	x	x	1	2	3.7	7E-04	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	673	71277	5.2	N
1366	gi|4505293	MYB-related protein B	1	2	3.6	4E-05	x	x	x	x	x	x	x	x	x	x	x	x	1	2	3.6	7E-04	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	700	78764	6.9	N
1367	gi|2449762	signal recognition par	1	2	3.5	4E-05	x	x	x	x	x	x	x	x	x	x	x	x	1	2	3.5	8E-04	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	627	70730	8.6	N
1368	gi|2274913	serum response facto	1	2	3.3	6E-05	x	x	x	x	x	x	x	x	x	x	x	x	1	2	3.3	0.001	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	427	48359	9.6	N
1369	gi|3857009	hypothetical protein L	1	2	2.7	4E-05	x	x	x	x	x	x	x	x	x	x	x	x	1	2	2.7	6E-04	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	776	86436	5.9	N
1370	gi|4885105	chromatin assembly f	1	2	2.7	5E-05	x	x	x	x	x	x	x	x	x	x	x	x	1	2	2.7	9E-04	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	559	61493	7.5	N
1372	gi|3335654	minichromosome mai	1	2	2.4	3E-05	x	x	x	x	x	x	x	x	x	x	x	x	1	2	2.4	6E-04	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	904	101896	5.5	N
1373	gi|1138615	TEA domain family m	1	2	2.4	7E-05	x	x	x	x	x	x	x	x	x	x	x	x	1	2	2.4	0.001	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	411	46369	8.6	N
1374	gi|2773506	hypothetical protein L	2	2	2.2	4E-05	x	x	x	x	x	x	x	x	x	x	x	x	2	2	2.2	7E-04	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	679	75357	6.8	N
1376	gi|4489006	hypothetical protein L	1	2	2	3E-05	x	x	x	x	x	x	x	x	x	x	x	x	1	2	2	5E-04	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	1045	114989	9.2	N
1377	gi|3457712	nuclear factor kappa-	1	2	1.9	3E-05	x	x	x	x	x	x	x	x	x	x	x	x	1	2	1.9	5E-04	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	969	105427	5.4	N
1378	gi|1349116	pumilio 1 isoform 2 [H	2	2	1.8	2E-05	x	x	x	x	x	x	x	x	x	x	x	x	2	2	1.8	4E-04	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	1186	126473	6.8	N
1380	gi|1598712	hypothetical protein L	1	2	1.8	2E-05	x	x	x	x	x	x	x	x	x	x	x	x	1	2	1.8	4E-04	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	1297	143732	8.8	N
1381	gi|4271627	CCR4-NOT transcript	1	2	1	1E-05	x	x	x	x	x	x	x	x	x	x	x	x	1	2	1	2E-04	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	2376	266937	7.1	N
1382	gi|1992328	AT-binding transcripti	2	2	0.9	7E-06	x	x	x	x	x	x	x	x	x	x	x	x	2	2	0.9	1E-04	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	3703	404474	6.2	N
1383	gi|1518716	lacritin precursor [Ho	1	2	8	2E-04	1	2	8	0.013	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	138	14246	5.5	N
		Total_SpectralCount	33208				548				47				822				1678				721				65				1098				1915				1930				1610				382				419				2049				963				841				248				463				447				1212				2214				262				374				1064				936				1255				1240				1802				1523				532				1860				999				328				309				518				534							
		False Discovery Rate (%)	0.054				0				0				0				0				0				0				0.182				0.104				0				0				0.522				0				0.098				0.415				0				0				0				0				0				0.09				0.76				0				0				0				0				0				0				0				0				0.107				0				0				0				0				0							
		SHUFFLED_SpectralCount	9				0				0				0				0				0				0				1				1				0				0				1				0				1				2				0				0				0				0				0				1				1				0				0				0				0				0				0				0				0				1				0				0				0				0				0							
646	SHUFFLE	FALSE POSITIVE	1	3	1.2		x	x	x		x	x	x		x	x	x		x	x	x		x	x	x		x	x	x		x	x	x		1	1	1.2		x	x	x		x	x	x		x	x	x		x	x	x		1	1	1.2		1	1	1.2		x	x	x		x	x	x		x	x	x		x	x	x		x	x	x		x	x	x		x	x	x		x	x	x		x	x	x		x	x	x		x	x	x		x	x	x		x	x	x		x	x	x		x	x	x		x	x	x		x	x	x		x	x	x		x	x	x		x	x	x		x	x	x		689	78439	9	N
649	SHUFFLE	FALSE POSITIVE	1	3	1.6		x	x	x		x	x	x		x	x	x		x	x	x		x	x	x		x	x	x		1	1	1.6		x	x	x		x	x	x		x	x	x		1	1	1.6		x	x	x		x	x	x		1	1	1.6		x	x	x		x	x	x		x	x	x		x	x	x		x	x	x		x	x	x		x	x	x		x	x	x		x	x	x		x	x	x		x	x	x		x	x	x		x	x	x		x	x	x		x	x	x		x	x	x		x	x	x		x	x	x		x	x	x		x	x	x		x	x	x		492	53132	9.4	N
560	SHUFFLE	FALSE POSITIVE	1	3	3.2		x	x	x		x	x	x		x	x	x		x	x	x		x	x	x		x	x	x		x	x	x		x	x	x		x	x	x		x	x	x		x	x	x		x	x	x		x	x	x		x	x	x		x	x	x		x	x	x		x	x	x		x	x	x		x	x	x		1	1	3.2		1	1	3.2		x	x	x		x	x	x		x	x	x		x	x	x		x	x	x		x	x	x		x	x	x		x	x	x		1	1	3.2		x	x	x		x	x	x		x	x	x		x	x	x		x	x	x		595	69690	6.5	N

Supporting Table 2B. Detailed List of Proteins and Peptides Detected in the Combined Negative Control Dataset.

Proteins with peptides passing the selection criteria described in the table below are listed by decreasing sequence coverage (percent of the protein sequence covered by the detected peptides).

Criteria Set	Parameter	Value
	Minimum +1 XCorr	1.8
	Minimum +2 XCorr	2.5
	Minimum +3 XCorr	3.5
	Minimum DeltCN	0.08
	Minimum charge state	1
	Maximum charge state	3
	Minimum ion proportion	0
	Maximum Sp rank	10
	Minimum Sp score	-1
	Modified peptide inclusion	Include
	Tryptic status requirement	Full
	Multiple, ambiguous IDs allowed	FALSE
	Minimum sequence length	7
	Maximum sequence length	100
	Sequence completeness required	0
	Purge duplicate peptides by protein	XCorr
	Include only loci with unique peptide	FALSE
	Remove subset proteins	TRUE
	Exclude protein names matching	Contaminant
	Exclude protein descriptions matching	KERATIN
	Minimum modified peptides per locus	0
	Minimum redundancy for low coverage loci	2
	Minimum peptides per locus	2

Locus	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Validation Status	Descriptive Name			
Unique	**FileName**	**XCorr**	**DeltCN**	**M+H+**	**CalcM+H+**	**TotalIntensity**	**SpRank**	**SpScore**	**IonProportion**	**Redundancy**	**Sequence**
gi|Flag_peptide	3	31	1	8	1013	4.3	U	[FLAG peptide]			
	HsHeLa_Control_Ti_101.00	2.6722	0.0932	1013.73	1013.99	5017.2	5	514.6	71.4	5	-.DYKDDDDK.-
	HsHeLa_Control-MG_Ti_10	2.682	0.1398	1013.82	1013.99	5124.1	5	588.4	71.4	24	-.DYKDDDDK.-
	HsFLAG-Control_HeLa_NE	3.0205	0.1185	1014.29	1013.99	5542.3	8	982.2	92.9	2	-.DYKDDDDK.-
gi|32455264|ref|	43	144	0.744	199	22110	8.1	U	peroxiredoxin 1 [Homo sapiens]			
gi|4505591|ref|N	43	144	0.744	199	22110	8.1	U	peroxiredoxin 1 [Homo sapiens]			
gi|32455266|ref|	43	144	0.744	199	22110	8.1	U	peroxiredoxin 1 [Homo sapiens]			
	HsFLAG-MOCK_300mM_T	2.2031	0.2368	980.6	981.142	4209.2	1	374.8	62.5	19	K.IGHPAPNFK.A
	HsFLAG-MOCK_300mM_T	2.0955	0.3208	1164.37	1165.35	5596.2	4	386.3	55	2	K.ATAVMPDGQFK.D
	HsHeLa_Control-MG_Ti_20	5.2246	0.4433	3095.93	3095.53	6416.5	1	905	45.8	3	K.YVVFFFYPLDFTFVCPTEIIAFSDR.A
	HsHeLa_Control-MG_Ti_20	5.0478	0.324	3097.25	3095.53	8398.6	1	1831.3	37.5	1	K.YVVFFFYPLDFTFVCPTEIIAFSDR.A
	HsHeLa_Control-MG_Ti_20	5.0651	0.495	2753.49	2755.04	7512.7	1	1240.9	52.2	2	K.LNCQVIGASVDSHFCHLAWVNTPK.K
	HsGST-MOCK_Ti_105.217	3.6616	0.2129	2755.75	2755.04	4902.9	3	612.5	31.5	1	K.LNCQVIGASVDSHFCHLAWVNTPK.K
	Hs293FLP_Ti_306.2691.26	4.023	0.3898	1753.15	1752.08	2715.2	1	541.5	65.6	1	K.KQGGLGPMNIPLVSDPK.R
	HsGST-MOCK_Ti_304.273	3.9108	0.3212	1622.89	1623.91	6549.5	1	1467.3	73.3	10	K.QGGLGPMNIPLVSDPK.R
	Hs293FLP-MG_Ti_306.237	2.617	0.1722	1263.45	1264.47	3157.2	6	277.8	65	1	K.RTIAQDYGVLK.A
	Hs293FLP-MG_Ti_204.178	3.1781	0.1557	1264.12	1264.47	5099.3	1	1072.2	85	6	K.RTIAQDYGVLK.A
	Hs293FLP-MG_Ti_306.238	3.0703	0.1576	1264.94	1264.47	4744.6	1	1041.1	80	5	K.RTIAQDYGVLK.A
	Hs293FLP-MG_Ti_202.210	2.0427	0.1032	1107.51	1108.28	9469.2	6	755.6	66.7	1	R.TIAQDYGVLK.A
	HsFLAG-MOCK_300mM_T	2.9813	0.2931	1108.42	1108.28	2778	1	627.2	88.9	4	R.TIAQDYGVLK.A
	Hs293FLP-MG_Ti_202.212	2.6848	0.2549	1108.43	1108.28	2869.9	1	577.4	83.3	1	R.TIAQDYGVLK.A
	HsFLAG-MOCK_300mM_T	3.5927	0.4618	1984.93	1984.22	6468.7	1	1153.3	61.8	2	R.TIAQDYGVLKADEGISFR.G
	HsFLAG-MOCK_300mM_T	2.8872	0.1391	894.47	894.96	4120.3	1	877.3	92.9	2	K.ADEGISFR.G
	Hs293FLP_TREX_Ti_102.1	3.0279	0.27	1212.5	1212.39	5952.5	1	1083.6	90	8	R.QITVNDLPVGR.S
	HsHeLa_Control-MG_Ti_20	3.0729	0.2001	1196.33	1197.38	5817.7	3	564.6	72.2	2	R.LVQAFQFTDK.H
	HsFLAG-Control_293_Ti_2	3.3774	0.2123	1196.35	1197.38	7910.3	1	723	72.2	4	R.LVQAFQFTDK.H
	Hs293FLP-MG_Ti_202.237	2.6414	0.228	1196.49	1197.38	8302.4	3	675.4	66.7	4	R.LVQAFQFTDK.H
	Hs293FLP_Ti_302.1968.19	3.2418	0.2584	1196.64	1197.38	7065.2	1	754	77.8	1	R.LVQAFQFTDK.H
	HsGST-MOCK_Ti_403.239	3.3922	0.2225	1196.81	1197.38	6452.4	1	945	77.8	2	R.LVQAFQFTDK.H
	HsFLAG-Control_293_Ti_2	3.5748	0.2081	1197.21	1197.38	6721.4	1	1351.9	88.9	5	R.LVQAFQFTDK.H
	HsFLAG-MOCK_300mM_T	3.4805	0.3193	1197.31	1197.38	6183.1	1	1274.2	88.9	4	R.LVQAFQFTDK.H
	HsHeLa_Control-MG_Ti_20	3.9172	0.2871	1197.43	1197.38	6133.9	1	1309.7	88.9	4	R.LVQAFQFTDK.H
	Hs293FLP-MG_Ti_202.238	3.5969	0.2004	1197.48	1197.38	6621.3	1	1248.7	88.9	1	R.LVQAFQFTDK.H
	HsFLAG-Control_MG_293_	3.0269	0.2236	1197.54	1197.38	8776.2	2	799	72.2	2	R.LVQAFQFTDK.H
	Hs293FLP_Ti_302.1967.19	3.6331	0.2333	1197.83	1197.38	5315.5	1	1112.3	88.9	2	R.LVQAFQFTDK.H
	HsHeLa_Control_Ti_103.22	3.6438	0.2315	1198.06	1197.38	5374.1	1	1111.5	88.9	3	R.LVQAFQFTDK.H
	HsFLAG-Control_HeLa_NE	2.7029	0.201	1198.55	1197.38	7491.3	1	632.6	72.2	1	R.LVQAFQFTDK.H
	HsFLAG-MOCK_300mM_T	5.9345	0.364	3585.09	3586.01	8608.1	1	912.2	26.6	3	R.LVQAFQFTDKHGEVCPAGWKPGSDTIKPDVQK.S
	HsHeLa_Control-MG_Ti_20	2.8933	0.2991	1140.68	1141.24	7169.4	1	913.8	77.8	3	K.HGEVCPAGWK.P
	HsGST-MOCK_Ti_104.147	5.1791	0.3778	2406.71	2407.65	7436.1	1	1142	52.4	4	K.HGEVCPAGWKPGSDTIKPDVQK.S
	HsFLAG-MOCK_300mM_T	4.5815	0.2891	2406.98	2407.65	6657.6	1	868	50	2	K.HGEVCPAGWKPGSDTIKPDVQK.S
	Hs293FLP_Ti_306.2354.23	5.1329	0.3059	2407.24	2407.65	7230.9	1	1504.8	59.5	2	K.HGEVCPAGWKPGSDTIKPDVQK.S
	HsGST-MOCK_Ti_104.147	5.3094	0.3884	2407.36	2407.65	7793.5	1	1904.9	42.9	2	K.HGEVCPAGWKPGSDTIKPDVQK.S

	HsFLAG-MOCK_300mM_T	5.2741	0.4359	2407.4	2407.65	7989.4		1	1533.5	57.1	4	K.HGEVCPAGWKPGSDTIKPDVQK.S
	HsHeLa_Control-MG_Ti_20	5.0675	0.3685	2407.6	2407.65	8247.9		1	1457.9	57.1	6	K.HGEVCPAGWKPGSDTIKPDVQK.S
	Hs293FLP_Ti_306.2355.23	5.0679	0.3312	2407.81	2407.65	7154.2		1	1497.8	40.5	3	K.HGEVCPAGWKPGSDTIKPDVQK.S
	HsHeLa_Control-MG_Ti_20	5.4248	0.4064	2408.09	2407.65	8569.4		1	1767.9	40.5	3	K.HGEVCPAGWKPGSDTIKPDVQK.S
	HsFLAG-MOCK_300mM_T	5.0147	0.2616	2408.67	2407.65	7629.3		1	1638.2	41.7	2	K.HGEVCPAGWKPGSDTIKPDVQK.S
	HsFLAG-MOCK_300mM_T	4.1506	0.1762	2409.55	2407.65	6661		2	786.5	33.3	1	K.HGEVCPAGWKPGSDTIKPDVQK.S
	HsHeLa_Control-MG_Ti_20	3.9564	0.1671	1285.31	1285.44	7908.9		1	1520.8	81.8	5	K.PGSDTIKPDVQK.S
gi|29788785|ref|N	98	648	0.707	444	49671	4.9	U	tubulin, beta polypeptide [Homo sapiens]				
*	HsFLAG-Control_HeLa_S1	6.5234	0.3157	3102.49	3104.27	7959.4		1	1262.6	34.6	28	K.FWEVISDEHGIDPTGTYHGDSDLQLDR.I
*	Hs293FLP-MG_Ti_204.283	5.5919	0.2892	3102.85	3104.27	6486.5		1	572.2	27.9	4	K.FWEVISDEHGIDPTGTYHGDSDLQLDR.I
*	Hs293FLP-MG_Ti_203.297	3.9055	0.2996	3103.04	3104.27	4284.6		3	270.9	34.6	2	K.FWEVISDEHGIDPTGTYHGDSDLQLDR.I
*	HsHeLa_Control-MG_Ti_10	2.7152	0.2812	3103.1	3104.27	3161.6		4	192.7	30.8	1	K.FWEVISDEHGIDPTGTYHGDSDLQLDR.I
*	HsHeLa_Control-MG_Ti_20	5.7535	0.3132	3103.97	3104.27	5903		1	817.8	32.7	7	K.FWEVISDEHGIDPTGTYHGDSDLQLDR.I
*	HsFLAG-Control_293_Ti_1	4.7657	0.2504	3105.41	3104.27	10089.4		2	895.9	27.9	3	K.FWEVISDEHGIDPTGTYHGDSDLQLDR.I
*	HsFLAG-Control_293_Ti_1	3.2978	0.0863	3105.54	3104.27	5296.9		2	285.7	32.7	1	K.FWEVISDEHGIDPTGTYHGDSDLQLDR.I
*	HsFLAG-Control_HeLa_S1	2.6089	0.2408	1301.44	1302.43	7267.7		1	529.6	59.1	1	R.ISVYYNEATGGK.Y
*	HsFLAG-Control_293_Ti_2	2.9076	0.2466	1301.48	1302.43	6252.1		1	662.5	68.2	6	R.ISVYYNEATGGK.Y
*	HsHeLa_Control-MG_Ti_20	2.8028	0.2907	1301.6	1302.43	5328.6		1	452.5	63.6	2	R.ISVYYNEATGGK.Y
*	HsFLAG-Control_HeLa_S1	3.4511	0.3687	1301.74	1302.43	6610.2		1	978.9	72.7	23	R.ISVYYNEATGGK.Y
*	Hs283FLP_Ti_102.1523.15	3.0796	0.2118	1302.41	1302.43	4736.5		1	813.3	72.7	1	R.ISVYYNEATGGK.Y
*	HsFLAG-Control_HeLa_S1	3.8701	0.3447	1302.45	1302.43	5644.6		1	1218.5	81.8	6	R.ISVYYNEATGGK.Y
	HsF-IP-293-MG_Ti_102.233	4.2116	0.3257	1617.72	1616.87	4090.1		1	901.5	75	15	R.AILVDLEPGTMDSVR.S
	HsFLAG-Control_293_Ti_1	4.3497	0.4199	2798.44	2800.07	7089.6		1	789.7	42	2	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G
	HsFLAG-Control_Hela_Ti_1	7.086	0.3585	2798.77	2800.07	8023.8		1	2007.6	39	1	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G
	HsHeLa_Control_Ti_106.35	3.3717	0.284	2799.08	2800.07	7040.2		1	509.9	34	1	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G
	HsFLAG-Control_HeLa_NE	5.559	0.4744	2799.13	2800.07	8777.8		1	1234	44	3	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G
	Hs293FLP_Ti_306.3134.31	4.4896	0.3405	2799.39	2800.07	5985.1		1	712.5	40	3	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G
	HsFLAG-Control_HeLa_S1	5.0217	0.2644	2799.44	2800.07	9812.3		1	1983	35	4	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G
	HsFLAG-Control_Hela_Ti_1	4.9745	0.3403	2799.45	2800.07	9442		1	1330.7	46	2	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G
	Hs293FLP-MG_Ti_206.324	5.6902	0.3542	2799.53	2800.07	9458.1		1	2291.7	38	3	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G
	HsFLAG-Control_293_Ti_1	6.1007	0.3859	2799.74	2800.07	9348.5		1	3099.1	42	2	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G
	HsFLAG-Control_HeLa_S1	5.4454	0.3567	2799.89	2800.07	7677.5		1	1212.9	46	3	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G
	HsHeLa_Control-MG_Ti_20	5.2597	0.3817	2799.92	2800.07	8298.5		1	1407.9	48	8	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G
	HsFLAG-Control_HeLa_S1	4.9984	0.3992	2799.99	2800.07	8366		1	1288.2	46	5	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G
	HsHeLa_Control_Ti_106.35	5.7438	0.2886	2800.05	2800.07	8407.2		1	2280	38	3	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G
	HsFLAG-Control_HeLa_S1	6.1803	0.4125	2800.31	2800.07	9515.8		1	2575.2	39	10	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G
	Hs293FLP-MG_Ti_206.324	4.0474	0.285	2800.79	2800.07	6819.9		1	693.4	38	4	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G
	Hs293FLP_Ti_306.3122.31	5.4056	0.2637	2801.19	2800.07	8261.6		1	1963.1	38	2	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G
	HsHeLa_Control-MG_Ti_20	6.5624	0.445	2801.2	2800.07	8704.9		1	2240.6	38	7	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G
	HsFLAG-Control_HeLa_NE	6.3579	0.3994	2801.45	2800.07	8898.9		1	2491.9	40	3	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G
	HsGST-MOCK_Ti_102.286	3.2049	0.3313	1958.45	1960.15	8017.5		1	762.8	52.9	1	K.GHYTEGAELVDSVLDVVR.K
	HsFLAG-Control_HeLa_S1	4.1642	0.2955	1959.3	1960.15	8544.6		2	1215.8	38.2	2	K.GHYTEGAELVDSVLDVVR.K
	HsGST-MOCK_Ti_403.395	4.7164	0.3422	1959.33	1960.15	10548.9		1	1301.9	55.9	1	K.GHYTEGAELVDSVLDVVR.K
	HsFLAG-Control_HeLa_NE	5.3562	0.4242	1959.63	1960.15	11243.1		1	2825.8	70.6	3	K.GHYTEGAELVDSVLDVVR.K
	Hs293FLP_Ti_303.3357.33	4.1617	0.1819	1959.92	1960.15	7405		2	1468.9	42.6	6	K.GHYTEGAELVDSVLDVVR.K
	HsHeLa_Control-MG_Ti_10	6.1452	0.4266	1959.96	1960.15	8101.6		1	2856.7	79.4	5	K.GHYTEGAELVDSVLDVVR.K
	Hs293FLP-MG_Ti_205.353	4.315	0.1813	1959.98	1960.15	9417.8		1	1643	41.2	5	K.GHYTEGAELVDSVLDVVR.K
	Hs293FLP-MG_Ti_204.367	6.6846	0.431	1959.98	1960.15	10282.1		1	3961.5	82.4	8	K.GHYTEGAELVDSVLDVVR.K
	Hs293FLP_Ti_306.3198.31	6.98	0.3863	1960.01	1960.15	9148.7		1	3744.2	85.3	7	K.GHYTEGAELVDSVLDVVR.K

	HsFLAG-Control_HeLa_S1	4.5919	0.2553	1960.03	1960.15	7594.6	1	1242.3	41.2	2	K.GHYTEGAELVDSVLDVVR.K
	HsHeLa_Control-MG_Ti_10	3.5165	0.1922	1960.13	1960.15	6171.6	3	834.7	35.3	1	K.GHYTEGAELVDSVLDVVR.K
	HsHeLa_Control-MG_Ti_20	4.3353	0.2198	1960.22	1960.15	8005.9	1	1897.4	47.1	2	K.GHYTEGAELVDSVLDVVR.K
	HsFLAG-Control_HeLa_S1	5.8707	0.417	1960.53	1960.15	9914.1	1	3928.7	82.4	2	K.GHYTEGAELVDSVLDVVR.K
	HsHeLa_Control-MG_Ti_20	6.9239	0.4578	1960.6	1960.15	10283.3	1	4222.7	85.3	8	K.GHYTEGAELVDSVLDVVR.K
	HsHeLa_Control_Ti_105.38	6.5934	0.4301	1960.92	1960.15	9241.8	1	3541.4	82.4	7	K.GHYTEGAELVDSVLDVVR.K
	HsFLAG-Control_HeLa_NE	4.632	0.1653	1961.1	1960.15	7796.1	7	1433.4	44.1	1	K.GHYTEGAELVDSVLDVVR.K
	HsHeLa_Control_Ti_105.38	3.9939	0.1774	1961.13	1960.15	6245.6	2	1192.6	45.6	2	K.GHYTEGAELVDSVLDVVR.K
	HsFLAG-Control_HeLa_S1	4.764	0.2325	1961.21	1960.15	8029.8	1	1535	42.6	2	K.GHYTEGAELVDSVLDVVR.K
	HsFLAG-Control_HeLa_S1	6.9041	0.4463	1961.25	1960.15	11475.7	1	4165.7	82.4	14	K.GHYTEGAELVDSVLDVVR.K
	HsFLAG-Control_HeLa_S1	5.9828	0.4073	1961.57	1960.15	10193.9	1	3020.1	76.5	5	K.GHYTEGAELVDSVLDVVR.K
	HsGST-MOCK_Ti_102.285	4.2626	0.1599	1962	1960.15	7062.2	4	1185.6	41.2	1	K.GHYTEGAELVDSVLDVVR.K
	Hs293FLP_Ti_306.3098.30	6.1016	0.4085	2088.19	2088.33	9030.4	1	2434	72.2	2	K.GHYTEGAELVDSVLDVVRK.E
	HsHeLa_Control_Ti_106.36	2.6425	0.3564	2089.18	2088.33	10954.4	1	669	41.7	1	K.GHYTEGAELVDSVLDVVRK.E
	HsFLAG-MOCK_300mM_T	4.8098	0.3951	2089.85	2088.33	6163.4	1	1098.1	41.7	3	K.GHYTEGAELVDSVLDVVRK.E
	Hs293FLP_Ti_305.3017.30	5.121	0.3371	2090.41	2088.33	6587.3	1	1579.1	48.6	9	K.GHYTEGAELVDSVLDVVRK.E
	HsFLAG-Control_HeLa_S1	2.9498	0.2063	1077.69	1078.17	5287.5	3	749.1	85.7	5	K.IREEYPDR.I
	HsFLAG-MOCK_300mM_T	2.7654	0.1191	2380.24	2379.74	5288.7	1	385.4	44.7	2	K.IREEYPDRIMNTFSVVPSPK.V
	HsFLAG-Control_MG_293_	4.3284	0.3282	1320.01	1320.59	8983.2	1	1855	86.4	18	R.IMNTFSVVPSPK.V
	HsFLAG-Control_HeLa_S1	5.2299	0.4574	4594.42	4595.9	5984.7	1	689.3	24.3	26	K.VSDTVVEPYNATLSVHQLVENTDETYCIDNEALYDICF R.T
	HsGST-MOCK_Ti_305.408	4.8022	0.4628	2708.4	2710.04	7804.4	1	972	43.8	1	K.LTTPTYGDLNHLVSATMSGVTTCLR.F
	Hs293FLP-MG_Ti_204.386	5.4701	0.3771	2708.64	2710.04	9092.1	1	1386.9	45.8	2	K.LTTPTYGDLNHLVSATMSGVTTCLR.F
	HsF-IP-293-MG_Ti_106.26	5.1039	0.31	2708.65	2710.04	6253.5	1	929.3	45.8	6	K.LTTPTYGDLNHLVSATMSGVTTCLR.F
	Hs293FLP-MG_Ti_204.386	3.7503	0.32	2709.13	2710.04	7710.2	1	762.9	29.2	1	K.LTTPTYGDLNHLVSATMSGVTTCLR.F
	HsHeLa_Control-MG_Ti_10	4.2137	0.4906	2709.32	2710.04	6602.6	1	706.6	39.6	1	K.LTTPTYGDLNHLVSATMSGVTTCLR.F
	HsFLAG-MOCK_300mM_T	3.5898	0.1924	2709.57	2710.04	8016.1	2	734.5	28.1	1	K.LTTPTYGDLNHLVSATMSGVTTCLR.F
	HsF-IP-293-MG_Ti_106.26	3.9395	0.217	2709.94	2710.04	7857.5	1	880.7	30.2	1	K.LTTPTYGDLNHLVSATMSGVTTCLR.F
	HsHeLa3_Ti_105.3722.372	4.5547	0.4711	2710.06	2710.04	7677.4	1	1059.3	43.8	3	K.LTTPTYGDLNHLVSATMSGVTTCLR.F
	HsHeLa_Control-MG_Ti_10	4.0048	0.2452	2712.04	2710.04	8274.3	1	1108.1	33.3	1	K.LTTPTYGDLNHLVSATMSGVTTCLR.F
	HsFLAG-Control_293_Ti_2	2.3562	0.2676	1130.49	1131.28	3790.3	1	334.2	72.2	1	R.FPGQLNADLR.K
	HsFLAG-Control_HeLa_S1	3.3308	0.1729	1130.86	1131.28	4313.3	1	873.6	88.9	23	R.FPGQLNADLR.K
	HsFLAG-Control_MG_293_	3.206	0.113	1130.88	1131.28	3899.4	1	816.9	88.9	6	R.FPGQLNADLR.K
	HsFLAG-Control_HeLa_S1	2.9598	0.1628	1259.33	1259.45	6893.9	1	1452.3	90	5	R.FPGQLNADLRK.L
	HsHeLa_Control-MG_Ti_10	3.4275	0.2361	1272.73	1272.59	5940.6	2	973.4	75	2	R.KLAVNMVPFPR.L
	HsF-IP-293-MG_Ti_104.21	3.5921	0.3097	1145.56	1144.42	4625.3	1	875.9	88.9	19	K.LAVNMVPFPR.L
	HsGST-MOCK_Ti_102.257	3.0182	0.4314	1621.6	1621.94	4033.6	1	699.6	69.2	2	R.LHFFMPGFAPLTSR.G
*	HsFLAG-Control_HeLa_S1	3.7113	0.3398	1660.48	1660.91	4103.1	1	587.1	64.3	4	R.ALTVPELTQQVFDAK.N
*	HsF-IP-293-MG_Ti_102.26	4.0023	0.2995	1660.57	1660.91	3003.5	1	516.3	71.4	12	R.ALTVPELTQQVFDAK.N
*	HsFLAG-Control_HeLa_S1	3.5243	0.335	1661.25	1660.91	4187.5	1	667.9	67.9	8	R.ALTVPELTQQVFDAK.N
*	HsFLAG-Control_HeLa_S1	4.0003	0.3286	1661.47	1660.91	6963.9	2	1179.9	48.2	2	R.ALTVPELTQQVFDAK.N
*	HsFlag1P_Ti_102.3255.32	4.1345	0.2164	1661.56	1660.91	3304	1	549.2	67.9	38	R.ALTVPELTQQVFDAK.N
*	HsFLAG-Control_HeLa_S1	3.9345	0.3293	1661.69	1660.91	6050.2	1	887	48.2	1	R.ALTVPELTQQVFDAK.N
*	HsFLAG-Control_HeLa_S1	3.5036	0.1847	1663.51	1660.91	6802.9	1	1027.4	48.2	1	R.ALTVPELTQQVFDAK.N
	HsHeLa-FLAG-IP_S100_Ti	2.9555	0.2199	1068.25	1066.2	7345.1	2	1221.1	81.2	2	K.NMMAACDPR.H
	HsFLAG-Control_HeLa_NE	3.3095	0.3087	1040.83	1040.25	5846.9	1	1088.4	93.8	50	R.YLTVAAVFR.G
	HsGST-MOCK_Ti_402.200	3.2807	0.1162	1445.58	1447.6	4353.1	1	621.9	77.3	1	K.EVDEQMLNVQNK.N
	HsFLAG-Control_293_Ti_2	3.0439	0.1965	1446.48	1447.6	5427.8	1	667.1	72.7	2	K.EVDEQMLNVQNK.N
	HsHeLa_Control_Ti_102.15	2.3866	0.11	1446.59	1447.6	3600.8	3	304.9	63.6	1	K.EVDEQMLNVQNK.N

	HsFLAG-Control_MG_293_	3.1945	0.1644	1447.26	1447.6	5122.2		1	556.1	68.2	1	K.EVDEQMLNVQNK.N
	HsHeLa-FLAG-IP_S100_Ti_	4.4378	0.162	1447.32	1447.6	7508.9		6	1453	77.3	14	K.EVDEQMLNVQNK.N
	HsFLAG-Control_HeLa_S1	2.6394	0.1147	1447.42	1447.6	5226.8		1	438.1	63.6	2	K.EVDEQMLNVQNK.N
	Hs293FLP-MG_Ti_102.177	3.6404	0.1591	1447.47	1447.6	6074.7		1	1112.2	72.7	2	K.EVDEQMLNVQNK.N
	HsFLAG-Control_HeLa_S1	4.4307	0.2086	1449.29	1447.6	7304.9		1	1751.9	86.4	2	K.EVDEQMLNVQNK.N
	HsFLAG-Control_HeLa_S1	4.2481	0.345	1697.72	1697.89	5597.6		1	913.8	69.2	79	K.NSSYFVEWIPNNVK.T
	HsHeLa-FLAG-IP_S100_Ti_	2.8782	0.1885	1029.7	1029.15	5615.6		1	1184.8	87.5	8	K.TAVCDIPPR.G
*	HsGST-MOCK_Ti_403.422	5.0814	0.456	1870.76	1871.2	7723.1		1	1992.8	71.9	23	K.MAVTFIGNSTAIQELFK.R
	HsHeLa_Control-MG_Ti_10	3.5998	0.3059	1388.48	1386.61	7275		1	1173.3	80	3	K.RISEQFTAMFR.R
gi|6005814|ref|N	204	1626	0.684	465	54190	7.2	U	serine/threonine kinase 38 [Homo sapiens]				
*	HsFLAG-Control_HeLa_S1	4.9334	0.3902	2062.85	2064.26	7844.9		1	1440.9	65.6	8	K.VTLENFYSNLIAQHEER.E
*	HsFLAG-MOCK_150mM_T	4.3519	0.1851	2062.96	2064.26	4406.1		1	1017.9	50	5	K.VTLENFYSNLIAQHEER.E
*	HsFLAG-MOCK_300mM_T	5.6916	0.4795	2063.56	2064.26	7180		1	1942.3	75	12	K.VTLENFYSNLIAQHEER.E
*	HsFLAG-Control_HeLa_S1	5.14	0.429	2063.56	2064.26	8421.8		1	1218.7	62.5	17	K.VTLENFYSNLIAQHEER.E
*	HsFlag1P_Ti_105.3138.313	5.2846	0.4385	2063.58	2064.26	7655		1	1760.6	71.9	7	K.VTLENFYSNLIAQHEER.E
*	HsFLAG-Control_HeLa_NE	5.1143	0.4089	2063.66	2064.26	8101.1		1	1478.4	65.6	18	K.VTLENFYSNLIAQHEER.E
*	HsFlag1P_Ti_105.3147.314	4.0704	0.199	2063.75	2064.26	6297.5		1	1759.8	54.7	2	K.VTLENFYSNLIAQHEER.E
*	HsFLAG-Control_HeLa_S1	4.7778	0.4211	2063.79	2064.26	8072		1	1178.1	59.4	28	K.VTLENFYSNLIAQHEER.E
*	HsFLAG-Control_HeLa_S1	4.0208	0.2775	2064.01	2064.26	5360.5		2	1092.5	46.9	1	K.VTLENFYSNLIAQHEER.E
*	Hs293FLP-MG_Ti_203.327	3.6924	0.1638	2064.05	2064.26	4451.6		1	863.7	46.9	1	K.VTLENFYSNLIAQHEER.E
*	HsHeLa_Control-MG_Ti_20	4.1787	0.2334	2064.1	2064.26	5075.6		1	1025	48.4	1	K.VTLENFYSNLIAQHEER.E
*	HsF-IP-293-MG_Ti_106.24	5.4612	0.5032	2064.16	2064.26	6424.6		1	1383	68.8	20	K.VTLENFYSNLIAQHEER.E
*	HsFLAG-Control_HeLa_NE	3.9943	0.244	2064.18	2064.26	5533.6		2	1249.3	48.4	3	K.VTLENFYSNLIAQHEER.E
*	HsHeLa_Control-MG_Ti_20	5.6595	0.4541	2064.31	2064.26	7446.6		1	1578.6	68.8	6	K.VTLENFYSNLIAQHEER.E
*	HsFLAG-MOCK_300mM_T	3.6345	0.123	2064.5	2064.26	4164.5		1	916.6	46.9	1	K.VTLENFYSNLIAQHEER.E
*	HsFLAG-Control_HeLa_S1	3.9541	0.1355	2065.67	2064.26	5180.8		2	830.3	40.6	4	K.VTLENFYSNLIAQHEER.E
*	HsHeLa_Control_Ti_105.34	5.1825	0.4029	2065.87	2064.26	7053.7		1	1437.6	65.6	42	K.VTLENFYSNLIAQHEER.E
*	HsFLAG-Control_Hela_Ti_1	4.1552	0.1588	2066.04	2064.26	4343.1		1	847.5	46.9	2	K.VTLENFYSNLIAQHEER.E
*	HsFLAG-MOCK_300mM_T	4.3947	0.241	1436.4	1436.57	9062.4		1	2019.2	86.4	20	K.VMEEEGLKDEEK.R
*	HsFlag1P_Ti_102.1627.162	4.3785	0.2716	1593.28	1592.76	9261.9		1	2237.6	79.2	7	K.VMEEEGLKDEEKR.L
*	HsFlag1P_Ti_105.2528.252	3.9601	0.2971	1409.61	1408.59	6077.5		1	1286.7	81.8	11	R.TRLGLEDFESLK.V
*	HsFLAG-Control_HeLa_S1	2.4953	0.2388	1150.45	1151.3	8708.6		3	724.2	66.7	1	R.LGLEDFESLK.V
*	HsFLAG-Control_HeLa_NE	2.769	0.1711	1150.49	1151.3	9603.8		1	930.3	72.2	2	R.LGLEDFESLK.V
*	HsFlag1P_Ti_102.2890.28	2.9387	0.1798	1150.5	1151.3	8421.8		1	791	72.2	3	R.LGLEDFESLK.V
*	HsFLAG-Control_HeLa_NE	2.5409	0.106	1150.52	1151.3	7149.5		1	686.1	72.2	3	R.LGLEDFESLK.V
*	HsFLAG-MOCK_300mM_T	2.5861	0.1201	1150.52	1151.3	7006.4		4	590	66.7	2	R.LGLEDFESLK.V
*	Hs283FLP_Ti_102.2438.24	2.8714	0.1487	1150.58	1151.3	7133.1		1	704.8	72.2	2	R.LGLEDFESLK.V
*	HsFLAG-MOCK_150mM_T	2.6574	0.1761	1150.64	1151.3	8198.7		2	734.7	72.2	3	R.LGLEDFESLK.V
*	Hs293FLP-MG_Ti_102.302	3.6038	0.2182	1150.67	1151.3	5377.8		2	1025.2	88.9	5	R.LGLEDFESLK.V
*	Hs293FLP_Ti_302.2646.26	2.7967	0.1206	1150.71	1151.3	7667.1		3	719.5	72.2	2	R.LGLEDFESLK.V
*	HsHeLa_Control-MG_Ti_10	2.6701	0.1897	1150.72	1151.3	6179.3		2	571.2	72.2	3	R.LGLEDFESLK.V
*	Hs293FLP-MG_Ti_102.295	2.1544	0.1091	1150.73	1151.3	7427.9		2	581.1	66.7	1	R.LGLEDFESLK.V
*	HsHeLa_Control-MG_Ti_20	3.4627	0.1766	1151.14	1151.3	6068.1		5	1006.5	83.3	4	R.LGLEDFESLK.V
*	HsFLAG-Control_HeLa_S1	3.6234	0.1446	1151.19	1151.3	6336.9		1	1233.5	88.9	8	R.LGLEDFESLK.V
*	HsFLAG-Control_HeLa_NE	3.3148	0.2925	1151.21	1151.3	6855.7		2	1076	83.3	16	R.LGLEDFESLK.V
*	HsFLAG-Control_HeLa_NE	3.7265	0.235	1151.38	1151.3	5732.1		1	1196.7	88.9	7	R.LGLEDFESLK.V
*	HsFLAG-MOCK_300mM_T	3.4432	0.2051	1151.4	1151.3	4724.1		3	947.4	83.3	3	R.LGLEDFESLK.V
*	Hs283FLP_Ti_103.2279.22	3.1896	0.1636	1151.42	1151.3	4505.5		1	1002.3	88.9	4	R.LGLEDFESLK.V
*	Hs293FLP_Ti_302.2642.26	3.247	0.1087	1151.5	1151.3	4357.1		2	928	83.3	2	R.LGLEDFESLK.V

*	HsFLAG-MOCK_150mM_T	3.5719	0.1926	1151.52	1151.3	4955.5	1	1138.4	88.9	2	R.LGLEDFESLK.V
*	HsFLAG-Control_293_Ti_2	2.4831	0.1222	1152.61	1151.3	7451.1	2	582.4	66.7	1	R.LGLEDFESLK.V
*	HsFLAG-Control_293_Ti_2	3.42	0.2484	1152.67	1151.3	5344	3	1092.9	88.9	25	R.LGLEDFESLK.V
*	HsHeLa-FLAG-IP_S100_Ti_	3.6351	0.2162	1152.98	1151.3	4539.9	1	991.1	88.9	89	R.LGLEDFESLK.V
*	HsFlag1P_Ti_106.2849.284	4.655	0.4147	1575.8	1576.83	8723.8	1	2206.7	80.8	4	R.LGLEDFESLKVIGR.G
*	HsFLAG-Control_293_Ti_2	2.7915	0.3415	1149.57	1150.34	6569.7	1	683.8	66.7	6	K.KDTGHVYAMK.I
*	HsF-IP-293-MG_Ti_103.118	2.2643	0.2318	1021.34	1022.16	5592.7	1	744.8	68.8	3	K.DTGHVYAMK.I
*	HsHeLa-FLAG-IP_S100_Ti_	2.6361	0.1611	1022.23	1022.16	7088.3	2	899.8	87.5	1	K.DTGHVYAMK.I
*	HsFLAG-Control_HeLa_NE_	2.5583	0.2486	1023.38	1022.16	6372.7	1	792.7	68.8	7	K.DTGHVYAMK.I
*	HsFlag1P_Ti_106.2276.227	4.9294	0.4106	1654.21	1654.93	8414.1	1	2336.4	84.6	1	R.KADMLEKEQVGHIR.A
*	HsFlag1P_Ti_106.2120.212	2.5182	0.1345	1194.78	1195.32	5759.7	4	555.2	77.8	1	K.EQVGHIRAER.D
*	HsFlag1P_Ti_106.2901.290	5.0794	0.3802	1844.61	1844.12	8415.4	1	2384.2	80	6	R.AERDILVEADSLWVVK.M
*	HsFlag1P_Ti_104.3539.353	5.2372	0.2624	1486.53	1487.74	8265.5	1	2564.1	87.5	11	R.DILVEADSLWVVK.M
*	Hs283FLP_Ti_106.2641.264	2.8804	0.3221	1486.72	1487.74	9047.1	1	1340.2	70.8	1	R.DILVEADSLWVVK.M
*	HsFLAG-Control_Hela_Ti_1	2.6063	0.239	1486.77	1487.74	7414.3	1	758.7	62.5	1	R.DILVEADSLWVVK.M
*	HsFLAG-Control_HeLa_NE_	5.6598	0.2186	1487.42	1487.74	7868.5	1	2550.6	87.5	65	R.DILVEADSLWVVK.M
*	Hs283FLP_Ti_104.2787.27	5.4767	0.2557	1487.58	1487.74	6993	1	2191.4	87.5	14	R.DILVEADSLWVVK.M
	HsHeLa_Control-MG_Ti_10	2.3171	0.1532	1065.57	1066.22	6077.8	6	529.4	71.4	3	K.MFYSFQDK.L
*	HsHeLa_Control-MG_Ti_20	7.3841	0.2715	3619.21	3620.05	10348.7	1	3165.6	37.5	16	K.KDTLTEEETQFYIAETVLAIDSIHQLGFIHR.D
*	HsFLAG-MOCK_300mM_T	6.2328	0.3063	3491.37	3491.88	7147.5	1	962	27.6	35	K.DTLTEEETQFYIAETVLAIDSIHQLGFIHR.D
*	HsFLAG-Control_HeLa_S1	2.2427	0.1847	1370.45	1371.57	7138.4	3	535	59.1	1	R.DIKPDNLLLDSK.G
*	HsFLAG-Control_293_Ti_2	2.4949	0.2532	1370.49	1371.57	6485.7	1	678.9	63.6	2	R.DIKPDNLLLDSK.G
*	HsFLAG-Control_HeLa_NE_	2.9936	0.243	1370.66	1371.57	6289.6	1	814.8	68.2	2	R.DIKPDNLLLDSK.G
*	HsFLAG-Control_HeLa_NE_	2.8242	0.2634	1370.71	1371.57	7289.9	1	757.9	63.6	2	R.DIKPDNLLLDSK.G
*	HsFLAG-Control_HeLa_NE_	2.4132	0.2248	1370.72	1371.57	7508.5	1	722.9	63.6	2	R.DIKPDNLLLDSK.G
*	HsHeLa_Control-MG_Ti_10	2.0152	0.1916	1370.74	1371.57	5548.3	3	490.7	54.5	1	R.DIKPDNLLLDSK.G
*	HsFLAG-Control_293_Ti_2	3.4334	0.1844	1371.08	1371.57	3413.3	2	502.1	72.7	31	R.DIKPDNLLLDSK.G
*	HsFlag1P_Ti_105.2216.221	3.2861	0.169	1371.38	1371.57	3851.5	2	810.7	81.8	5	R.DIKPDNLLLDSK.G
*	HsHeLa_Control-MG_Ti_20	3.3575	0.1683	1371.52	1371.57	3777.7	1	584.4	72.7	13	R.DIKPDNLLLDSK.G
*	HsFlag1P_Ti_102.2283.228	2.8374	0.1057	1371.64	1371.57	4945.8	1	648.1	68.2	2	R.DIKPDNLLLDSK.G
*	HsHeLa_Control_Ti_103.21	2.8054	0.1729	1371.67	1371.57	4863.6	1	601.8	68.2	2	R.DIKPDNLLLDSK.G
*	HsFLAG-Control_HeLa_S1	3.166	0.1906	1371.7	1371.57	3575.3	1	456	68.2	15	R.DIKPDNLLLDSK.G
*	HsFLAG-Control_HeLa_NE_	3.5379	0.1499	1371.7	1371.57	3841.1	1	721.5	77.3	11	R.DIKPDNLLLDSK.G
*	HsFLAG-Control_HeLa_NE_	3.3765	0.1747	1371.76	1371.57	3451.3	1	666.8	77.3	4	R.DIKPDNLLLDSK.G
*	HsFLAG-Control_Hela_Ti_1	2.8272	0.1721	1371.78	1371.57	3420.5	1	455.6	68.2	2	R.DIKPDNLLLDSK.G
*	HsFLAG-Control_HeLa_NE_	3.6515	0.2182	1372.69	1371.57	3441.8	1	606.2	77.3	5	R.DIKPDNLLLDSK.G
*	HsFlag1P_Ti_106.2416.241	4.0489	0.3299	1793.46	1793.07	6149.6	1	861.2	60	2	R.DIKPDNLLLDSKGHVK.L
*	HsFLAG-Control_HeLa_NE_	2.7142	0.1639	1014.24	1015.15	8054.2	1	786.1	75	7	K.PDNLLLDSK.G
	HsFLAG-Control_293_Ti_2	2.6151	0.2965	1210.33	1211.37	5258.2	1	695.6	70	4	K.LSDFGLCTGLK.K
	HsFLAG-Control_HeLa_NE_	2.5471	0.2723	1210.38	1211.37	5294.4	1	605	65	5	K.LSDFGLCTGLK.K
	HsHeLa_Control-MG_Ti_20	2.5733	0.2852	1210.38	1211.37	4203.2	1	377.7	55	2	K.LSDFGLCTGLK.K
	HsFLAG-Control_MG_293_	2.5821	0.3547	1210.39	1211.37	5238.7	1	636.4	65	4	K.LSDFGLCTGLK.K
	Hs293FLP_TREX_Ti_102.2	2.6622	0.2892	1210.4	1211.37	4466	1	478.7	60	2	K.LSDFGLCTGLK.K
	Hs293FLP-MG_Ti_202.251	2.3237	0.2827	1210.45	1211.37	4990	1	490.7	60	1	K.LSDFGLCTGLK.K
	HsFLAG-MOCK_300mM_T	2.6108	0.361	1210.47	1211.37	4601.5	1	551.2	65	3	K.LSDFGLCTGLK.K
	HsF-IP-293-MG_Ti_102.197	2.4689	0.2527	1210.49	1211.37	4535	1	547.2	65	2	K.LSDFGLCTGLK.K
	HsHeLa-FLAG-IP_S100_Ti_	1.8467	0.1459	1210.53	1211.37	4890.3	1	392	55	1	K.LSDFGLCTGLK.K
	Hs283FLP_Ti_102.2003.20	2.6768	0.2557	1210.55	1211.37	4679.7	1	568.8	65	2	K.LSDFGLCTGLK.K
	HsFLAG-Control_HeLa_NE_	2.5274	0.3029	1210.58	1211.37	5048.5	1	631.1	70	2	K.LSDFGLCTGLK.K

	HsFLAG-Control_HeLa_S1	2.3076	0.2541	1210.58	1211.37	5353.8	2	480.4	60	2	K.LSDFGLCTGLK.K
	HsFLAG-Control_Hela_Ti_1	2.1004	0.2798	1210.61	1211.37	5239.4	4	310.3	50	2	K.LSDFGLCTGLK.K
	HsHeLa_Control_Ti_103.23	2.6092	0.2765	1210.62	1211.37	4162.2	1	422.2	60	2	K.LSDFGLCTGLK.K
	HsFLAG-MOCK_150mM_T	2.5559	0.2977	1210.63	1211.37	4371.3	1	557.2	65	2	K.LSDFGLCTGLK.K
	Hs293FLP_Ti_302.2103.21	2.4897	0.2237	1210.7	1211.37	4081.1	1	469.5	60	2	K.LSDFGLCTGLK.K
	HsHeLa_Control-MG_Ti_10	2.4806	0.2699	1210.72	1211.37	3999.7	1	436.9	60	2	K.LSDFGLCTGLK.K
	Hs293FLP-MG_Ti_102.243	2.2777	0.1812	1210.73	1211.37	4149.3	2	375.8	55	2	K.LSDFGLCTGLK.K
	HsFLAG-Control_293_Ti_2	4.0226	0.2724	1211.17	1211.37	6036.8	1	1564.9	90	3	K.LSDFGLCTGLK.K
	HsFLAG-Control_HeLa_NE	3.8264	0.3062	1211.23	1211.37	5545	2	1300	85	9	K.LSDFGLCTGLK.K
	HsFLAG-Control_HeLa_NE	3.9803	0.2422	1211.24	1211.37	6010.2	1	1532.1	90	6	K.LSDFGLCTGLK.K
	Hs293FLP_TREX_Ti_102.2	3.8489	0.3113	1211.25	1211.37	5383.6	1	1329.4	85	4	K.LSDFGLCTGLK.K
	HsFLAG-Control_HeLa_S1	4.022	0.2854	1211.26	1211.37	5874	2	1516.2	90	11	K.LSDFGLCTGLK.K
	HsHeLa-FLAG-IP_S100_Ti_	4.1443	0.3235	1211.29	1211.37	5663.3	1	1567.1	90	52	K.LSDFGLCTGLK.K
	HsF-IP-293-MG_Ti_102.19	3.8997	0.3475	1211.31	1211.37	5359.9	1	1521.9	90	4	K.LSDFGLCTGLK.K
	Hs293FLP-MG_Ti_202.252	4.1153	0.3165	1211.32	1211.37	6077.1	1	1604.4	90	1	K.LSDFGLCTGLK.K
	HsFLAG-Control_HeLa_NE	4.0494	0.2091	1211.32	1211.37	5901.1	1	1581.2	90	2	K.LSDFGLCTGLK.K
	HsFLAG-MOCK_150mM_T	3.9522	0.2989	1211.44	1211.37	5985.5	1	1555.7	90	2	K.LSDFGLCTGLK.K
	HsHeLa_Control-MG_Ti_20	3.9398	0.2841	1211.46	1211.37	7189.5	1	1564.6	85	2	K.LSDFGLCTGLK.K
	Hs283FLP_Ti_102.2001.20	4.0562	0.3185	1211.48	1211.37	5413.7	1	1513.2	90	2	K.LSDFGLCTGLK.K
	HsFlag1P_Ti_103.2474.247	2.3605	0.2426	1211.55	1211.37	5138.1	1	478.4	60	3	K.LSDFGLCTGLK.K
	HsHeLa_Control-MG_Ti_10	3.9558	0.3415	1211.65	1211.37	5209.5	1	1430.3	90	2	K.LSDFGLCTGLK.K
	HsHeLa_Control_Ti_103.23	3.7085	0.2509	1212.02	1211.37	5631.6	1	1225.4	85	2	K.LSDFGLCTGLK.K
	HsFlag1P_Ti_102.2452.245	3.9867	0.2505	1212.23	1211.37	5494	1	1425.2	90	6	K.LSDFGLCTGLK.K
	HsFLAG-MOCK_300mM_T	3.9448	0.2963	1212.46	1211.37	5598.4	1	1438.9	90	3	K.LSDFGLCTGLK.K
	HsFLAG-Control_MG_293_	3.8678	0.3049	1212.47	1211.37	6343.4	1	1641.9	90	5	K.LSDFGLCTGLK.K
	Hs293FLP-MG_Ti_102.242	3.5428	0.1193	1212.59	1211.37	5107.3	1	1225.1	85	3	K.LSDFGLCTGLK.K
	Hs293FLP_Ti_302.2102.21	3.8678	0.244	1212.73	1211.37	5175.9	1	1388.9	90	4	K.LSDFGLCTGLK.K
	HsFLAG-MOCK_300mM_T	2.772	0.2874	1338.65	1339.54	5388.3	1	426.2	59.1	1	K.LSDFGLCTGLKK.A
	HsFlag1P_Ti_106.2458.245	2.8721	0.312	1338.78	1339.54	5464	1	449.3	59.1	1	K.LSDFGLCTGLKK.A
	HsFlag1P_Ti_106.2456.245	3.7584	0.3281	1339.14	1339.54	6523.9	1	1077.5	81.8	6	K.LSDFGLCTGLKK.A
	HsFLAG-MOCK_300mM_T	3.1443	0.2011	1339.66	1339.54	6422.2	1	903.1	77.3	7	K.LSDFGLCTGLKK.A
	HsFlag1P_Ti_106.2201.220	3.0143	0.24	1079.47	1080.19	7686.1	3	798.5	78.6	1	K.AHRTEFYR.N
*	HsFLAG-MOCK_300mM_T	5.0208	0.4079	2093.81	2095.29	5022.1	1	1162	67.6	4	R.NLNHSLPSDFTFQNMNSK.R
*	HsFlag1P_Ti_106.2554.255	4.9427	0.4438	2094.2	2095.29	4451.5	1	1100.9	70.6	6	R.NLNHSLPSDFTFQNMNSK.R
*	HsFLAG-MOCK_150mM_T	4.821	0.4031	2094.66	2095.29	4434.7	1	892.7	64.7	10	R.NLNHSLPSDFTFQNMNSK.R
*	HsHeLa_Control-MG_Ti_10	4.5128	0.4003	2095.02	2095.29	3969.5	1	805.5	64.7	3	R.NLNHSLPSDFTFQNMNSK.R
*	HsHeLa_Control-MG_Ti_10	4.3607	0.3463	2095.19	2095.29	7462.7	1	1542.5	44.1	2	R.NLNHSLPSDFTFQNMNSK.R
*	Hs293FLP-MG_Ti_205.226	5.3089	0.3427	2095.23	2095.29	7769.5	1	1316.8	41.2	1	R.NLNHSLPSDFTFQNMNSK.R
*	HsFLAG-MOCK_300mM_T	5.6252	0.3347	2095.29	2095.29	8235	1	1663.1	45.6	1	R.NLNHSLPSDFTFQNMNSK.R
*	HsFLAG-MOCK_150mM_T	4.6399	0.3646	2095.35	2095.29	9343.2	2	1342.9	41.2	1	R.NLNHSLPSDFTFQNMNSK.R
*	HsFLAG-Control_293_Ti_2	5.4474	0.4371	2095.42	2095.29	4796.3	1	1109.2	67.6	8	R.NLNHSLPSDFTFQNMNSK.R
*	HsHeLa_Control_Ti_105.27	4.1661	0.233	2095.47	2095.29	8825.1	1	1968.7	44.1	2	R.NLNHSLPSDFTFQNMNSK.R
*	HsFlag1P_Ti_106.2949.294	3.2234	0.3182	2777.6	2779.14	5870.1	1	388.3	35.4	2	R.QLAFSTVGTPDYIAPEVFMQTGYNK.L
*	HsFlag1P_Ti_106.2950.295	4.2259	0.3193	2778.05	2779.14	9184	1	995.6	31.2	2	R.QLAFSTVGTPDYIAPEVFMQTGYNK.L
*	HsFLAG-Control_293_Ti_2	3.3016	0.2179	2779.57	2779.14	5518.4	1	205.4	27.1	2	R.QLAFSTVGTPDYIAPEVFMQTGYNK.L
*	HsFLAG-Control_293_Ti_2	5.1235	0.3577	2780.83	2779.14	9865	1	1762.4	35.4	1	R.QLAFSTVGTPDYIAPEVFMQTGYNK.L
*	HsFlag1P_Ti_106.2769.276	4.2104	0.4544	2245.51	2246.63	4918.2	1	742.5	55.6	3	K.VMNWKETLTFPPEVPISEK.A
*	HsFLAG-Control_Hela_Ti_1	2.4355	0.283	1586.67	1587.81	3936.9	1	292.7	53.8	5	K.ETLTFPPEVPISEK.A
*	HsFLAG-Control_HeLa_NE	3.6567	0.1966	1586.7	1587.81	3340.1	1	377.8	61.5	8	K.ETLTFPPEVPISEK.A

*	HsFLAG-MOCK_300mM_T	2.5034	0.2891	1587.48	1587.81	4148	2	225.8	50	1	K.ETLTFPPEVPISEK.A
*	HsFlag1P_Ti_102.2859.285	3.7279	0.131	1587.54	1587.81	3283.6	1	453.6	65.4	4	K.ETLTFPPEVPISEK.A
*	HsFLAG-Control_HeLa_NE	2.4856	0.1175	1587.65	1587.81	4488.8	4	245.4	46.2	2	K.ETLTFPPEVPISEK.A
*	HsHeLa-FLAG-IP_S100_Ti	3.6116	0.1325	1588.07	1587.81	3437.3	2	435.1	65.4	111	K.ETLTFPPEVPISEK.A
*	HsFLAG-Control_293_Ti_2	3.6365	0.2172	1588.25	1587.81	3828.4	1	663.4	73.1	21	K.ETLTFPPEVPISEK.A
*	HsFLAG-Control_293_Ti_2	2.0557	0.1367	1223.42	1224.25	7285.9	4	370.4	64.3	1	R.FCCEWEHR.I
*	HsFLAG-Control_293_Ti_2	2.8071	0.1854	1225.25	1224.25	5488.4	1	947.6	92.9	4	R.FCCEWEHR.I
*	HsFLAG-MOCK_300mM_T	3.0809	0.2383	1226.81	1224.25	5239.4	1	977.3	92.9	14	R.FCCEWEHR.I
*	HsFLAG-Control_Hela_Ti_1	2.3225	0.2183	1012.39	1013.18	4619	1	519.1	66.7	1	R.IGAPGVEEIK.S
*	HsF-IP-293-MG_Ti_102.15	1.8868	0.1867	1012.4	1013.18	4550.1	2	427.6	61.1	1	R.IGAPGVEEIK.S
*	HsFLAG-Control_HeLa_S1	2.0988	0.1736	1012.42	1013.18	5624.9	3	427.1	61.1	1	R.IGAPGVEEIK.S
*	HsFLAG-Control_293_Ti_2	2.3254	0.1615	1012.44	1013.18	5051.2	1	632.6	72.2	2	R.IGAPGVEEIK.S
*	HsFLAG-MOCK_300mM_T	1.9512	0.176	1012.44	1013.18	4680.4	1	505	66.7	1	R.IGAPGVEEIK.S
*	HsFLAG-Control_HeLa_NE	2.0855	0.1684	1012.45	1013.18	5219.8	1	651.6	72.2	3	R.IGAPGVEEIK.S
*	HsF-IP-293_Ti_103.1481.1	2.0787	0.1626	1012.46	1013.18	4576.2	1	514.1	66.7	1	R.IGAPGVEEIK.S
*	HsFLAG-Control_HeLa_S1	2.2144	0.1625	1012.48	1013.18	4236.2	9	350	55.6	1	R.IGAPGVEEIK.S
*	HsFLAG-Control_HeLa_S1	2.5374	0.2182	1012.48	1013.18	4482	1	480.7	66.7	1	R.IGAPGVEEIK.S
*	Hs293FLP-MG_Ti_302.140	2.0867	0.1935	1012.49	1013.18	4457.5	7	349.7	55.6	1	R.IGAPGVEEIK.S
*	HsFLAG-Control_HeLa_NE	2.4087	0.1421	1012.49	1013.18	4878.2	1	511.8	66.7	2	R.IGAPGVEEIK.S
*	HsHeLa-FLAG-IP_S100_Ti	1.8813	0.1292	1012.51	1013.18	3880.4	1	376.5	61.1	1	R.IGAPGVEEIK.S
*	HsFLAG-Control_MG_293_	2.2337	0.1937	1012.54	1013.18	4767.6	1	492.8	66.7	2	R.IGAPGVEEIK.S
*	HsFLAG-Control_HeLa_NE	2.2722	0.2151	1012.56	1013.18	4103.6	8	398.4	61.1	2	R.IGAPGVEEIK.S
*	HsFLAG-Control_HeLa_S1	2.5211	0.2113	1012.56	1013.18	5112.3	2	456.4	61.1	2	R.IGAPGVEEIK.S
*	HsHelaFlag1P_Ti_102.152	2.2821	0.2326	1012.63	1013.18	3927.9	1	449.7	61.1	2	R.IGAPGVEEIK.S
*	HsFLAG-Control_HeLa_NE	2.4581	0.1755	1012.71	1013.18	5184.8	1	429.8	61.1	1	R.IGAPGVEEIK.S
*	Hs283FLP_Ti_102.1517.15	2.3896	0.2159	1012.74	1013.18	4582.6	1	507.4	66.7	1	R.IGAPGVEEIK.S
*	HsFLAG-MOCK_150mM_T	3.3017	0.3097	1013.11	1013.18	3291.3	1	953.8	94.4	5	R.IGAPGVEEIK.S
*	HsFLAG-Control_HeLa_NE	3.3913	0.299	1013.22	1013.18	3885.4	1	942.2	88.9	4	R.IGAPGVEEIK.S
*	HsFLAG-Control_HeLa_S1	3.2374	0.272	1013.24	1013.18	4099.3	1	906.8	88.9	3	R.IGAPGVEEIK.S
*	HsFLAG-Control_293_Ti_2	3.2737	0.3126	1013.27	1013.18	4114.8	1	1114.5	94.4	2	R.IGAPGVEEIK.S
*	Hs293FLP_TREX_Ti_102.1	3.3545	0.331	1013.29	1013.18	3234.2	1	919.9	94.4	3	R.IGAPGVEEIK.S
*	HsFLAG-Control_HeLa_NE	3.2549	0.3165	1013.3	1013.18	4312	1	961.2	88.9	2	R.IGAPGVEEIK.S
*	HsFLAG-Control_MG_293_	3.4436	0.3071	1013.32	1013.18	3937.6	1	813.8	83.3	1	R.IGAPGVEEIK.S
*	HsF-IP-293_Ti_103.1480.1	3.2435	0.2673	1013.32	1013.18	3051.8	1	916.3	94.4	3	R.IGAPGVEEIK.S
*	HsFLAG-Control_Hela_Ti_1	3.3428	0.2726	1013.35	1013.18	3331.3	1	743.7	83.3	2	R.IGAPGVEEIK.S
*	HsFLAG-MOCK_300mM_T	3.5317	0.2917	1013.35	1013.18	3439.3	1	954.9	94.4	4	R.IGAPGVEEIK.S
*	HsHeLa-FLAG-IP_S100_Ti	3.3198	0.2995	1013.36	1013.18	3303.7	1	835.6	88.9	14	R.IGAPGVEEIK.S
*	HsHelaFlag1P_Ti_102.153	2.8178	0.3099	1013.43	1013.18	2897.8	1	646.8	83.3	2	R.IGAPGVEEIK.S
*	HsFLAG-Control_HeLa_S1	3.072	0.2911	1013.43	1013.18	4136.9	1	740.5	83.3	2	R.IGAPGVEEIK.S
*	HsFLAG-Control_HeLa_NE	3.5715	0.2865	1013.47	1013.18	4057.1	1	1084.9	94.4	23	R.IGAPGVEEIK.S
*	HsFLAG-Control_HeLa_NE	3.2599	0.234	1013.67	1013.18	4009.3	1	916.2	88.9	2	R.IGAPGVEEIK.S
*	HsFLAG-Control_HeLa_S1	3.3693	0.3001	1014.49	1013.18	4368.1	1	890.7	88.9	2	R.IGAPGVEEIK.S
*	HsF-IP-293-MG_Ti_102.15	3.235	0.3032	1014.57	1013.18	3017	1	777.1	88.9	2	R.IGAPGVEEIK.S
*	HsFLAG-Control_HeLa_NE	3.6024	0.2732	1723.44	1723.84	5149.2	1	792.3	46.2	1	K.SNSFFEGVDWEHIR.E
*	HsFlag1P_Ti_103.3074.307	4.517	0.4319	1723.48	1723.84	6566.9	1	1642	80.8	51	K.SNSFFEGVDWEHIR.E
*	HsFLAG-Control_HeLa_S1	4.2447	0.4356	1723.61	1723.84	7136.3	1	1528.6	76.9	7	K.SNSFFEGVDWEHIR.E
*	HsFLAG-MOCK_300mM_T	4.3497	0.4512	1723.75	1723.84	6862.8	1	1515.4	76.9	44	K.SNSFFEGVDWEHIR.E
*	HsFLAG-Control_HeLa_S1	3.5274	0.3246	1723.86	1723.84	5442.8	1	821.6	46.2	1	K.SNSFFEGVDWEHIR.E
*	HsFLAG-Control_HeLa_S1	4.3004	0.3587	1724.07	1723.84	6615.4	1	1144.9	73.1	10	K.SNSFFEGVDWEHIR.E

*	HsFLAG-Control_HeLa_S1	3.5031	0.2014	1724.8	1723.84	6102		2	723.6	42.3	1	K.SNSFFEGVDWEHIR.E
*	HsFlag1P_Ti_105.2022.202	2.3156	0.1725	1226.58	1227.45	2922.3		1	282.2	65	1	R.ERPAAISIEIK.S
*	HsFLAG-Control_HeLa_S1	2.2275	0.1785	1226.63	1227.45	3366.2		1	368.5	70	1	R.ERPAAISIEIK.S
*	HsFLAG-Control_HeLa_NE	2.4001	0.205	1226.64	1227.45	3912.9		8	297.3	60	2	R.ERPAAISIEIK.S
*	HsFLAG-MOCK_300mM_T	2.3409	0.1904	1226.7	1227.45	2954.1		1	337.5	70	2	R.ERPAAISIEIK.S
*	HsFLAG-Control_HeLa_S1	3.1836	0.1437	1227.47	1227.45	5644.3		4	836	80	6	R.ERPAAISIEIK.S
*	HsFLAG-Control_HeLa_NE	3.404	0.1655	1227.64	1227.45	5847.1		4	789.7	75	4	R.ERPAAISIEIK.S
*	HsFLAG-Control_HeLa_NE	2.9378	0.1563	1227.7	1227.45	3398.1		1	365.6	70	1	R.ERPAAISIEIK.S
*	HsFLAG-MOCK_150mM_T	3.3454	0.1913	1227.83	1227.45	4908.3		7	723.2	75	6	R.ERPAAISIEIK.S
*	HsFlag1P_Ti_105.2021.202	3.0319	0.1382	1228.65	1227.45	5303.5		3	763.6	80	5	R.ERPAAISIEIK.S
*	Hs283FLP_Ti_104.1552.15	3.0893	0.1368	1228.72	1227.45	4596.8		5	734.3	80	17	R.ERPAAISIEIK.S
*	HsFLAG-Control_HeLa_NE	3.1797	0.3476	2072.48	2073.17	7106.4		5	357.9	38.2	1	K.SIDDTSNFDEFPESDILK.P
*	HsFLAG-Control_293_Ti_2	6.0631	0.4272	3613.27	3614.81	9910.5		1	1346.4	28.2	196	K.SIDDTSNFDEFPESDILKPTVATSNHPETDYK.N
*	HsFlag1P_Ti_103.2789.278	5.6454	0.4279	3855.47	3857.09	10749.3		1	1649.2	27.3	3	K.SIDDTSNFDEFPESDILKPTVATSNHPETDYKNK.D
*	HsFLAG-MOCK_300mM_T	4.518	0.2905	1590.76	1591.81	5924.4		1	1335.9	81.8	30	K.NKDWVFINYTYK.R
*	HsFLAG-Control_HeLa_NE	1.9742	0.1527	949.47	950.085	2705.8		4	271	71.4	1	K.RFEGLTAR.G
*	HsFLAG-Control_HeLa_NE	3.3945	0.2032	950.31	950.085	8107.4		3	1154.5	92.9	7	K.RFEGLTAR.G
*	HsHeLa_Control-MG_Ti_10	3.5432	0.1908	950.77	950.085	7704.4		1	1521.3	100	35	K.RFEGLTAR.G
gi|4757756|ref|N	26	85	0.684	339	38604	7.8	U	annexin A2 isoform 2 [Homo sapiens]				
gi|50845388|ref|N	26	85	0.65	357	40411	8.4	U	annexin A2 isoform 1 [Homo sapiens]				
gi|50845386|ref|N	26	85	0.684	339	38604	7.8	U	annexin A2 isoform 2 [Homo sapiens]				
	HsFLAG-MOCK_300mM_T	4.268	0.4276	1845.98	1846	3638.2		1	578.7	55.9	5	K.LSLEGDHSTPPSAYGSVK.A
	HsFLAG-MOCK_300mM_T	4.2043	0.3048	2155.9	2156.36	8075.5		1	1062.5	50	11	K.AYTNFDAERDALNIETAIK.T
	HsHeLa3_Ti_104.3283.328	4.825	0.3095	1543.18	1543.76	8832.7		1	2037.6	76.9	13	K.GVDEVTIVNILTNR.S
	HsHeLa3_Ti_105.3252.325	2.433	0.3352	1543.78	1543.76	4183.5		1	350.4	57.7	1	K.GVDEVTIVNILTNR.S
	HsFLAG-MOCK_300mM_T	4.5115	0.3113	1669.25	1668.81	5713.7		1	1014.8	65.4	2	R.SNAQRQDIAFAYQR.R
	HsHeLa_Control-MG_Ti_20	4.4167	0.4638	1651.48	1651.99	7356.8		1	1398.8	70	1	K.SALSGHLETVILGLLK.T
	HsHeLa3_Ti_106.3094.309	5.3085	0.3059	1652.2	1651.99	7224.2		1	1505.9	66.7	2	K.SALSGHLETVILGLLK.T
	HsFLAG-MOCK_300mM_T	5.2665	0.3729	1653.51	1651.99	6072.3		1	1291.4	66.7	4	K.SALSGHLETVILGLLK.T
	HsFLAG-MOCK_300mM_T	3.7196	0.2901	1653.62	1651.99	4379.5		4	647.2	45	1	K.SALSGHLETVILGLLK.T
	HsHeLa3_Ti_106.3103.310	3.6224	0.2925	1654.15	1651.99	4328.2		2	705.3	43.3	1	K.SALSGHLETVILGLLK.T
	HsHeLa3_Ti_102.1502.150	2.8318	0.2667	1222.62	1223.33	4581.5		2	346.8	65	2	K.TPAQYDASELK.A
	HsHeLa3_Ti_102.1507.150	3.743	0.2367	1223.64	1223.33	4641.9		1	997.9	85	1	K.TPAQYDASELK.A
	HsHeLa3_Ti_103.3348.335	4.5892	0.3586	1779.68	1778.92	8304.4		1	1140.3	56.7	13	K.GLGTDEDSLIEIICSR.T
	HsHeLa3_Ti_103.1402.140	3.7777	0.1216	1246.49	1245.34	5277.9		8	873.8	83.3	2	R.TNQELQEINR.V
	HsHeLa3_Ti_103.1787.178	2.6367	0.2559	1355.51	1354.46	5327.2		1	886.9	72.7	1	K.DIISDTSGDFRK.L
	HsGST-MOCK_Ti_102.183	4.0785	0.3124	2066.51	2066.19	6064		1	801.8	55.9	1	R.RAEDGSVIDYELIDQDAR.D
	HsGST-MOCK_Ti_302.244	4.3545	0.2487	1909.12	1910	5571.9		1	943.8	65.6	6	R.AEDGSVIDYELIDQDAR.D
	HsHeLa3_Ti_102.1538.153	1.8449	0.1443	880.77	880.973	5062.1		9	550.8	71.4	1	R.DLYDAGVK.R
	HsHeLa3_Ti_103.2136.213	2.5317	0.0893	1037.22	1036.23	3553.3		4	488.6	78.6	1	K.WISIMTER.S
	HsHeLa3_Ti_103.2923.292	3.4501	0.2687	1463	1461.63	5905.1		1	1002.5	77.3	3	K.SYSPYDMLESIR.K
	HsGST-MOCK_Ti_403.483	5.0793	0.3331	1977.98	1977.19	8364.7		1	1635.2	65.6	6	K.GDLENAFLNLVQCIQNK.P
	HsGST-MOCK_Ti_103.441	3.5664	0.1119	3577.16	3578.04	7791.8		1	499.7	23.3	1	K.GDLENAFLNLVQCIQNKPLYFADRLYDSMK.G
	HsHeLa3_Ti_103.2026.202	2.6086	0.286	1421.61	1422.58	5420.1		1	626.2	70	2	K.SLYYYIQQDTK.G
	HsHeLa3_Ti_103.2027.202	4.2236	0.2887	1424.6	1422.58	7304.7		1	1586.8	85	2	K.SLYYYIQQDTK.G
	HsFLAG-MOCK_300mM_T	2.8202	0.3575	2014.53	2014.2	5215.9		1	535.8	60	1	K.SLYYYIQQDTKGDYQK.A
	HsHeLa3_Ti_102.2329.232	1.9477	0.2948	1096.47	1097.18	6430.5		3	617.9	61.1	1	K.ALLYLCGGDD.-
gi|13699824|ref|N	236	1845	0.671	1056	119159	5.6	U	kinesin family member 11 [Homo sapiens]				
*	Hs293FLP_Ti_306.2367.23	2.7675	0.1956	1164.66	1163.29	4415.4		7	476.6	75	8	R.CRPFNLAER.K

*	HsHeLa_Control-MG_Ti_20	4.2132	0.3683	1570.69	1569.72	4993.6	1	940.3	73.1	2	R.KASAHSIVECDPVR.K
*	HsFLAG-Control_293_Ti_2	3.048	0.3599	1440.3	1441.55	6141.6	1	430.8	54.2	2	K.ASAHSIVECDPVR.K
*	HsFLAG-Control_293_Ti_2	4.0562	0.3892	1441	1441.55	8686	1	1467.3	70.8	8	K.ASAHSIVECDPVR.K
*	Hs293FLP_Ti_303.1390.13	3.9637	0.4261	1441.87	1441.55	7211.3	1	1125.6	66.7	4	K.ASAHSIVECDPVR.K
*	HsHeLa_Control-MG_Ti_20	3.7186	0.3774	1569.42	1569.72	7537.4	1	906.7	61.5	19	K.ASAHSIVECDPVRK.E
*	Hs293FLP_Ti_304.1395.13	3.5406	0.3469	1570.28	1569.72	5882.6	1	738.9	42.3	1	K.ASAHSIVECDPVRK.E
*	Hs293FLP-MG_Ti_105.141	3.6323	0.2996	1570.45	1569.72	5713	1	884.7	65.4	28	K.ASAHSIVECDPVRK.E
*	HsF-IP-293_Ti_206.2508.2	3.7693	0.3706	1468.6	1468.66	5843.3	1	927.6	75	13	K.TYTFDMVFGASTK.Q
*	Hs293FLP-MG_Ti_203.493	4.3549	0.5216	3094.99	3095.47	8627.9	1	1052.2	40.7	2	R.SVVCPILDEVIMGYNCTIFAYGQTGTGK.T
*	HsF-IP-293-MG_Ti_106.28	3.8623	0.2042	3095.09	3095.47	9849.1	3	520.4	22.2	1	R.SVVCPILDEVIMGYNCTIFAYGQTGTGK.T
*	Hs293FLP-MG_Ti_204.459	5.9418	0.4457	3096.02	3095.47	10407.3	1	2080	32.4	6	R.SVVCPILDEVIMGYNCTIFAYGQTGTGK.T
*	HsFLAG-MOCK_300mM_T	3.969	0.3191	3169.22	3169.45	7275.8	1	851.8	29.8	3	K.TFTMEGERSPNEEYTWEEDPLAGIIPR.T
*	HsFLAG-Control_293_Ti_2	4.0082	0.38	2216.26	2217.4	8365.8	1	1473	38.9	4	R.SPNEEYTWEEDPLAGIIPR.T
*	HsHeLa_Control-MG_Ti_20	4.5917	0.29	2217.56	2217.4	7651.2	1	1477.9	41.7	1	R.SPNEEYTWEEDPLAGIIPR.T
*	HsFLAG-Control_293_Ti_2	6.1181	0.4799	2217.85	2217.4	7752.3	1	2042.4	69.4	92	R.SPNEEYTWEEDPLAGIIPR.T
*	HsHeLa_Control-MG_Ti_20	5.7373	0.4912	2218.12	2217.4	8885.8	1	2058.9	66.7	23	R.SPNEEYTWEEDPLAGIIPR.T
*	HsF-IP-293-MG_Ti_102.33	5.5157	0.4774	2219.72	2217.4	8897.4	1	1457.9	58.3	26	R.SPNEEYTWEEDPLAGIIPR.T
*	HsFLAG-Control_293_Ti_2	2.199	0.1448	1015.42	1016.19	4753.3	6	494	71.4	2	R.TLHQIFEK.L
*	HsFLAG-Control_MG_293_	2.1243	0.1608	1015.47	1016.19	4995	2	400.5	64.3	1	R.TLHQIFEK.L
*	Hs293FLP-MG_Ti_205.164	2.1995	0.1159	1015.49	1016.19	5937.6	3	524.6	71.4	1	R.TLHQIFEK.L
*	Hs283FLP_Ti_105.1401.14	1.8289	0.1237	1015.52	1016.19	5187.7	9	436.3	64.3	1	R.TLHQIFEK.L
*	HsF-IP-293-MG_Ti_104.15	2.095	0.1216	1015.52	1016.19	5008.8	3	422.3	64.3	2	R.TLHQIFEK.L
*	Hs293FLP_Ti_305.1501.15	2.2159	0.1357	1015.63	1016.19	4792.3	6	498.4	71.4	3	R.TLHQIFEK.L
*	HsHeLa_Control_Ti_106.27	2.19	0.1693	1015.89	1016.19	4875	7	489.6	71.4	1	R.TLHQIFEK.L
*	HsFLAG-Control_MG_293_	2.5715	0.1225	1016.21	1016.19	4660.5	3	528.9	85.7	1	R.TLHQIFEK.L
*	Hs293FLP-MG_Ti_205.164	3.0191	0.1368	1016.27	1016.19	3644.6	1	567.5	92.9	1	R.TLHQIFEK.L
*	HsFLAG-Control_293_Ti_2	2.8404	0.1358	1016.3	1016.19	4983.7	1	575.9	85.7	1	R.TLHQIFEK.L
*	Hs283FLP_Ti_105.1409.14	2.8789	0.0892	1016.4	1016.19	4680	1	693.5	92.9	4	R.TLHQIFEK.L
*	HsF-IP-293-MG_Ti_104.15	2.8206	0.1396	1016.4	1016.19	4000.5	3	568.6	85.7	2	R.TLHQIFEK.L
*	HsFLAG-Control_HeLa_S1	2.8715	0.132	1016.53	1016.19	5211.7	2	727.9	92.9	9	R.TLHQIFEK.L
*	Hs293FLP_Ti_305.1502.15	2.6175	0.0845	1016.66	1016.19	4111.5	1	641.4	92.9	2	R.TLHQIFEK.L
*	HsFLAG-Control_293_Ti_2	2.3788	0.1652	1210.42	1211.31	5462.4	3	436.9	65	1	K.LTDNGTEFSVK.V
*	Hs293FLP-MG_Ti_202.188	2.1966	0.1928	1210.46	1211.31	6912.1	1	619	65	1	K.LTDNGTEFSVK.V
*	HsHeLa_Control_Ti_102.15	2.0332	0.1718	1210.6	1211.31	5608.1	1	428.4	60	1	K.LTDNGTEFSVK.V
*	HsFLAG-Control_MG_293_	3.5267	0.1806	1210.87	1211.31	6064.9	5	829.9	75	2	K.LTDNGTEFSVK.V
*	HsFLAG-MOCK_300mM_T	3.2455	0.2909	1211.21	1211.31	5869.5	3	744.1	75	6	K.LTDNGTEFSVK.V
*	HsFLAG-Control_293_Ti_2	2.868	0.2528	1211.3	1211.31	6138	2	775.7	75	1	K.LTDNGTEFSVK.V
*	Hs283FLP_Ti_104.3965.39	3.998	0.1565	2781.87	2783.06	6293.1	6	476.5	27.2	4	K.VSLLEIYNEELFDLLNPSSDVSER.L
*	HsHeLa_Control-MG_Ti_20	4.7897	0.2829	2782.59	2783.06	6874.6	2	880.4	45.7	18	K.VSLLEIYNEELFDLLNPSSDVSER.L
*	HsFLAG-Control_HeLa_NE	3.8435	0.2578	2782.61	2783.06	8326.5	1	970.3	31.5	1	K.VSLLEIYNEELFDLLNPSSDVSER.L
*	HsF-IP-293-MG_Ti_104.02	5.3498	0.3256	2782.96	2783.06	7800.1	1	1019.8	45.7	37	K.VSLLEIYNEELFDLLNPSSDVSER.L
*	HsFLAG-Control_293_Ti_2	4.9199	0.3587	2783.09	2783.06	7200.8	1	1341.8	52.2	21	K.VSLLEIYNEELFDLLNPSSDVSER.L
*	HsFLAG-Control_HeLa_S1	4.9425	0.2776	2783.21	2783.06	8529.8	3	940.9	43.5	7	K.VSLLEIYNEELFDLLNPSSDVSER.L
*	HsFLAG-Control_HeLa_S1	4.4185	0.2831	2783.22	2783.06	7808.2	1	993.5	33.7	1	K.VSLLEIYNEELFDLLNPSSDVSER.L
*	HsFLAG-MOCK_300mM_T	4.2828	0.2295	2783.37	2783.06	6442.5	1	751.7	43.5	8	K.VSLLEIYNEELFDLLNPSSDVSER.L
*	HsHeLa_Control_Ti_102.48	5.1409	0.2741	2783.54	2783.06	7440	2	941.8	45.7	13	K.VSLLEIYNEELFDLLNPSSDVSER.L
*	Hs293FLP-MG_Ti_204.492	5.0737	0.1861	2783.59	2783.06	8484.2	1	1192.6	32.6	3	K.VSLLEIYNEELFDLLNPSSDVSER.L
*	HsFLAG-Control_293_Ti_2	5.4965	0.316	2784.33	2783.06	7360.8	1	1216.7	37	1	K.VSLLEIYNEELFDLLNPSSDVSER.L
*	HsHeLa_Control-MG_Ti_10	3.7501	0.1935	2785.3	2783.06	6170.2	1	693.9	30.4	1	K.VSLLEIYNEELFDLLNPSSDVSER.L

*	HsFLAG-Control_293_Ti_2	3.0711	0.2175	1021.95	1022.16	3919	8	601	78.6	4	R.LQMFDDPR.N
*	Hs293FLP-MG_Ti_204.262	5.0064	0.4074	2257.73	2258.53	7340.7	1	840.9	50	12	K.GLEEITVHNKDEVYQILEK.G
*	HsHeLa_Control-MG_Ti_20	5.1385	0.3859	2257.75	2258.53	7844	1	1294.2	58.3	6	K.GLEEITVHNKDEVYQILEK.G
*	HsFlag1P_Ti_103.2885.288	4.5502	0.3522	2257.87	2258.53	9411.4	1	1419.6	55.6	4	K.GLEEITVHNKDEVYQILEK.G
*	Hs293FLP-MG_Ti_203.282	4.829	0.4223	2258.55	2258.53	7527.3	1	1513.7	44.4	6	K.GLEEITVHNKDEVYQILEK.G
*	HsHeLa_Control-MG_Ti_10	4.9557	0.3975	2259.04	2258.53	6575.3	1	1159.6	58.3	1	K.GLEEITVHNKDEVYQILEK.G
*	HsHeLa_Control_Ti_105.30	4.8122	0.3953	2259.54	2258.53	8398.4	1	1103.5	36.1	2	K.GLEEITVHNKDEVYQILEK.G
*	HsHeLa_Control-MG_Ti_20	5.2707	0.4211	2259.54	2258.53	9390.7	1	1952.8	44.4	6	K.GLEEITVHNKDEVYQILEK.G
*	HsHeLa_Control-MG_Ti_10	4.2296	0.3014	2260.58	2258.53	8036.8	1	1568.6	43.1	2	K.GLEEITVHNKDEVYQILEK.G
*	HsF-IP-293_Ti_102.1728.17	3.0289	0.131	1137.23	1137.28	4654.8	4	899.2	81.2	2	K.DEVYQILEK.G
*	HsF-IP-293-MG_Ti_106.20	4.8698	0.4607	1543.29	1543.74	6117.7	1	1207.9	76.9	11	K.RTTAATLMNAYSSR.S
*	HsFLAG-Control_293_Ti_2	2.4052	0.1818	1386.47	1387.55	3249.4	6	121.8	50	1	R.TTAATLMNAYSSR.S
*	HsFLAG-Control_293_Ti_2	4.2331	0.3317	1386.94	1387.55	6643.6	1	1296.5	79.2	6	R.TTAATLMNAYSSR.S
*	HsFlag1P_Ti_103.2197.21	4.2961	0.332	1387.02	1387.55	8275.5	1	1756.2	83.3	6	R.TTAATLMNAYSSR.S
*	HsFlag1P_Ti_106.2633.26	5.5472	0.4145	1770	1770.04	7819.9	1	2545.5	78.1	2	K.IGKLNLVDLAGSENIGR.S
*	HsHeLa_Control-MG_Ti_20	2.1568	0.2076	1470.51	1471.65	3120.7	2	189.7	50	1	K.LNLVDLAGSENIGR.S
*	HsFLAG-Control_293_Ti_2	2.9849	0.0972	1470.62	1471.65	3824.2	1	318.7	57.7	1	K.LNLVDLAGSENIGR.S
*	HsFLAG-Control_HeLa_NE	5.1959	0.219	1470.62	1471.65	8447.9	1	2329.2	84.6	24	K.LNLVDLAGSENIGR.S
*	Hs293FLP_Ti_302.2543.25	2.4482	0.1117	1470.68	1471.65	2778.8	4	199.3	53.8	1	K.LNLVDLAGSENIGR.S
*	HsFlag1P_Ti_102.2790.27	5.5066	0.2119	1470.79	1471.65	9070.1	1	2724.8	88.5	3	K.LNLVDLAGSENIGR.S
*	HsHeLa_Control_Ti_103.27	2.6447	0.1578	1470.84	1471.65	2757.7	4	255.6	57.7	1	K.LNLVDLAGSENIGR.S
*	HsFlag1P_Ti_102.2795.27	2.6629	0.1484	1471.03	1471.65	3012.9	2	244.7	53.8	1	K.LNLVDLAGSENIGR.S
*	HsF-IP-293-MG_Ti_102.24	5.1081	0.2297	1471.18	1471.65	7574.3	1	1792.9	80.8	63	K.LNLVDLAGSENIGR.S
*	HsHeLa_Control-MG_Ti_20	5.4225	0.2225	1471.51	1471.65	7380.1	1	1955.2	84.6	13	K.LNLVDLAGSENIGR.S
*	Hs293FLP_Ti_302.2534.25	4.3326	0.1535	1471.79	1471.65	6846.6	1	1719.6	80.8	3	K.LNLVDLAGSENIGR.S
*	HsFLAG-Control_293_Ti_2	3.8419	0.3048	2028.62	2029.26	8061.7	1	902.4	52.6	3	K.LNLVDLAGSENIGRSGAVDK.R
*	HsFlag1P_Ti_106.2509.250	4.9416	0.3893	1714.37	1713.94	8492.2	1	2042.4	76.7	2	R.AREAGNINQSLLTLGR.V
*	HsFLAG-Control_293_Ti_2	4.6518	0.4161	1485.81	1486.67	7641.8	1	1367.7	76.9	68	R.EAGNINQSLLTLGR.V
*	HsF-IP-293_Ti_103.1529.15	3.0713	0.1626	901.35	901.094	3661.7	3	720.4	92.9	4	R.VITALVER.T
*	Hs293FLP-MG_Ti_302.128	2.1533	0.1941	958.41	959.09	3726.6	2	348.8	75	2	R.ILQDSLGGR.T
*	HsFLAG-Control_293_Ti_2	2.1698	0.2523	958.51	959.09	4446.2	2	312.4	62.5	2	R.ILQDSLGGR.T
*	HsFLAG-Control_293_Ti_2	2.8034	0.1115	958.79	959.09	4606.4	1	1022.3	87.5	6	R.ILQDSLGGR.T
*	HsF-IP-293_Ti_102.1316.13	3.1109	0.1888	959.39	959.09	4250.3	1	1007.2	93.8	2	R.ILQDSLGGR.T
*	HsF-IP-293-MG_Ti_106.26	3.9262	0.3391	2831.33	2832.18	7406.2	1	609.7	36	20	R.TSIIATISPASLNLEETLSTLEYAHR.A
*	HsFLAG-Control_HeLa_S1	4.4265	0.3235	2833.12	2832.18	4946.1	2	433.9	26	3	R.TSIIATISPASLNLEETLSTLEYAHR.A
*	HsHeLa_Control_Ti_106.37	3.9567	0.3801	2833.29	2832.18	8061	1	695.5	36	4	R.TSIIATISPASLNLEETLSTLEYAHR.A
*	HsFLAG-Control_HeLa_NE	3.5761	0.183	1297.46	1297.5	6307.6	6	1000.4	80	8	K.NILNKPEVNQK.L
*	HsFlag1P_Ti_106.2418.241	4.0148	0.2916	1623.07	1622.86	6314.2	1	1497.5	83.3	1	K.KALIKEYTEEIER.L
*	HsFlag1P_Ti_103.2221.222	4.1641	0.3696	1494.22	1494.69	4860.3	1	1036.6	81.8	3	K.ALIKEYTEEIER.L
*	HsFLAG-Control_MG_293_	3.1114	0.207	1327.48	1328.42	3347	1	292.9	70	1	K.NGVYISEENFR.V
*	Hs293FLP_Ti_302.1771.17	2.7373	0.1362	1327.6	1328.42	2242.2	1	235.4	75	2	K.NGVYISEENFR.V
*	Hs293FLP-MG_Ti_102.203	1.8228	0.1737	1327.74	1328.42	2206.8	3	134.4	65	1	K.NGVYISEENFR.V
*	HsF-IP-293-MG_Ti_102.17	3.6064	0.3172	1328.12	1328.42	4622	1	1067.2	80	6	K.NGVYISEENFR.V
*	HsFLAG-Control_293_Ti_2	2.7315	0.1317	1328.28	1328.42	3107.9	6	182.1	60	4	K.NGVYISEENFR.V
*	HsFLAG-Control_MG_293_	3.6243	0.0901	1328.32	1328.42	4543.6	1	978.3	80	1	K.NGVYISEENFR.V
*	Hs293FLP-MG_Ti_202.214	3.4714	0.0967	1328.4	1328.42	6791.2	1	1353	80	1	K.NGVYISEENFR.V
*	HsF-IP-293_Ti_102.1603.1	3.4341	0.2018	1328.47	1328.42	4593.4	1	1056.2	80	14	K.NGVYISEENFR.V
*	HsFlag1P_Ti_102.2218.221	2.7759	0.2086	1328.63	1328.42	2644.7	1	249.4	65	1	K.NGVYISEENFR.V
*	Hs293FLP_Ti_302.1766.17	3.2331	0.1888	1328.79	1328.42	4148.8	1	1103.9	85	2	K.NGVYISEENFR.V

*	HsHeLa_Control-MG_Ti_20	5.5676	0.2805	1672.46	1671.93	8984.1	1	2449	84.6	96	K.LTVQEEQIVELIEK.I
*	Hs293FLP-MG_Ti_302.139	2.4214	0.1589	1129.33	1130.24	3063.7	2	252.5	66.7	2	K.IGAVEEELNR.V
*	HsF-IP-293-MG_Ti_102.15	1.9857	0.1984	1129.47	1130.24	3700.6	3	279.9	66.7	1	K.IGAVEEELNR.V
*	HsFLAG-Control_MG_293_	2.6143	0.1874	1129.5	1130.24	4315.6	1	431.1	72.2	2	K.IGAVEEELNR.V
*	HsHeLa_Control-MG_Ti_20	2.4056	0.1491	1129.61	1130.24	2871	1	259.1	72.2	2	K.IGAVEEELNR.V
*	Hs293FLP-MG_Ti_202.187	2.3776	0.2118	1129.66	1130.24	4012.5	1	336.3	66.7	2	K.IGAVEEELNR.V
*	HsHeLa_Control_Ti_102.15	2.4344	0.217	1129.77	1130.24	3051.5	1	295.7	66.7	1	K.IGAVEEELNR.V
*	Hs293FLP_Ti_302.1536.15	1.9777	0.2645	1129.86	1130.24	2978.9	1	226.6	61.1	1	K.IGAVEEELNR.V
*	HsFLAG-Control_293_Ti_2	3.7943	0.2692	1129.94	1130.24	5900.9	1	1272.5	88.9	4	K.IGAVEEELNR.V
*	HsFLAG-Control_MG_293_	3.7897	0.2201	1130.03	1130.24	5606.4	1	1322.5	94.4	2	K.IGAVEEELNR.V
*	Hs293FLP-MG_Ti_202.187	3.1894	0.1307	1130.41	1130.24	6471.1	1	1143.1	83.3	2	K.IGAVEEELNR.V
*	HsFLAG-MOCK_300mM_T	3.674	0.2286	1130.42	1130.24	5296.6	1	1275.9	94.4	5	K.IGAVEEELNR.V
*	Hs293FLP-MG_Ti_102.173	3.8477	0.2596	1131.07	1130.24	4990.9	1	1236.2	94.4	3	K.IGAVEEELNR.V
*	HsHeLa_Control-MG_Ti_20	3.9001	0.1757	1131.35	1130.24	6363.2	1	1461.9	94.4	5	K.IGAVEEELNR.V
*	HsFLAG-MOCK_150mM_T	5.0839	0.3843	3096.24	3096.4	10648.5	1	1577.9	33	3	K.IGAVEEELNRVTELFMDNKNELDQCK.S
*	HsFLAG-Control_293_Ti_2	2.8075	0.2367	1096.43	1097.27	5867.1	9	458.1	68.8	2	R.VTELFMDNK.N
*	HsFLAG-Control_MG_293_	3.5789	0.2141	1984.88	1985.18	10025.8	4	1021.9	38.3	1	R.VTELFMDNKNELDQCK.S
*	Hs293FLP-MG_Ti_306.241	4.9133	0.4539	1985.02	1985.18	6336.2	1	1270.5	70	2	R.VTELFMDNKNELDQCK.S
*	HsFLAG-Control_293_Ti_2	5.1145	0.4847	1985.79	1985.18	8353.1	1	1365	63.3	53	R.VTELFMDNKNELDQCK.S
*	Hs293FLP-MG_Ti_206.316	4.2227	0.3431	3670.45	3671.1	10037.2	1	629.6	21.8	1	K.HLQETKLQLVKEEYITSALESTEEKLHDAASK.L
*	HsFLAG-Control_293_Ti_2	5.945	0.5211	2209.83	2211.47	7921.7	1	2527.4	75	4	K.LQLVKEEYITSALESTEEK.L
*	Hs293FLP-MG_Ti_204.279	5.2603	0.4108	2210.32	2211.47	10203.6	1	1194.7	34.7	5	K.LQLVKEEYITSALESTEEK.L
*	Hs293FLP-MG_Ti_203.292	6.0707	0.4811	2210.86	2211.47	9737.8	1	3585.2	77.8	5	K.LQLVKEEYITSALESTEEK.L
*	HsHeLa_Control-MG_Ti_20	6.2662	0.4915	2210.91	2211.47	7651.9	1	1554	63.9	8	K.LQLVKEEYITSALESTEEK.L
*	Hs283FLP_Ti_106.2387.23	6.6612	0.4623	2211.01	2211.47	7723.6	1	2680.5	75	4	K.LQLVKEEYITSALESTEEK.L
*	Hs293FLP_Ti_303.2555.25	6.2866	0.4435	2211.06	2211.47	7726.9	1	2639.6	75	8	K.LQLVKEEYITSALESTEEK.L
*	HsHeLa_Control-MG_Ti_10	5.3929	0.4987	2211.09	2211.47	7040.5	1	1776.4	66.7	6	K.LQLVKEEYITSALESTEEK.L
*	HsHeLa_Control-MG_Ti_10	4.4045	0.3684	2211.38	2211.47	7386.6	1	1198.4	38.9	1	K.LQLVKEEYITSALESTEEK.L
*	HsF-IP-293-MG_Ti_106.23	4.893	0.3498	2211.47	2211.47	7914.7	1	1183.5	38.9	2	K.LQLVKEEYITSALESTEEK.L
*	HsHeLa_Control-MG_Ti_20	5.5885	0.3812	2211.49	2211.47	8465.2	1	1499.8	43.1	5	K.LQLVKEEYITSALESTEEK.L
*	Hs293FLP_Ti_303.2554.25	5.5633	0.2874	2211.76	2211.47	8180.4	1	1374.9	40.3	8	K.LQLVKEEYITSALESTEEK.L
*	HsHeLa_Control_Ti_106.32	5.8934	0.4442	2212.85	2211.47	8704.8	1	2849.8	75	9	K.LQLVKEEYITSALESTEEK.L
*	Hs283FLP_Ti_106.2392.23	5.0537	0.4115	2213.19	2211.47	7494.1	1	1076.5	38.9	2	K.LQLVKEEYITSALESTEEK.L
*	HsHeLa_Control_Ti_105.31	5.6928	0.3351	2213.21	2211.47	7503.4	1	1320.5	41.7	5	K.LQLVKEEYITSALESTEEK.L
*	Hs293FLP-MG_Ti_204.342	6.6876	0.4417	2934.07	2934.27	9093	1	1265.8	33	8	K.LQLVKEEYITSALESTEEKLHDAASK.L
*	HsF-IP-293_Ti_102.1738.1	5.0592	0.3464	1630.45	1629.72	6874.9	1	1772.8	80.8	39	K.EEYITSALESTEEK.L
*	HsHeLa_Control-MG_Ti_20	2.3609	0.0934	1147.48	1148.3	6393.1	8	433.7	66.7	1	K.LLNTVEETTK.D
*	HsFLAG-Control_MG_293_	2.6737	0.1741	1147.52	1148.3	8159.6	5	542.6	66.7	2	K.LLNTVEETTK.D
*	Hs293FLP-MG_Ti_102.160	2.5442	0.255	1147.64	1148.3	6231.6	6	457.7	72.2	1	K.LLNTVEETTK.D
*	HsFLAG-Control_MG_293_	3.1493	0.2104	1148.21	1148.3	5012.6	4	821.6	83.3	1	K.LLNTVEETTK.D
*	HsFLAG-MOCK_300mM_T	3.4947	0.2445	1148.23	1148.3	5165.5	1	1067.6	88.9	1	K.LLNTVEETTK.D
*	HsHeLa_Control-MG_Ti_20	3.5594	0.289	1148.23	1148.3	4769.3	9	777.2	83.3	4	K.LLNTVEETTK.D
*	Hs293FLP-MG_Ti_202.176	3.1137	0.111	1148.41	1148.3	5398.5	5	913.5	83.3	1	K.LLNTVEETTK.D
*	HsFlag1P_Ti_105.2100.21	4.1778	0.4173	1971.32	1972.2	9629.9	1	1521.7	61.8	2	K.LLNTVEETTKDVSGLHSK.L
*	Hs293FLP-MG_Ti_205.146	2.0362	0.2243	1226.61	1227.36	4464.6	7	304.2	55	1	K.DVSGLHSKLDR.K
*	Hs293FLP-MG_Ti_205.146	3.2403	0.3825	1227.65	1227.36	8599.6	1	1353.5	85	1	K.DVSGLHSKLDR.K
*	Hs293FLP_Ti_304.1334.13	3.4089	0.3332	1227.78	1227.36	6992.2	1	1203.2	90	5	K.DVSGLHSKLDR.K
*	HsFlag1P_Ti_106.2329.232	5.2939	0.3914	1771.15	1771.93	9386.9	1	1902	70	1	K.KAVDQHNAEAQDIFGK.N
*	HsF-IP-293-MG_Ti_103.16	4.9912	0.4323	1643.39	1643.75	8457.1	1	2111.1	75	40	K.AVDQHNAEAQDIFGK.N

*	HsFLAG-Control_MG_293_	5.0854	0.395	1643.47	1643.75	8726.1	1	1697.4	67.9	52	K.AVDQHNAEAQDIFGK.N
*	Hs293FLP-MG_Ti_203.175	3.8252	0.1872	1645.52	1643.75	3876.3	1	773.3	46.4	1	K.AVDQHNAEAQDIFGK.N
*	Hs293FLP_Ti_302.3946.39	4.76	0.3238	1679.89	1679.93	5110.3	1	944.1	73.1	62	K.NLNSLFNNMEELIK.D
*	Hs293FLP-MG_Ti_203.461	4.5714	0.2302	1269.95	1270.56	7744	1	1625.2	85	54	K.TVLQELINVLK.T
*	Hs293FLP-MG_Ti_205.008	3.5703	0.1215	2160.81	2160.62	5448.9	1	514.6	39.5	1	K.TDLLSSLEMILSPTVVSILK.I
*	HsFLAG-Control_293_Ti_2	3.0618	0.2173	1447.64	1448.61	5382.7	1	681.7	66.7	3	K.TSLTVADKIEDQK.K
*	HsFLAG-Control_293_Ti_2	4.1341	0.2359	1448.3	1448.61	6053.7	1	1074.2	75	13	K.TSLTVADKIEDQK.K
*	HsHeLa_Control-MG_Ti_20	4.0324	0.2349	1448.54	1448.61	5097.4	2	1114.4	79.2	1	K.TSLTVADKIEDQK.K
*	Hs293FLP-MG_Ti_204.155	4.2392	0.1413	1576.54	1576.79	6566.7	2	1333.6	73.1	35	K.TSLTVADKIEDQKK.E
*	HsHeLa_Control-MG_Ti_20	5.7585	0.3909	3533.7	3533.89	7910.6	1	1126.8	28.4	7	K.KELDGFLSILCNNLHELQENTICSLVESQK.Q
*	Hs293FLP-MG_Ti_205.000	6.4379	0.4491	3406.37	3405.72	9862.6	1	1429.6	30.4	49	K.ELDGFLSILCNNLHELQENTICSLVESQK.Q
*	HsFLAG-Control_293_Ti_2	2.7063	0.2301	1177.81	1178.25	4779.8	1	692.3	88.9	3	K.QCGNLTEDLK.T
*	HsFLAG-Control_MG_293_	2.1343	0.1663	1062.46	1063.26	4859.3	2	259.2	71.4	1	K.LMNLWTER.F
*	Hs293FLP_Ti_302.1378.13	2.3117	0.0809	896.59	896.982	8004.7	5	895.9	83.3	3	R.FCALEEK.C
*	HsF-IP-293-MG_Ti_102.14	2.5679	0.0803	897.34	896.982	3336.4	1	685.1	100	1	R.FCALEEK.C
*	HsFlag1P_Ti_105.2224.222	6.1771	0.4206	3022.08	3022.31	5527.6	1	1335.5	39.6	5	R.FCALEEKCENIQKPLSSVQENIQQK.S
*	HsHeLa_Control-MG_Ti_20	5.666	0.3109	2143.38	2144.36	5239.5	1	1435.4	73.5	6	K.CENIQKPLSSVQENIQQK.S
*	HsFLAG-Control_MG_293_	4.6153	0.2146	2143.49	2144.36	4892.7	1	780.5	61.8	5	K.CENIQKPLSSVQENIQQK.S
*	HsF-IP-293-MG_Ti_104.15	5.0989	0.3068	2143.65	2144.36	4560.6	1	1293.3	76.5	4	K.CENIQKPLSSVQENIQQK.S
*	HsFLAG-Control_293_Ti_2	5.3789	0.2339	2143.76	2144.36	5027.2	1	1296.4	70.6	7	K.CENIQKPLSSVQENIQQK.S
*	Hs293FLP-MG_Ti_105.165	4.0264	0.2806	2143.94	2144.36	4009.7	1	693	64.7	1	K.CENIQKPLSSVQENIQQK.S
*	HsHeLa_Control-MG_Ti_20	6.4512	0.3109	2144.06	2144.36	9266.4	1	3494.6	54.4	3	K.CENIQKPLSSVQENIQQK.S
*	HsFLAG-Control_293_Ti_2	6.1535	0.2842	2144.46	2144.36	8718.7	1	2925.5	52.9	2	K.CENIQKPLSSVQENIQQK.S
*	HsF-IP-293-MG_Ti_104.15	6.0556	0.3439	2144.89	2144.36	8627	1	2873.9	52.9	2	K.CENIQKPLSSVQENIQQK.S
*	Hs293FLP-MG_Ti_105.166	5.4647	0.2965	2145.15	2144.36	6607.4	1	2734.8	55.9	2	K.CENIQKPLSSVQENIQQK.S
*	HsF-IP-293_Ti_103.1378.1	3.3954	0.2816	1371.27	1371.53	7687.6	1	1184.1	77.3	1	K.PLSSVQENIQQK.S
*	HsFLAG-Control_293_Ti_2	2.128	0.2044	1531.37	1532.57	3716.9	4	224.2	45.8	1	K.FCADSDGFSQELR.N
*	Hs293FLP-MG_Ti_202.220	1.876	0.1539	1531.39	1532.57	4179.3	7	263	50	1	K.FCADSDGFSQELR.N
*	HsFLAG-Control_MG_293_	1.9991	0.2202	1531.4	1532.57	4506.2	1	274.4	50	1	K.FCADSDGFSQELR.N
*	HsF-IP-293-MG_Ti_102.17	4.7453	0.5049	1532.39	1532.57	5741.6	1	1508.9	83.3	6	K.FCADSDGFSQELR.N
*	HsHeLa_Control-MG_Ti_10	4.922	0.3685	1532.81	1532.57	5583.7	1	1626.6	87.5	23	K.FCADSDGFSQELR.N
*	HsFLAG-Control_MG_293_	4.6077	0.4468	1533.06	1532.57	6490	1	1974.2	91.7	3	K.FCADSDGFSQELR.N
*	Hs293FLP-MG_Ti_202.220	4.1554	0.383	1534.47	1532.57	6419.6	1	1321.5	79.2	2	K.FCADSDGFSQELR.N
*	Hs293FLP-MG_Ti_203.254	2.8564	0.2351	2450.73	2451.53	8619.9	6	301.5	32.5	2	K.FCADSDGFSQELRNFNQEGTK.L
*	Hs293FLP-MG_Ti_203.395	4.7694	0.4167	3237.36	3236.44	9405.3	1	889.2	25.9	1	K.FCADSDGFSQELRNFNQEGTKLVEESVK.H
*	HsFlag1P_Ti_103.2206.220	5.0402	0.2835	1723.59	1722.89	8761.7	1	2065.2	78.6	6	R.NFNQEGTKLVEESVK.H
*	HsFlag1P_Ti_103.1694.16	3.5818	0.1442	1851.43	1851.93	7279.6	3	674	57.1	1	K.ISQETEQRCESLNTR.T
*	Hs293FLP-MG_Ti_204.301	4.9037	0.4363	1846.62	1846.01	8289.5	1	1657.5	75	32	R.TVYFSEQWVSSLNER.E
*	Hs293FLP-MG_Ti_203.321	4.5095	0.3855	2905.89	2907.05	7534.2	1	846.2	43.8	8	R.EQELHNLLEVVSQCCEASSSDITEK.S
*	HsHeLa_Control-MG_Ti_20	6.681	0.4644	2906.14	2907.05	7323.6	1	2238.7	42.7	7	R.EQELHNLLEVVSQCCEASSSDITEK.S
*	HsF-IP-293-MG_Ti_106.24	5.0163	0.32	2906.31	2907.05	9906.1	1	2161.9	37.5	2	R.EQELHNLLEVVSQCCEASSSDITEK.S
*	Hs293FLP-MG_Ti_203.318	6.7841	0.4495	2906.55	2907.05	9533.1	1	2593.5	40.6	14	R.EQELHNLLEVVSQCCEASSSDITEK.S
*	HsFLAG-Control_293_Ti_2	4.8282	0.2897	2906.56	2907.05	10380.2	2	705.8	37.5	2	R.EQELHNLLEVVSQCCEASSSDITEK.S
*	HsHeLa_Control_Ti_104.34	5.8576	0.3674	2907.01	2907.05	8318.3	1	1766.6	37.5	4	R.EQELHNLLEVVSQCCEASSSDITEK.S
*	HsHeLa_Control_Ti_105.33	3.8042	0.1598	2907.13	2907.05	6387.4	2	400.5	33.3	3	R.EQELHNLLEVVSQCCEASSSDITEK.S
*	HsHeLa_Control-MG_Ti_20	4.5113	0.3924	2907.29	2907.05	8114.9	1	808.5	39.6	6	R.EQELHNLLEVVSQCCEASSSDITEK.S
*	HsFLAG-Control_293_Ti_2	4.0192	0.3179	1848.02	1848.04	8601.9	1	935.1	60.7	5	K.QHNIFLDQMTIDEDK.L
*	Hs293FLP-MG_Ti_205.349	4.8632	0.2992	3327.15	3328.76	8202.6	1	959.2	29.6	16	K.QHNIFLDQMTIDEDKLIAQNLELNETIK.I
*	HsFLAG-Control_MG_293_	3.6538	0.1884	1498.51	1499.75	6621.7	2	631.2	62.5	4	K.LIAQNLELNETIK.I

*	HsHeLa_Control-MG_Ti_20	3.2416	0.2145	1498.51	1499.75	5717.2		2	507.9	62.5	2	K.LIAQNLELNETIK.I
*	HsFLAG-Control_293_Ti_2	3.6181	0.1419	1498.51	1499.75	6615.7		1	576.8	58.3	4	K.LIAQNLELNETIK.I
*	Hs293FLP-MG_Ti_202.247	2.6663	0.1743	1498.53	1499.75	7825.1		2	636	58.3	1	K.LIAQNLELNETIK.I
*	HsHeLa_Control_Ti_103.22	3.1666	0.1342	1498.68	1499.75	5062.6		1	480	62.5	1	K.LIAQNLELNETIK.I
*	Hs293FLP_Ti_302.2060.20	3.0015	0.1211	1498.82	1499.75	4737.2		8	316	54.2	2	K.LIAQNLELNETIK.I
*	HsFLAG-Control_MG_293_	4.5709	0.1881	1498.86	1499.75	7442.6		1	1817.5	83.3	39	K.LIAQNLELNETIK.I
*	HsFLAG-Control_293_Ti_2	4.5816	0.1976	1499.23	1499.75	6865.5		1	1793.1	87.5	42	K.LIAQNLELNETIK.I
*	Hs293FLP-MG_Ti_202.247	4.4361	0.1862	1499.56	1499.75	6734.8		1	1582.9	83.3	4	K.LIAQNLELNETIK.I
*	HsFLAG-Control_HeLa_S1	4.4016	0.1738	1499.65	1499.75	6752.2		1	1328.7	79.2	8	K.LIAQNLELNETIK.I
*	Hs293FLP_Ti_302.2058.20	4.2465	0.1623	1499.71	1499.75	6055.7		1	1523	83.3	2	K.LIAQNLELNETIK.I
*	HsHeLa_Control-MG_Ti_20	4.5665	0.1684	1499.83	1499.75	7209.2		1	1672.1	83.3	15	K.LIAQNLELNETIK.I
*	HsHeLa_Control-MG_Ti_10	3.4436	0.1248	1279.68	1280.43	6282		8	651.2	72.2	1	K.LNCFLEQDLK.L
*	HsFLAG-Control_HeLa_S1	3.7336	0.1439	1280.32	1280.43	7853.8		3	1441.5	88.9	5	K.LNCFLEQDLK.L
*	HsF-IP-293-MG_Ti_102.19	3.7523	0.1743	1280.45	1280.43	7463.9		3	1491.3	88.9	18	K.LNCFLEQDLK.L
*	HsFlag1P_Ti_106.2766.27	5.4534	0.3819	2459.78	2460.76	7683.4		1	1191.1	52.5	4	K.LNCFLEQDLKLDIPTGTTPQR.K
*	Hs293FLP-MG_Ti_205.273	3.6665	0.2414	2587.87	2588.93	7886.2		5	501.8	35.7	1	K.LNCFLEQDLKLDIPTGTTPQRK.S
*	Hs293FLP-MG_Ti_205.272	5.3142	0.3147	2588.17	2588.93	8538.1		1	1435.1	36.9	2	K.LNCFLEQDLKLDIPTGTTPQRK.S
*	HsFLAG-MOCK_300mM_T	3.1591	0.1522	1199.25	1199.35	4231.5		6	533.3	75	1	K.LDIPTGTTPQR.K
*	HsFlag1P_Ti_106.2440.244	3.0151	0.1486	1327.62	1327.57	4977.5		2	639.6	65	2	R.KSYLYPSTLVR.T
*	Hs283FLP_Ti_102.1923.19	2.8433	0.126	1199.69	1199.39	3471.9		7	491.6	72.2	2	K.SYLYPSTLVR.T
*	Hs293FLP-MG_Ti_206.293	3.5079	0.2132	2659.45	2660.05	5725.9		1	549.8	31	1	K.SYLYPSTLVRTEPREHLLDQLK.R
*	HsHeLa_Control-MG_Ti_20	2.549	0.1902	995.37	996.152	2353.7		4	162.2	71.4	3	R.EHLLDQLK.R
*	Hs293FLP-MG_Ti_205.168	2.6317	0.1402	1151.64	1152.34	3513.9		3	246.2	68.8	2	R.EHLLDQLKR.K
*	Hs293FLP-MG_Ti_205.168	2.5472	0.1725	1151.66	1152.34	4809.9		2	573.7	81.2	1	R.EHLLDQLKR.K
*	HsFlag1P_Ti_106.2366.23	2.8849	0.2001	1151.94	1152.34	4669.8		1	574.9	81.2	3	R.EHLLDQLKR.K
*	Hs293FLP-MG_Ti_205.189	3.3845	0.2843	2285.76	2285.56	7912.3		3	358	39.5	2	R.GINTLERSKVEETTEHLVTK.S
*	HsHeLa_Control-MG_Ti_20	2.5968	0.4073	1500.49	1501.68	3683.1		8	244.2	45.8	2	R.SKVEETTEHLVTK.S
*	Hs293FLP-MG_Ti_204.147	2.0322	0.2589	1500.56	1501.68	5525.8		7	369.1	50	1	R.SKVEETTEHLVTK.S
*	HsFLAG-Control_MG_293_	2.3703	0.2814	1500.57	1501.68	5874.6		2	435.3	54.2	1	R.SKVEETTEHLVTK.S
*	HsFLAG-Control_293_Ti_2	4.9122	0.3104	1500.62	1501.68	7865		1	2079.7	87.5	24	R.SKVEETTEHLVTK.S
*	HsFLAG-Control_293_Ti_2	3.0025	0.1337	1500.72	1501.68	4873.4		1	454.1	58.3	2	R.SKVEETTEHLVTK.S
*	Hs293FLP-MG_Ti_204.147	4.8443	0.3004	1501.04	1501.68	8253.1		1	2222.4	87.5	2	R.SKVEETTEHLVTK.S
*	Hs293FLP-MG_Ti_306.226	2.4665	0.239	1501.45	1501.68	3808		3	348.2	54.2	1	R.SKVEETTEHLVTK.S
*	HsFlag1P_Ti_104.1798.17	4.7562	0.2566	1501.62	1501.68	8192.3		1	1906.2	83.3	15	R.SKVEETTEHLVTK.S
*	Hs283FLP_Ti_105.1301.13	5.0565	0.2866	1501.67	1501.68	7311.4		1	1622	79.2	11	R.SKVEETTEHLVTK.S
*	Hs293FLP-MG_Ti_204.147	4.3597	0.3706	1502.08	1501.68	5109.9		2	849.6	50	2	R.SKVEETTEHLVTK.S
*	HsFLAG-Control_MG_293_	4.5572	0.2857	1502.27	1501.68	8181.7		1	1876.1	83.3	23	R.SKVEETTEHLVTK.S
*	Hs293FLP-MG_Ti_306.225	4.548	0.3087	1503.17	1501.68	6703.3		1	1584.3	83.3	1	R.SKVEETTEHLVTK.S
*	Hs293FLP-MG_Ti_103.124	3.8194	0.2674	1287.64	1286.43	7431.1		1	1373.3	80	4	K.VEETTEHLVTK.S
gi|5174735|ref|N	87	532	0.667	445	49831	4.9	U	tubulin, beta, 2 [Homo sapiens]				
	HsHeLa_Control-MG_Ti_10	3.167	0.2606	3117.27	3118.3	3315.1		1	242.8	32.7	2	K.FWEVISDEHGIDPTGTYHGDSDLQLER.I
	Hs293FLP-MG_Ti_203.296	6.0012	0.2864	3117.83	3118.3	8093.8		1	1675.5	37.5	7	K.FWEVISDEHGIDPTGTYHGDSDLQLER.I
	HsFLAG-Control_HeLa_S1	5.6644	0.367	3117.88	3118.3	8579.6		1	912.3	28.8	15	K.FWEVISDEHGIDPTGTYHGDSDLQLER.I
*	HsFLAG-Control_HeLa_S1	2.8883	0.2416	1328.42	1329.45	6895.9		1	497.7	59.1	2	R.INVYYNEATGGK.Y
*	HsFLAG-Control_HeLa_S1	2.4601	0.2357	1328.45	1329.45	6448.3		1	497.3	59.1	1	R.INVYYNEATGGK.Y
*	HsHeLa_Control-MG_Ti_10	1.8417	0.2504	1328.55	1329.45	5416.6		1	325	54.5	1	R.INVYYNEATGGK.Y
*	HsFLAG-Control_HeLa_S1	3.5461	0.3202	1329.1	1329.45	5511.6		1	1202.8	81.8	6	R.INVYYNEATGGK.Y
*	HsFLAG-Control_HeLa_S1	3.232	0.2695	1329.32	1329.45	5673.1		2	946	77.3	2	R.INVYYNEATGGK.Y
*	HsFLAG-Control_HeLa_S1	3.4415	0.2029	1329.33	1329.45	5054.6		1	934.9	77.3	10	R.INVYYNEATGGK.Y

HsHeLa-FLAG-IP_S100_Ti	3.8964	0.3342	1603.75	1602.84	4509.3	1	1068	75	18	R.AVLVDLEPGTMDSVR.S
HsFLAG-Control_293_Ti_1	4.3497	0.4199	2798.44	2800.07	7089.6	1	789.7	42	2	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G
HsFLAG-Control_Hela_Ti_1	7.086	0.3585	2798.77	2800.07	8023.8	1	2007.6	39	1	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G
HsHeLa_Control_Ti_106.35	3.3717	0.284	2799.08	2800.07	7040.2	1	509.9	34	1	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G
HsFLAG-Control_HeLa_NE	5.559	0.4744	2799.13	2800.07	8777.8	1	1234	44	3	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G
Hs293FLP_Ti_306.3134.31	4.4896	0.3405	2799.39	2800.07	5985.1	1	712.5	40	3	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G
HsFLAG-Control_HeLa_S1	5.0217	0.2644	2799.44	2800.07	9812.3	1	1983	35	4	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G
HsFLAG-Control_Hela_Ti_1	4.9745	0.3403	2799.45	2800.07	9442	1	1330.7	46	2	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G
Hs293FLP-MG_Ti_206.324	5.6902	0.3542	2799.53	2800.07	9458.1	1	2291.7	38	3	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G
HsFLAG-Control_293_Ti_1	6.1007	0.3859	2799.74	2800.07	9348.5	1	3099.1	42	2	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G
HsFLAG-Control_HeLa_S1	5.4454	0.3567	2799.89	2800.07	7677.5	1	1212.9	46	3	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G
HsHeLa_Control-MG_Ti_20	5.2597	0.3817	2799.92	2800.07	8298.5	1	1407.9	48	8	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G
HsFLAG-Control_HeLa_S1	4.9984	0.3992	2799.99	2800.07	8366	1	1288.2	46	5	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G
HsHeLa_Control_Ti_106.35	5.7438	0.2886	2800.05	2800.07	8407.2	1	2280	38	3	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G
HsFLAG-Control_HeLa_S1	6.1803	0.4125	2800.31	2800.07	9515.8	1	2575.2	39	10	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G
Hs293FLP-MG_Ti_206.324	4.0474	0.285	2800.79	2800.07	6819.9	1	693.4	38	4	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G
Hs293FLP_Ti_306.3122.31	5.4056	0.2637	2801.19	2800.07	8261.6	1	1963.1	38	2	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G
HsHeLa_Control-MG_Ti_20	6.5624	0.445	2801.2	2800.07	8704.9	1	2240.6	38	7	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G
HsFLAG-Control_HeLa_NE	6.3579	0.3994	2801.45	2800.07	8898.9	1	2491.9	40	3	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G
HsGST-MOCK_Ti_102.286	3.2049	0.3313	1958.45	1960.15	8017.5	1	762.8	52.9	1	K.GHYTEGAELVDSVLDVVR.K
HsFLAG-Control_HeLa_S1	4.1642	0.2955	1959.3	1960.15	8544.6	2	1215.8	38.2	2	K.GHYTEGAELVDSVLDVVR.K
HsGST-MOCK_Ti_403.395	4.7164	0.3422	1959.33	1960.15	10548.9	1	1301.9	55.9	1	K.GHYTEGAELVDSVLDVVR.K
HsFLAG-Control_HeLa_NE	5.3562	0.4242	1959.63	1960.15	11243.1	1	2825.8	70.6	3	K.GHYTEGAELVDSVLDVVR.K
Hs293FLP_Ti_303.3357.33	4.1617	0.1819	1959.92	1960.15	7405	2	1468.9	42.6	6	K.GHYTEGAELVDSVLDVVR.K
HsHeLa_Control-MG_Ti_10	6.1452	0.4266	1959.96	1960.15	8101.6	1	2856.7	79.4	5	K.GHYTEGAELVDSVLDVVR.K
Hs293FLP-MG_Ti_205.353	4.315	0.1813	1959.98	1960.15	9417.8	1	1643	41.2	5	K.GHYTEGAELVDSVLDVVR.K
Hs293FLP-MG_Ti_204.367	6.6846	0.431	1959.98	1960.15	10282.1	1	3961.5	82.4	8	K.GHYTEGAELVDSVLDVVR.K
Hs293FLP_Ti_306.3198.31	6.98	0.3863	1960.01	1960.15	9148.7	1	3744.2	85.3	7	K.GHYTEGAELVDSVLDVVR.K
HsFLAG-Control_HeLa_S1	4.5919	0.2553	1960.03	1960.15	7594.6	1	1242.3	41.2	2	K.GHYTEGAELVDSVLDVVR.K
HsHeLa_Control-MG_Ti_10	3.5165	0.1922	1960.13	1960.15	6171.6	3	834.7	35.3	1	K.GHYTEGAELVDSVLDVVR.K
HsHeLa_Control-MG_Ti_20	4.3353	0.2198	1960.22	1960.15	8005.9	1	1897.4	47.1	2	K.GHYTEGAELVDSVLDVVR.K
HsFLAG-Control_HeLa_S1	5.8707	0.417	1960.53	1960.15	9914.1	1	3928.7	82.4	2	K.GHYTEGAELVDSVLDVVR.K
HsHeLa_Control-MG_Ti_20	6.9239	0.4578	1960.6	1960.15	10283.3	1	4222.7	85.3	8	K.GHYTEGAELVDSVLDVVR.K
HsHeLa_Control_Ti_105.38	6.5934	0.4301	1960.92	1960.15	9241.8	1	3541.4	82.4	7	K.GHYTEGAELVDSVLDVVR.K
HsFLAG-Control_HeLa_NE	4.632	0.1653	1961.1	1960.15	7796.1	7	1433.4	44.1	1	K.GHYTEGAELVDSVLDVVR.K
HsHeLa_Control_Ti_105.38	3.9939	0.1774	1961.13	1960.15	6245.6	2	1192.6	45.6	2	K.GHYTEGAELVDSVLDVVR.K
HsFLAG-Control_HeLa_S1	4.764	0.2325	1961.21	1960.15	8029.8	1	1535	42.6	2	K.GHYTEGAELVDSVLDVVR.K
HsFLAG-Control_HeLa_S1	6.9041	0.4463	1961.25	1960.15	11475.7	1	4165.7	82.4	14	K.GHYTEGAELVDSVLDVVR.K
HsFLAG-Control_HeLa_S1	5.9828	0.4073	1961.57	1960.15	10193.9	1	3020.1	76.5	5	K.GHYTEGAELVDSVLDVVR.K
HsGST-MOCK_Ti_102.285	4.2626	0.1599	1962	1960.15	7062.2	4	1185.6	41.2	1	K.GHYTEGAELVDSVLDVVR.K
Hs293FLP_Ti_306.3098.30	6.1016	0.4085	2088.19	2088.33	9030.4	1	2434	72.2	2	K.GHYTEGAELVDSVLDVVRK.E
HsHeLa_Control_Ti_106.36	2.6425	0.3564	2089.18	2088.33	10954.4	1	669	41.7	1	K.GHYTEGAELVDSVLDVVRK.E
HsFLAG-MOCK_300mM_T	4.8098	0.3951	2089.85	2088.33	6163.4	1	1098.1	41.7	3	K.GHYTEGAELVDSVLDVVRK.E
Hs293FLP_Ti_305.3017.30	5.121	0.3371	2090.41	2088.33	6587.3	1	1579.1	48.6	9	K.GHYTEGAELVDSVLDVVRK.E
HsFLAG-Control_HeLa_S1	2.9498	0.2063	1077.69	1078.17	5287.5	3	749.1	85.7	5	K.IREEYPDR.I
HsFLAG-MOCK_300mM_T	2.7654	0.1191	2380.24	2379.74	5288.7	1	385.4	44.7	2	K.IREEYPDRIMNTFSVVPSPK.V
HsFLAG-Control_MG_293_	4.3284	0.3282	1320.01	1320.59	8983.2	1	1855	86.4	18	R.IMNTFSVVPSPK.V
HsFLAG-Control_HeLa_S1	5.2299	0.4574	4594.42	4595.9	5984.7	1	689.3	24.3	26	K.VSDTVVEPYNATLSVHQLVENTDETYCIDNEALYDICFR.T

	HsGST-MOCK_Ti_305.408	4.8022	0.4628	2708.4	2710.04	7804.4		1	972	43.8	1	K.LTTPTYGDLNHLVSATMSGVTTCLR.F
	Hs293FLP-MG_Ti_204.386	5.4701	0.3771	2708.64	2710.04	9092.1		1	1386.9	45.8	2	K.LTTPTYGDLNHLVSATMSGVTTCLR.F
	HsF-IP-293-MG_Ti_106.26	5.1039	0.31	2708.65	2710.04	6253.5		1	929.3	45.8	6	K.LTTPTYGDLNHLVSATMSGVTTCLR.F
	Hs293FLP-MG_Ti_204.386	3.7503	0.32	2709.13	2710.04	7710.2		1	762.9	29.2	1	K.LTTPTYGDLNHLVSATMSGVTTCLR.F
	HsHeLa_Control-MG_Ti_10	4.2137	0.4906	2709.32	2710.04	6602.6		1	706.6	39.6	1	K.LTTPTYGDLNHLVSATMSGVTTCLR.F
	HsFLAG-MOCK_300mM_T	3.5898	0.1924	2709.57	2710.04	8016.1		2	734.5	28.1	1	K.LTTPTYGDLNHLVSATMSGVTTCLR.F
	HsF-IP-293-MG_Ti_106.26	3.9395	0.217	2709.94	2710.04	7857.5		1	880.7	30.2	1	K.LTTPTYGDLNHLVSATMSGVTTCLR.F
	HsHeLa3_Ti_105.3722.372	4.5547	0.4711	2710.06	2710.04	7677.4		1	1059.3	43.8	3	K.LTTPTYGDLNHLVSATMSGVTTCLR.F
	HsHeLa_Control-MG_Ti_10	4.0048	0.2452	2712.04	2710.04	8274.3		1	1108.1	33.3	1	K.LTTPTYGDLNHLVSATMSGVTTCLR.F
	HsFLAG-Control_293_Ti_2	2.3562	0.2676	1130.49	1131.28	3790.3		1	334.2	72.2	1	R.FPGQLNADLR.K
	HsFLAG-Control_HeLa_S1	3.3308	0.1729	1130.86	1131.28	4313.3		1	873.6	88.9	23	R.FPGQLNADLR.K
	HsFLAG-Control_MG_293_	3.206	0.113	1130.88	1131.28	3899.4		1	816.9	88.9	6	R.FPGQLNADLR.K
	HsFLAG-Control_HeLa_S1	2.9598	0.1628	1259.33	1259.45	6893.9		1	1452.3	90	5	R.FPGQLNADLRK.L
	HsHeLa_Control-MG_Ti_10	3.4275	0.2361	1272.73	1272.59	5940.6		2	973.4	75	2	R.KLAVNMVPFPR.L
	HsF-IP-293-MG_Ti_104.21	3.5921	0.3097	1145.56	1144.42	4625.3		1	875.9	88.9	19	K.LAVNMVPFPR.L
	HsGST-MOCK_Ti_102.257	3.0182	0.4314	1621.6	1621.94	4033.6		1	699.6	69.2	2	R.LHFFMPGFAPLTSR.G
	HsHeLa-FLAG-IP_S100_Ti_	3.5217	0.3098	1692.35	1692.97	3844.5		1	610.2	67.9	9	R.ALTVPELTQQMFDAK.N
	HsHeLa-FLAG-IP_S100_Ti_	2.9555	0.2199	1068.25	1066.2	7345.1		2	1221.1	81.2	2	K.NMMAACDPR.H
	HsFLAG-Control_HeLa_NE	3.3095	0.3087	1040.83	1040.25	5846.9		1	1088.4	93.8	50	R.YLTVAAVFR.G
	HsGST-MOCK_Ti_402.200	3.2807	0.1162	1445.58	1447.6	4353.1		1	621.9	77.3	1	K.EVDEQMLNVQNK.N
	HsFLAG-Control_293_Ti_2	3.0439	0.1965	1446.48	1447.6	5427.8		1	667.1	72.7	2	K.EVDEQMLNVQNK.N
	HsHeLa_Control_Ti_102.15	2.3866	0.11	1446.59	1447.6	3600.8		3	304.9	63.6	1	K.EVDEQMLNVQNK.N
	HsFLAG-Control_MG_293_	3.1945	0.1644	1447.26	1447.6	5122.2		1	556.1	68.2	1	K.EVDEQMLNVQNK.N
	HsHeLa-FLAG-IP_S100_Ti_	4.4378	0.162	1447.32	1447.6	7508.9		6	1453	77.3	14	K.EVDEQMLNVQNK.N
	HsFLAG-Control_HeLa_S1	2.6394	0.1147	1447.42	1447.6	5226.8		1	438.1	63.6	2	K.EVDEQMLNVQNK.N
	Hs293FLP-MG_Ti_102.177	3.6404	0.1591	1447.47	1447.6	6074.7		1	1112.2	72.7	2	K.EVDEQMLNVQNK.N
	HsFLAG-Control_HeLa_S1	4.4307	0.2086	1449.29	1447.6	7304.9		1	1751.9	86.4	2	K.EVDEQMLNVQNK.N
	HsFLAG-Control_HeLa_S1	4.2481	0.345	1697.72	1697.89	5597.6		1	913.8	69.2	79	K.NSSYFVEWIPNNVK.T
	HsHeLa-FLAG-IP_S100_Ti_	2.8782	0.1885	1029.7	1029.15	5615.6		1	1184.8	87.5	8	K.TAVCDIPPR.G
	HsHeLa_Control-MG_Ti_10	3.5998	0.3059	1388.48	1386.61	7275		1	1173.3	80	3	K.RISEQFTAMFR.R
gi|7669492|ref|NI	20	48	0.66	335	36053	8.5	U	glyceraldehyde-3-phosphate dehydrogenase [Homo sapiens]				
*	HsHeLa3_Ti_106.3590.359	4.6218	0.2169	3310.76	3310.76	4307.5		1	719	33.3	1	K.VDIVAINDPFIDLNYMVYMFQYDSTHGK.F
*	HsHeLa_Control-MG_Ti_20	4.5202	0.3701	1615.5	1614.89	7610.1		1	1338.7	73.1	1	K.LVINGNPITIFQER.D
*	HsHeLa3_Ti_105.2662.266	3.9883	0.4385	2043.55	2042.34	6257.3		1	723.4	50	9	K.LVINGNPITIFQERDPSK.I
*	HsHeLa3_Ti_105.3258.325	4.5645	0.4998	2277.65	2278.5	6914.8		1	1572.2	60	3	K.WGDAGAEYVVESTGVFTTMEK.A
*	HsHeLa3_Ti_105.0788.079	2.5921	0.2134	909.73	910.021	4142.7		1	515.7	66.7	1	K.AGAHLQGGAK.R
*	HsHeLa3_Ti_104.1747.174	4.3035	0.2564	1836.04	1835.04	6074.9		1	1254	62.5	6	K.IISNASCTTNCLAPLAK.V
*	HsHeLa3_Ti_106.3163.316	5.531	0.4502	2595.53	2597	7601.4		1	1586	56.5	3	K.VIHDNFGIVEGLMTTVHAITATQK.T
*	HsHeLa3_Ti_106.3155.315	5.9431	0.4566	2598.58	2597	7308.4		1	1300.1	35.9	2	K.VIHDNFGIVEGLMTTVHAITATQK.T
*	Hs293FLP_TREX_Ti_103.1	2.7633	0.2817	1411.39	1412.63	3896.5		1	416.6	57.1	1	R.GALQNIIPASTGAAK.A
*	HsFLAG-Control_MG_293_	2.9577	0.2479	1411.56	1412.63	4827.2		3	448.5	57.1	1	R.GALQNIIPASTGAAK.A
*	HsFLAG-Control_293_Ti_2	3.3718	0.1432	1412.15	1412.63	4241.8		1	605	67.9	2	R.GALQNIIPASTGAAK.A
*	HsFlag1P_Ti_105.2182.218	3.3392	0.2255	1412.25	1412.63	5342.3		1	747	67.9	2	R.GALQNIIPASTGAAK.A
*	HsHeLa3_Ti_106.2575.257	4.1696	0.346	2308.28	2308.67	4186.2		1	471.3	50	2	K.LTGMAFRVPTANVSVVDLTCR.L
*	HsHeLa3_Ti_103.1979.197	2.2105	0.2875	1530.75	1531.72	4260		5	208	46.2	2	R.VPTANVSVVDLTCR.L
*	HsHeLa3_Ti_103.1974.197	3.6911	0.2615	1531.91	1531.72	5595.7		1	759.4	61.5	3	R.VPTANVSVVDLTCR.L
*	HsHeLa3_Ti_105.2319.231	4.6438	0.3872	1901.83	1902.16	6754.3		1	1037.6	59.4	1	R.VPTANVSVVDLTCRLEK.P
*	HsHeLa3_Ti_106.3800.380	3.5139	0.2187	4039.87	4039.32	11722.6		1	850.9	20.9	1	K.GILGYTEHQVVSSDFNSDTHSSTFDAGAGIALNDHFV K.L

*	HsHeLa3_Ti_103.2616.261	4.207	0.3451	1766.32	1764.89	7142.2		1	1227.8	69.2	2	K.LISWYDNEFGYSNR.V
*	HsHeLa3_Ti_104.1797.179	2.7996	0.3241	1330.61	1331.59	5786.7		1	764.2	63.6	2	R.VVDLMAHMASKE.-
*	HsHeLa3_Ti_104.1791.179	4.1343	0.399	1333	1331.59	8588.3		1	2065.5	86.4	3	R.VVDLMAHMASKE.-
gi|5453854|ref|N	28	178	0.643	356	37526	7.1	U		poly(rC) binding protein 1 [Homo sapiens]			
	HsFLAG-MOCK_300mM_T	3.7768	0.4013	1482.96	1482.83	6028.7		1	1195.7	76.9	2	R.LLMHGKEVGSIIGK.K
	HsFLAG-Control_HeLa_NE	4.0721	0.1996	1289.32	1289.35	6636.7		1	1467.5	85	25	R.INISEGNCPER.I
*	HsFLAG-Control_Hela_Ti_1	3.6999	0.2829	1388.52	1389.68	6003		1	826.6	66.7	23	R.IITLTGPTNAIFK.A
*	HsHeLa3_Ti_105.2578.257	2.6483	0.1456	1388.72	1389.68	6787.6		8	469.5	54.2	1	R.IITLTGPTNAIFK.A
*	HsFlag1P_Ti_106.2705.270	3.5084	0.1563	1389.29	1389.68	6667.9		1	918.4	70.8	1	R.IITLTGPTNAIFK.A
*	HsGST-MOCK_Ti_405.288	3.6479	0.2065	1389.44	1389.68	5710.3		4	586.7	62.5	2	R.IITLTGPTNAIFK.A
*	HsGST-MOCK_Ti_405.288	3.204	0.3397	1389.61	1389.68	5200		1	417	58.3	2	R.IITLTGPTNAIFK.A
*	HsFLAG-Control_HeLa_S1	2.9727	0.1913	1389.76	1389.68	8626.4		9	574.8	54.2	1	R.IITLTGPTNAIFK.A
*	HsFLAG-Control_HeLa_S1	3.919	0.246	1390.67	1389.68	5321.7		1	557.4	62.5	25	R.IITLTGPTNAIFK.A
*	HsFLAG-MOCK_300mM_T	3.6211	0.1013	3382.83	3380.86	7482.6		1	1361.9	30	1	K.AFAMIIDKLEEDINSSMTNSTAASRPPVTLR.L
*	HsFLAG-Control_HeLa_NE	3.4887	0.3209	1443.07	1443.69	4183.9		1	818.2	80.8	13	R.LVVPATQCGSLIGK.G
*	HsFLAG-MOCK_300mM_T	2.9765	0.3942	1847.67	1846.11	4089.8		1	462.9	55.9	1	R.LVVPATQCGSLIGKGGCK.I
	HsGST-MOCK_Ti_402.221	4.9595	0.4065	2090.84	2091.26	6640.2		1	1123.5	57.9	9	R.ESTGAQVQVAGDMLPNSTER.A
*	HsFLAG-Control_HeLa_NE	3.3786	0.2379	1675.77	1673.91	3331.3		1	525.3	66.7	6	R.AITIAGVPQSVTECVK.Q
*	HsFlag1P_Ti_106.2868.286	3.9102	0.3213	1960.39	1961.25	9202.7		1	1851.1	68.8	4	K.QICLVMLETLSQSPQGR.V
*	HsGST-MOCK_Ti_305.265	3.2328	0.1608	2476.73	2476.83	5640.9		3	317.7	38.6	5	R.VMTIPYQPMPASSPVICAGGQDR.C
*	HsFLAG-MOCK_300mM_T	3.2162	0.2821	2607.96	2607.88	8553.2		1	527.7	35.4	2	R.QQSHFAMMHGGTGFAGIDSSSPEVK.G
*	HsFLAG-Control_HeLa_NE	2.6697	0.1274	1015.45	1015.11	4576.3		9	476.3	87.5	2	R.QGANINEIR.Q
*	HsFLAG-Control_HeLa_NE	1.92	0.1222	1086.63	1087.18	6335.1		1	472.1	65	1	K.IANPVEGSSGR.Q
*	HsFLAG-Control_HeLa_S1	2.9209	0.1875	1087.22	1087.18	5252.7		1	856.7	80	9	K.IANPVEGSSGR.Q
*	HsHeLa3_Ti_103.1324.132	2.5211	0.1814	1087.68	1087.18	4880.5		1	700.3	75	1	K.IANPVEGSSGR.Q
*	HsFLAG-Control_HeLa_S1	5.2006	0.443	2178.18	2178.49	8009.3		1	1216.5	37.5	2	R.QVTITGSAASISLAQYLINAR.L
*	HsFLAG-Control_HeLa_NE	5.3258	0.4747	2178.32	2178.49	8518.4		1	1324.6	55	9	R.QVTITGSAASISLAQYLINAR.L
*	HsFLAG-Control_HeLa_S1	3.9746	0.3195	2179.03	2178.49	8915.3		9	791.5	31.2	1	R.QVTITGSAASISLAQYLINAR.L
*	HsFLAG-Control_HeLa_S1	4.0234	0.386	2179.25	2178.49	8828		1	561.8	40	1	R.QVTITGSAASISLAQYLINAR.L
*	HsFLAG-Control_HeLa_NE	5.9485	0.4232	2179.68	2178.49	6692.3		1	1547.7	62.5	13	R.QVTITGSAASISLAQYLINAR.L
*	HsGST-MOCK_Ti_404.390	5.385	0.4275	2180.02	2178.49	7139.2		1	1240.6	57.5	10	R.QVTITGSAASISLAQYLINAR.L
*	HsFLAG-Control_HeLa_NE	5.4215	0.4277	2180.6	2178.49	9444.7		1	1696.7	40	6	R.QVTITGSAASISLAQYLINAR.L
gi|13129110|ref|N	91	912	0.643	342	36724	5.2	U		methylosome protein 50 [Homo sapiens]			
*	HsHeLa_Control-MG_Ti_20	2.5695	0.3433	1372.56	1373.64	3555.4		1	355.5	58.3	1	R.KETPPPLVPPAAR.E
*	HsFLAG-Control_293_Ti_2	2.3426	0.2261	1372.59	1373.64	5832		9	340.3	50	2	R.KETPPPLVPPAAR.E
*	HsF-IP-293-MG_Ti_106.20	1.8225	0.1866	1372.63	1373.64	5070.9		2	357.4	54.2	1	R.KETPPPLVPPAAR.E
*	HsFLAG-Control_293_Ti_2	3.3503	0.2436	1373.33	1373.64	7206.4		4	757.6	62.5	1	R.KETPPPLVPPAAR.E
*	Hs293FLP-MG_Ti_206.256	2.9851	0.2265	1373.41	1373.64	7115.5		4	577.3	54.2	1	R.KETPPPLVPPAAR.E
*	HsF-IP-293_Ti_206.2111.2	2.1987	0.2397	1373.59	1373.64	5722.6		7	401.5	54.2	1	R.KETPPPLVPPAAR.E
*	HsHeLa_Control-MG_Ti_20	3.056	0.2335	1373.69	1373.64	6134.5		4	630.7	62.5	1	R.KETPPPLVPPAAR.E
*	HsF-IP-293_Ti_206.2108.2	3.2839	0.1374	1375.71	1373.64	6560.4		9	605	58.3	4	R.KETPPPLVPPAAR.E
*	HsFLAG-Control_MG_293_	2.4613	0.2512	1244.56	1245.46	2860.3		7	184.9	59.1	9	K.ETPPPLVPPAAR.E
*	HsFLAG-Control_MG_293_	3.6616	0.1439	1685.65	1685.86	4335.9		2	428.7	61.5	24	R.EWNLPPNAPACMER.Q
*	HsFLAG-Control_293_Ti_1	4.1659	0.3168	1723.46	1723.93	6145.2		1	1324.3	68.8	12	R.YRSDGALLLGASSLSGR.C
*	HsFLAG-Control_293_Ti_2	4.9156	0.3678	1723.48	1723.93	6103		1	2470	84.4	7	R.YRSDGALLLGASSLSGR.C
*	HsFLAG-Control_MG_293_	4.5491	0.3422	1723.59	1723.93	6450.1		1	2048.9	78.1	3	R.YRSDGALLLGASSLSGR.C
*	Hs283FLP_Ti_106.2193.21	4.8078	0.2991	1723.84	1723.93	5431		1	1902.8	81.2	11	R.YRSDGALLLGASSLSGR.C
*	Hs293FLP-MG_Ti_205.223	4.2603	0.2431	1724.03	1723.93	5783.3		1	1197.2	45.3	4	R.YRSDGALLLGASSLSGR.C
*	HsFLAG-Control_293_Ti_1	4.3961	0.2626	1724.19	1723.93	7096.2		1	1453.5	45.3	1	R.YRSDGALLLGASSLSGR.C

*	HsHeLa_Control-MG_Ti_20	4.0451	0.2991	1724.22	1723.93	7750.8	1	1660.6	45.3	2	R.YRSDGALLLGASSLSGR.C
*	HsHeLa_Control-MG_Ti_20	4.5179	0.3268	1724.42	1723.93	5332.3	1	1475.7	75	6	R.YRSDGALLLGASSLSGR.C
*	Hs293FLP_Ti_304.2029.20	4.0697	0.1265	1724.91	1723.93	7606.5	4	1081.9	37.5	3	R.YRSDGALLLGASSLSGR.C
*	HsHeLa_Control-MG_Ti_10	4.1275	0.2227	1724.97	1723.93	6261.8	1	1281	42.2	2	R.YRSDGALLLGASSLSGR.C
*	HsHeLa_Control_Ti_105.27	5.0428	0.282	1725.14	1723.93	5257.6	1	1486	75	10	R.YRSDGALLLGASSLSGR.C
*	HsFLAG-Control_293_Ti_2	1.9328	0.2005	1404.02	1404.56	2634.6	3	231.4	53.6	1	R.SDGALLLGASSLSGR.C
*	HsFLAG-Control_293_Ti_1	5.3567	0.4425	1404.38	1404.56	6904.9	1	1885.5	82.1	9	R.SDGALLLGASSLSGR.C
*	HsFLAG-Control_293_Ti_1	2.4155	0.1854	1404.68	1404.56	2537.2	1	236	57.1	1	R.SDGALLLGASSLSGR.C
*	HsHeLa_Control_Ti_103.23	4.9503	0.4005	1404.96	1404.56	5803	1	1402.9	75	73	R.SDGALLLGASSLSGR.C
*	HsFLAG-Control_293_Ti_2	5.2513	0.4063	1405.34	1404.56	5942.2	1	1515.7	78.6	56	R.SDGALLLGASSLSGR.C
*	HsHeLa_Control-MG_Ti_10	2.4926	0.2297	1267.78	1268.47	3592.2	3	221.7	61.1	1	R.CWAGSLWLFK.D
*	HsFLAG-Control_Hela_Ti_1	2.9653	0.0949	1268.18	1268.47	4530.7	1	781.2	83.3	4	R.CWAGSLWLFK.D
*	Hs293FLP-MG_Ti_204.362	3.0286	0.153	1268.19	1268.47	4849.3	1	932.6	88.9	4	R.CWAGSLWLFK.D
*	HsF-IP-293-MG_Ti_106.26	2.512	0.1274	1268.55	1268.47	3880.8	6	215.9	61.1	2	R.CWAGSLWLFK.D
*	Hs293FLP_Ti_304.3282.32	3.569	0.2116	1269.01	1268.47	4124.9	1	679.4	83.3	24	R.CWAGSLWLFK.D
*	Hs293FLP-MG_Ti_203.330	4.9557	0.4059	3164.65	3166.32	7604.5	1	977	43.1	9	K.DPCAAPNEGFCSAGVQTEAGVADLTWVGER.G
*	Hs293FLP-MG_Ti_205.306	3.8772	0.3632	3165.59	3166.32	10306.2	1	1006.3	27.6	1	K.DPCAAPNEGFCSAGVQTEAGVADLTWVGER.G
*	HsFLAG-Control_293_Ti_2	5.5596	0.4698	3165.88	3166.32	8768.7	1	1530.8	46.6	6	K.DPCAAPNEGFCSAGVQTEAGVADLTWVGER.G
*	HsFLAG-Control_293_Ti_1	5.0886	0.4506	3166.07	3166.32	8697.9	1	1121.4	41.4	56	K.DPCAAPNEGFCSAGVQTEAGVADLTWVGER.G
*	HsFLAG-Control_293_Ti_2	5.0908	0.3357	3166.34	3166.32	10361.7	1	1128.8	27.6	1	K.DPCAAPNEGFCSAGVQTEAGVADLTWVGER.G
*	HsFLAG-Control_293_Ti_1	4.7969	0.3433	3167.91	3166.32	9808	1	1021.6	26.7	1	K.DPCAAPNEGFCSAGVQTEAGVADLTWVGER.G
*	Hs293FLP-MG_Ti_206.338	5.333	0.3742	2789.79	2789.11	8485.7	1	854.3	40	49	R.GILVASDSGAVELWELDENETLIVSK.F
*	Hs293FLP-MG_Ti_205.379	5.2763	0.4056	2790.95	2789.11	6449.4	1	876.5	31	1	R.GILVASDSGAVELWELDENETLIVSK.F
*	HsHeLa_Control-MG_Ti_20	4.816	0.3918	2901.95	2903.14	7952.5	1	1476.2	34.6	4	K.FCKYEHDDIVSTVSVLSSGTQAVSGSK.D
*	Hs293FLP_Ti_305.2273.22	4.9654	0.3444	2902.13	2903.14	6605.2	1	1348.5	46.2	4	K.FCKYEHDDIVSTVSVLSSGTQAVSGSK.D
*	HsHeLa_Control-MG_Ti_10	5.6784	0.4445	2902.29	2903.14	6648.8	1	1636.5	50	6	K.FCKYEHDDIVSTVSVLSSGTQAVSGSK.D
*	Hs293FLP-MG_Ti_205.249	4.9764	0.3045	2902.33	2903.14	8363.2	1	2062.2	39.4	5	K.FCKYEHDDIVSTVSVLSSGTQAVSGSK.D
*	Hs293FLP-MG_Ti_204.258	5.0079	0.4577	2902.7	2903.14	7131	1	1780.9	51.9	2	K.FCKYEHDDIVSTVSVLSSGTQAVSGSK.D
*	HsHeLa_Control_Ti_105.30	4.3129	0.2888	2903	2903.14	6844.5	1	872.5	31.7	2	K.FCKYEHDDIVSTVSVLSSGTQAVSGSK.D
*	Hs293FLP_Ti_305.2269.22	4.6182	0.2012	2903.69	2903.14	6483.5	1	1367.6	36.5	4	K.FCKYEHDDIVSTVSVLSSGTQAVSGSK.D
*	HsHeLa_Control-MG_Ti_20	5.5522	0.4382	2903.82	2903.14	7095.9	1	1668.8	51.9	7	K.FCKYEHDDIVSTVSVLSSGTQAVSGSK.D
*	HsHeLa_Control-MG_Ti_10	4.3906	0.2922	2904	2903.14	6498.4	1	1024.7	31.7	3	K.FCKYEHDDIVSTVSVLSSGTQAVSGSK.D
*	HsF-IP-293_Ti_202.0018.0	6.1762	0.5637	2466.69	2467.65	8078.3	1	1781.8	56.5	19	K.YEHDDIVSTVSVLSSGTQAVSGSK.D
*	HsF-IP-293-MG_Ti_106.23	6.6828	0.5114	2466.76	2467.65	8294.8	1	2246.4	63	22	K.YEHDDIVSTVSVLSSGTQAVSGSK.D
*	Hs293FLP_Ti_305.2297.22	6.1869	0.5108	2467.31	2467.65	7508.4	1	2039.8	60.9	15	K.YEHDDIVSTVSVLSSGTQAVSGSK.D
*	HsFLAG-Control_293_Ti_1	4.7338	0.3916	2467.38	2467.65	11091.8	1	1480	32.6	6	K.YEHDDIVSTVSVLSSGTQAVSGSK.D
*	HsHeLa_Control-MG_Ti_20	6.8193	0.544	2467.69	2467.65	9064.9	1	2641.6	65.2	47	K.YEHDDIVSTVSVLSSGTQAVSGSK.D
*	HsF-IP-293-MG_Ti_105.24	3.5523	0.3613	2467.8	2467.65	9316.9	1	934.2	30.4	1	K.YEHDDIVSTVSVLSSGTQAVSGSK.D
*	Hs293FLP-MG_Ti_206.295	7.0252	0.5579	2467.83	2467.65	9396.7	1	3214.6	67.4	23	K.YEHDDIVSTVSVLSSGTQAVSGSK.D
*	Hs293FLP_Ti_305.2298.22	3.7286	0.2295	2467.99	2467.65	7513.3	1	780.7	29.3	1	K.YEHDDIVSTVSVLSSGTQAVSGSK.D
*	Hs283FLP_Ti_105.2089.20	4.6147	0.3891	2468.05	2467.65	8784.8	1	1065.7	31.5	2	K.YEHDDIVSTVSVLSSGTQAVSGSK.D
*	HsFLAG-Control_293_Ti_1	6.3625	0.4656	2468.18	2467.65	11373.9	1	1983.1	54.3	41	K.YEHDDIVSTVSVLSSGTQAVSGSK.D
*	HsF-IP-293_Ti_202.0003.0	4.1796	0.3125	2468.37	2467.65	8745.3	1	927.2	29.3	2	K.YEHDDIVSTVSVLSSGTQAVSGSK.D
*	Hs283FLP_Ti_104.2095.20	6.0949	0.4904	2468.82	2467.65	6648.7	1	1619.9	58.7	6	K.YEHDDIVSTVSVLSSGTQAVSGSK.D
*	HsHeLa_Control-MG_Ti_20	3.7803	0.3151	2469.6	2467.65	9718.5	1	1049.5	30.4	1	K.YEHDDIVSTVSVLSSGTQAVSGSK.D
*	HsF-IP-293_Ti_202.0122.0	5.8109	0.2755	1665.53	1664.9	7326.3	1	2652.6	88.5	144	K.VWDLAQQVVLSSYR.A
*	HsF-IP-293_Ti_206.1956.1	3.5097	0.4435	1547.48	1548.71	5334.2	1	773.3	64.3	2	R.AHAAQVTCVAASPHK.D
*	HsF-IP-293-MG_Ti_106.18	3.9482	0.4516	1547.54	1548.71	5069.6	1	662.4	60.7	2	R.AHAAQVTCVAASPHK.D
*	HsHeLa_Control-MG_Ti_20	2.6462	0.3069	1547.55	1548.71	3867.2	1	374.3	57.1	1	R.AHAAQVTCVAASPHK.D

*	HsFLAG-Control_293_Ti_2	3.7486	0.3991	1547.7	1548.71	6165.5		1	814.6	64.3	3	R.AHAAQVTCVAASPHK.D
*	HsFLAG-Control_MG_293_	5.2403	0.4226	1547.89	1548.71	9747.9		1	2829.2	82.1	2	R.AHAAQVTCVAASPHK.D
*	HsHeLa_Control-MG_Ti_10	3.2046	0.2567	1547.96	1548.71	5980		2	464.8	53.6	2	R.AHAAQVTCVAASPHK.D
*	HsFLAG-Control_293_Ti_1	4.659	0.3733	1547.96	1548.71	9297.8		1	1973.9	75	3	R.AHAAQVTCVAASPHK.D
*	Hs283FLP_Ti_106.1795.17	5.3534	0.4751	1548.44	1548.71	8228.1		1	2421.8	82.1	7	R.AHAAQVTCVAASPHK.D
*	HsFLAG-Control_293_Ti_1	1.837	0.1604	1548.45	1548.71	6313.6		8	271.1	42.9	1	R.AHAAQVTCVAASPHK.D
*	HsFLAG-Control_293_Ti_2	5.0098	0.4273	1548.48	1548.71	9513.2		1	2848.5	82.1	2	R.AHAAQVTCVAASPHK.D
*	HsF-IP-293_Ti_206.1955.1	5.2774	0.4043	1548.49	1548.71	9082.8		1	2583.4	78.6	3	R.AHAAQVTCVAASPHK.D
*	HsFLAG-Control_MG_293_	4.1412	0.3208	1548.5	1548.71	6968.1		1	936.2	60.7	4	R.AHAAQVTCVAASPHK.D
*	HsFLAG-Control_Hela_Ti_1	3.0088	0.3227	1548.57	1548.71	6228.2		1	462	50	4	R.AHAAQVTCVAASPHK.D
*	HsF-IP-293-MG_Ti_106.18	5.3713	0.4146	1548.69	1548.71	8329.7		1	2815.6	85.7	2	R.AHAAQVTCVAASPHK.D
*	Hs293FLP-MG_Ti_306.215	4.4915	0.4381	1548.81	1548.71	7948.3		1	1933.3	82.1	2	R.AHAAQVTCVAASPHK.D
*	HsFLAG-MOCK_300mM_T	5.0209	0.4408	1548.93	1548.71	7546		1	2088	78.6	4	R.AHAAQVTCVAASPHK.D
*	HsHeLa_Control-MG_Ti_20	5.0364	0.3925	1549.15	1548.71	9577.1		1	2272.4	75	2	R.AHAAQVTCVAASPHK.D
*	HsF-IP-293_Ti_206.1960.1	4.3406	0.4479	1549.28	1548.71	6322.5		1	1514.3	51.8	1	R.AHAAQVTCVAASPHK.D
*	HsFLAG-Control_MG_293_	4.9973	0.3782	1549.54	1548.71	7627.3		1	1720.3	51.8	1	R.AHAAQVTCVAASPHK.D
*	HsF-IP-293-MG_Ti_106.18	4.8488	0.4245	1549.6	1548.71	6148.7		1	1660.8	55.4	2	R.AHAAQVTCVAASPHK.D
*	HsHeLa_Control-MG_Ti_10	5.0533	0.4544	1549.96	1548.71	7614.1		1	2410.8	82.1	2	R.AHAAQVTCVAASPHK.D
*	HsHeLa_Control-MG_Ti_20	4.2804	0.4139	1551.16	1548.71	8419.6		2	1035.9	41.1	2	R.AHAAQVTCVAASPHK.D
*	HsHeLa_Control-MG_Ti_10	4.5496	0.4174	2960.54	2959.13	5561.6		1	955.8	32.7	1	R.AHAAQVTCVAASPHKDSVFLSCSEDNR.I
*	HsHeLa_Control-MG_Ti_20	2.621	0.1616	1428.39	1429.45	2354.8		7	140.5	59.1	2	K.DSVFLSCSEDNR.I
*	HsFLAG-Control_293_Ti_1	2.519	0.3027	1428.53	1429.45	3041.3		5	192.4	54.5	1	K.DSVFLSCSEDNR.I
*	HsF-IP-293-MG_Ti_102.16	4.1484	0.3546	1429.24	1429.45	5892.3		1	1067.2	77.3	14	K.DSVFLSCSEDNR.I
*	HsHeLa_Control_Ti_102.16	3.919	0.3475	1429.58	1429.45	4899.7		2	786.7	72.7	16	K.DSVFLSCSEDNR.I
*	HsHeLa_Control-MG_Ti_20	4.2038	0.4171	1431.05	1429.45	7712.5		1	1498.2	81.8	15	K.DSVFLSCSEDNR.I
*	Hs293FLP-MG_Ti_205.359	5.3897	0.378	4490.96	4492.91	7384.5		1	743.2	20.7	37	K.PASQIGCSAPGYLPTSLAWHPQQSEVFVFGDENGTVSLVDTK.S
gi|20070220|ref|N	178	1423	0.641	637	72684	6.3	U		SKB1 homolog [Homo sapiens]			
*	HsFlag1P_Ti_103.2910.291	4.6361	0.3047	2272.22	2273.52	7176.9		1	1520.8	54.8	5	R.VSSGRDLNCVPEIADTLGAVAK.Q
*	Hs293FLP-MG_Ti_203.286	3.896	0.3434	2274	2273.52	8748.7		1	659.5	38.1	8	R.VSSGRDLNCVPEIADTLGAVAK.Q
*	HsFlag1P_Ti_103.2935.293	4.208	0.2323	2274.75	2273.52	5942.7		1	1259.1	38.1	2	R.VSSGRDLNCVPEIADTLGAVAK.Q
*	Hs293FLP-MG_Ti_302.278	2.9379	0.1918	1786.59	1786.99	2519.4		3	329.4	59.4	1	R.DLNCVPEIADTLGAVAK.Q
*	Hs293FLP_Ti_303.2949.29	4.2351	0.2492	1786.78	1786.99	2558.4		1	581.2	71.9	7	R.DLNCVPEIADTLGAVAK.Q
*	Hs293FLP-MG_Ti_202.348	3.0188	0.2174	1786.84	1786.99	3900		3	525.1	56.2	2	R.DLNCVPEIADTLGAVAK.Q
*	HsF-IP-293-MG_Ti_102.27	4.7831	0.2725	1786.84	1786.99	8106.6		1	2416	56.2	2	R.DLNCVPEIADTLGAVAK.Q
*	HsFLAG-Control_293_Ti_1	4.2693	0.22	1786.96	1786.99	10455.7		1	2377.4	48.4	2	R.DLNCVPEIADTLGAVAK.Q
*	HsHeLa-FLAG-IP_S100_Ti_	4.4005	0.3883	1787.09	1786.99	2879.2		1	651.8	71.9	51	R.DLNCVPEIADTLGAVAK.Q
*	Hs293FLP-MG_Ti_202.354	4.1197	0.2063	1787.4	1786.99	9312.4		3	1179.8	42.2	1	R.DLNCVPEIADTLGAVAK.Q
*	HsF-IP-293_Ti_202.0140.0	4.6834	0.224	1787.45	1786.99	7750.4		1	1678.8	48.4	1	R.DLNCVPEIADTLGAVAK.Q
*	HsFLAG-Control_293_Ti_2	4.5563	0.4307	1787.61	1786.99	3607		1	974.6	81.2	15	R.DLNCVPEIADTLGAVAK.Q
*	Hs293FLP_Ti_305.3193.31	3.5602	0.2322	1753.85	1752.01	5849.7		2	842.9	44.2	1	K.QGFDFLCMPVFHPR.F
*	HsHeLa_Control-MG_Ti_20	3.2485	0.164	1393.12	1393.63	4994.4		1	775.9	80	1	R.FKREFIQEPAK.N
*	Hs293FLP-MG_Ti_204.145	2.7255	0.1352	1118.25	1118.28	4401.9		1	833.1	93.8	2	K.REFIQEPAK.N
*	Hs293FLP-MG_Ti_202.173	2.668	0.0805	961.47	962.09	4058.9		9	374.5	78.6	1	R.EFIQEPAK.N
*	HsFlag1P_Ti_106.2829.282	5.4079	0.3255	1887.56	1888.17	7914.5		1	1910	71.9	16	R.SDLLLSGRDWNTLIVGK.L
*	HsF-IP-293-MG_Ti_106.24	4.7411	0.2808	1888.61	1888.17	7112.9		1	1418.1	65.6	5	R.SDLLLSGRDWNTLIVGK.L
*	Hs293FLP_Ti_304.2878.28	3.8518	0.2126	1889.34	1888.17	5213.2		3	904.2	43.8	2	R.SDLLLSGRDWNTLIVGK.L
*	HsHeLa_Control-MG_Ti_20	3.6325	0.1062	3427.18	3424.97	8949.9		2	711	25.9	1	R.SDLLLSGRDWNTLIVGKLSPWIRPDSKVEK.I
*	HsFLAG-Control_293_Ti_2	2.7879	0.1389	1045.48	1046.21	7300.1		1	939.2	81.2	18	R.DWNTLIVGK.L

*	Hs293FLP-MG_Ti_102.253	2.0933	0.0923	1046.02	1046.21	6254.7	2	808.5	81.2	2	R.DWNTLIVGK.L
*	HsF-IP-293-MG_Ti_102.20	3.2098	0.0978	1046.4	1046.21	4444.5	2	1073.9	87.5	1	R.DWNTLIVGK.L
*	Hs283FLP_Ti_106.2020.20	3.44	0.2711	1555.9	1555.82	6242.7	1	842	70.8	14	K.LSPWIRPDSKVEK.I
*	HsHeLa_Control-MG_Ti_20	5.2777	0.3941	4005.21	4006.53	6679	1	572.2	25	3	R.RNSEAAMLQELNFGAYLGLPAFLLPLNQEDNTNLAR.V
*	HsF-IP-293-MG_Ti_106.29	7.0087	0.3965	3851.71	3850.34	7559.5	1	1630.5	30.9	47	R.NSEAAMLQELNFGAYLGLPAFLLPLNQEDNTNLAR.V
*	Hs293FLP_TREX_Ti_102.1	2.198	0.2868	1108.47	1109.31	3818.4	1	293.5	66.7	1	R.VPLVAPEDLR.D
*	HsF-IP-293_Ti_203.1864.1	1.9096	0.3059	1108.54	1109.31	3857.4	1	260.2	61.1	1	R.VPLVAPEDLR.D
*	HsF-IP-293-MG_Ti_103.17	2.4503	0.322	1108.6	1109.31	3909.3	4	295.2	66.7	3	R.VPLVAPEDLR.D
*	Hs293FLP-MG_Ti_203.203	2.2247	0.201	1108.61	1109.31	4142.6	1	315.9	66.7	2	R.VPLVAPEDLR.D
*	HsFLAG-Control_293_Ti_2	2.8853	0.2252	1108.62	1109.31	4229.6	1	450.1	72.2	2	R.VPLVAPEDLR.D
*	HsFLAG-Control_MG_293_	2.6749	0.2386	1108.65	1109.31	4345	2	374.5	72.2	2	R.VPLVAPEDLR.D
*	HsHeLa_Control-MG_Ti_10	2.234	0.2723	1108.79	1109.31	3313.3	9	199.8	55.6	2	R.VPLVAPEDLR.D
*	Hs293FLP-MG_Ti_103.196	2.5694	0.2286	1108.83	1109.31	3148.7	2	255.4	66.7	1	R.VPLVAPEDLR.D
*	HsFlag1P_Ti_104.2187.21	3.0181	0.2474	1109.04	1109.31	7428.5	1	1198.2	83.3	4	R.VPLVAPEDLR.D
*	HsHeLa-FLAG-IP_S100_Ti	3.5232	0.2959	1109.38	1109.31	6517.3	1	1243	83.3	17	R.VPLVAPEDLR.D
*	HsF-IP-293_Ti_103.1698.1	3.2889	0.2344	1109.4	1109.31	6780.2	1	1350	83.3	2	R.VPLVAPEDLR.D
*	HsFLAG-Control_293_Ti_2	3.4333	0.2528	1109.41	1109.31	6306.1	1	1104.8	77.8	3	R.VPLVAPEDLR.D
*	HsFLAG-Control_MG_293_	3.3966	0.2774	1109.44	1109.31	8224.2	1	1890.3	94.4	4	R.VPLVAPEDLR.D
*	Hs293FLP_TREX_Ti_102.1	3.1688	0.2702	1109.44	1109.31	6998.7	1	1108.3	83.3	3	R.VPLVAPEDLR.D
*	HsFLAG-Control_Hela_Ti_	2.2985	0.2357	1109.45	1109.31	3770.7	2	254.7	66.7	2	R.VPLVAPEDLR.D
*	Hs293FLP-MG_Ti_303.161	2.4961	0.3186	1109.48	1109.31	3016.5	2	248.2	72.2	1	R.VPLVAPEDLR.D
*	Hs293FLP-MG_Ti_203.203	3.0776	0.2246	1109.52	1109.31	6873.4	1	1086.5	77.8	2	R.VPLVAPEDLR.D
*	Hs293FLP-MG_Ti_103.196	2.86	0.2403	1109.53	1109.31	5336.8	2	777.8	72.2	2	R.VPLVAPEDLR.D
*	Hs283FLP_Ti_103.1675.16	3.2759	0.2589	1109.7	1109.31	6126.2	1	1286.1	88.9	6	R.VPLVAPEDLR.D
*	HsFLAG-Control_293_Ti_1	3.3445	0.2802	1110.33	1109.31	7798.3	1	1615.2	88.9	4	R.VPLVAPEDLR.D
*	HsF-IP-293-MG_Ti_103.17	3.3077	0.2151	1110.44	1109.31	6579.5	1	1601.3	94.4	4	R.VPLVAPEDLR.D
*	HsHeLa_Control-MG_Ti_20	2.0132	0.1449	1110.5	1109.31	2258.1	3	130.3	61.1	1	R.VPLVAPEDLR.D
*	HsHeLa_Control-MG_Ti_10	3.1675	0.2568	1110.69	1109.31	5718.8	2	883.3	77.8	3	R.VPLVAPEDLR.D
*	Hs293FLP_Ti_302.1826.18	2.4607	0.2543	1110.83	1109.31	3120.7	1	218.8	66.7	2	R.VPLVAPEDLR.D
*	Hs293FLP_Ti_305.2467.24	5.6747	0.3586	3369.25	3369.62	6804	1	1137.6	31.9	10	R.VPLVAPEDLRDDIIENAPTTHTEEYSGEEK.T
*	HsFLAG-Control_MG_293_	5.6536	0.4799	2278.63	2279.33	4817.8	1	985.6	60.5	2	R.DDIIENAPTTHTEEYSGEEK.T
*	Hs293FLP-MG_Ti_202.189	4.0991	0.2478	2279.42	2279.33	5230.9	4	809.5	36.8	1	R.DDIIENAPTTHTEEYSGEEK.T
*	HsFLAG-Control_293_Ti_1	5.4054	0.433	2279.97	2279.33	5652.8	1	1123.7	60.5	97	R.DDIIENAPTTHTEEYSGEEK.T
*	HsFLAG-Control_MG_293_	3.9849	0.1401	2281.32	2279.33	5021.4	1	1010.9	43.4	3	R.DDIIENAPTTHTEEYSGEEK.T
*	Hs293FLP-MG_Ti_303.142	4.5343	0.3684	2282.16	2279.33	4428.3	1	931	60.5	1	R.DDIIENAPTTHTEEYSGEEK.T
*	HsHeLa_Control-MG_Ti_10	2.6985	0.3246	1364.73	1364.57	5764.1	1	821.8	81.2	1	K.TWMWWHNFR.T
*	HsHeLa_Control-MG_Ti_20	4.4653	0.1854	2160.89	2160.48	5636	1	1025.1	40.8	5	K.RIAVALEIGADLPSNHVIDR.W
*	HsFLAG-Control_293_Ti_1	5.014	0.2404	2003.4	2004.29	8051.3	2	1872.4	43.1	6	R.IAVALEIGADLPSNHVIDR.W
*	HsFLAG-Control_293_Ti_1	5.4232	0.363	2003.98	2004.29	8000.7	1	2004.3	69.4	51	R.IAVALEIGADLPSNHVIDR.W
*	Hs293FLP-MG_Ti_203.527	4.7032	0.1495	2004.76	2004.29	7750.3	6	1628.4	41.7	6	R.IAVALEIGADLPSNHVIDR.W
*	Hs283FLP_Ti_106.2355.23	5.418	0.4088	2004.79	2004.29	6096.4	1	1370.3	63.9	5	R.IAVALEIGADLPSNHVIDR.W
*	HsHeLa_Control-MG_Ti_20	4.4978	0.2469	2004.94	2004.29	7382.3	1	2038.5	47.2	6	R.IAVALEIGADLPSNHVIDR.W
*	HsF-IP-293-MG_Ti_106.25	5.6778	0.4361	2005.79	2004.29	5576.8	1	1265.4	63.9	33	R.IAVALEIGADLPSNHVIDR.W
*	Hs293FLP_Ti_305.2482.24	4.8741	0.2224	2006.2	2004.29	7133.8	5	1790.2	44.4	3	R.IAVALEIGADLPSNHVIDR.W
*	HsHeLa_Control-MG_Ti_20	4.8381	0.3558	2006.31	2004.29	6949.1	1	1321.8	61.1	26	R.IAVALEIGADLPSNHVIDR.W
*	HsF-IP-293-MG_Ti_103.26	4.1539	0.4045	1388.3	1389.68	3161.4	1	883.3	83.3	34	K.AAILPTSIFLTNK.K
*	HsFLAG-Control_Hela_Ti_	2.3892	0.3618	1388.43	1389.68	7015.7	1	639.5	58.3	1	K.AAILPTSIFLTNK.K

*	HsHeLa_Control-MG_Ti_20	2.5492	0.3214	1388.63	1389.68	5499.8	1	341.4	50	2	K.AAILPTSIFLTNK.K
*	HsF-IP-293-MG_Ti_103.25	1.978	0.2638	1388.64	1389.68	5358.4	1	421.6	54.2	2	K.AAILPTSIFLTNK.K
*	HsHeLa_Control_Ti_104.34	2.2752	0.1538	1388.8	1389.68	5080.8	2	274.6	45.8	1	K.AAILPTSIFLTNK.K
*	Hs293FLP_Ti_304.2829.28	2.2217	0.2821	1388.8	1389.68	5331.5	1	446.2	54.2	2	K.AAILPTSIFLTNK.K
*	HsHeLa-FLAG-IP_S100_Ti	2.1511	0.2487	1388.83	1389.68	7377.9	1	528.7	54.2	1	K.AAILPTSIFLTNK.K
*	HsHeLa_Control_Ti_104.34	3.8316	0.3117	1389.4	1389.68	3248.8	1	638.8	75	3	K.AAILPTSIFLTNK.K
*	HsFlag1P_Ti_106.2828.282	4.0652	0.3943	1389.41	1389.68	3233	1	861.8	83.3	2	K.AAILPTSIFLTNK.K
*	HsFLAG-Control_293_Ti_2	2.8431	0.3204	1389.49	1389.68	7181.4	1	656.2	58.3	6	K.AAILPTSIFLTNK.K
*	HsFLAG-Control_HeLa_S1	4.2497	0.4033	1389.51	1389.68	3095.1	1	757	83.3	17	K.AAILPTSIFLTNK.K
*	Hs293FLP-MG_Ti_204.314	4.1984	0.4206	1389.55	1389.68	3354.7	1	732.9	79.2	7	K.AAILPTSIFLTNK.K
*	HsFLAG-Control_Hela_Ti_1	4.0233	0.3455	1389.56	1389.68	3296.4	1	854.3	83.3	5	K.AAILPTSIFLTNK.K
*	Hs293FLP-MG_Ti_203.322	2.6651	0.3623	1389.63	1389.68	6492	1	456.7	54.2	1	K.AAILPTSIFLTNK.K
*	HsFLAG-Control_293_Ti_1	2.4494	0.3369	1389.75	1389.68	7548	1	516.9	54.2	4	K.AAILPTSIFLTNK.K
*	HsFLAG-Control_293_Ti_1	4.1074	0.3361	1390.05	1389.68	3914.3	1	883.2	79.2	6	K.AAILPTSIFLTNK.K
*	Hs293FLP_Ti_304.2825.28	3.8537	0.3951	1390.15	1389.68	2806.2	1	687	79.2	9	K.AAILPTSIFLTNK.K
*	HsFLAG-Control_293_Ti_2	4.3207	0.3987	1390.68	1389.68	4459.4	1	1004.7	79.2	70	K.AAILPTSIFLTNK.K
*	HsHeLa_Control-MG_Ti_20	4.0939	0.3621	1390.97	1389.68	3540.8	1	819.2	79.2	22	K.AAILPTSIFLTNK.K
*	HsHeLa_Control-MG_Ti_20	2.9322	0.2677	1516.64	1517.85	4474	3	353.3	53.8	2	K.AAILPTSIFLTNKK.G
*	HsF-IP-293-MG_Ti_106.23	3.0644	0.2403	1517.65	1517.85	4904.1	8	305.4	50	2	K.AAILPTSIFLTNKK.G
*	HsFLAG-Control_HeLa_S1	3.0982	0.3536	1517.7	1517.85	3653.7	1	447.4	61.5	3	K.AAILPTSIFLTNKK.G
*	Hs293FLP_Ti_306.2827.28	2.7355	0.0899	1518.95	1517.85	4659.2	6	308.9	50	1	K.AAILPTSIFLTNKK.G
*	Hs293FLP_Ti_305.2401.24	2.8358	0.3104	1520.49	1517.85	3310.4	2	298.7	57.7	1	K.AAILPTSIFLTNKK.G
*	HsHeLa_Control-MG_Ti_20	3.6009	0.2589	1520.61	1517.85	3711	1	537	69.2	2	K.AAILPTSIFLTNKK.G
*	Hs293FLP_Ti_306.2376.23	2.0561	0.1153	874.86	876.087	3510.9	3	454.5	71.4	1	K.KGFPVLSK.M
*	HsF-IP-293_Ti_206.2158.2	1.9683	0.1441	875.4	876.087	3160.2	4	411.9	71.4	2	K.KGFPVLSK.M
*	HsHeLa_Control-MG_Ti_20	1.8244	0.1604	875.42	876.087	2934.9	7	290	64.3	1	K.KGFPVLSK.M
*	HsFLAG-Control_MG_293_	2.2148	0.1259	875.54	876.087	3762.5	3	467	71.4	1	K.KGFPVLSK.M
*	Hs293FLP-MG_Ti_206.261	1.8398	0.1513	875.57	876.087	4553.6	1	489.5	71.4	1	K.KGFPVLSK.M
*	HsFLAG-Control_293_Ti_2	2.1047	0.1681	875.58	876.087	3685.3	3	452.5	71.4	2	K.KGFPVLSK.M
*	Hs293FLP-MG_Ti_306.233	2.0188	0.1253	875.66	876.087	3493.1	2	429.5	71.4	2	K.KGFPVLSK.M
*	Hs283FLP_Ti_106.1991.19	2.0726	0.1207	875.67	876.087	3720.1	4	439.1	71.4	2	K.KGFPVLSK.M
*	HsHeLa_Control_Ti_106.27	2.4284	0.2036	875.88	876.087	3248.6	2	438.6	71.4	2	K.KGFPVLSK.M
*	HsHeLa_Control-MG_Ti_10	2.4254	0.1739	875.88	876.087	4025.3	5	456.8	71.4	3	K.KGFPVLSK.M
*	HsHeLa_Control-MG_Ti_20	3.2931	0.0976	876.23	876.087	4023.4	1	951.1	100	3	K.KGFPVLSK.M
*	HsFLAG-Control_MG_293_	3.1681	0.1046	876.32	876.087	4460.5	3	794.3	92.9	2	K.KGFPVLSK.M
*	HsFLAG-Control_293_Ti_2	3.2571	0.1165	876.32	876.087	3999.3	1	909	100	4	K.KGFPVLSK.M
*	HsHeLa_Control_Ti_106.27	3.0887	0.1012	876.36	876.087	3153.8	3	790.3	100	2	K.KGFPVLSK.M
*	HsF-IP-293_Ti_206.2159.2	3.2964	0.1038	876.36	876.087	3296.5	1	809.9	100	2	K.KGFPVLSK.M
*	Hs283FLP_Ti_106.1989.19	3.0123	0.1067	876.4	876.087	3318.8	1	691.5	92.9	1	K.KGFPVLSK.M
*	Hs293FLP-MG_Ti_206.261	3.0197	0.0987	876.49	876.087	4019.5	1	827.1	100	1	K.KGFPVLSK.M
*	HsHeLa_Control-MG_Ti_10	3.0852	0.0979	876.57	876.087	3092.1	1	835.5	100	2	K.KGFPVLSK.M
*	Hs293FLP_Ti_306.2379.23	3.2286	0.0915	876.8	876.087	3413.2	3	834.9	100	3	K.KGFPVLSK.M
*	Hs293FLP-MG_Ti_203.189	2.0294	0.0982	747.53	747.913	3241.3	4	379.1	75	2	K.GFPVLSK.M
*	HsHeLa_Control-MG_Ti_20	4.1801	0.2743	1855.11	1854.07	9829.9	6	749.8	50	7	K.LEVQFIITGTNHHSEK.E
*	Hs293FLP-MG_Ti_205.403	5.795	0.4932	3343.9	3342.7	7511.6	1	723.7	26.9	53	K.EFCSYLQYLEYLSQNRPPPNAYELFAK.G
*	HsFLAG-Control_293_Ti_2	5.2303	0.3998	3238.22	3238.55	8799.5	1	757.9	28.8	8	K.GYEDYLQSPLQPLMDNLESQTYEVFEK.D
*	Hs293FLP-MG_Ti_203.514	4.8306	0.2984	3690.57	3692.09	4931	1	585.7	26.7	4	K.GYEDYLQSPLQPLMDNLESQTYEVFEKDPIK.Y
*	HsHeLa_Control-MG_Ti_20	4.4715	0.3374	1744.88	1745.97	4471.2	1	782.7	76.9	6	K.DPIKYSQYQQAIYK.C
*	Hs293FLP-MG_Ti_302.135	3.0812	0.1932	1291.29	1292.43	7985.5	1	759.2	72.2	1	K.YSQYQQAIYK.C

*	HsFLAG-Control_293_Ti_2	2.7868	0.1666	1291.34	1292.43	9558.6	4	695.5	66.7	2	K.YSQYQQAIYK.C
*	Hs293FLP_TREX_Ti_102.1	2.9034	0.1568	1291.39	1292.43	9758.5	1	1072.5	77.8	1	K.YSQYQQAIYK.C
*	HsFLAG-Control_MG_293_	2.9198	0.0964	1291.39	1292.43	9874	7	742.1	66.7	2	K.YSQYQQAIYK.C
*	HsF-IP-293-MG_Ti_102.14	3.0123	0.162	1291.4	1292.43	8586.4	8	620.1	66.7	2	K.YSQYQQAIYK.C
*	HsFLAG-Control_293_Ti_1	2.4763	0.1621	1291.48	1292.43	8587.3	1	654.1	66.7	1	K.YSQYQQAIYK.C
*	Hs293FLP-MG_Ti_202.181	3.3002	0.2631	1291.51	1292.43	8856.3	2	848.2	72.2	2	K.YSQYQQAIYK.C
*	HsHeLa_Control-MG_Ti_10	2.7757	0.2108	1291.69	1292.43	7891.5	1	738.1	72.2	1	K.YSQYQQAIYK.C
*	HsFLAG-Control_HeLa_S1	2.6849	0.2141	1291.84	1292.43	10039.7	1	738.9	66.7	3	K.YSQYQQAIYK.C
*	HsFLAG-Control_293_Ti_2	3.8627	0.2582	1292.09	1292.43	6940.2	1	1365.8	88.9	3	K.YSQYQQAIYK.C
*	HsHeLa_Control-MG_Ti_20	3.9965	0.2813	1292.17	1292.43	7213.4	1	1408.5	88.9	7	K.YSQYQQAIYK.C
*	HsFLAG-Control_HeLa_S1	3.817	0.2602	1292.25	1292.43	7743.8	1	1355.2	88.9	3	K.YSQYQQAIYK.C
*	Hs293FLP-MG_Ti_202.182	3.8954	0.2108	1292.39	1292.43	6824	1	1252.4	88.9	3	K.YSQYQQAIYK.C
*	HsFLAG-Control_293_Ti_1	3.6182	0.3045	1292.39	1292.43	7172	1	1331.9	88.9	2	K.YSQYQQAIYK.C
*	Hs293FLP-MG_Ti_302.135	3.4723	0.2277	1292.48	1292.43	5934.5	1	1134.9	88.9	1	K.YSQYQQAIYK.C
*	HsFLAG-Control_Hela_Ti_1	3.1911	0.2357	1292.5	1292.43	8651.9	1	982	77.8	1	K.YSQYQQAIYK.C
*	HsHeLa_Control-MG_Ti_20	2.8473	0.1677	1292.5	1292.43	7023.7	1	698	72.2	2	K.YSQYQQAIYK.C
*	HsHelaFlag1P_Ti_102.147	3.086	0.2591	1292.87	1292.43	5077.5	1	931.1	88.9	2	K.YSQYQQAIYK.C
*	HsHeLa_Control-MG_Ti_10	3.749	0.2948	1293.02	1292.43	6394	1	1268	88.9	4	K.YSQYQQAIYK.C
*	HsFLAG-Control_MG_293_	3.8109	0.2533	1293.47	1292.43	6925.3	1	1252.2	88.9	2	K.YSQYQQAIYK.C
*	Hs293FLP_Ti_302.1496.14	3.426	0.2723	1293.66	1292.43	6148.9	1	1163.8	88.9	2	K.YSQYQQAIYK.C
*	Hs293FLP-MG_Ti_102.165	3.8265	0.2605	1293.8	1292.43	5696.5	1	1112.1	88.9	4	K.YSQYQQAIYK.C
*	HsFLAG-Control_HeLa_NE	3.6841	0.3521	1294.06	1292.43	7696.8	1	1338.9	88.9	22	K.YSQYQQAIYK.C
*	HsFLAG-Control_293_Ti_1	4.2991	0.1467	1388.2	1388.53	6562.3	3	1383.9	85	42	K.CLLDRVPEEEK.D
*	Hs293FLP-MG_Ti_204.323	5.4671	0.336	2843.96	2843.23	9079	1	983.7	29.2	11	K.CLLDRVPEEEKDTNVQVLMVLGAGR.G
*	HsHeLa_Control-MG_Ti_10	2.9192	0.2186	2185.4	2185.5	7019	1	532.7	44.7	1	R.VPEEEKDTNVQVLMVLGAGR.G
*	HsF-IP-293_Ti_206.2504.2	3.6218	0.3273	1472.52	1473.73	3958.6	1	318.4	57.7	1	K.DTNVQVLMVLGAGR.G
*	HsFLAG-Control_293_Ti_2	3.2577	0.3519	1472.58	1473.73	4002.7	1	376.8	61.5	1	K.DTNVQVLMVLGAGR.G
*	Hs293FLP_Ti_302.2863.28	5.2146	0.3683	1472.72	1473.73	6524.8	1	1989.1	84.6	12	K.DTNVQVLMVLGAGR.G
*	HsF-IP-293-MG_Ti_104.25	5.1166	0.4174	1473.3	1473.73	6914.2	1	1639.4	80.8	40	K.DTNVQVLMVLGAGR.G
*	HsHeLa_Control-MG_Ti_20	4.6194	0.3801	1473.36	1473.73	8064.4	1	2186.2	80.8	2	K.DTNVQVLMVLGAGR.G
*	HsFLAG-Control_HeLa_S1	2.2063	0.1701	926.52	927.092	3556.8	3	230.4	75	1	R.GPLVNASLR.A
*	HsFLAG-Control_HeLa_S1	3.1189	0.2736	927.3	927.092	5117.6	2	1000.5	87.5	6	R.GPLVNASLR.A
*	Hs293FLP-MG_Ti_204.165	3.3187	0.2773	927.39	927.092	4857.1	4	807	81.2	31	R.GPLVNASLR.A
*	HsFLAG-Control_293_Ti_1	1.9513	0.1931	858.49	858.969	3377.7	8	276.7	83.3	2	R.EWVAPEK.A
*	HsHeLa_Control-MG_Ti_10	4.2729	0.2038	4131.37	4130.56	5762	1	497.9	21.5	1	R.EWVAPEKADIIVSELLGSFADNELSPECLDGAQHFLK.D
*	HsHeLa_Control-MG_Ti_20	6.112	0.4032	3289.45	3290.62	6778.1	1	1194.8	32.8	103	K.ADIIVSELLGSFADNELSPECLDGAQHFLK.D
*	HsHeLa-FLAG-IP_S100_Ti_	4.7584	0.5291	2173.47	2171.37	3808.2	1	658.1	57.5	113	K.DDGVSIPGEYTSFLAPISSSK.L
*	HsFlag1P_Ti_103.2505.25	3.0279	0.1609	2109.68	2110.35	5689.6	3	415.7	50	2	R.EKDRDPEAQFEMPYVVR.L
*	Hs293FLP-MG_Ti_203.253	4.1426	0.3606	1852.46	1853.06	5656.9	1	793.4	67.9	2	K.DRDPEAQFEMPYVVR.L
*	HsF-IP-293_Ti_206.2366.2	3.996	0.2957	1852.62	1853.06	5209.2	1	815	67.9	2	K.DRDPEAQFEMPYVVR.L
*	Hs293FLP-MG_Ti_306.252	3.7747	0.3117	1852.65	1853.06	4732.1	1	660.2	64.3	2	K.DRDPEAQFEMPYVVR.L
*	Hs293FLP-MG_Ti_203.254	3.8113	0.1445	1852.7	1853.06	5401.7	1	1056.5	48.2	1	K.DRDPEAQFEMPYVVR.L
*	HsHeLa_Control-MG_Ti_10	4.0584	0.3554	1853.04	1853.06	4992.1	1	770.2	67.9	6	K.DRDPEAQFEMPYVVR.L
*	HsHeLa_Control-MG_Ti_20	4.3383	0.1715	1853.05	1853.06	8070.7	5	1307.2	44.6	1	K.DRDPEAQFEMPYVVR.L
*	HsF-IP-293_Ti_206.2379.2	3.9201	0.0917	1853.06	1853.06	6107.5	1	1362.9	51.8	1	K.DRDPEAQFEMPYVVR.L
*	HsHeLa_Control-MG_Ti_10	4.0857	0.1115	1853.48	1853.06	5072.6	1	1305.4	53.6	2	K.DRDPEAQFEMPYVVR.L
*	HsHeLa_Control-MG_Ti_20	3.9313	0.3333	1853.56	1853.06	5292.4	1	844.5	67.9	3	K.DRDPEAQFEMPYVVR.L
*	Hs293FLP_Ti_302.2490.24	4.4171	0.3103	1853.99	1853.06	4804.3	1	796	71.4	48	K.DRDPEAQFEMPYVVR.L

*	HsF-IP-293-MG_Ti_105.29	4.2399	0.1602	1854.53	1853.06	7466		1	1618.8	53.6	4	K.DRDPEAQFEMPYVVR.L
*	HsFLAG-Control_293_Ti_2	3.0653	0.2298	1580.64	1581.78	10996		3	814.6	50	1	R.DPEAQFEMPYVVR.L
*	Hs293FLP-MG_Ti_206.303	2.998	0.2467	2543.77	2543.85	6806.7		1	429.2	38.1	1	K.KVWYEWAVTAPVCSAIHNPTGR.S
*	Hs293FLP_Ti_306.2858.28	4.7647	0.4139	2544.16	2543.85	4740.3		1	1053.2	59.5	4	K.KVWYEWAVTAPVCSAIHNPTGR.S
*	HsHeLa_Control-MG_Ti_10	5.0151	0.3899	2544.38	2543.85	4972.9		1	1152.5	61.9	2	K.KVWYEWAVTAPVCSAIHNPTGR.S
*	Hs293FLP_Ti_306.2856.28	4.8388	0.3042	2544.43	2543.85	8344.7		1	1882.7	39.3	2	K.KVWYEWAVTAPVCSAIHNPTGR.S
*	HsHeLa_Control-MG_Ti_10	5.3141	0.2506	2544.54	2543.85	8112.4		1	1970	40.5	1	K.KVWYEWAVTAPVCSAIHNPTGR.S
*	HsFLAG-Control_293_Ti_1	4.4129	0.4244	2413.78	2415.68	4942.7		1	819.6	55	7	K.VWYEWAVTAPVCSAIHNPTGR.S
*	Hs293FLP-MG_Ti_205.302	3.5923	0.1879	2414.83	2415.68	6285.2		1	1064.2	36.2	2	K.VWYEWAVTAPVCSAIHNPTGR.S
*	HsHeLa_Control-MG_Ti_20	4.7415	0.4154	2415.36	2415.68	5164.8		1	693	52.5	17	K.VWYEWAVTAPVCSAIHNPTGR.S
*	HsFLAG-Control_293_Ti_1	3.9845	0.2774	2416.43	2415.68	8358.1		1	1307.5	35	1	K.VWYEWAVTAPVCSAIHNPTGR.S
*	Hs293FLP-MG_Ti_205.302	4.2435	0.3895	2416.44	2415.68	5849.6		1	697.8	47.5	5	K.VWYEWAVTAPVCSAIHNPTGR.S
*	HsHeLa_Control-MG_Ti_20	4.4578	0.2642	2416.68	2415.68	6370.2		1	1014.6	35	2	K.VWYEWAVTAPVCSAIHNPTGR.S
gi|17986283|ref|	39	745	0.641	451	50136	5.1	U	tubulin, alpha 3 [Homo sapiens]				
	HsFLAG-Control_HeLa_S1	5.6931	0.4653	2009.21	2009.09	9324.1		1	1749.3	63.2	204	K.TIGGGDDSFNTFFSETGAGK.H
	HsF-IP-293-MG_Ti_102.27	5.0334	0.4399	1702.32	1702.95	4530		1	1284.8	82.1	22	R.AVFVDLEPTVIDEVR.T
	HsFLAG-Control_HeLa_S1	4.9427	0.335	1702.54	1702.95	7851		1	1529.4	50	5	R.AVFVDLEPTVIDEVR.T
	HsFLAG-Control_HeLa_S1	4.0389	0.2932	1703.03	1702.95	8687.1		1	1386.4	46.4	2	R.AVFVDLEPTVIDEVR.T
	HsHeLa-FLAG-IP_S100_Ti_	5.2915	0.4169	1703.58	1702.95	4669.1		1	1294.9	82.1	56	R.AVFVDLEPTVIDEVR.T
	HsFLAG-Control_HeLa_S1	4.7409	0.3371	1703.91	1702.95	5321.1		1	1259.1	78.6	16	R.AVFVDLEPTVIDEVR.T
	HsFLAG-Control_HeLa_NE	4.1691	0.3052	1704.24	1702.95	8886.6		1	1330.2	44.6	1	R.AVFVDLEPTVIDEVR.T
	HsHeLa_Control_Ti_102.30	5.091	0.2766	1704.76	1702.95	4122.7		1	1098.9	82.1	19	R.AVFVDLEPTVIDEVR.T
	HsFLAG-Control_HeLa_S1	4.2449	0.3005	2415.72	2416.66	8163.2		1	1212.2	36.2	4	R.QLFHPEQLITGKEDAANNYAR.G
	HsHeLa_Control-MG_Ti_10	3.4137	0.2652	2416.42	2416.66	7726.4		1	627.9	45	8	R.QLFHPEQLITGKEDAANNYAR.G
	HsGST-MOCK_Ti_103.173	4.1081	0.2897	2416.8	2416.66	6806.6		1	1048.6	36.2	1	R.QLFHPEQLITGKEDAANNYAR.G
	HsFLAG-Control_HeLa_NE	3.5321	0.3633	2417.37	2416.66	8286.1		1	502	42.5	3	R.QLFHPEQLITGKEDAANNYAR.G
	HsFLAG-Control_HeLa_S1	3.3565	0.0828	1086.26	1086.27	6338.4		2	941.8	87.5	18	K.EIIDLVLDR.I
	Hs293FLP-MG_Ti_206.350	4.9972	0.3758	3392.79	3392.78	9865.2		1	1364.1	27.4	5	K.LADQCTGLQGFLVFHSFGGGTGSGFTSLLMER.L
	HsFLAG-Control_MG_293_	3.4903	0.1725	1719.53	1719.9	7713.5		1	803	61.5	17	R.NLDIERPTYTNLNR.L
	HsFLAG-Control_HeLa_NE	5.8208	0.383	2410.89	2410.69	6224.2		1	1491.8	62.5	149	R.FDGALNVDLTEFQTNLVPYPR.I
	HsFLAG-Control_HeLa_S1	3.7053	0.2052	1757.29	1758.07	4837.7		5	804.3	45	1	R.IHFPLATYAPVISAEK.A
	HsFLAG-Control_HeLa_NE	4.2732	0.3578	1757.6	1758.07	4681.9		1	893.2	70	13	R.IHFPLATYAPVISAEK.A
	HsHeLa_Control-MG_Ti_20	4.3621	0.4339	1757.74	1758.07	4584.4		1	1152	76.7	16	R.IHFPLATYAPVISAEK.A
	HsFLAG-Control_HeLa_S1	4.2526	0.2613	1757.75	1758.07	5170.2		2	1162.9	48.3	1	R.IHFPLATYAPVISAEK.A
	HsFLAG-Control_HeLa_S1	4.411	0.4766	1758.41	1758.07	4071.6		1	935.5	73.3	3	R.IHFPLATYAPVISAEK.A
	HsHeLa_Control-MG_Ti_10	4.4041	0.3426	2753.23	2752.04	7001.1		1	1357.7	52.2	2	K.AYHEQLSVAEITNACFEPANQMVK.C
	Hs293FLP-MG_Ti_103.214	3.0177	0.1953	1251.47	1250.43	4064.5		1	618.2	81.2	2	K.YMACCLLYR.G
	HsFLAG-Control_HeLa_S1	2.3439	0.2742	1015.45	1016.18	7798		1	652.7	72.2	2	K.DVNAAIATIK.T
	HsFLAG-Control_293_Ti_2	2.4919	0.2722	1015.46	1016.18	6406.7		1	644.8	77.8	4	K.DVNAAIATIK.T
	HsFLAG-Control_HeLa_S1	2.1932	0.1673	1015.48	1016.18	6826.5		6	502	66.7	1	K.DVNAAIATIK.T
	HsHeLa_Control_Ti_102.17	2.4787	0.2338	1015.71	1016.18	5846.2		1	557.5	77.8	3	K.DVNAAIATIK.T
	HsFLAG-Control_HeLa_S1	3.6128	0.2873	1016.27	1016.18	5362.6		1	1163.9	88.9	1	K.DVNAAIATIK.T
	HsFLAG-Control_HeLa_S1	3.5311	0.2771	1016.35	1016.18	5480.7		1	1193.4	88.9	2	K.DVNAAIATIK.T
	HsFLAG-Control_HeLa_S1	3.5176	0.2784	1016.38	1016.18	5208.6		1	1029	83.3	1	K.DVNAAIATIK.T
	HsHeLa-FLAG-IP_S100_Ti_	3.4285	0.2973	1016.56	1016.18	5657.7		1	925.2	77.8	12	K.DVNAAIATIK.T
	HsFLAG-Control_HeLa_S1	2.1618	0.2038	1017.63	1016.18	6803		6	446.1	66.7	2	K.DVNAAIATIK.T
	HsHeLa_Control-MG_Ti_20	3.7919	0.422	1755.69	1755.98	6153.4		1	806.5	65.4	7	K.RTIQFVDWCPTGFK.V
	HsFLAG-Control_HeLa_S1	4.5938	0.4395	1599.28	1599.79	7004.1		1	1203.6	75	4	R.TIQFVDWCPTGFK.V
	HsHeLa-FLAG-IP_S100_Ti_	4.1491	0.409	1825.53	1826.1	3764.8		1	755.9	64.7	121	K.VGINYQPPTVVPGGDLAK.V

	HsF-IP-293-MG_Ti_104.26	2.8488	0.3461	1865.28	1866.11	9656.2		1	1217.8	59.4	2	R.AVCMLSNTTAIAEAWAR.L
	HsGST-MOCK_Ti_404.302	2.6983	0.1597	2332.29	2331.52	9294.4		1	579.2	42.1	1	R.AFVHWYVGEGMEEGEFSEAR.E
	HsFLAG-Control_HeLa_S1	2.1109	0.2465	906.43	907.026	5999.8		4	545.2	78.6	1	R.EDMAALEK.D
	HsGST-MOCK_Ti_402.032	5.1595	0.5167	2350.05	2350.28	9303.1		1	2231.4	65	13	K.DYEEVGVDSVEGEGEEEGEEY.-
gi|57242777|ref|N	31	111	0.641	103	11967	5.9	U	c-myc binding protein [Homo sapiens]				
*	HsHeLa_Control-MG_Ti_10	1.8718	0.1038	932.77	934.078	6130.4		2	456.3	62.5	1	K.SGVLDTLTK.V
*	HsFLAG-Control_HeLa_NE	2.2287	0.1557	933.49	934.078	6953.2		4	570.9	68.8	3	K.SGVLDTLTK.V
*	Hs293FLP_Ti_302.1770.17	1.8315	0.11	933.84	934.078	6868.8		7	505.7	68.8	1	K.SGVLDTLTK.V
*	HsHeLa-FLAG-IP_S100_Ti_	2.8055	0.285	934.2	934.078	3315		2	1060.5	93.8	2	K.SGVLDTLTK.V
*	Hs283FLP_Ti_102.1718.17	2.6346	0.2574	934.28	934.078	3435.5		2	1116.1	93.8	1	K.SGVLDTLTK.V
*	HsF-IP-293-MG_Ti_102.17	2.8264	0.2854	934.42	934.078	3086.2		2	1044.3	93.8	1	K.SGVLDTLTK.V
*	HsF-IP-293-MG_Ti_106.25	4.6434	0.321	2275.03	2276.64	5195.1		1	591.4	52.6	5	K.VLVALYEEPEKPNSALDFLK.H
*	HsHeLa_Control-MG_Ti_20	4.1032	0.2697	2275.52	2276.64	6566.6		5	525.6	42.1	3	K.VLVALYEEPEKPNSALDFLK.H
*	HsHeLa_Control-MG_Ti_20	4.8105	0.3376	2275.63	2276.64	5431.5		1	824.6	39.5	4	K.VLVALYEEPEKPNSALDFLK.H
*	HsFlag1P_Ti_105.3196.31	3.7964	0.3032	2275.7	2276.64	5283.9		3	708.3	35.5	1	K.VLVALYEEPEKPNSALDFLK.H
*	HsHeLa_Control-MG_Ti_10	4.0297	0.2718	2276.28	2276.64	4858		6	315.2	39.5	5	K.VLVALYEEPEKPNSALDFLK.H
*	HsFlag1P_Ti_105.3182.31	4.9703	0.3337	2276.93	2276.64	5615.1		1	765.1	55.3	7	K.VLVALYEEPEKPNSALDFLK.H
*	HsHeLa_Control_Ti_103.32	4.4326	0.2926	2277	2276.64	4757.1		1	520.1	47.4	17	K.VLVALYEEPEKPNSALDFLK.H
*	Hs293FLP-MG_Ti_203.333	5.0189	0.3308	2277.15	2276.64	6442.8		1	1332.5	43.4	4	K.VLVALYEEPEKPNSALDFLK.H
*	Hs293FLP_Ti_305.2871.28	4.9835	0.2992	2277.61	2276.64	5090.9		1	888.8	39.5	6	K.VLVALYEEPEKPNSALDFLK.H
*	Hs293FLP_Ti_305.2869.28	4.712	0.3062	2277.78	2276.64	4528		1	592.2	55.3	6	K.VLVALYEEPEKPNSALDFLK.H
*	HsFLAG-MOCK_300mM_T	3.8829	0.288	2278.23	2276.64	4759.2		2	610.6	36.8	2	K.VLVALYEEPEKPNSALDFLK.H
*	HsHeLa_Control-MG_Ti_10	4.1419	0.2895	2278.69	2276.64	4335.2		1	682.9	39.5	1	K.VLVALYEEPEKPNSALDFLK.H
*	HsHeLa_Control-MG_Ti_20	3.7221	0.303	1897.15	1898.13	6623.8		1	1361.8	71.9	2	K.HHLGAATPENPEIELLR.L
*	Hs293FLP-MG_Ti_206.277	4.13	0.2925	1897.66	1898.13	6648.9		1	1156.2	65.6	6	K.HHLGAATPENPEIELLR.L
*	HsHeLa_Control-MG_Ti_20	4.481	0.2553	1897.98	1898.13	7663.2		1	1923.3	48.4	2	K.HHLGAATPENPEIELLR.L
*	Hs293FLP-MG_Ti_206.278	3.9915	0.1388	1898.15	1898.13	7573.5		1	1701.6	48.4	1	K.HHLGAATPENPEIELLR.L
*	HsHeLa_Control-MG_Ti_10	3.9586	0.1942	1898.76	1898.13	6063.7		1	1048.3	65.6	2	K.HHLGAATPENPEIELLR.L
*	HsHeLa_Control-MG_Ti_10	3.5319	0.1867	1899.4	1898.13	5851.6		1	1168.1	45.3	1	K.HHLGAATPENPEIELLR.L
*	Hs283FLP_Ti_102.1294.12	2.7832	0.1096	1094.49	1095.19	6645.8		2	736.7	75	3	K.YEAIVEENK.K
*	HsHeLa_Control_Ti_102.12	2.5205	0.1896	1094.53	1095.19	6487.6		3	738.4	75	2	K.YEAIVEENK.K
*	HsHeLa-FLAG-IP_S100_Ti_	2.591	0.1182	1095.11	1095.19	5670.3		1	956.5	87.5	1	K.YEAIVEENK.K
*	HsFLAG-Control_Hela_Ti_1	2.0223	0.2616	1331.47	1332.45	3973		3	390.3	65	1	K.LAQYEPPQEEK.R
*	Hs293FLP-MG_Ti_202.168	2.4056	0.1318	1331.58	1332.45	3981.4		6	296.3	55	1	K.LAQYEPPQEEK.R
*	HsHeLa_Control_Ti_102.13	3.0521	0.2152	1332.02	1332.45	3289.9		1	587.5	80	1	K.LAQYEPPQEEK.R
*	HsHeLa-FLAG-IP_S100_Ti_	3.5046	0.1803	1332.35	1332.45	3938.8		5	517.3	70	18	K.LAQYEPPQEEK.R
gi|4505813|ref|N	7	15	0.64	89	10366	7.4	U	cytoplasmic dynein light polypeptide [Homo sapiens]				
*	HsHeLa3_Ti_102.2402.240	4.4049	0.4002	2516.07	2515.65	9925.5		1	1374	50	2	K.NADMSEEMQQDSVECATQALEK.Y
*	HsFLAG-Control_HeLa_NE	1.8987	0.1463	767.53	767.903	3278.1		1	454.1	83.3	2	K.DIAAHIK.K
*	HsFLAG-MOCK_300mM_T	4.1091	0.3533	1417.72	1415.63	10275.7		1	1836	86.4	3	K.DIAAHIKKEFDK.K
	HsGST-MOCK_Ti_106.215	2.9763	0.2661	1531.28	1531.72	5223.3		1	1038.2	81.8	1	K.KYNPTWHCIVGR.N
	HsFLAG-Control_HeLa_NE	2.7353	0.2141	1282.67	1283.38	5483		1	487.8	65	2	R.NFGSYVTHETK.H
	HsFLAG-Control_HeLa_NE	3.2281	0.3104	1284.39	1283.38	6420.5		2	737.8	70	2	R.NFGSYVTHETK.H
	HsFLAG-Control_HeLa_NE	2.9627	0.3019	1284.57	1283.38	6332		1	751.6	75	3	R.NFGSYVTHETK.H
gi|57013276|ref|N	45	852	0.636	451	50152	5.1	U	tubulin, alpha, ubiquitous [Homo sapiens]				
	HsFLAG-Control_HeLa_S1	5.6931	0.4653	2009.21	2009.09	9324.1		1	1749.3	63.2	204	K.TIGGGDDSFNTFFSETGAGK.H
	HsF-IP-293-MG_Ti_102.27	5.0334	0.4399	1702.32	1702.95	4530		1	1284.8	82.1	22	R.AVFVDLEPTVIDEVR.T
	HsFLAG-Control_HeLa_S1	4.9427	0.335	1702.54	1702.95	7851		1	1529.4	50	5	R.AVFVDLEPTVIDEVR.T
	HsFLAG-Control_HeLa_S1	4.0389	0.2932	1703.03	1702.95	8687.1		1	1386.4	46.4	2	R.AVFVDLEPTVIDEVR.T

	HsHeLa-FLAG-IP_S100_Ti_	5.2915	0.4169	1703.58	1702.95	4669.1	1	1294.9	82.1	56	R.AVFVDLEPTVIDEVR.T
	HsFLAG-Control_HeLa_S1	4.7409	0.3371	1703.91	1702.95	5321.1	1	1259.1	78.6	16	R.AVFVDLEPTVIDEVR.T
	HsFLAG-Control_HeLa_NE	4.1691	0.3052	1704.24	1702.95	8886.6	1	1330.2	44.6	1	R.AVFVDLEPTVIDEVR.T
	HsHeLa_Control_Ti_102.30	5.091	0.2766	1704.76	1702.95	4122.7	1	1098.9	82.1	19	R.AVFVDLEPTVIDEVR.T
	HsFLAG-Control_HeLa_S1	4.2449	0.3005	2415.72	2416.66	8163.2	1	1212.2	36.2	4	R.QLFHPEQLITGKEDAANNYAR.G
	HsHeLa_Control-MG_Ti_10	3.4137	0.2652	2416.42	2416.66	7726.4	1	627.9	45	8	R.QLFHPEQLITGKEDAANNYAR.G
	HsGST-MOCK_Ti_103.173	4.1081	0.2897	2416.8	2416.66	6806.6	1	1048.6	36.2	1	R.QLFHPEQLITGKEDAANNYAR.G
	HsFLAG-Control_HeLa_NE	3.5321	0.3633	2417.37	2416.66	8286.1	1	502	42.5	3	R.QLFHPEQLITGKEDAANNYAR.G
	HsFLAG-Control_HeLa_S1	3.3565	0.0828	1086.26	1086.27	6338.4	2	941.8	87.5	18	K.EIIDLVLDR.I
	Hs293FLP-MG_Ti_206.350	4.9972	0.3758	3392.79	3392.78	9865.2	1	1364.1	27.4	5	K.LADQCTGLQGFLVFHSFGGGTGSGFTSLLMER.L
	HsFLAG-Control_MG_293_	3.4903	0.1725	1719.53	1719.9	7713.5	1	803	61.5	17	R.NLDIERPTYTNLNR.L
	HsFLAG-Control_HeLa_S1	4.6066	0.4074	1488.47	1488.77	7506.5	1	1467.1	76.9	9	R.LISQIVSSITASLR.F
	HsFLAG-Control_HeLa_S1	4.684	0.43	1488.49	1488.77	7157.4	1	1312.2	73.1	22	R.LISQIVSSITASLR.F
	HsHeLa_Control-MG_Ti_20	5.0495	0.4454	1488.53	1488.77	8030.6	1	1907.4	80.8	39	R.LISQIVSSITASLR.F
	HsFLAG-Control_HeLa_S1	4.722	0.3946	1488.57	1488.77	8151.1	1	1172.8	69.2	9	R.LISQIVSSITASLR.F
	HsFLAG-Control_HeLa_S1	4.3035	0.346	1488.75	1488.77	5615.6	1	1324.7	55.8	2	R.LISQIVSSITASLR.F
	HsFLAG-Control_HeLa_S1	4.1471	0.2471	1489.29	1488.77	5256.5	3	867.3	50	2	R.LISQIVSSITASLR.F
	HsFLAG-Control_HeLa_NE	4.6049	0.3537	1489.3	1488.77	6361.1	1	1211.5	73.1	15	R.LISQIVSSITASLR.F
	HsFLAG-Control_HeLa_NE	4.3453	0.2295	1489.54	1488.77	5799.3	1	1231.8	53.8	2	R.LISQIVSSITASLR.F
	HsFLAG-Control_HeLa_S1	3.7596	0.3173	1490.02	1488.77	5380.1	1	894.9	50	1	R.LISQIVSSITASLR.F
	HsFLAG-Control_HeLa_NE	5.8208	0.383	2410.89	2410.69	6224.2	1	1491.8	62.5	149	R.FDGALNVDLTEFQTNLVPYPR.I
	HsHeLa_Control-MG_Ti_10	4.4041	0.3426	2753.23	2752.04	7001.1	1	1357.7	52.2	2	K.AYHEQLSVAEITNACFEPANQMVK.C
	Hs293FLP-MG_Ti_103.214	3.0177	0.1953	1251.47	1250.43	4064.5	1	618.2	81.2	2	K.YMACCLLYR.G
	HsFLAG-Control_HeLa_S1	2.3439	0.2742	1015.45	1016.18	7798	1	652.7	72.2	2	K.DVNAAIATIK.T
	HsFLAG-Control_293_Ti_2	2.4919	0.2722	1015.46	1016.18	6406.7	1	644.8	77.8	4	K.DVNAAIATIK.T
	HsFLAG-Control_HeLa_S1	2.1932	0.1673	1015.48	1016.18	6826.5	6	502	66.7	1	K.DVNAAIATIK.T
	HsHeLa_Control_Ti_102.17	2.4787	0.2338	1015.71	1016.18	5846.2	1	557.5	77.8	3	K.DVNAAIATIK.T
	HsFLAG-Control_HeLa_S1	3.6128	0.2873	1016.27	1016.18	5362.6	1	1163.9	88.9	1	K.DVNAAIATIK.T
	HsFLAG-Control_HeLa_S1	3.5311	0.2771	1016.35	1016.18	5480.7	1	1193.4	88.9	2	K.DVNAAIATIK.T
	HsFLAG-Control_HeLa_S1	3.5176	0.2784	1016.38	1016.18	5208.6	1	1029	83.3	1	K.DVNAAIATIK.T
	HsHeLa-FLAG-IP_S100_Ti_	3.4285	0.2973	1016.56	1016.18	5657.7	1	925.2	77.8	12	K.DVNAAIATIK.T
	HsFLAG-Control_HeLa_S1	2.1618	0.2038	1017.63	1016.18	6803	6	446.1	66.7	2	K.DVNAAIATIK.T
	HsFLAG-Control_HeLa_S1	4.2609	0.3792	1742.64	1741.95	6595.1	1	848.5	61.5	13	K.RSIQFVDWCPTGFK.V
	HsHeLa_Control-MG_Ti_10	2.0279	0.2794	1584.51	1585.77	5859.1	2	301.2	41.7	1	R.SIQFVDWCPTGFK.V
	HsFLAG-Control_HeLa_S1	4.2773	0.4207	1585.41	1585.77	5673	1	1071.3	75	19	R.SIQFVDWCPTGFK.V
	HsHeLa_Control-MG_Ti_10	4.2534	0.4251	1587.43	1585.77	4819.9	1	915.9	75	18	R.SIQFVDWCPTGFK.V
	HsHeLa-FLAG-IP_S100_Ti_	4.1491	0.409	1825.53	1826.1	3764.8	1	755.9	64.7	121	K.VGINYQPPTVVPGGDLAK.V
	HsF-IP-293-MG_Ti_104.26	2.8488	0.3461	1865.28	1866.11	9656.2	1	1217.8	59.4	2	R.AVCMLSNTTAIAEAWAR.L
	HsGST-MOCK_Ti_404.302	2.6983	0.1597	2332.29	2331.52	9294.4	1	579.2	42.1	1	R.AFVHWYVGEGMEEGEFSEAR.E
	HsFLAG-Control_HeLa_S1	2.1109	0.2465	906.43	907.026	5999.8	4	545.2	78.6	1	R.EDMAALEK.D
	HsGST-MOCK_Ti_402.032	5.1595	0.5167	2350.05	2350.28	9303.1	1	2231.4	65	13	K.DYEEVGVDSVEGEGEEEGEEY.-
gi|4885431|ref|N	119	605	0.635	641	70025	5.6	U	heat shock 70kDa protein 1B [Homo sapiens]			
	Hs293FLP-MG_Ti_204.283	3.2702	0.2947	2265.63	2266.53	8694.6	2	578.6	40.5	4	K.AAAIGIDLGTTYSCVGVFQHGK.V
	HsF-IP-293-MG_Ti_102.17	2.6315	0.2566	1487.66	1488.59	3419.2	1	176.5	58.3	2	R.TTPSYVAFTDTER.L
	Hs293FLP-MG_Ti_202.217	3.2886	0.3043	1487.89	1488.59	4372.6	1	860.7	83.3	12	R.TTPSYVAFTDTER.L
	HsFLAG-Control_HeLa_NE	3.2444	0.2808	1487.89	1488.59	4634.5	1	570.4	66.7	57	R.TTPSYVAFTDTER.L
	HsHeLa_Control-MG_Ti_20	2.4813	0.2055	1488.47	1488.59	3249.8	1	121.1	50	1	R.TTPSYVAFTDTER.L
	HsHeLa_Control-MG_Ti_20	3.6044	0.4296	1489.1	1488.59	3675.9	1	589.8	75	9	R.TTPSYVAFTDTER.L
	HsFLAG-MOCK_300mM_T	3.2112	0.1491	2159.14	2157.39	6487.7	1	523.9	44.7	2	R.TTPSYVAFTDTERLIGDAAK.N

	HsFLAG-Control_HeLa_NE	4.9019	0.3489	1660.59	1659.84	5531	1	994.8	71.4	42	K.NQVALNPQNTVFDAK.R
	Hs293FLP_Ti_302.1600.16	3.5544	0.3409	1223.7	1223.39	4705	2	1008.8	85	2	K.FGDPVVQSDMK.H
	HsGST-MOCK_Ti_406.270	3.0808	0.2337	1681.64	1681.89	4124.2	1	538.8	65.4	2	K.HWPFQVINDGDKPK.V
	HsHeLa_Control_Ti_106.31	2.769	0.2496	1681.82	1681.89	3194.8	1	355.5	57.7	1	K.HWPFQVINDGDKPK.V
	HsGST-MOCK_Ti_103.166	4.5852	0.1849	1682.23	1681.89	5199.4	1	1240	53.8	1	K.HWPFQVINDGDKPK.V
	HsHeLa_Control-MG_Ti_20	3.6708	0.2074	1682.59	1681.89	5824	2	990.2	48.1	1	K.HWPFQVINDGDKPK.V
	HsFLAG-MOCK_300mM_T	4.3972	0.3004	1682.6	1681.89	4758.1	1	1009.5	51.9	2	K.HWPFQVINDGDKPK.V
	Hs293FLP-MG_Ti_206.285	4.0055	0.3067	1682.73	1681.89	4323.9	1	887.7	76.9	7	K.HWPFQVINDGDKPK.V
	HsHeLa_Control-MG_Ti_10	3.2443	0.2897	1682.79	1681.89	3614.5	1	510.4	65.4	3	K.HWPFQVINDGDKPK.V
*	HsFLAG-Control_MG_293_	2.676	0.2572	1138.42	1139.29	6100	3	519.3	66.7	1	K.VQVSYKGETK.A
*	Hs293FLP-MG_Ti_104.114	3.1041	0.2251	1140.53	1139.29	4332.1	8	587.1	72.2	3	K.VQVSYKGETK.A
	HsGST-MOCK_Ti_302.323	3.467	0.4254	1615.76	1615.88	4904.2	1	879.9	76.9	1	K.AFYPEEISSMVLTK.M
	HsFLAG-Control_HeLa_NE	2.6584	0.1973	3001.48	3003.34	6084.6	1	341.5	30.8	1	K.EIAEAYLGYPVTNAVITVPAYFNDSQR.Q
	Hs293FLP-MG_Ti_202.419	3.988	0.4419	3001.65	3003.34	4865	1	660.7	42.3	5	K.EIAEAYLGYPVTNAVITVPAYFNDSQR.Q
	HsHeLa_Control-MG_Ti_20	3.9441	0.314	3002.47	3003.34	4789.9	1	549.7	42.3	2	K.EIAEAYLGYPVTNAVITVPAYFNDSQR.Q
	HsFLAG-Control_HeLa_S1	3.7718	0.2522	3002.63	3003.34	4631.4	1	489.2	29.8	1	K.EIAEAYLGYPVTNAVITVPAYFNDSQR.Q
	Hs293FLP-MG_Ti_202.419	3.9208	0.3228	3003.18	3003.34	4032.5	1	421.3	29.8	2	K.EIAEAYLGYPVTNAVITVPAYFNDSQR.Q
	Hs283FLP_Ti_102.3387.33	3.3026	0.1464	3003.31	3003.34	4716.6	2	362.3	34.6	4	K.EIAEAYLGYPVTNAVITVPAYFNDSQR.Q
	HsGST-MOCK_Ti_302.395	3.5482	0.2999	3003.39	3003.34	5075	1	460.2	38.5	2	K.EIAEAYLGYPVTNAVITVPAYFNDSQR.Q
	HsGST-MOCK_Ti_403.415	4.0344	0.288	3003.52	3003.34	4580	1	578.1	31.7	1	K.EIAEAYLGYPVTNAVITVPAYFNDSQR.Q
	HsFLAG-Control_HeLa_NE	3.9805	0.2081	3003.55	3003.34	4327.2	2	391.5	28.8	2	K.EIAEAYLGYPVTNAVITVPAYFNDSQR.Q
	HsFLAG-Control_HeLa_S1	3.6967	0.2344	3003.74	3003.34	4957.1	2	329.7	32.7	4	K.EIAEAYLGYPVTNAVITVPAYFNDSQR.Q
	HsHeLa_Control-MG_Ti_20	4.0641	0.1086	3003.9	3003.34	4274.4	1	498	31.7	1	K.EIAEAYLGYPVTNAVITVPAYFNDSQR.Q
	HsFLAG-Control_HeLa_S1	3.444	0.306	3004.11	3003.34	5315.9	3	298.6	32.7	2	K.EIAEAYLGYPVTNAVITVPAYFNDSQR.Q
	HsFLAG-Control_293_Ti_2	4.0252	0.2246	3004.15	3003.34	4916.1	1	458.1	36.5	8	K.EIAEAYLGYPVTNAVITVPAYFNDSQR.Q
	HsFLAG-Control_HeLa_S1	3.966	0.2705	3004.53	3003.34	4838.8	1	590.9	32.7	1	K.EIAEAYLGYPVTNAVITVPAYFNDSQR.Q
	Hs283FLP_Ti_103.3091.30	4.383	0.2231	3005.21	3003.34	3917.1	1	461.2	29.8	3	K.EIAEAYLGYPVTNAVITVPAYFNDSQR.Q
	HsFLAG-Control_293_Ti_2	3.9403	0.1343	3006.04	3003.34	4464.8	5	413.7	28.8	1	K.EIAEAYLGYPVTNAVITVPAYFNDSQR.Q
	Hs293FLP-MG_Ti_202.302	2.4988	0.215	1197.55	1198.41	3227.7	3	256.7	59.1	2	K.DAGVIAGLNVLR.I
	HsFLAG-Control_HeLa_S1	4.4911	0.242	1198.36	1198.41	6241.2	1	1789.9	90.9	34	K.DAGVIAGLNVLR.I
	Hs293FLP-MG_Ti_202.302	4.3885	0.222	1198.53	1198.41	6626.9	1	1848	90.9	8	K.DAGVIAGLNVLR.I
	Hs293FLP-MG_Ti_202.294	4.8775	0.4462	1687.76	1688.92	5341.9	1	1731.2	83.3	3	R.IINEPTAAAIAYGLDR.T
	HsGST-MOCK_Ti_303.271	5.3019	0.4188	1687.89	1688.92	6005.7	1	1770	80	5	R.IINEPTAAAIAYGLDR.T
	HsFLAG-Control_293_Ti_2	4.1753	0.1988	1687.96	1688.92	6399	1	1885.4	51.7	1	R.IINEPTAAAIAYGLDR.T
	HsFLAG-Control_HeLa_S1	4.903	0.4088	1688.25	1688.92	7186.8	1	1733	73.3	10	R.IINEPTAAAIAYGLDR.T
	HsFLAG-Control_HeLa_S1	3.9936	0.1641	1688.33	1688.92	7417.7	1	1534	45	1	R.IINEPTAAAIAYGLDR.T
	HsFLAG-Control_HeLa_S1	5.0183	0.3954	1688.36	1688.92	5572.8	1	1466.9	76.7	6	R.IINEPTAAAIAYGLDR.T
	Hs283FLP_Ti_102.2353.23	3.8797	0.1309	1688.68	1688.92	7756.8	2	1564.1	46.7	1	R.IINEPTAAAIAYGLDR.T
	HsFLAG-Control_HeLa_NE	4.519	0.1849	1688.87	1688.92	8251.2	1	1695	48.3	2	R.IINEPTAAAIAYGLDR.T
	Hs293FLP_Ti_302.2512.25	5.4892	0.4056	1689.01	1688.92	4983.8	1	1547.6	80	6	R.IINEPTAAAIAYGLDR.T
	HsF-IP-293-MG_Ti_102.22	4.8927	0.3179	1689.03	1688.92	5477.4	1	1448.1	76.7	2	R.IINEPTAAAIAYGLDR.T
	HsF-IP-293-MG_Ti_102.23	4.2375	0.1806	1689.14	1688.92	8011.1	1	1686.5	46.7	1	R.IINEPTAAAIAYGLDR.T
	Hs293FLP-MG_Ti_202.294	5.0798	0.1684	1689.4	1688.92	8497.4	1	2183.9	51.7	2	R.IINEPTAAAIAYGLDR.T
	HsFLAG-Control_HeLa_S1	3.5964	0.1281	1689.42	1688.92	8134.2	1	1438.2	45	1	R.IINEPTAAAIAYGLDR.T
	HsFLAG-Control_HeLa_NE	5.5152	0.4246	1689.75	1688.92	5197.5	1	1487.3	76.7	18	R.IINEPTAAAIAYGLDR.T
	HsHeLa_Control-MG_Ti_10	5.0746	0.318	1689.79	1688.92	5333.8	1	1131.8	70	9	R.IINEPTAAAIAYGLDR.T
	HsFLAG-Control_293_Ti_2	4.5503	0.4103	1677.37	1676.7	7130.1	1	1456.7	70	19	K.ATAGDTHLGGEDFDNR.L
	Hs293FLP-MG_Ti_204.200	2.4977	0.2506	1261.52	1262.45	5742.7	3	369.7	55.6	2	R.LVNHFVEEFK.R
	HsFLAG-Control_HeLa_NE	2.4484	0.2621	1261.58	1262.45	6474.4	2	519.7	61.1	2	R.LVNHFVEEFK.R

Hs283FLP_Ti_105.1687.16	2.3922	0.2357	1261.59	1262.45	5641.6	1	471.2	61.1	1	R.LVNHFVEEFK.R
HsFLAG-Control_MG_293_	2.5907	0.2398	1261.63	1262.45	5790.7	1	510.2	66.7	2	R.LVNHFVEEFK.R
Hs293FLP_Ti_304.1822.18	2.5334	0.2709	1261.64	1262.45	6628.4	1	523	61.1	2	R.LVNHFVEEFK.R
HsGST-MOCK_Ti_305.212	2.5835	0.1943	1261.66	1262.45	4109.2	3	355	61.1	1	R.LVNHFVEEFK.R
HsFLAG-Control_293_Ti_2	2.5369	0.2325	1261.67	1262.45	6890.5	3	474.8	55.6	2	R.LVNHFVEEFK.R
Hs293FLP-MG_Ti_204.199	3.6059	0.266	1262.13	1262.45	7431.6	1	1201.7	83.3	1	R.LVNHFVEEFK.R
HsGST-MOCK_Ti_305.211	3.5635	0.2773	1262.24	1262.45	6917.9	1	1154.1	83.3	4	R.LVNHFVEEFK.R
HsFLAG-Control_MG_293_	3.8991	0.2729	1262.43	1262.45	6976.8	1	1190.2	83.3	33	R.LVNHFVEEFK.R
Hs293FLP_TREX_Ti_105.1	3.7395	0.2763	1262.43	1262.45	7099.4	1	1398	88.9	6	R.LVNHFVEEFK.R
HsFLAG-Control_HeLa_NE	3.4435	0.2104	1262.57	1262.45	8132	1	1323.1	83.3	4	R.LVNHFVEEFK.R
HsFLAG-Control_HeLa_NE	3.8151	0.3148	1262.58	1262.45	8917.1	1	1383.3	83.3	10	R.LVNHFVEEFK.R
Hs293FLP_Ti_304.1818.18	3.4238	0.2773	1262.64	1262.45	6805.9	1	1174.1	83.3	2	R.LVNHFVEEFK.R
HsFLAG-Control_293_Ti_2	3.6997	0.2789	1262.73	1262.45	7600.5	1	1014.7	77.8	5	R.LVNHFVEEFK.R
Hs293FLP_Ti_305.1718.17	3.1455	0.3209	1420.05	1418.64	6349.5	1	760.9	70	6	R.LVNHFVEEFKR.K
HsFLAG-Control_HeLa_NE	5.1596	0.3539	2982.25	2983.26	7427.5	1	1240.4	48.1	6	R.TLSSSTQASLEIDSLFEGIDFYTSITR.A
HsFLAG-Control_HeLa_S1	4.5252	0.4278	2983.55	2983.26	9450.9	1	989.4	38.5	3	R.TLSSSTQASLEIDSLFEGIDFYTSITR.A
HsFLAG-Control_HeLa_NE	5.2765	0.3259	2983.84	2983.26	10601.4	1	2210.9	34.6	1	R.TLSSSTQASLEIDSLFEGIDFYTSITR.A
HsGST-MOCK_Ti_404.277	3.9207	0.2533	1543.5	1543.69	5188.1	1	843.1	72.7	4	R.ARFEELCSDLFR.S
HsGST-MOCK_Ti_102.200	3.7463	0.1191	1543.86	1543.69	7015	1	1515	52.3	1	R.ARFEELCSDLFR.S
Hs293FLP_Ti_303.2415.24	4.2742	0.302	1545.2	1543.69	4892.3	1	1270.4	86.4	21	R.ARFEELCSDLFR.S
HsFLAG-Control_HeLa_S1	3.4883	0.2705	1316.29	1316.42	7134.9	5	1058.9	77.8	8	R.FEELCSDLFR.S
HsFLAG-Control_HeLa_NE	2.0048	0.1567	902.47	903.02	4539.8	5	443.3	71.4	4	R.STLEPVEK.A
HsFLAG-Control_MG_293_	3.5139	0.1965	1110.11	1110.26	6808.4	1	1199.2	87.5	27	K.LLQDFFNGR.D
HsGST-MOCK_Ti_403.434	4.8873	0.4836	2303.72	2305.61	7751.9	1	1475.4	54.5	11	K.SINPDEAVAYGAAVQAAILMGDK.S
HsGST-MOCK_Ti_403.436	5.5284	0.3617	2305.81	2305.61	9393.7	1	2713.4	44.3	1	K.SINPDEAVAYGAAVQAAILMGDK.S
HsFLAG-Control_293_Ti_1	3.2967	0.3581	3181.76	3182.74	6743.4	1	554.7	33.3	3	K.SENVQDLLLLDVAPLSLGLETAGGVMTALIK.R
HsHeLa_Control-MG_Ti_20	6.3425	0.4536	3181.94	3182.74	10797.9	1	2183	31.7	7	K.SENVQDLLLLDVAPLSLGLETAGGVMTALIK.R
HsFLAG-Control_293_Ti_1	4.742	0.3629	3182.17	3182.74	10758.3	1	1110.1	26.7	1	K.SENVQDLLLLDVAPLSLGLETAGGVMTALIK.R
HsGST-MOCK_Ti_306.054	5.6551	0.3649	3182.29	3182.74	9743.4	1	1523.6	30.8	5	K.SENVQDLLLLDVAPLSLGLETAGGVMTALIK.R
HsF-IP-293-MG_Ti_106.33	4.4641	0.3484	3182.3	3182.74	4557.5	1	394.1	35	7	K.SENVQDLLLLDVAPLSLGLETAGGVMTALIK.R
HsHeLa_Control-MG_Ti_20	4.1527	0.4037	3182.72	3182.74	6057.5	1	702.4	38.3	4	K.SENVQDLLLLDVAPLSLGLETAGGVMTALIK.R
HsGST-MOCK_Ti_303.335	2.5776	0.2963	2786.6	2788.04	7450.8	1	473.9	37	1	K.QTQIFTTYSDNQPGVLIQVYEGER.A
Hs293FLP-MG_Ti_204.321	4.2945	0.5036	2787.69	2788.04	6064.2	1	769.6	45.7	4	K.QTQIFTTYSDNQPGVLIQVYEGER.A
Hs293FLP-MG_Ti_205.311	5.4004	0.3198	2788.58	2788.04	11083.1	1	1393.9	33.7	2	K.QTQIFTTYSDNQPGVLIQVYEGER.A
HsFLAG-Control_HeLa_S1	3.5026	0.3748	2788.84	2788.04	6443.9	1	586	41.3	2	K.QTQIFTTYSDNQPGVLIQVYEGER.A
HsFLAG-Control_HeLa_NE	3.9327	0.3083	2788.9	2788.04	14432.1	5	820.7	26.1	2	K.QTQIFTTYSDNQPGVLIQVYEGER.A
Hs293FLP_Ti_302.3136.31	4.1608	0.366	2789.84	2788.04	7098.1	1	800.1	31.5	1	K.QTQIFTTYSDNQPGVLIQVYEGER.A
HsFLAG-Control_MG_293_	2.37	0.1055	1183.56	1184.38	4415.4	2	447.5	65	2	R.FELSGIPPAPR.G
HsFLAG-Control_MG_293_	3.253	0.2405	1184.35	1184.38	3642.9	1	911.3	80	11	R.FELSGIPPAPR.G
HsFLAG-Control_MG_293_	3.8888	0.3065	1289.5	1288.46	6627.1	1	1451.2	85	5	K.NALESYAFNMK.S
HsFLAG-Control_HeLa_NE	2.1567	0.1434	947.4	948.018	9862.3	6	694	62.5	3	K.SAVEDEGLK.G
HsGST-MOCK_Ti_102.232	3.7854	0.3557	2663.49	2663.87	7161.2	1	876.9	47.6	2	K.CQEVISWLDANTLAEKDEFEHK.R
Hs293FLP-MG_Ti_205.284	4.6951	0.3329	3185.32	3185.53	8783.5	1	1540	31.5	1	R.KELEQVCNPIISGLYQGAGGPGPGGFGAQGPK.G
HsGST-MOCK_Ti_405.327	4.7798	0.3593	3055.46	3057.36	7871.6	1	1607.6	34.2	1	K.ELEQVCNPIISGLYQGAGGPGPGGFGAQGPK.G
HsHeLa_Control-MG_Ti_20	3.4944	0.4245	3055.59	3057.36	7975.4	1	838.4	35	1	K.ELEQVCNPIISGLYQGAGGPGPGGFGAQGPK.G
HsF-IP-293_Ti_204.2917.2	2.8978	0.2397	3055.78	3057.36	7958.5	1	462.5	30	1	K.ELEQVCNPIISGLYQGAGGPGPGGFGAQGPK.G
Hs293FLP-MG_Ti_203.336	4.3577	0.3974	3055.86	3057.36	9217.9	1	878.5	36.7	2	K.ELEQVCNPIISGLYQGAGGPGPGGFGAQGPK.G
HsHeLa3_Ti_104.3109.310	3.8407	0.4989	3056.05	3057.36	5236.2	1	614.8	40	2	K.ELEQVCNPIISGLYQGAGGPGPGGFGAQGPK.G
HsFLAG-Control_293_Ti_1	6.8367	0.4432	3056.18	3057.36	9398.5	1	1848.1	34.2	2	K.ELEQVCNPIISGLYQGAGGPGPGGFGAQGPK.G

	Hs293FLP_Ti_303.2947.29	4.0835	0.4932	3056.26	3057.36	6503.7		1	820.1	40	2	K.ELEQVCNPIISGLYQGAGGPGPGGFGAQGPK.G
	HsFLAG-Control_293_Ti_1	5.1265	0.4028	3056.32	3057.36	6353.9		1	876.7	43.3	2	K.ELEQVCNPIISGLYQGAGGPGPGGFGAQGPK.G
	Hs293FLP-MG_Ti_203.336	6.9009	0.436	3056.42	3057.36	8440.5		1	2521.9	37.5	2	K.ELEQVCNPIISGLYQGAGGPGPGGFGAQGPK.G
	HsHeLa_Control-MG_Ti_20	6.5314	0.4244	3056.43	3057.36	8158.6		1	2297.5	38.3	2	K.ELEQVCNPIISGLYQGAGGPGPGGFGAQGPK.G
	HsFLAG-Control_293_Ti_2	4.7242	0.4588	3056.75	3057.36	7695.8		1	1186.7	43.3	1	K.ELEQVCNPIISGLYQGAGGPGPGGFGAQGPK.G
	Hs283FLP_Ti_104.2544.25	6.3147	0.4418	3056.86	3057.36	9055.8		1	2279.7	36.7	2	K.ELEQVCNPIISGLYQGAGGPGPGGFGAQGPK.G
	HsGST-MOCK_Ti_405.328	3.9418	0.3045	3056.9	3057.36	8303		1	624.7	31.7	1	K.ELEQVCNPIISGLYQGAGGPGPGGFGAQGPK.G
	HsFLAG-Control_HeLa_NE	7.2394	0.4746	3056.99	3057.36	10678.3		1	4070.1	41.7	14	K.ELEQVCNPIISGLYQGAGGPGPGGFGAQGPK.G
	HsF-IP-293-MG_Ti_103.27	4.3936	0.3195	3057.06	3057.36	8142.5		1	1078.8	30	3	K.ELEQVCNPIISGLYQGAGGPGPGGFGAQGPK.G
	Hs293FLP_Ti_303.2945.29	6.9596	0.3371	3057.08	3057.36	8400.8		1	2283.8	36.7	3	K.ELEQVCNPIISGLYQGAGGPGPGGFGAQGPK.G
	HsHeLa_Control-MG_Ti_10	5.8796	0.3096	3057.29	3057.36	8102.1		1	1828.9	35	2	K.ELEQVCNPIISGLYQGAGGPGPGGFGAQGPK.G
	HsHeLa_Control_Ti_104.35	6.6676	0.3746	3057.45	3057.36	9233.7		1	2250.6	36.7	2	K.ELEQVCNPIISGLYQGAGGPGPGGFGAQGPK.G
	HsHeLa_Control_Ti_104.35	4.4827	0.4406	3058	3057.36	5486.1		1	736.9	40	1	K.ELEQVCNPIISGLYQGAGGPGPGGFGAQGPK.G
	HsHeLa_Control-MG_Ti_10	4.4422	0.3802	3058.19	3057.36	5565		1	715.2	41.7	2	K.ELEQVCNPIISGLYQGAGGPGPGGFGAQGPK.G
gi|29788768|ref|	77	422	0.631	445	49953	4.9	U	tubulin, beta polypeptide paralog [Homo sapiens]				
	HsF-IP-293-MG_Ti_102.23	4.2116	0.3257	1617.72	1616.87	4090.1		1	901.5	75	15	R.AILVDLEPGTMDSVR.S
	HsFLAG-Control_293_Ti_1	4.3497	0.4199	2798.44	2800.07	7089.6		1	789.7	42	2	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G
	HsFLAG-Control_Hela_Ti_1	7.086	0.3585	2798.77	2800.07	8023.8		1	2007.6	39	1	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G
	HsHeLa_Control_Ti_106.35	3.3717	0.284	2799.08	2800.07	7040.2		1	509.9	34	1	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G
	HsFLAG-Control_HeLa_NE	5.559	0.4744	2799.13	2800.07	8777.8		1	1234	44	3	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G
	Hs293FLP_Ti_306.3134.31	4.4896	0.3405	2799.39	2800.07	5985.1		1	712.5	40	3	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G
	HsFLAG-Control_HeLa_S1	5.0217	0.2644	2799.44	2800.07	9812.3		1	1983	35	4	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G
	HsFLAG-Control_Hela_Ti_1	4.9745	0.3403	2799.45	2800.07	9442		1	1330.7	46	2	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G
	Hs293FLP-MG_Ti_206.324	5.6902	0.3542	2799.53	2800.07	9458.1		1	2291.7	38	3	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G
	HsFLAG-Control_293_Ti_1	6.1007	0.3859	2799.74	2800.07	9348.5		1	3099.1	42	2	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G
	HsFLAG-Control_HeLa_S1	5.4454	0.3567	2799.89	2800.07	7677.5		1	1212.9	46	3	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G
	HsHeLa_Control-MG_Ti_20	5.2597	0.3817	2799.92	2800.07	8298.5		1	1407.9	48	8	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G
	HsFLAG-Control_HeLa_S1	4.9984	0.3992	2799.99	2800.07	8366		1	1288.2	46	5	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G
	HsHeLa_Control_Ti_106.35	5.7438	0.2886	2800.05	2800.07	8407.2		1	2280	38	3	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G
	HsFLAG-Control_HeLa_S1	6.1803	0.4125	2800.31	2800.07	9515.8		1	2575.2	39	10	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G
	Hs293FLP-MG_Ti_206.324	4.0474	0.285	2800.79	2800.07	6819.9		1	693.4	38	4	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G
	Hs293FLP_Ti_306.3122.31	5.4056	0.2637	2801.19	2800.07	8261.6		1	1963.1	38	2	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G
	HsHeLa_Control-MG_Ti_20	6.5624	0.445	2801.2	2800.07	8704.9		1	2240.6	38	7	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G
	HsFLAG-Control_HeLa_NE	6.3579	0.3994	2801.45	2800.07	8898.9		1	2491.9	40	3	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G
	HsGST-MOCK_Ti_102.286	3.2049	0.3313	1958.45	1960.15	8017.5		1	762.8	52.9	1	K.GHYTEGAELVDSVLDVVR.K
	HsFLAG-Control_HeLa_S1	4.1642	0.2955	1959.3	1960.15	8544.6		2	1215.8	38.2	2	K.GHYTEGAELVDSVLDVVR.K
	HsGST-MOCK_Ti_403.395	4.7164	0.3422	1959.33	1960.15	10548.9		1	1301.9	55.9	1	K.GHYTEGAELVDSVLDVVR.K
	HsFLAG-Control_HeLa_NE	5.3562	0.4242	1959.63	1960.15	11243.1		1	2825.8	70.6	3	K.GHYTEGAELVDSVLDVVR.K
	Hs293FLP_Ti_303.3357.33	4.1617	0.1819	1959.92	1960.15	7405		2	1468.9	42.6	6	K.GHYTEGAELVDSVLDVVR.K
	HsHeLa_Control-MG_Ti_10	6.1452	0.4266	1959.96	1960.15	8101.6		1	2856.7	79.4	5	K.GHYTEGAELVDSVLDVVR.K
	Hs293FLP-MG_Ti_205.353	4.315	0.1813	1959.98	1960.15	9417.8		1	1643	41.2	5	K.GHYTEGAELVDSVLDVVR.K
	Hs293FLP-MG_Ti_204.367	6.6846	0.431	1959.98	1960.15	10282.1		1	3961.5	82.4	8	K.GHYTEGAELVDSVLDVVR.K
	Hs293FLP_Ti_306.3198.31	6.98	0.3863	1960.01	1960.15	9148.7		1	3744.2	85.3	7	K.GHYTEGAELVDSVLDVVR.K
	HsFLAG-Control_HeLa_S1	4.5919	0.2553	1960.03	1960.15	7594.6		1	1242.3	41.2	2	K.GHYTEGAELVDSVLDVVR.K
	HsHeLa_Control-MG_Ti_10	3.5165	0.1922	1960.13	1960.15	6171.6		3	834.7	35.3	1	K.GHYTEGAELVDSVLDVVR.K
	HsHeLa_Control-MG_Ti_20	4.3353	0.2198	1960.22	1960.15	8005.9		1	1897.4	47.1	2	K.GHYTEGAELVDSVLDVVR.K
	HsFLAG-Control_HeLa_S1	5.8707	0.417	1960.53	1960.15	9914.1		1	3928.7	82.4	2	K.GHYTEGAELVDSVLDVVR.K
	HsHeLa_Control-MG_Ti_20	6.9239	0.4578	1960.6	1960.15	10283.3		1	4222.7	85.3	8	K.GHYTEGAELVDSVLDVVR.K
	HsHeLa_Control_Ti_105.38	6.5934	0.4301	1960.92	1960.15	9241.8		1	3541.4	82.4	7	K.GHYTEGAELVDSVLDVVR.K

	HsFLAG-Control_HeLa_NE	4.632	0.1653	1961.1	1960.15	7796.1		7	1433.4	44.1	1	K.GHYTEGAELVDSVLDVVR.K
	HsHeLa_Control_Ti_105.38	3.9939	0.1774	1961.13	1960.15	6245.6		2	1192.6	45.6	2	K.GHYTEGAELVDSVLDVVR.K
	HsFLAG-Control_HeLa_S1(	4.764	0.2325	1961.21	1960.15	8029.8		1	1535	42.6	2	K.GHYTEGAELVDSVLDVVR.K
	HsFLAG-Control_HeLa_S1(	6.9041	0.4463	1961.25	1960.15	11475.7		1	4165.7	82.4	14	K.GHYTEGAELVDSVLDVVR.K
	HsFLAG-Control_HeLa_S1(	5.9828	0.4073	1961.57	1960.15	10193.9		1	3020.1	76.5	5	K.GHYTEGAELVDSVLDVVR.K
	HsGST-MOCK_Ti_102.285!	4.2626	0.1599	1962	1960.15	7062.2		4	1185.6	41.2	1	K.GHYTEGAELVDSVLDVVR.K
	Hs293FLP_Ti_306.3098.30	6.1016	0.4085	2088.19	2088.33	9030.4		1	2434	72.2	2	K.GHYTEGAELVDSVLDVVRK.E
	HsHeLa_Control_Ti_106.36	2.6425	0.3564	2089.18	2088.33	10954.4		1	669	41.7	1	K.GHYTEGAELVDSVLDVVRK.E
	HsFLAG-MOCK_300mM_T	4.8098	0.3951	2089.85	2088.33	6163.4		1	1098.1	41.7	3	K.GHYTEGAELVDSVLDVVRK.E
	Hs293FLP_Ti_305.3017.30	5.121	0.3371	2090.41	2088.33	6587.3		1	1579.1	48.6	9	K.GHYTEGAELVDSVLDVVRK.E
	Hs293FLP_Ti_303.2883.28	4.8438	0.3042	3329.53	3329.59	8954.5		1	943.2	25	1	K.ESESCDCLQGFQLTHSLGGGTGSGMGTLLISK.I
	HsFLAG-Control_HeLa_S1(	2.9498	0.2063	1077.69	1078.17	5287.5		3	749.1	85.7	5	K.IREEYPDR.I
	HsFLAG-Control_MG_293_	3.7383	0.2202	1352.31	1352.65	8028.9		1	1182	72.7	2	R.IMNTFSVMPSPK.V
	HsFLAG-Control_HeLa_S1(	5.2299	0.4574	4594.42	4595.9	5984.7		1	689.3	24.3	26	K.VSDTVVEPYNATLSVHQLVENTDETYCIDNEALYDICFR.T
	HsGST-MOCK_Ti_305.408	4.8022	0.4628	2708.4	2710.04	7804.4		1	972	43.8	1	K.LTTPTYGDLNHLVSATMSGVTTCLR.F
	Hs293FLP-MG_Ti_204.386	5.4701	0.3771	2708.64	2710.04	9092.1		1	1386.9	45.8	2	K.LTTPTYGDLNHLVSATMSGVTTCLR.F
	HsF-IP-293-MG_Ti_106.26	5.1039	0.31	2708.65	2710.04	6253.5		1	929.3	45.8	6	K.LTTPTYGDLNHLVSATMSGVTTCLR.F
	Hs293FLP-MG_Ti_204.386	3.7503	0.32	2709.13	2710.04	7710.2		1	762.9	29.2	1	K.LTTPTYGDLNHLVSATMSGVTTCLR.F
	HsHeLa_Control-MG_Ti_10	4.2137	0.4906	2709.32	2710.04	6602.6		1	706.6	39.6	1	K.LTTPTYGDLNHLVSATMSGVTTCLR.F
	HsFLAG-MOCK_300mM_T	3.5898	0.1924	2709.57	2710.04	8016.1		2	734.5	28.1	1	K.LTTPTYGDLNHLVSATMSGVTTCLR.F
	HsF-IP-293-MG_Ti_106.26	3.9395	0.217	2709.94	2710.04	7857.5		1	880.7	30.2	1	K.LTTPTYGDLNHLVSATMSGVTTCLR.F
	HsHeLa3_Ti_105.3722.372	4.5547	0.4711	2710.06	2710.04	7677.4		1	1059.3	43.8	3	K.LTTPTYGDLNHLVSATMSGVTTCLR.F
	HsHeLa_Control-MG_Ti_10	4.0048	0.2452	2712.04	2710.04	8274.3		1	1108.1	33.3	1	K.LTTPTYGDLNHLVSATMSGVTTCLR.F
	HsFLAG-Control_293_Ti_2(	2.3562	0.2676	1130.49	1131.28	3790.3		1	334.2	72.2	1	R.FPGQLNADLR.K
	HsFLAG-Control_HeLa_S1(	3.3308	0.1729	1130.86	1131.28	4313.3		1	873.6	88.9	23	R.FPGQLNADLR.K
	HsFLAG-Control_MG_293_	3.206	0.113	1130.88	1131.28	3899.4		1	816.9	88.9	6	R.FPGQLNADLR.K
	HsFLAG-Control_HeLa_S1(	2.9598	0.1628	1259.33	1259.45	6893.9		1	1452.3	90	5	R.FPGQLNADLRK.L
	HsHeLa_Control-MG_Ti_10	3.4275	0.2361	1272.73	1272.59	5940.6		2	973.4	75	2	R.KLAVNMVPFPR.L
	HsF-IP-293-MG_Ti_104.21	3.5921	0.3097	1145.56	1144.42	4625.3		1	875.9	88.9	19	K.LAVNMVPFPR.L
	HsGST-MOCK_Ti_102.257!	3.0182	0.4314	1621.6	1621.94	4033.6		1	699.6	69.2	2	R.LHFFMPGFAPLTSR.G
	HsFLAG-Control_HeLa_S1(	3.2928	0.2951	1708.57	1708.97	4062.4		1	387.6	57.1	15	R.ALTVPELTQQMFDSK.N
	HsHeLa-FLAG-IP_S100_Ti_	2.9555	0.2199	1068.25	1066.2	7345.1		2	1221.1	81.2	2	K.NMMAACDPR.H
	HsGST-MOCK_Ti_402.200	3.2807	0.1162	1445.58	1447.6	4353.1		1	621.9	77.3	1	K.EVDEQMLNVQNK.N
	HsFLAG-Control_293_Ti_2(	3.0439	0.1965	1446.48	1447.6	5427.8		1	667.1	72.7	2	K.EVDEQMLNVQNK.N
	HsHeLa_Control_Ti_102.15	2.3866	0.11	1446.59	1447.6	3600.8		3	304.9	63.6	1	K.EVDEQMLNVQNK.N
	HsFLAG-Control_MG_293_	3.1945	0.1644	1447.26	1447.6	5122.2		1	556.1	68.2	1	K.EVDEQMLNVQNK.N
	HsHeLa-FLAG-IP_S100_Ti_	4.4378	0.162	1447.32	1447.6	7508.9		6	1453	77.3	14	K.EVDEQMLNVQNK.N
	HsFLAG-Control_HeLa_S1(	2.6394	0.1147	1447.42	1447.6	5226.8		1	438.1	63.6	2	K.EVDEQMLNVQNK.N
	Hs293FLP-MG_Ti_102.177	3.6404	0.1591	1447.47	1447.6	6074.7		1	1112.2	72.7	2	K.EVDEQMLNVQNK.N
	HsFLAG-Control_HeLa_S1(	4.4307	0.2086	1449.29	1447.6	7304.9		1	1751.9	86.4	2	K.EVDEQMLNVQNK.N
	HsFLAG-Control_HeLa_S1(	4.2481	0.345	1697.72	1697.89	5597.6		1	913.8	69.2	79	K.NSSYFVEWIPNNVK.T
	HsHeLa-FLAG-IP_S100_Ti_	2.8782	0.1885	1029.7	1029.15	5615.6		1	1184.8	87.5	8	K.TAVCDIPPR.G
	HsHeLa_Control-MG_Ti_10	3.5998	0.3059	1388.48	1386.61	7275		1	1173.3	80	3	K.RISEQFTAMFR.R
gi|50592994|ref|N	21	60	0.629	105	11737	4.9	U	thioredoxin [Homo sapiens]				
*	HsHeLa_Control_Ti_102.20	3.3435	0.3901	1336.52	1337.43	8359.5		1	1164.5	66.7	2	K.TAFQEALDAAGDK.L
*	HsHeLa_Control-MG_Ti_10	2.9578	0.2839	1336.64	1337.43	6841		1	741.1	62.5	2	K.TAFQEALDAAGDK.L
*	HsHeLa_Control-MG_Ti_20	4.1492	0.324	1337.1	1337.43	7916.5		1	2193.2	83.3	9	K.TAFQEALDAAGDK.L
*	HsFLAG-Control_Hela_Ti_1	2.8875	0.3608	1337.32	1337.43	7862		1	847.8	62.5	4	K.TAFQEALDAAGDK.L

*	HsFLAG-Control_HeLa_NE	3.889	0.3334	1338.25	1337.43	7944.9		1	2199.3	83.3	15	K.TAFQEALDAAGDK.L
*	HsHeLa_Control_Ti_102.20	3.6903	0.3284	1338.87	1337.43	6440.1		1	1646.8	79.2	3	K.TAFQEALDAAGDK.L
*	HsGST-MOCK_Ti_104.231	3.5719	0.4214	1740.08	1739.94	6837.1		1	682.2	57.1	2	K.LVVVDFSATWCGPCK.M
*	HsHeLa_Control-MG_Ti_20	2.6602	0.1892	1091.46	1092.24	3911.9		3	399.9	75	1	K.PFFHSLSEK.Y
*	Hs283FLP_Ti_106.2047.20	2.5599	0.2203	1091.55	1092.24	5791.9		6	502.1	68.8	2	K.PFFHSLSEK.Y
*	HsHeLa_Control-MG_Ti_10	2.9018	0.1683	1091.65	1092.24	6019.9		3	593.4	75	1	K.PFFHSLSEK.Y
*	Hs293FLP_Ti_305.1634.16	2.6892	0.1889	1091.78	1092.24	6016.9		2	603.9	75	2	K.PFFHSLSEK.Y
*	HsHeLa_Control_Ti_106.28	2.5456	0.1519	1091.84	1092.24	5102.4		1	512.9	75	1	K.PFFHSLSEK.Y
*	Hs293FLP_TREX_Ti_105.1	3.0961	0.2806	1092.1	1092.24	5078.6		1	734.9	81.2	1	K.PFFHSLSEK.Y
*	HsHeLa_Control-MG_Ti_20	2.9273	0.2509	1092.26	1092.24	5642.8		1	785.3	81.2	1	K.PFFHSLSEK.Y
*	HsHeLa_Control-MG_Ti_10	2.8934	0.2602	1092.65	1092.24	4162.4		1	651.5	81.2	2	K.PFFHSLSEK.Y
*	Hs293FLP_Ti_305.1633.16	2.9315	0.2394	1092.99	1092.24	4433.4		2	713.6	81.2	2	K.PFFHSLSEK.Y
*	HsHeLa_Control_Ti_106.28	3.1852	0.2499	1094	1092.24	4151.8		1	761	87.5	3	K.PFFHSLSEK.Y
*	HsGST-MOCK_Ti_405.307	2.7162	0.3148	1206.15	1206.41	2803.2		1	510.4	81.2	1	K.CMPTFQFFK.K
*	HsFLAG-Control_Hela_Ti_1	3.2113	0.1961	909.52	908.987	6888.4		1	1430.1	93.8	1	K.VGEFSGANK.E
*	HsFlag1P_Ti_105.3223.322	2.6133	0.1474	2149.65	2149.41	10329.3		2	601.4	39.5	2	K.VGEFSGANKEKLEATINELV.-
*	HsHeLa_Control-MG_Ti_20	3.877	0.1777	1260.57	1259.44	9965		3	1944.3	90	3	K.EKLEATINELV.-
gi|4501885|ref|N	44	365	0.627	375	41737	5.5	U	beta actin [Homo sapiens]				
gi|4501887|ref|N	44	365	0.627	375	41793	5.5	U	actin, gamma 1 propeptide [Homo sapiens]				
	HsFLAG-Control_HeLa_S1	2.2896	0.2133	976.42	977.021	5697.3		5	418.5	61.1	1	K.AGFAGDDAPR.A
	HsFLAG-Control_Hela_Ti_1	3.0127	0.1884	976.63	977.021	5102.4		1	1237.5	88.9	9	K.AGFAGDDAPR.A
	HsHeLa_Control_Ti_102.11	2.1727	0.108	976.67	977.021	4557.8		2	513.5	66.7	1	K.AGFAGDDAPR.A
	HsFLAG-MOCK_150mM_T	3.2886	0.2636	978.67	977.021	5248.4		1	1406.5	88.9	20	K.AGFAGDDAPR.A
	HsFLAG-Control_HeLa_S1	2.6516	0.2088	946.02	946.137	3258.8		2	623.5	87.5	1	R.AVFPSIVGR.P
	HsFLAG-MOCK_300mM_T	3.5305	0.3215	1199.52	1199.44	7004.5		2	801.6	75	15	R.AVFPSIVGRPR.H
	HsFLAG-MOCK_300mM_T	2.8034	0.3247	1171.52	1172.41	5485.7		1	609.4	65	3	R.HQGVMVGMGQK.D
	HsHeLa3_Ti_106.1966.196	2.937	0.3448	1171.61	1172.41	5543.4		1	647.3	65	2	R.HQGVMVGMGQK.D
	HsHeLa3_Ti_106.1967.196	3.1676	0.3309	1172.92	1172.41	4063.3		1	693.8	80	1	R.HQGVMVGMGQK.D
	HsFLAG-MOCK_300mM_T	3.105	0.361	1173.72	1172.41	4167.5		1	841.2	85	2	R.HQGVMVGMGQK.D
	HsFLAG-MOCK_300mM_T	5.2956	0.4824	2351.94	2352.6	7863.3		1	2199.1	66.7	2	R.HQGVMVGMGQKDSYVGDEAQSK.R
	HsFLAG-Control_HeLa_S1	3.424	0.33	1199.08	1199.22	4776.6		2	971.4	85	4	K.DSYVGDEAQSK.R
	HsFLAG-Control_Hela_Ti_1	3.2795	0.3331	1515.45	1516.7	7777.5		1	997.2	75	12	K.IWHHTFYNELR.V
	HsFLAG-MOCK_300mM_T	2.4013	0.1049	1515.69	1516.7	5047.5		1	338.5	60	1	K.IWHHTFYNELR.V
	HsHeLa_Control-MG_Ti_10	3.3547	0.3682	1518.65	1516.7	5691.8		1	740.7	75	4	K.IWHHTFYNELR.V
	HsFLAG-Control_Hela_Ti_1	3.8269	0.0974	1954.23	1955.26	7101.3		7	678.1	35.3	1	R.VAPEEHPVLLTEAPLNPK.A
	HsFLAG-Control_Hela_Ti_1	4.4739	0.3418	1954.47	1955.26	5423.1		1	777.4	58.8	12	R.VAPEEHPVLLTEAPLNPK.A
	HsFLAG-Control_HeLa_NE	4.4438	0.3998	1954.64	1955.26	5966.4		1	906.2	61.8	6	R.VAPEEHPVLLTEAPLNPK.A
	HsGST-MOCK_Ti_405.231	3.9785	0.3952	1954.64	1955.26	5779.6		1	1049.7	61.8	4	R.VAPEEHPVLLTEAPLNPK.A
	HsFLAG-Control_MG_293_	4.2926	0.3247	1954.65	1955.26	5827.3		1	937	61.8	60	R.VAPEEHPVLLTEAPLNPK.A
	HsFLAG-Control_HeLa_NE	4.4704	0.2283	1954.69	1955.26	5597.7		1	725.8	58.8	4	R.VAPEEHPVLLTEAPLNPK.A
	Hs293FLP_TREX_Ti_105.1	4.5388	0.3216	1954.7	1955.26	4902.1		1	936.6	64.7	5	R.VAPEEHPVLLTEAPLNPK.A
	HsFLAG-Control_HeLa_S1	4.6473	0.2961	1954.79	1955.26	5345.4		1	959.7	64.7	20	R.VAPEEHPVLLTEAPLNPK.A
	HsFLAG-Control_MG_293_	3.6843	0.1385	1955.26	1955.26	5777.1		4	796.8	41.2	2	R.VAPEEHPVLLTEAPLNPK.A
	HsFLAG-Control_HeLa_NE	3.7445	0.1366	1955.27	1955.26	6564.5		7	873.5	41.2	1	R.VAPEEHPVLLTEAPLNPK.A
	Hs293FLP_TREX_Ti_104.1	3.6692	0.1216	1955.37	1955.26	5613.2		1	815.8	41.2	1	R.VAPEEHPVLLTEAPLNPK.A
	HsHeLa_Control-MG_Ti_20	4.5848	0.3256	1955.51	1955.26	6431.6		1	1337.4	70.6	13	R.VAPEEHPVLLTEAPLNPK.A
	Hs283FLP_Ti_105.1739.17	3.5091	0.1499	1955.54	1955.26	5622.7		5	612.3	36.8	1	R.VAPEEHPVLLTEAPLNPK.A
	HsFLAG-Control_HeLa_S1	3.8414	0.1501	1956.46	1955.26	6047.5		7	626.7	38.2	2	R.VAPEEHPVLLTEAPLNPK.A
	HsFLAG-Control_HeLa_NE	4.2177	0.1933	1956.92	1955.26	6916.3		2	647.7	39.7	1	R.VAPEEHPVLLTEAPLNPK.A

	HsHeLa3_Ti_106.2603.260	4.5221	0.3038	3185.19	3185.62	3947.7		1	407.6	36.2	2	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L
	HsHeLa_Control-MG_Ti_20	5.6034	0.4079	3185.37	3185.62	8847.7		1	1345	31	8	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L
	HsHeLa_Control_Ti_105.33	6.0472	0.4346	3185.58	3185.62	9179.9		1	1261.4	29.3	2	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L
	HsFLAG-Control_293_Ti_2	2.3671	0.1397	1000.32	999.167	7387.7		9	624.4	71.4	2	R.DLTDYLMK.I
	HsFLAG-Control_HeLa_S1	3.2887	0.3754	1132.75	1133.2	6769.6		1	1138.7	83.3	26	R.GYSFTTTAER.E
	HsFLAG-MOCK_300mM_T	5.7804	0.3874	2551.51	2551.79	8558.6		1	2302.9	56.8	20	K.LCYVALDFEQEMATAASSSSLEK.S
	HsHeLa_Control-MG_Ti_20	5.1912	0.2593	1792.4	1791.96	5309.1		1	1957.5	86.7	61	K.SYELPDGQVITIGNER.F
	HsFLAG-MOCK_300mM_T	5.6387	0.4443	3536.82	3536.97	6318.9		1	919.9	29.3	3	R.FRCPEALFQPSFLGMESCGIHETTFNSIMK.C
	HsHeLa3_Ti_105.3498.349	4.399	0.2568	3233.57	3233.61	4293.9		1	705.7	31.5	1	R.CPEALFQPSFLGMESCGIHETTFNSIMK.C
	HsFLAG-MOCK_300mM_T	4.9064	0.4874	2343.92	2344.65	6226.7		1	1722.2	64.3	2	R.KDLYANTVLSGGTTMYPGIADR.M
	HsFLAG-MOCK_300mM_T	4.3364	0.3584	2346.26	2344.65	5622.9		2	591.4	33.3	1	R.KDLYANTVLSGGTTMYPGIADR.M
	HsFLAG-MOCK_150mM_T	4.7935	0.5235	2215.81	2216.47	7675.6		1	763.5	50	14	K.DLYANTVLSGGTTMYPGIADR.M
	HsHeLa_Control-MG_Ti_10	2.6274	0.294	1161.67	1162.39	4080.9		1	437	65	10	K.EITALAPSTMK.I
	HsFLAG-Control_Hela_Ti_1	2.701	0.0863	1517.89	1517.6	5879.3		1	499.9	58.3	1	K.QEYDESGPSIVHR.K
gi|31742498|ref|	80	582	0.623	717	80311	6.7	U		unc-84 homolog B [Homo sapiens]			
*	HsF-IP-293_Ti_102.1500.1	6.142	0.4716	2512.37	2512.52	8480.2		1	1440.3	50	21	R.YSQGDDDGSSSSGGSSVAGSQSTLFK.D
*	HsF-IP-293_Ti_206.2292.2	4.686	0.4006	1928.57	1929.01	6497.8		1	1632	71.9	11	R.SSLEELHGDANWGEDLR.V
*	HsF-IP-293-MG_Ti_106.21	4.6737	0.3774	1928.71	1929.01	6103.8		1	2152	81.2	4	R.SSLEELHGDANWGEDLR.V
*	Hs283FLP_Ti_105.1810.18	4.0428	0.1293	1930.33	1929.01	6252.9		1	978.3	39.1	1	R.SSLEELHGDANWGEDLR.V
*	HsF-IP-293_Ti_206.2259.2	5.3197	0.515	3555.31	3555.57	7012.3		1	1102.7	28.1	3	R.KATEDFLGSSSGYSSEDDYVGYSDVDQQSSSSR.L
*	Hs283FLP_Ti_106.2743.27	4.0575	0.3243	1617.58	1616.86	7502.1		1	1253.5	72.7	2	R.LLYWWAGTTWYR.L
*	Hs283FLP_Ti_104.3371.33	4.889	0.352	1621.74	1620.93	7726.9		1	1361.6	71.4	13	R.LTTAASLLDVFVLTR.R
*	Hs283FLP_Ti_103.1208.12	1.9266	0.2356	1115.56	1116.18	3152.7		1	211.3	56.2	1	R.RPDEGWEAR.D
*	Hs293FLP_TREX_Ti_103.1	3.1	0.1815	1116.44	1116.18	5645.4		2	958.7	87.5	5	R.RPDEGWEAR.D
*	HsHeLa_Control-MG_Ti_10	2.9958	0.1689	1117.13	1116.18	5686.2		1	897.7	81.2	2	R.RPDEGWEAR.D
*	Hs283FLP_Ti_103.1110.11	2.5872	0.3508	1301.55	1302.35	2923.2		1	272.1	60	2	R.DSSPHFQAEQR.V
*	Hs293FLP_TREX_Ti_102.1	3.1576	0.3374	1302.47	1302.35	6803.9		2	942	75	10	R.DSSPHFQAEQR.V
*	HsHeLa_Control-MG_Ti_10	3.3076	0.2467	1302.61	1302.35	6148.4		1	786.4	70	2	R.DSSPHFQAEQR.V
*	Hs283FLP_Ti_106.2360.23	5.5293	0.4717	1750.76	1750.95	9385.2		1	2144.9	78.6	6	R.RLEALAAEFSSNWQK.E
*	HsF-IP-293-MG_Ti_102.24	4.9074	0.3831	1594.64	1594.76	8466.4		1	2103	80.8	9	R.LEALAAEFSSNWQK.E
*	HsF-IP-293-MG_Ti_106.25	3.5132	0.353	2576.86	2577.81	4989.7		1	270.9	32.7	2	R.QGAPGQGGGGGLSHEDTLALLEGLVSR.R
*	Hs293FLP-MG_Ti_204.356	4.4306	0.2825	2577.25	2577.81	6066.1		1	580.9	26	2	R.QGAPGQGGGGGLSHEDTLALLEGLVSR.R
*	Hs293FLP-MG_Ti_204.356	3.8706	0.4394	2578.08	2577.81	8229.7		1	429.9	32.7	2	R.QGAPGQGGGGGLSHEDTLALLEGLVSR.R
*	HsF-IP-293-MG_Ti_106.25	4.642	0.2933	2578.24	2577.81	5397.2		1	864.7	32.7	2	R.QGAPGQGGGGGLSHEDTLALLEGLVSR.R
*	HsHeLa_Control-MG_Ti_20	3.074	0.3302	2578.4	2577.81	2923.6		2	117.7	32.7	1	R.QGAPGQGGGGGLSHEDTLALLEGLVSR.R
*	HsFLAG-Control_Hela_Ti_1	3.7546	0.3881	2578.41	2577.81	5918		1	619.1	26.9	1	R.QGAPGQGGGGGLSHEDTLALLEGLVSR.R
*	HsHeLa_Control_Ti_104.38	3.7867	0.362	2578.47	2577.81	7156		1	418.2	32.7	3	R.QGAPGQGGGGGLSHEDTLALLEGLVSR.R
*	HsFLAG-Control_Hela_Ti_1	3.0055	0.3391	2578.48	2577.81	9435.5		1	423.9	32.7	1	R.QGAPGQGGGGGLSHEDTLALLEGLVSR.R
*	HsHeLa_Control_Ti_104.38	3.7384	0.2154	2579.16	2577.81	4968.5		1	589.6	27.9	1	R.QGAPGQGGGGGLSHEDTLALLEGLVSR.R
*	Hs293FLP_Ti_303.3269.32	4.7609	0.2823	2580.12	2577.81	4303.5		3	464.4	26.9	7	R.QGAPGQGGGGGLSHEDTLALLEGLVSR.R
*	Hs283FLP_Ti_106.2161.21	4.2075	0.3133	2487.93	2487.69	7128.9		1	614.7	42.5	1	R.IQEELSALRAEHQQDSEDLFK.K
*	HsF-IP-293-MG_Ti_106.22	4.5062	0.3187	2489.26	2487.69	5733.4		1	1123	40	1	R.IQEELSALRAEHQQDSEDLFK.K
*	Hs283FLP_Ti_102.1487.14	3.6156	0.3002	1447.61	1447.5	6499.5		1	1287.5	81.8	1	R.AEHQQDSEDLFK.K
*	Hs283FLP_Ti_104.1277.12	3.9067	0.3724	1575.77	1575.68	9173.9		1	1690	79.2	4	R.AEHQQDSEDLFKK.I
*	HsF-IP-293-MG_Ti_104.18	4.7357	0.4502	2019.78	2019.15	7437.9		1	1185.7	62.5	13	K.SEWQSMTQESFQESSVK.E
*	Hs293FLP-MG_Ti_204.425	5.185	0.3172	2079.65	2081.42	6746.3		1	1737.2	66.7	5	R.RLEDQLAGLQQELAALALK.Q
*	HsHeLa_Control-MG_Ti_20	4.8613	0.3997	2080.08	2081.42	7794.6		1	2433.6	72.2	3	R.RLEDQLAGLQQELAALALK.Q
*	Hs293FLP-MG_Ti_204.422	6.0426	0.3036	2080.7	2081.42	9532.4		1	3156	51.4	2	R.RLEDQLAGLQQELAALALK.Q

*	HsFLAG-Control_Hela_Ti_1	4.6457	0.4157	2080.74	2081.42	8299		1	1842.1	66.7	18	R.RLEDQLAGLQQELAALALK.Q
*	HsHeLa_Control_Ti_105.42	6.9015	0.2504	2080.92	2081.42	7879		1	2733.1	51.4	4	R.RLEDQLAGLQQELAALALK.Q
*	Hs293FLP_Ti_305.3695.36	5.2037	0.3459	2081.39	2081.42	6444		1	1923.5	69.4	5	R.RLEDQLAGLQQELAALALK.Q
*	HsHeLa_Control-MG_Ti_10	6.2679	0.2595	2081.46	2081.42	8023.4		1	3295.1	54.2	3	R.RLEDQLAGLQQELAALALK.Q
*	HsHeLa_Control_Ti_106.38	5.7375	0.337	2081.58	2081.42	8151.2		1	2673.8	75	8	R.RLEDQLAGLQQELAALALK.Q
*	HsHeLa_Control-MG_Ti_20	6.1532	0.2982	2081.87	2081.42	8425.1		1	2264.5	45.8	2	R.RLEDQLAGLQQELAALALK.Q
*	Hs293FLP_Ti_303.3857.38	6.909	0.3045	2083.56	2081.42	8066.1		1	2551.4	48.6	5	R.RLEDQLAGLQQELAALALK.Q
*	Hs293FLP_Ti_302.4004.40	5.3946	0.3503	1926.81	1925.23	4251.3		1	885.8	64.7	16	R.LEDQLAGLQQELAALALK.Q
*	HsF-IP-293_Ti_202.0114.0	3.8926	0.1987	2052.81	2053.32	4643.4		1	848.7	63.9	7	K.QSSVAEEVGLLPQQIQAVR.D
*	Hs293FLP-MG_Ti_202.324	3.7047	0.283	2052.96	2053.32	4975.9		1	697.2	55.6	2	K.QSSVAEEVGLLPQQIQAVR.D
*	Hs283FLP_Ti_102.2591.25	4.3656	0.2452	2053.67	2053.32	4247.9		1	787.4	40.3	1	K.QSSVAEEVGLLPQQIQAVR.D
*	HsF-IP-293-MG_Ti_102.25	4.4326	0.2753	2053.9	2053.32	4667.4		1	1104.8	66.7	2	K.QSSVAEEVGLLPQQIQAVR.D
*	HsF-IP-293-MG_Ti_102.25	4.5051	0.2453	2055.4	2053.32	4441.6		1	997.6	43.1	1	K.QSSVAEEVGLLPQQIQAVR.D
*	HsHeLa_Control-MG_Ti_20	4.9307	0.351	4045.21	4044.51	5995.5		1	531.2	21.4	4	K.QSSVAEEVGLLPQQIQAVRDDVESQFPAWISQFLAR.G
*	Hs293FLP-MG_Ti_202.504	4.8808	0.4424	2009.22	2010.21	4736.7		1	1018.1	68.8	2	R.DDVESQFPAWISQFLAR.G
*	HsHeLa_Control-MG_Ti_20	3.8701	0.2031	2009.49	2010.21	9415.8		1	1699.6	43.8	1	R.DDVESQFPAWISQFLAR.G
*	Hs283FLP_Ti_104.3633.36	5.4705	0.2818	2009.5	2010.21	4144		1	980	68.8	14	R.DDVESQFPAWISQFLAR.G
*	HsHeLa_Control-MG_Ti_20	4.8622	0.2937	2009.52	2010.21	5834.9		1	1047.7	65.6	7	R.DDVESQFPAWISQFLAR.G
*	Hs283FLP_Ti_103.3743.37	4.1924	0.1796	2009.7	2010.21	8567.1		1	1229.8	43.8	2	R.DDVESQFPAWISQFLAR.G
*	HsF-IP-293-MG_Ti_102.40	4.3393	0.2854	2010.66	2010.21	7677.8		2	1141.8	43.8	3	R.DDVESQFPAWISQFLAR.G
*	Hs293FLP_Ti_302.4430.44	4.1678	0.281	2011.56	2010.21	3954.1		1	643.1	59.4	8	R.DDVESQFPAWISQFLAR.G
*	HsF-IP-293-MG_Ti_104.14	2.9761	0.263	1226.45	1227.46	5541.2		1	857.3	70	2	K.ILTHVAEMQGK.S
*	HsF-IP-293_Ti_205.1567.1	2.4039	0.2839	1226.45	1227.46	6211.6		1	544.5	55	3	K.ILTHVAEMQGK.S
*	Hs293FLP-MG_Ti_105.145	3.0324	0.2682	1226.7	1227.46	6172.1		1	1000.8	70	2	K.ILTHVAEMQGK.S
*	HsFLAG-Control_293_Ti_2	2.9755	0.3764	1226.97	1227.46	8260.8		1	985.3	70	2	K.ILTHVAEMQGK.S
*	Hs293FLP_TREX_Ti_104.1	3.7987	0.4243	1227.33	1227.46	6375.9		1	1627.1	90	5	K.ILTHVAEMQGK.S
*	HsFLAG-Control_293_Ti_2	3.0711	0.2881	1227.42	1227.46	7340		1	957.9	70	4	K.ILTHVAEMQGK.S
*	HsF-IP-293-MG_Ti_104.14	2.9994	0.3643	1228.38	1227.46	6491		1	1538.1	90	2	K.ILTHVAEMQGK.S
*	Hs293FLP-MG_Ti_105.145	3.0333	0.2461	1229.3	1227.46	6089.4		1	1383.8	85	3	K.ILTHVAEMQGK.S
*	Hs283FLP_Ti_102.1799.17	3.5903	0.2835	1233.47	1232.42	6589.2		1	1393.4	86.4	9	R.EAAASLSLTLQK.E
*	HsF-IP-293-MG_Ti_106.22	4.0328	0.3565	1774.72	1775.02	7714.2		1	657.6	50	14	K.EGVIGVTEEQVHHIVK.Q
*	Hs293FLP-MG_Ti_202.316	5.1113	0.4707	1880.23	1881.09	8616		1	1889.7	63.9	3	R.IGLADYALESGGASVISTR.C
*	HsF-IP-293-MG_Ti_102.26	5.2138	0.5069	1880.75	1881.09	8145.1		1	1849.7	66.7	34	R.IGLADYALESGGASVISTR.C
*	HsF-IP-293-MG_Ti_102.24	3.901	0.3255	1881.18	1881.09	5648		1	1210.4	44.4	1	R.IGLADYALESGGASVISTR.C
*	HsHeLa_Control-MG_Ti_20	5.5212	0.4364	1881.46	1881.09	9954.6		1	2422.7	66.7	39	R.IGLADYALESGGASVISTR.C
*	Hs283FLP_Ti_104.2236.22	4.2104	0.273	1882.11	1881.09	5673.4		1	1290	43.1	6	R.IGLADYALESGGASVISTR.C
*	HsHeLa_Control-MG_Ti_20	3.9111	0.3384	2186.94	2187.55	3943.6		1	311.2	44.4	4	K.TALLSLFGIPLWYHSQSPR.V
*	Hs293FLP-MG_Ti_206.355	3.31	0.3151	2187.18	2187.55	4151		1	366.9	44.4	1	K.TALLSLFGIPLWYHSQSPR.V
*	Hs293FLP_Ti_306.3495.34	3.3151	0.1938	2188.85	2187.55	3030.9		1	416.3	55.6	2	K.TALLSLFGIPLWYHSQSPR.V
*	Hs293FLP_Ti_306.3499.34	3.5735	0.2465	2189.01	2187.55	6115.6		1	1138.3	43.1	1	K.TALLSLFGIPLWYHSQSPR.V
*	HsHeLa_Control-MG_Ti_20	3.6716	0.2277	2189.05	2187.55	6699.3		3	855.8	37.5	1	K.TALLSLFGIPLWYHSQSPR.V
*	HsFLAG-Control_Hela_Ti_1	3.1362	0.3552	2793.12	2794.15	5698.8		1	347.2	33.3	1	R.VILQPDVHPGNCWAFQGPQGFAVVR.L
*	Hs293FLP_TREX_Ti_106.2	3.7183	0.2738	1461.78	1461.75	4249.6		3	510.6	62.5	12	R.IRPTAVTLEHVPK.A
*	HsF-IP-293_Ti_206.2870.2	6.7284	0.486	2243.73	2244.46	9538.5		1	2681.8	71.1	153	K.DFAIFGFDEDLQQEGTLLGK.F
*	HsF-IP-293-MG_Ti_106.25	5.5466	0.4251	3435.12	3434.8	4401		1	691.1	32.1	6	K.FTYDQDGEPIQTFHFQAPTMATYQVVELR.I
*	HsHeLa_Control-MG_Ti_20	4.3931	0.3552	1923.44	1924.13	4394		1	598.2	64.3	10	R.ILTNWGHPEYTCIYR.F
*	Hs283FLP_Ti_106.1784.17	2.8277	0.1803	1051.8	1050.17	5153.2		2	852.2	87.5	3	R.FRVHGEPAH.-
gi|14165435|ref|	57	489	0.579	463	50976	5.5	U	heterogeneous nuclear ribonucleoprotein K isoform b [Homo sapiens]				

gi|14165439|ref|N	57	489	0.578	464	51028	5.3	U	heterogeneous nuclear ribonucleoprotein K isoform a [Homo sapiens]			
gi|14165437|ref|N	57	489	0.578	464	51028	5.3	U	heterogeneous nuclear ribonucleoprotein K isoform a [Homo sapiens]			
	Hs293FLP_Ti_303.1398.13	4.125	0.4016	1581.63	1580.71	8342.4	1	1509.3	75	2	K.RPAEDMEEEQAFK.R
	HsHeLa_Control-MG_Ti_10	1.8661	0.1184	729.7	729.855	4355.3	2	448.9	71.4	1	K.NAGAVIGK.G
	HsFLAG-MOCK_300mM_T	4.6585	0.4487	2122.19	2122.26	4379.4	1	829.8	63.2	3	K.ALRTDYNASVSVPDSSGPER.I
	HsFLAG-Control_HeLa_S1(	3.8982	0.3134	1783.58	1781.83	4744.9	1	749.1	62.5	49	R.TDYNASVSVPDSSGPER.I
	HsGST-MOCK_Ti_403.493(	5.5662	0.4069	1715.37	1716.03	8511.8	1	2870	86.7	33	R.ILSISADIETIGEILK.K
	HsFlag1P_Ti_106.3252.325	4.5083	0.4231	1843.64	1844.2	7684.5	1	1191.7	62.5	10	R.ILSISADIETIGEILKK.I
	HsHeLa_Control-MG_Ti_20	6.1958	0.3966	4186.73	4185.68	10495.6	1	1614.6	27.1	9	K.KIIPTLEEGLQLPSPTATSQLPLESDAVECLNYQHYK.G
	HsFLAG-Control_HeLa_NE	4.7403	0.2501	4058.44	4057.51	5222.2	1	722.3	25.7	2	K.IIPTLEEGLQLPSPTATSQLPLESDAVECLNYQHYK.G
	HsFLAG-Control_HeLa_NE	3.3812	0.2918	1099.36	1099.11	6403.8	2	840	81.2	4	K.GSDFDCELR.L
	HsFLAG-MOCK_300mM_T	4.0678	0.089	1520.07	1519.87	6386.5	1	1186.2	71.4	1	R.LLIHQSLAGGIIGVK.G
	HsFLAG-MOCK_300mM_T	3.9093	0.3144	1576.93	1574.82	8825.2	1	1003.8	66.7	2	K.IKELRENTQTTIK.L
	HsFLAG-Control_HeLa_S1(	3.3954	0.1969	1550.2	1550.6	8903.9	1	898.6	63.6	8	K.LFQECCPHSTDR.V
	HsGST-MOCK_Ti_104.155	4.7776	0.3436	2585.57	2585.86	8732.1	1	2149.3	42.9	4	K.LFQECCPHSTDRVVLIGGKPDR.V
	HsGST-MOCK_Ti_105.169(	5.3324	0.3238	3313.39	3314.71	10946.8	1	1282.4	29.6	1	K.LFQECCPHSTDRVVLIGGKPDRVVECIK.I
	HsFLAG-Control_HeLa_NE	2.903	0.1272	1054.26	1054.28	4823.1	7	812.4	77.8	7	R.VVLIGGKPDR.V
	HsFLAG-Control_HeLa_NE	3.129	0.1936	1340.67	1341.63	7595.8	1	803.7	68.2	2	K.IILDLISESPIK.G
	HsHeLa3_Ti_103.3088.309	3.2485	0.3183	1340.74	1341.63	5664.4	1	612.6	68.2	1	K.IILDLISESPIK.G
	HsFLAG-Control_HeLa_NE	4.6739	0.2464	1341.35	1341.63	8587.7	2	1790.9	81.8	18	K.IILDLISESPIK.G
	HsHeLa3_Ti_103.3098.309	4.6155	0.253	1341.39	1341.63	8229.6	1	1821.8	81.8	3	K.IILDLISESPIK.G
	HsFLAG-Control_HeLa_NE	4.7883	0.2517	1341.5	1341.63	8184.8	1	2378	90.9	7	K.IILDLISESPIK.G
	HsFLAG-Control_HeLa_NE	3.4068	0.2917	1341.72	1341.63	8161.3	1	1046.2	72.7	2	K.IILDLISESPIK.G
	HsFlag1P_Ti_106.2756.275	4.9341	0.2674	1555.51	1554.87	6667.6	1	1614.5	80.8	3	K.IILDLISESPIKGR.A
	HsGST-MOCK_Ti_302.397	3.3339	0.3087	3058.83	3060.25	5564.9	1	562.7	41.7	1	R.AQPYDPNFYDETYDYGGFTMMFDDR.R
	HsFLAG-Control_HeLa_NE	5.5832	0.4356	1918.46	1918.2	7846	1	1559.2	63.9	150	R.GSYGDLGGPIITTQVTIPK.D
	HsFLAG-Control_HeLa_NE	1.9673	0.1718	873.4	874.025	6526.9	3	592.1	68.8	1	K.DLAGSIIGK.G
	HsFLAG-Control_HeLa_NE	2.5195	0.0931	874.12	874.025	3318	4	566.2	75	1	K.DLAGSIIGK.G
	HsFLAG-Control_HeLa_S1(	2.272	0.1671	874.4	874.025	7075.2	1	668	75	2	K.DLAGSIIGK.G
	HsFLAG-Control_HeLa_NE	4.5825	0.4231	2069.73	2070.18	6988.6	1	1409.6	66.7	1	R.HESGASIKIDEPLEGSEDR.I
	HsFLAG-MOCK_300mM_T	4.1154	0.2853	4643.15	4642.09	8763.1	3	454.8	17.7	3	R.HESGASIKIDEPLEGSEDRIITITGTQDQIQNAQYLLQNSVK.Q
	HsFLAG-MOCK_300mM_T	3.5682	0.2518	1260.91	1260.3	5151.1	1	1328.7	90	10	K.IDEPLEGSEDR.I
	HsFLAG-Control_HeLa_NE	5.1841	0.4623	3830.99	3832.21	9203.5	1	1030	25	3	K.IDEPLEGSEDRIITITGTQDQIQNAQYLLQNSVK.Q
	HsFLAG-Control_HeLa_NE	5.5052	0.455	2589.06	2590.94	8616.2	1	1540	52.3	26	R.IITITGTQDQIQNAQYLLQNSVK.Q
	HsFLAG-Control_HeLa_S1(	4.6911	0.4184	2589.26	2590.94	11012.9	1	1112.6	43.2	2	R.IITITGTQDQIQNAQYLLQNSVK.Q
	HsFLAG-Control_HeLa_NE	5.9379	0.4364	2589.39	2590.94	8598.3	1	1220.1	47.7	17	R.IITITGTQDQIQNAQYLLQNSVK.Q
	HsFLAG-MOCK_300mM_T	5.4014	0.4145	2589.67	2590.94	9405.2	1	1228	45.5	5	R.IITITGTQDQIQNAQYLLQNSVK.Q
	Hs293FLP-MG_Ti_202.373	4.969	0.3921	2589.79	2590.94	8402.9	1	1248.9	50	3	R.IITITGTQDQIQNAQYLLQNSVK.Q
	HsGST-MOCK_Ti_303.354	5.2735	0.3229	2589.88	2590.94	8521.1	1	1597.1	54.5	5	R.IITITGTQDQIQNAQYLLQNSVK.Q
	HsFLAG-Control_HeLa_S1(	5.7198	0.3938	2589.9	2590.94	8909.4	1	1626.4	54.5	2	R.IITITGTQDQIQNAQYLLQNSVK.Q
	HsFLAG-Control_HeLa_NE	5.576	0.3414	2589.96	2590.94	9026.4	1	1725.7	54.5	8	R.IITITGTQDQIQNAQYLLQNSVK.Q
	Hs283FLP_Ti_102.3029.30	5.8915	0.3684	2590	2590.94	10034.3	1	2403.9	38.6	3	R.IITITGTQDQIQNAQYLLQNSVK.Q
	HsFLAG-Control_HeLa_S1(	5.5057	0.4653	2590.01	2590.94	11190.3	1	1848.3	35.2	3	R.IITITGTQDQIQNAQYLLQNSVK.Q
	HsFLAG-Control_HeLa_S1(	5.6849	0.5239	2590.02	2590.94	11265.5	1	2437.3	39.8	5	R.IITITGTQDQIQNAQYLLQNSVK.Q
	HsFLAG-Control_HeLa_S1(	3.5156	0.2385	2590.04	2590.94	8841	1	603.1	38.6	2	R.IITITGTQDQIQNAQYLLQNSVK.Q
	HsHeLa3_Ti_103.3274.327	5.171	0.2764	2590.1	2590.94	8517.9	1	1125.8	47.7	3	R.IITITGTQDQIQNAQYLLQNSVK.Q

	HsFLAG-Control_HeLa_NE	5.8708	0.4456	2590.24	2590.94	12528.2		1	2390.2	36.4	6	R.IITITGTQDQIQNAQYLLQNSVK.Q
	HsGST-MOCK_Ti_403.364	4.8814	0.3598	2590.42	2590.94	12566.1		1	2070.6	35.2	1	R.IITITGTQDQIQNAQYLLQNSVK.Q
	HsF-IP-293-MG_Ti_102.29	4.3221	0.313	2590.55	2590.94	9953.5		1	915.1	43.2	3	R.IITITGTQDQIQNAQYLLQNSVK.Q
	Hs293FLP_Ti_302.3294.32	5.3785	0.3078	2590.57	2590.94	8567.8		1	1095.5	45.5	8	R.IITITGTQDQIQNAQYLLQNSVK.Q
	Hs293FLP-MG_Ti_202.374	6.1841	0.4296	2590.6	2590.94	11582.4		1	2313.6	38.6	2	R.IITITGTQDQIQNAQYLLQNSVK.Q
	HsFLAG-Control_HeLa_S1	5.9962	0.522	2590.64	2590.94	9169		1	1610.2	36.4	2	R.IITITGTQDQIQNAQYLLQNSVK.Q
	Hs283FLP_Ti_102.3034.30	5.5693	0.309	2590.77	2590.94	7795.5		1	1233.6	50	10	R.IITITGTQDQIQNAQYLLQNSVK.Q
	HsFLAG-Control_293_Ti_2	4.5893	0.4092	2590.9	2590.94	11683		1	1309.9	30.7	1	R.IITITGTQDQIQNAQYLLQNSVK.Q
	HsFLAG-Control_HeLa_NE	6.3998	0.4438	2591.14	2590.94	11931.7		1	2624.6	38.6	6	R.IITITGTQDQIQNAQYLLQNSVK.Q
	HsF-IP-293-MG_Ti_102.29	4.9498	0.3334	2591.91	2590.94	13548.7		1	1719	31.8	1	R.IITITGTQDQIQNAQYLLQNSVK.Q
	HsFLAG-Control_HeLa_NE	6.6576	0.4918	2592.01	2590.94	10530.5		1	2474.9	39.8	18	R.IITITGTQDQIQNAQYLLQNSVK.Q
	HsHeLa3_Ti_103.3275.327	5.3202	0.4116	2592.12	2590.94	9207.4		1	1945.2	38.6	2	R.IITITGTQDQIQNAQYLLQNSVK.Q
	HsFLAG-MOCK_300mM_T	5.7003	0.353	2593.14	2590.94	10676.5		1	1750.3	34.1	1	R.IITITGTQDQIQNAQYLLQNSVK.Q
gi|5729877|ref|N	94	552	0.567	646	70898	5.5	U	heat shock 70kDa protein 8 isoform 1 [Homo sapiens]				
	HsHeLa3_Ti_106.2448.244	4.4054	0.1675	2265.02	2264.51	7546.1		1	625.1	40.5	1	K.GPAVGIDLGTTYSCVGVFQHGK.V
	HsHeLa_Control-MG_Ti_20	4.6995	0.211	2265.07	2264.51	10915.3		1	1590.6	54.8	4	K.GPAVGIDLGTTYSCVGVFQHGK.V
	HsFLAG-Control_HeLa_S1	3.9247	0.2716	2265.96	2264.51	4306.6		1	618.7	33.3	2	K.GPAVGIDLGTTYSCVGVFQHGK.V
	HsF-IP-293-MG_Ti_102.17	2.6315	0.2566	1487.66	1488.59	3419.2		1	176.5	58.3	2	R.TTPSYVAFTDTER.L
	HsFLAG-Control_HeLa_NE	3.2444	0.2808	1487.89	1488.59	4634.5		1	570.4	66.7	57	R.TTPSYVAFTDTER.L
	Hs293FLP-MG_Ti_202.217	3.2886	0.3043	1487.89	1488.59	4372.6		1	860.7	83.3	12	R.TTPSYVAFTDTER.L
	HsHeLa_Control-MG_Ti_20	2.4813	0.2055	1488.47	1488.59	3249.8		1	121.1	50	1	R.TTPSYVAFTDTER.L
	HsHeLa_Control-MG_Ti_20	3.6044	0.4296	1489.1	1488.59	3675.9		1	589.8	75	9	R.TTPSYVAFTDTER.L
	HsFLAG-MOCK_300mM_T	3.2112	0.1491	2159.14	2157.39	6487.7		1	523.9	44.7	2	R.TTPSYVAFTDTERLIGDAAK.N
	HsGST-MOCK_Ti_303.207	4.9627	0.4058	1650.02	1650.85	5724.7		1	1649.5	82.1	10	K.NQVAMNPTNTVFDAK.R
	HsFLAG-MOCK_300mM_T	3.7693	0.4006	1411.8	1411.57	5298.5		1	1194.1	81.8	3	R.RFDDAVVQSDMK.H
	HsGST-MOCK_Ti_105.174	3.2636	0.4169	1654.63	1654.93	3707.1		1	650.1	73.1	2	K.HWPFMVVNDAGRPK.V
	HsGST-MOCK_Ti_105.175	4.3692	0.3384	1655.25	1654.93	5147.8		1	1559.1	57.7	2	K.HWPFMVVNDAGRPK.V
	Hs293FLP_TREX_Ti_103.1	3.1894	0.2192	1181.34	1181.33	4945.8		3	857.3	83.3	5	K.VQVEYKGETK.S
	HsGST-MOCK_Ti_302.287	4.164	0.3308	1617.96	1617.85	4190.6		1	927.1	80.8	6	K.SFYPEEVSSMVLTK.M
	HsFLAG-Control_HeLa_NE	2.4761	0.1642	993.42	994.133	4988.2		5	428.3	68.8	5	K.EIAEAYLGK.T
	HsFLAG-Control_HeLa_NE	3.3552	0.2398	1981.96	1983.19	4191.9		1	456	52.9	13	K.TVTNAVVTVPAYFNDSQR.Q
	HsGST-MOCK_Ti_403.272	3.2923	0.3398	1982.49	1983.19	4326.7		1	456.9	55.9	5	K.TVTNAVVTVPAYFNDSQR.Q
	HsFLAG-Control_HeLa_S1	4.0683	0.3035	1982.58	1983.19	7541.4		1	1251.8	45.6	1	K.TVTNAVVTVPAYFNDSQR.Q
	HsFLAG-Control_HeLa_S1	3.206	0.2753	1982.72	1983.19	4452.9		1	461.8	50	2	K.TVTNAVVTVPAYFNDSQR.Q
	HsFLAG-Control_HeLa_S1	3.8087	0.2803	1982.86	1983.19	7156.3		2	1073.8	41.2	2	K.TVTNAVVTVPAYFNDSQR.Q
	HsFLAG-Control_HeLa_S1	3.2873	0.2476	1983.41	1983.19	4951.1		1	399.1	50	4	K.TVTNAVVTVPAYFNDSQR.Q
	HsFLAG-Control_HeLa_S1	3.9221	0.3572	1983.79	1983.19	6926.6		1	1016.7	42.6	1	K.TVTNAVVTVPAYFNDSQR.Q
	HsHeLa_Control-MG_Ti_20	5.5061	0.3911	1661.88	1660.91	4282.5		1	1591.7	86.7	75	R.IINEPTAAAIAYGLDK.K
	HsFlag1P_Ti_105.2426.242	5.1147	0.1386	1787.95	1789.08	4898.2		1	1086.6	71.9	5	R.IINEPTAAAIAYGLDKK.V
	HsHeLa_Control-MG_Ti_10	3.2344	0.2825	1236.5	1236.47	5739.6		1	870.4	72.2	4	R.MVNHFIAEFK.R
	HsFLAG-Control_HeLa_S1	3.5464	0.2955	2999.08	2999.26	8277.7		1	604	34.6	1	R.TLSSSTQASIEIDSLYEGIDFYTSITR.A
	HsGST-MOCK_Ti_102.194	4.0503	0.2122	1481.42	1481.65	6150.3		2	1322.4	54.5	2	R.ARFEELNADLFR.G
	HsGST-MOCK_Ti_404.268	3.9815	0.2532	1481.49	1481.65	5240.4		1	1202.9	86.4	2	R.ARFEELNADLFR.G
	HsHeLa_Control-MG_Ti_10	4.2431	0.2761	1483.66	1481.65	4363.8		1	928.3	81.8	24	R.ARFEELNADLFR.G
	HsFLAG-Control_HeLa_S1	3.8164	0.214	1254.28	1254.39	7085		1	1542.2	88.9	7	R.FEELNADLFR.G
	HsFLAG-Control_293_Ti_2	3.8559	0.4528	1481.52	1482.68	5943.4		1	846.1	65.4	2	K.SQIHDIVLVGGSTR.I
	HsFLAG-Control_MG_293_	3.1916	0.398	1481.61	1482.68	6462.3		1	617	53.8	1	K.SQIHDIVLVGGSTR.I
	Hs293FLP-MG_Ti_204.184	3.3162	0.4067	1481.69	1482.68	6234.7		1	644.6	57.7	2	K.SQIHDIVLVGGSTR.I
	HsFLAG-Control_HeLa_NE	3.7225	0.4672	1481.73	1482.68	6211.4		1	888	65.4	4	K.SQIHDIVLVGGSTR.I

Hs293FLP_Ti_304.1698.16	3.2524	0.4446	1481.82	1482.68	5265.7	1	766.2	65.4	2	K.SQIHDIVLVGGSTR.I
HsFLAG-MOCK_300mM_T	3.041	0.3696	1481.86	1482.68	4795.5	1	703.9	65.4	1	K.SQIHDIVLVGGSTR.I
HsHeLa_Control-MG_Ti_10	3.3098	0.3886	1481.89	1482.68	5062.8	1	824.4	69.2	2	K.SQIHDIVLVGGSTR.I
HsHeLa_Control-MG_Ti_20	4.946	0.3344	1481.93	1482.68	7702.9	1	2340.2	84.6	11	K.SQIHDIVLVGGSTR.I
HsFLAG-Control_HeLa_NE	4.5597	0.3068	1482.26	1482.68	8854.8	1	1742	69.2	9	K.SQIHDIVLVGGSTR.I
HsFLAG-Control_HeLa_S1	4.7635	0.3224	1482.41	1482.68	8130.9	1	1893.2	73.1	18	K.SQIHDIVLVGGSTR.I
Hs293FLP-MG_Ti_204.184	4.6886	0.312	1482.5	1482.68	8678.4	1	2057.2	76.9	1	K.SQIHDIVLVGGSTR.I
HsFLAG-Control_293_Ti_2	4.2856	0.3071	1482.56	1482.68	8116.9	1	1808.6	73.1	2	K.SQIHDIVLVGGSTR.I
HsGST-MOCK_Ti_405.205	2.287	0.322	1482.57	1482.68	3388.1	1	321.2	57.7	1	K.SQIHDIVLVGGSTR.I
HsFLAG-Control_HeLa_S1	3.4799	0.3599	1482.7	1482.68	7228.3	4	606	53.8	3	K.SQIHDIVLVGGSTR.I
HsHeLa3_Ti_105.1744.174	4.2829	0.4085	1482.73	1482.68	5309.1	1	1023.6	73.1	2	K.SQIHDIVLVGGSTR.I
HsFLAG-Control_HeLa_NE	4.593	0.3103	1482.76	1482.68	8234.6	1	2366.9	80.8	5	K.SQIHDIVLVGGSTR.I
HsFLAG-MOCK_300mM_T	4.0466	0.2571	1482.83	1482.68	7009.9	1	1435.8	69.2	3	K.SQIHDIVLVGGSTR.I
HsGST-MOCK_Ti_101.080	4.6702	0.295	1482.99	1482.68	7872.8	1	2390.2	80.8	6	K.SQIHDIVLVGGSTR.I
HsFLAG-Control_HeLa_S1	3.9658	0.3945	1483.02	1482.68	7100.2	1	1215.4	69.2	1	K.SQIHDIVLVGGSTR.I
HsGST-MOCK_Ti_405.205	5.092	0.3507	1483.61	1482.68	8554.1	1	2381.3	80.8	2	K.SQIHDIVLVGGSTR.I
Hs293FLP_Ti_305.1686.16	4.6099	0.2866	1483.98	1482.68	7164.7	1	2599.1	88.5	4	K.SQIHDIVLVGGSTR.I
HsFLAG-Control_HeLa_S1	4.4395	0.2709	1485.01	1482.68	9405.6	1	1871.4	69.2	3	K.SQIHDIVLVGGSTR.I
HsFLAG-Control_MG_293_	3.1449	0.1938	1082.22	1082.24	5278.9	5	835.3	87.5	7	K.LLQDFFNGK.E
HsFLAG-MOCK_300mM_T	3.5405	0.2578	1568.26	1566.8	8502.8	1	1323.3	75	1	K.LLQDFFNGKELNK.S
HsFLAG-Control_HeLa_S1	5.6097	0.5339	2260.52	2261.49	7975	1	1606.5	56.8	7	K.SINPDEAVAYGAAVQAAILSGDK.S
HsFLAG-Control_HeLa_NE	5.9557	0.404	2260.63	2261.49	8563.7	1	1874.8	39.8	5	K.SINPDEAVAYGAAVQAAILSGDK.S
Hs293FLP-MG_Ti_202.417	5.1297	0.5251	2260.66	2261.49	7167	1	1540.4	59.1	4	K.SINPDEAVAYGAAVQAAILSGDK.S
HsGST-MOCK_Ti_302.392	5.314	0.5256	2260.67	2261.49	7971.5	1	1811	63.6	5	K.SINPDEAVAYGAAVQAAILSGDK.S
HsFLAG-Control_HeLa_S1	5.818	0.3302	2260.73	2261.49	8332.9	1	1455.8	37.5	6	K.SINPDEAVAYGAAVQAAILSGDK.S
HsFLAG-Control_HeLa_S1	5.8344	0.5087	2260.74	2261.49	7587.2	1	1617.1	59.1	24	K.SINPDEAVAYGAAVQAAILSGDK.S
HsFLAG-Control_HeLa_S1	5.4821	0.4976	2260.84	2261.49	7522	1	2005.7	61.4	10	K.SINPDEAVAYGAAVQAAILSGDK.S
Hs293FLP_Ti_302.3692.36	4.5818	0.435	2260.97	2261.49	7687.7	1	1220.3	36.4	1	K.SINPDEAVAYGAAVQAAILSGDK.S
HsHeLa_Control_Ti_102.36	4.6448	0.4625	2261.06	2261.49	6095.4	1	1146.3	54.5	1	K.SINPDEAVAYGAAVQAAILSGDK.S
Hs293FLP-MG_Ti_202.419	5.2834	0.4054	2261.06	2261.49	8657.2	1	1434.6	36.4	1	K.SINPDEAVAYGAAVQAAILSGDK.S
HsFLAG-Control_HeLa_S1	6.5692	0.5503	2261.2	2261.49	9040.4	1	2484.3	44.3	5	K.SINPDEAVAYGAAVQAAILSGDK.S
HsGST-MOCK_Ti_302.393	6.0016	0.4796	2261.29	2261.49	8073.8	1	1980.4	40.9	1	K.SINPDEAVAYGAAVQAAILSGDK.S
HsHeLa_Control-MG_Ti_20	5.8931	0.4265	2261.32	2261.49	8329.3	1	1959.5	40.9	2	K.SINPDEAVAYGAAVQAAILSGDK.S
HsFLAG-Control_293_Ti_2	5.4368	0.5221	2261.5	2261.49	7200.9	1	1253.6	54.5	12	K.SINPDEAVAYGAAVQAAILSGDK.S
HsF-IP-293-MG_Ti_102.33	5.2435	0.407	2261.56	2261.49	8035.6	1	1825.5	39.8	2	K.SINPDEAVAYGAAVQAAILSGDK.S
HsFLAG-Control_HeLa_NE	6.0796	0.4577	2261.56	2261.49	9546.8	1	2193.2	42	2	K.SINPDEAVAYGAAVQAAILSGDK.S
HsFLAG-Control_HeLa_S1	6.0208	0.4435	2261.57	2261.49	10483.8	1	2409.7	39.8	2	K.SINPDEAVAYGAAVQAAILSGDK.S
Hs283FLP_Ti_102.3377.33	5.611	0.4086	2261.58	2261.49	8393.8	1	1711.1	37.5	2	K.SINPDEAVAYGAAVQAAILSGDK.S
HsFLAG-Control_HeLa_NE	6.2814	0.4759	2261.82	2261.49	6695.3	1	1432.4	59.1	17	K.SINPDEAVAYGAAVQAAILSGDK.S
Hs283FLP_Ti_103.3082.30	6.1923	0.5078	2261.93	2261.49	6939.7	1	1751.5	61.4	11	K.SINPDEAVAYGAAVQAAILSGDK.S
HsHeLa3_Ti_102.3815.381	4.9635	0.4367	2262.11	2261.49	7595.2	1	1422.2	37.5	2	K.SINPDEAVAYGAAVQAAILSGDK.S
Hs293FLP_Ti_302.3683.36	4.8028	0.425	2262.33	2261.49	5824.5	1	1116.1	56.8	1	K.SINPDEAVAYGAAVQAAILSGDK.S
HsHeLa_Control-MG_Ti_20	6.5278	0.5401	2262.51	2261.49	7263.9	1	1852.4	63.6	4	K.SINPDEAVAYGAAVQAAILSGDK.S
HsFLAG-Control_HeLa_NE	6.0978	0.5559	2262.55	2261.49	7942.2	1	2036.6	63.6	18	K.SINPDEAVAYGAAVQAAILSGDK.S
HsHeLa3_Ti_102.3785.378	3.555	0.3286	2263.04	2261.49	7709.2	1	714.7	45.5	2	K.SINPDEAVAYGAAVQAAILSGDK.S
HsHeLa_Control_Ti_102.36	5.71	0.4624	2263.38	2261.49	7211.4	1	1448	36.4	2	K.SINPDEAVAYGAAVQAAILSGDK.S
HsHeLa_Control-MG_Ti_20	4.5969	0.3942	3239.63	3240.82	11123.7	1	1384.5	27.5	2	K.SENVQDLLLLDVTPLSLGIETAGGVMTVLIK.R
HsFLAG-Control_HeLa_S1	3.9516	0.3796	2775.78	2775.99	5840.8	1	436.6	37	5	K.QTQTFTTYSDNQPGVLIQVYEGER.A
HsFLAG-Control_HeLa_NE	4.4446	0.2549	2775.86	2775.99	11162.9	1	1419.2	32.6	3	K.QTQTFTTYSDNQPGVLIQVYEGER.A

	HsFLAG-Control_HeLa_NE	3.4583	0.3349	2775.88	2775.99	6152.6		1	471.2	37	2	K.QTQTFTTYSDNQPGVLIQVYEGER.A
*	HsFLAG-Control_HeLa_S1	3.215	0.0989	990.19	990.101	5523.5		3	856.7	92.9	4	R.LSKEDIER.M
*	HsFLAG-MOCK_300mM_T	3.8038	0.3146	1700.94	1698.89	5486		1	904.1	73.1	2	R.MVQEAEKYKAEDEK.Q
*	HsHeLa3_Ti_103.2103.210	2.8767	0.3146	1303.5	1304.46	4220.9		1	263.2	60	1	K.NSLESYAFNMK.A
*	HsGST-MOCK_Ti_403.248	3.8512	0.3573	1304.08	1304.46	6601.5		1	1373.6	85	4	K.NSLESYAFNMK.A
*	HsHeLa3_Ti_103.2100.210	3.4534	0.2336	1304.51	1304.46	6123.1		1	1194.7	85	2	K.NSLESYAFNMK.A
*	HsFLAG-Control_MG_293_	2.4955	0.1493	1306.36	1304.46	4600		1	348.3	65	1	K.NSLESYAFNMK.A
*	HsFLAG-Control_HeLa_NE	3.6803	0.2102	1305.94	1305.44	7123.7		2	1324.7	88.9	2	K.CNEIINWLDK.N
*	HsFLAG-Control_HeLa_NE	5.0042	0.2718	1746.62	1746.83	10402.5		1	1560.6	65.4	10	K.NQTAEKEEFEHQQK.E
*	HsFLAG-MOCK_300mM_T	5.469	0.1038	2246.04	2246.4	8090.7		1	856.7	52.9	1	K.NQTAEKEEFEHQQKELEK.V
gi|4503481|ref|NP	29	144	0.563	437	50119	6.7	U	eukaryotic translation elongation factor 1 gamma [Homo sapiens]				
*	HsGST-MOCK_Ti_404.196	4.9436	0.4465	1348.36	1348.55	9413.5		1	2236.6	79.2	32	K.ALIAAQYSGAQVR.V
	HsGST-MOCK_Ti_106.217	3.3089	0.4209	1707.81	1708.92	5891.1		1	836.9	64.3	1	R.VLSAPPHFHFGQTNR.T
	HsGST-MOCK_Ti_302.453	4.4819	0.4146	3198.69	3200.41	8401.2		1	994.2	40.7	9	K.VPAFEGDDGFCVFESNAIAYYVSNEELR.G
	HsGST-MOCK_Ti_303.465	5.6216	0.4227	3199.39	3200.41	8508.2		1	1425.5	32.4	3	K.VPAFEGDDGFCVFESNAIAYYVSNEELR.G
	HsGST-MOCK_Ti_103.240	3.3541	0.1422	1275.5	1275.58	5082.5		1	1165.5	85	5	R.RILGLLDAYLK.T
	HsGST-MOCK_Ti_303.354	3.6319	0.0894	1119.22	1119.39	3738.1		3	868.4	88.9	2	R.ILGLLDAYLK.T
	HsGST-MOCK_Ti_406.294	4.2496	0.3348	1610.4	1610.82	6506.5		1	1724.5	86.4	4	R.WFLTCINQPQFR.A
	HsGST-MOCK_Ti_302.221	5.0408	0.4796	2357.34	2358.5	5515.7		1	984.6	59.5	6	K.AAAPAPEEEMDECEQALAAEPK.A
	HsGST-MOCK_Ti_406.243	3.0281	0.0941	924.91	925.075	3427.9		6	632.1	92.9	1	K.DPFAHLPK.S
	Hs293FLP_TREX_Ti_102.2	2.185	0.1825	1085.38	1086.23	8062.3		2	610.5	68.8	1	K.STFVLDEFK.R
	HsGST-MOCK_Ti_302.232	2.7873	0.1742	1085.48	1086.23	5117.3		1	887.9	81.2	2	K.STFVLDEFK.R
	HsGST-MOCK_Ti_302.245	2.7543	0.1806	1085.49	1086.23	6792.6		1	675.9	75	1	K.STFVLDEFK.R
	HsGST-MOCK_Ti_402.265	2.8527	0.235	1086.18	1086.23	5825.1		4	894.9	81.2	2	K.STFVLDEFK.R
	Hs293FLP_TREX_Ti_102.2	2.7033	0.1174	1086.33	1086.23	5619.7		2	745.4	81.2	1	K.STFVLDEFK.R
	HsGST-MOCK_Ti_402.264	2.2858	0.1961	1086.52	1086.23	7087.3		8	457.6	62.5	1	K.STFVLDEFK.R
	HsGST-MOCK_Ti_303.233	2.636	0.1936	1242.21	1242.42	6208.1		3	826.9	72.2	1	K.STFVLDEFKR.K
	HsGST-MOCK_Ti_305.386	4.9402	0.4168	2589.93	2590.85	6842.3		1	803.9	50	2	R.KYSNEDTLSVALPYFWEHFDK.D
	HsGST-MOCK_Ti_404.425	4.3908	0.4458	2460.38	2462.68	4712.3		1	902.6	57.9	10	K.YSNEDTLSVALPYFWEHFDK.D
	HsGST-MOCK_Ti_404.424	4.0327	0.2749	2462.15	2462.68	7335.1		1	1139.7	39.5	3	K.YSNEDTLSVALPYFWEHFDK.D
	HsGST-MOCK_Ti_303.411	4.7388	0.2994	2462.51	2462.68	7279.1		1	1411	43.4	1	K.YSNEDTLSVALPYFWEHFDK.D
	HsGST-MOCK_Ti_304.349	4.3676	0.3903	2463.73	2462.68	5110.5		1	581.4	44.7	11	K.YSNEDTLSVALPYFWEHFDK.D
	HsGST-MOCK_Ti_302.305	4.1212	0.3956	1462.22	1462.56	7513.3		1	1411.1	80	6	K.DGWSLWYSEYR.F
	HsGST-MOCK_Ti_302.306	2.5435	0.1757	1462.58	1462.56	2757.8		1	219.8	60	1	K.DGWSLWYSEYR.F
	HsGST-MOCK_Ti_102.457	3.7247	0.3748	3993.05	3995.44	12032		1	1518.1	29	1	K.DGWSLWYSEYRFPEELTQTFMSCNLITGMFQR.L
	HsGST-MOCK_Ti_303.468	5.8493	0.4677	2552.37	2551.9	9621.9		1	1355.5	52.5	8	R.FPEELTQTFMSCNLITGMFQR.L
	HsFLAG-Control_HeLa_S1	3.8355	0.3598	2575.52	2574.9	10533.5		1	717.5	39.1	1	K.NAFASVILFGTNNSSSISGVWVFR.G
	HsGST-MOCK_Ti_302.398	4.9525	0.4169	2688.65	2688.91	7410.9		1	1184	54.8	18	R.GQELAFPLSPDWQVDYESYTWR.K
*	HsGST-MOCK_Ti_404.182	3.9437	0.3331	1573.59	1573.74	3508.2		1	971.3	88.5	3	R.KLDPGSEETQTLVR.E
	HsGST-MOCK_Ti_404.299	4.0081	0.3533	1685.94	1685.84	9076.2		1	1278.6	65.4	7	R.EYFSWEGAFQHVGK.A
gi|4502891|ref|NP	21	124	0.561	237	26215	4.1	U	chloride channel, nucleotide-sensitive, 1A [Homo sapiens]				
*	HsFlag1P_Ti_103.2305.230	4.4	0.4289	1338.37	1338.5	8016.3		1	1291.8	75	32	K.GLGTGTLYIAESR.L
*	Hs293FLP-MG_Ti_205.410	2.9104	0.3358	2719.84	2721.09	6556.6		1	319.8	29.2	2	R.LSWLDGSGLGFSLEYPTISLHALSR.D
*	HsFLAG-Control_Hela_Ti_1	3.5721	0.4091	2720.45	2721.09	6642.6		1	548.5	35.4	1	R.LSWLDGSGLGFSLEYPTISLHALSR.D
*	HsHeLa_Control-MG_Ti_20	5.7977	0.4083	2720.66	2721.09	7004.4		1	1496.7	37.5	7	R.LSWLDGSGLGFSLEYPTISLHALSR.D
*	HsFLAG-Control_293_Ti_1	5.4751	0.3674	2720.93	2721.09	7389.6		1	1519.5	37.5	2	R.LSWLDGSGLGFSLEYPTISLHALSR.D
*	Hs293FLP-MG_Ti_206.350	5.9236	0.4348	2720.95	2721.09	7612.8		1	1861.9	40.6	6	R.LSWLDGSGLGFSLEYPTISLHALSR.D
*	HsHeLa_Control-MG_Ti_10	3.0996	0.4355	2721.17	2721.09	5886.9		1	500.9	37.5	1	R.LSWLDGSGLGFSLEYPTISLHALSR.D
*	HsHeLa_Control-MG_Ti_20	4.6738	0.3949	2721.18	2721.09	8353.9		1	848.9	41.7	4	R.LSWLDGSGLGFSLEYPTISLHALSR.D

*	Hs293FLP_Ti_306.3455.34	3.8376	0.4276	2721.45	2721.09	5782.7		1	562.6	41.7	4	R.LSWLDGSGLGFSLEYPTISLHALSR.D
*	HsHeLa_Control_Ti_106.38	4.9922	0.4319	2721.5	2721.09	7131.4		1	1216.5	33.3	2	R.LSWLDGSGLGFSLEYPTISLHALSR.D
*	HsFLAG-Control_293_Ti_1	4.0698	0.3901	2721.64	2721.09	6741.9		1	654.1	39.6	3	R.LSWLDGSGLGFSLEYPTISLHALSR.D
*	HsHeLa_Control-MG_Ti_10	5.3233	0.3708	2721.75	2721.09	5393.1		1	1365.8	39.6	5	R.LSWLDGSGLGFSLEYPTISLHALSR.D
*	HsHeLa_Control_Ti_106.38	2.5935	0.4215	2721.86	2721.09	5891.1		1	331.6	33.3	1	R.LSWLDGSGLGFSLEYPTISLHALSR.D
*	Hs293FLP_Ti_306.3459.34	5.8601	0.4302	2722.27	2721.09	6257.5		1	1366.6	38.5	4	R.LSWLDGSGLGFSLEYPTISLHALSR.D
*	HsFLAG-MOCK_300mM_T	4.2541	0.372	2723.59	2721.09	5543.9		1	543.3	28.1	2	R.LSWLDGSGLGFSLEYPTISLHALSR.D
*	HsHeLa_Control-MG_Ti_10	3.7758	0.4268	2009.47	2008.22	9276.3		1	1283.9	62.5	2	R.DRSDCLGEHLYVMVNAK.F
*	Hs293FLP_Ti_304.2151.21	2.9273	0.276	1738.89	1736.95	6880.4		1	887.3	57.1	2	R.SDCLGEHLYVMVNAK.F
*	Hs283FLP_Ti_104.1825.18	6.3189	0.479	3315.79	3316.33	7291.3		1	1750.9	36.1	9	K.FEEESKEPVADEEEEDSDDDVEPITEFR.F
*	HsFLAG-Control_293_Ti_2	5.6155	0.4936	2057.41	2058.33	6835		1	1171.8	61.1	9	R.LEGMLSQSVSSQYNMAGVR.T
*	Hs293FLP_Ti_303.2391.23	5.8136	0.3528	3458.98	3459.54	5067.5		1	951.5	32.5	15	R.TEDSIRDYEDGMEVDTTPTVAGQFEDADVDH.-
*	Hs293FLP-MG_Ti_202.279	4.5214	0.441	2756.59	2757.81	5441.1		1	619.9	43.8	11	R.DYEDGMEVDTTPTVAGQFEDADVDH.-
gi|10800130|ref|	6	41	0.546	130	14107	10.9	U		histone 1, H2ad [Homo sapiens]			
gi|4504243|ref|	6	41	0.546	130	14091	10.9	U		H2A histone family, member I [Homo sapiens]			
gi|4504241|ref|	6	41	0.546	130	14091	10.9	U		H2A histone family, member D [Homo sapiens]			
gi|4504239|ref|	6	41	0.546	130	14091	10.9	U		H2A histone family, member C [Homo sapiens]			
gi|29553970|ref|	6	41	0.55	129	14019	10.9	U		H2A histone family, member J isoform 2 [Homo sapiens]			
gi|18105045|ref|	6	41	0.555	128	13906	10.9	U		H2A histone family member [Homo sapiens]			
gi|10800144|ref|	6	41	0.555	128	13936	10.9	U		H2A histone family, member E [Homo sapiens]			
gi|10800132|ref|	6	41	0.546	130	14091	10.9	U		H2A histone family, member P [Homo sapiens]			
	Hs293FLP-MG_Ti_104.190	2.3447	0.1182	944.77	945.109	4092.1		5	353.2	68.8	1	R.AGLQFPVGR.V
	HsHeLa_Control-MG_Ti_10	2.6626	0.17	945.58	945.109	3921		2	699.4	81.2	1	R.AGLQFPVGR.V
	HsFLAG-Control_HeLa_NE	4.5014	0.4747	2916.07	2917.38	7823.6		1	640.8	32.1	1	R.VGAGAPVYLAAVLEYLTAEILELAGNAAR.D
	HsFLAG-Control_HeLa_NE	6.3703	0.4516	2916.71	2917.38	9322.9		1	2302	36.6	3	R.VGAGAPVYLAAVLEYLTAEILELAGNAAR.D
	HsHeLa_Control-MG_Ti_10	3.6354	0.3585	1693.91	1693.9	7274.3		1	861.3	65.4	1	R.HLQLAIRNDEELNK.L
	HsFLAG-Control_HeLa_NE	4.9834	0.3335	1934.26	1932.36	4934.3		1	762.8	58.3	34	K.VTIAQGGVLPNIQAVLLPK.K
gi|29558022|ref|	21	122	0.545	387	42771	5.2	U		protein phosphatase 1B isoform 2 [Homo sapiens]			
	HsFLAG-Control_293_Ti_2	2.6531	0.2112	1103.33	1104.17	4101.4		1	403.1	75	1	K.HNAHGAGNGLR.Y
	HsFLAG-Control_293_Ti_1	3.2339	0.3453	1103.74	1104.17	8861.2		1	2265.7	95	2	K.HNAHGAGNGLR.Y
	HsHeLa_Control-MG_Ti_10	4.8821	0.4005	2423.08	2421.6	8031.9		1	1254.5	52.6	6	R.VANYCSTHLLEHITTNEDFR.A
	HsFLAG-Control_MG_293_	2.9992	0.2103	1332.24	1333.48	7647.4		1	699	62.5	6	K.SGSALELSVENVK.N
	HsFLAG-Control_293_Ti_2	2.9318	0.2077	1332.57	1333.48	8414.3		2	667.2	54.2	4	K.SGSALELSVENVK.N
	HsFLAG-Control_MG_293_	4.1643	0.3777	1333.09	1333.48	7152.2		1	1787	83.3	6	K.SGSALELSVENVK.N
	HsFLAG-Control_293_Ti_2	4.9454	0.3704	1333.37	1333.48	6398.8		1	1435.5	79.2	6	K.SGSALELSVENVK.N
	HsFLAG-Control_293_Ti_2	2.4622	0.2138	1233.46	1234.45	8679		8	612.3	54.2	1	R.SGSTAVGVMISPK.H
	HsHeLa_Control-MG_Ti_20	3.7095	0.2212	1382.45	1382.49	4556.8		1	868.1	85	12	K.HIYFINCGDSR.A
	HsFLAG-Control_293_Ti_2	3.3738	0.2339	2045.79	2046.14	6794.8		1	703	56.2	4	R.NGQVCFSTQDHKPCNPR.E
	HsFLAG-Control_MG_293_	2.5652	0.0862	1273.47	1274.48	5630		1	401.2	63.6	1	R.IQNAGGSVMIQR.V
	HsFLAG-Control_MG_293_	4.4413	0.3358	1273.86	1274.48	6627.4		1	1508.5	86.4	2	R.IQNAGGSVMIQR.V
	HsFLAG-Control_293_Ti_2	4.4046	0.2904	1275.28	1274.48	7129.4		1	1529.5	81.8	2	R.IQNAGGSVMIQR.V
	HsFLAG-Control_MG_293_	2.8295	0.1074	903.19	903.026	4555.8		1	951.5	93.8	2	R.VNGSLAVSR.A
	HsFLAG-Control_MG_293_	2.3432	0.1222	944.4	945.017	7578		5	674.3	71.4	4	R.ALGDYDYK.C
	HsFLAG-Control_293_Ti_2	3.7284	0.3198	2056.4	2057.31	5430.9		1	555.4	50	9	K.GPTEQLVSPEPEVYEILR.A
	HsHeLa_Control-MG_Ti_20	4.4558	0.2567	2788.68	2789.99	9630.6		1	1342	36.4	1	K.SRLEVSDDLENVCNWVVDTCLHK.G
	HsFLAG-Control_293_Ti_2	3.6227	0.3259	1528.53	1529.73	4073.7		1	564.8	65.4	5	K.SGEEGMPDLAHVMR.I
	HsFLAG-Control_293_Ti_2	4.1389	0.2668	1820.08	1819.11	4487.6		1	494.2	50	19	R.ILSAENIPNLPPGGGLAGK.R
	HsFLAG-Control_MG_293_	3.8182	0.2893	1207.2	1207.38	6196.9		1	990.8	83.3	28	K.RNVIEAVYSR.L
*	HsFLAG-Control_293_Ti_2	2.637	0.1658	1348.18	1348.32	3746.8		2	321.7	58.3	1	R.ESDGGAGDLEDPW.-

gi|14389309|ref|N	41	800	0.543	449	49895	5.1	U	tubulin alpha 6 [Homo sapiens]				
	HsFLAG-Control_HeLa_S1	5.6931	0.4653	2009.21	2009.09	9324.1		1	1749.3	63.2	204	K.TIGGGDDSFNTFFSETGAGK.H
	HsF-IP-293-MG_Ti_102.27	5.0334	0.4399	1702.32	1702.95	4530		1	1284.8	82.1	22	R.AVFVDLEPTVIDEVR.T
	HsFLAG-Control_HeLa_S1	4.9427	0.335	1702.54	1702.95	7851		1	1529.4	50	5	R.AVFVDLEPTVIDEVR.T
	HsFLAG-Control_HeLa_S1	4.0389	0.2932	1703.03	1702.95	8687.1		1	1386.4	46.4	2	R.AVFVDLEPTVIDEVR.T
	HsHeLa-FLAG-IP_S100_Ti_	5.2915	0.4169	1703.58	1702.95	4669.1		1	1294.9	82.1	56	R.AVFVDLEPTVIDEVR.T
	HsFLAG-Control_HeLa_S1	4.7409	0.3371	1703.91	1702.95	5321.1		1	1259.1	78.6	16	R.AVFVDLEPTVIDEVR.T
	HsFLAG-Control_HeLa_NE	4.1691	0.3052	1704.24	1702.95	8886.6		1	1330.2	44.6	1	R.AVFVDLEPTVIDEVR.T
	HsHeLa_Control_Ti_102.30	5.091	0.2766	1704.76	1702.95	4122.7		1	1098.9	82.1	19	R.AVFVDLEPTVIDEVR.T
	HsFLAG-Control_HeLa_S1	4.2449	0.3005	2415.72	2416.66	8163.2		1	1212.2	36.2	4	R.QLFHPEQLITGKEDAANNYAR.G
	HsHeLa_Control-MG_Ti_10	3.4137	0.2652	2416.42	2416.66	7726.4		1	627.9	45	8	R.QLFHPEQLITGKEDAANNYAR.G
	HsGST-MOCK_Ti_103.173	4.1081	0.2897	2416.8	2416.66	6806.6		1	1048.6	36.2	1	R.QLFHPEQLITGKEDAANNYAR.G
	HsFLAG-Control_HeLa_NE	3.5321	0.3633	2417.37	2416.66	8286.1		1	502	42.5	3	R.QLFHPEQLITGKEDAANNYAR.G
	HsFLAG-Control_HeLa_S1	3.3565	0.0828	1086.26	1086.27	6338.4		2	941.8	87.5	18	K.EIIDLVLDR.I
	Hs293FLP-MG_Ti_206.350	4.9972	0.3758	3392.79	3392.78	9865.2		1	1364.1	27.4	5	K.LADQCTGLQGFLVFHSFGGGTGSGFTSLLMER.L
	HsFLAG-Control_MG_293_	3.4903	0.1725	1719.53	1719.9	7713.5		1	803	61.5	17	R.NLDIERPTYTNLNR.L
	HsFLAG-Control_HeLa_S1	4.6066	0.4074	1488.47	1488.77	7506.5		1	1467.1	76.9	9	R.LISQIVSSITASLR.F
	HsFLAG-Control_HeLa_S1	4.684	0.43	1488.49	1488.77	7157.4		1	1312.2	73.1	22	R.LISQIVSSITASLR.F
	HsHeLa_Control-MG_Ti_20	5.0495	0.4454	1488.53	1488.77	8030.6		1	1907.4	80.8	39	R.LISQIVSSITASLR.F
	HsFLAG-Control_HeLa_S1	4.722	0.3946	1488.57	1488.77	8151.1		1	1172.8	69.2	9	R.LISQIVSSITASLR.F
	HsFLAG-Control_HeLa_S1	4.3035	0.346	1488.75	1488.77	5615.6		1	1324.7	55.8	2	R.LISQIVSSITASLR.F
	HsFLAG-Control_HeLa_S1	4.1471	0.2471	1489.29	1488.77	5256.5		3	867.3	50	2	R.LISQIVSSITASLR.F
	HsFLAG-Control_HeLa_NE	4.6049	0.3537	1489.3	1488.77	6361.1		1	1211.5	73.1	15	R.LISQIVSSITASLR.F
	HsFLAG-Control_HeLa_NE	4.3453	0.2295	1489.54	1488.77	5799.3		1	1231.8	53.8	2	R.LISQIVSSITASLR.F
	HsFLAG-Control_HeLa_S1	3.7596	0.3173	1490.02	1488.77	5380.1		1	894.9	50	1	R.LISQIVSSITASLR.F
	HsFLAG-Control_HeLa_NE	5.8208	0.383	2410.89	2410.69	6224.2		1	1491.8	62.5	149	R.FDGALNVDLTEFQTNLVPYPR.I
	Hs293FLP-MG_Ti_103.214	3.0177	0.1953	1251.47	1250.43	4064.5		1	618.2	81.2	2	K.YMACCLLYR.G
	HsFLAG-Control_HeLa_S1	2.3439	0.2742	1015.45	1016.18	7798		1	652.7	72.2	2	K.DVNAAIATIK.T
	HsFLAG-Control_293_Ti_2	2.4919	0.2722	1015.46	1016.18	6406.7		1	644.8	77.8	4	K.DVNAAIATIK.T
	HsFLAG-Control_HeLa_S1	2.1932	0.1673	1015.48	1016.18	6826.5		6	502	66.7	1	K.DVNAAIATIK.T
	HsHeLa_Control_Ti_102.17	2.4787	0.2338	1015.71	1016.18	5846.2		1	557.5	77.8	3	K.DVNAAIATIK.T
	HsFLAG-Control_HeLa_S1	3.6128	0.2873	1016.27	1016.18	5362.6		1	1163.9	88.9	1	K.DVNAAIATIK.T
	HsFLAG-Control_HeLa_S1	3.5311	0.2771	1016.35	1016.18	5480.7		1	1193.4	88.9	2	K.DVNAAIATIK.T
	HsFLAG-Control_HeLa_S1	3.5176	0.2784	1016.38	1016.18	5208.6		1	1029	83.3	1	K.DVNAAIATIK.T
	HsHeLa-FLAG-IP_S100_Ti_	3.4285	0.2973	1016.56	1016.18	5657.7		1	925.2	77.8	12	K.DVNAAIATIK.T
	HsFLAG-Control_HeLa_S1	2.1618	0.2038	1017.63	1016.18	6803		6	446.1	66.7	2	K.DVNAAIATIK.T
	HsHeLa_Control-MG_Ti_20	3.7919	0.422	1755.69	1755.98	6153.4		1	806.5	65.4	7	K.RTIQFVDWCPTGFK.V
	HsFLAG-Control_HeLa_S1	4.5938	0.4395	1599.28	1599.79	7004.1		1	1203.6	75	4	R.TIQFVDWCPTGFK.V
	HsHeLa-FLAG-IP_S100_Ti_	4.1491	0.409	1825.53	1826.1	3764.8		1	755.9	64.7	121	K.VGINYQPPTVVPGGDLAK.V
	HsGST-MOCK_Ti_404.302	2.6983	0.1597	2332.29	2331.52	9294.4		1	579.2	42.1	1	R.AFVHWYVGEGMEEGEFSEAR.E
	HsFLAG-Control_HeLa_S1	2.1109	0.2465	906.43	907.026	5999.8		4	545.2	78.6	1	R.EDMAALEK.D
*	HsFLAG-Control_HeLa_S1	4.5554	0.3766	2080.1	2079.95	6250.7		1	885	58.3	5	K.DYEEVGADSADGEDEGEEY.-
gi|14165464|ref|N	59	263	0.542	550	59037	9.2	U	polypyrimidine tract-binding protein 1 isoform b [Homo sapiens]				
gi|4506243|ref|N	59	263	0.535	557	59633	9.2	U	polypyrimidine tract-binding protein 1 isoform a [Homo sapiens]				
gi|14165466|ref|N	59	263	0.561	531	57221	9.2	U	polypyrimidine tract-binding protein 1 isoform c [Homo sapiens]				
	HsGST-MOCK_Ti_102.198	6.3264	0.3753	3451.63	3451.67	8131.1		1	1391.4	29.7	4	K.RGSDELFSTCVTNGPFIMSSNSASAANGNDSKK.F
	HsFLAG-Control_HeLa_NE	6.0654	0.5142	2112.79	2113.5	9098.1		1	3133	73.7	11	R.KLPIDVTEGEVISLGLPFGK.V
	HsHeLa3_Ti_106.2910.291	5.716	0.478	2113.22	2113.5	7768.8		1	2103.1	65.8	4	R.KLPIDVTEGEVISLGLPFGK.V
	HsFLAG-Control_HeLa_S1	3.8182	0.1819	2113.52	2113.5	6081.1		1	825.3	35.5	1	R.KLPIDVTEGEVISLGLPFGK.V

HsGST-MOCK_Ti_406.315	5.6388	0.5109	2113.8	2113.5	9176.1	1	2272.7	68.4	6	R.KLPIDVTEGEVISLGLPFGK.V
HsFLAG-Control_HeLa_S1	4.9072	0.499	2114.57	2113.5	8297.8	1	1896.8	63.2	2	R.KLPIDVTEGEVISLGLPFGK.V
HsHeLa3_Ti_105.3559.355	3.5469	0.1599	2115.25	2113.5	5872.6	1	733.9	34.2	1	R.KLPIDVTEGEVISLGLPFGK.V
HsFLAG-Control_HeLa_NE	4.3717	0.3222	2115.48	2113.5	6576.7	1	1205.2	39.5	3	R.KLPIDVTEGEVISLGLPFGK.V
HsFLAG-Control_HeLa_S1	5.7831	0.4791	1984.52	1985.33	10120	1	2833	72.2	32	K.LPIDVTEGEVISLGLPFGK.V
HsFLAG-Control_HeLa_NE	3.0179	0.1332	1431.53	1432.62	5054.4	1	428.8	63.6	1	R.GQPIYIQFSNHK.E
HsFLAG-Control_HeLa_NE	2.8591	0.0956	1431.57	1432.62	4754.1	1	426.2	63.6	1	R.GQPIYIQFSNHK.E
HsGST-MOCK_Ti_406.253	3.1579	0.1749	1433.39	1432.62	4082.8	1	664.7	81.8	8	R.GQPIYIQFSNHK.E
HsFLAG-Control_HeLa_NE	2.8596	0.2369	1433.83	1432.62	4876.8	1	673.5	72.7	3	R.GQPIYIQFSNHK.E
HsGST-MOCK_Ti_404.488	5.1903	0.4524	3681.44	3683.19	6521.7	1	1101.5	26.3	7	R.AQAALQAVNSVQSGNLALAASAAAVDAGMAMAGQSPVLR.I
HsFLAG-Control_HeLa_NE	3.7235	0.3185	2488.6	2489.96	4847.8	1	327.9	37.5	5	R.IIVENLFYPVTLDVLHQIFSK.F
HsFLAG-Control_HeLa_S1	3.9292	0.2219	2489.61	2489.96	4623.4	2	543.6	33.8	3	R.IIVENLFYPVTLDVLHQIFSK.F
HsFLAG-Control_HeLa_S1	3.6305	0.3224	2490.21	2489.96	4379.8	1	380.9	42.5	2	R.IIVENLFYPVTLDVLHQIFSK.F
HsFLAG-Control_HeLa_NE	4.3244	0.2846	2492.06	2489.96	4588.2	4	569.9	33.8	3	R.IIVENLFYPVTLDVLHQIFSK.F
HsFLAG-Control_HeLa_NE	5.2787	0.3686	2243.72	2244.47	7263.1	1	1646.5	65.8	6	K.NNQFQALLQYADPVSAQHAK.L
HsGST-MOCK_Ti_405.320	5.3317	0.4129	2243.73	2244.47	6065.1	1	1178.6	40.8	2	K.NNQFQALLQYADPVSAQHAK.L
HsHeLa3_Ti_105.2894.289	4.6285	0.3915	2243.97	2244.47	6987.9	1	1158.7	57.9	2	K.NNQFQALLQYADPVSAQHAK.L
HsFLAG-Control_HeLa_NE	4.9335	0.3289	2244.37	2244.47	7038.3	1	1177.2	39.5	6	K.NNQFQALLQYADPVSAQHAK.L
HsFLAG-Control_HeLa_S1	3.6924	0.3342	2244.58	2244.47	8883.4	1	666.3	42.1	1	K.NNQFQALLQYADPVSAQHAK.L
HsFLAG-Control_HeLa_S1	4.8845	0.2504	2244.61	2244.47	5886.4	2	860.1	38.2	3	K.NNQFQALLQYADPVSAQHAK.L
HsFLAG-MOCK_300mM_T	4.4406	0.4435	2244.7	2244.47	5611.7	1	603.7	47.4	2	K.NNQFQALLQYADPVSAQHAK.L
HsHeLa3_Ti_105.2895.289	4.6961	0.3277	2245.08	2244.47	7007.4	2	1014.5	39.5	2	K.NNQFQALLQYADPVSAQHAK.L
HsGST-MOCK_Ti_405.321	4.684	0.3838	2245.21	2244.47	7069.5	1	964.5	52.6	2	K.NNQFQALLQYADPVSAQHAK.L
HsFLAG-Control_HeLa_NE	3.8309	0.2629	2245.46	2244.47	7225.5	2	892.6	50	2	K.NNQFQALLQYADPVSAQHAK.L
HsFLAG-MOCK_300mM_T	4.6577	0.318	2245.62	2244.47	6222.9	1	990.4	39.5	3	K.NNQFQALLQYADPVSAQHAK.L
HsFLAG-Control_HeLa_NE	4.5737	0.2838	2247.14	2244.47	8476.6	1	1355.7	38.2	1	K.NNQFQALLQYADPVSAQHAK.L
HsFLAG-Control_HeLa_NE	4.1714	0.222	1898.62	1899.04	6235	1	976.3	63.3	11	K.LSLDGQNIYNACCTLR.I
HsFLAG-Control_HeLa_S1	4.2616	0.5106	2274.79	2276.64	5345.8	1	673.7	50	1	R.IAIPGLAGAGNSVLLVSNLNPER.V
HsFLAG-Control_HeLa_NE	5.4401	0.478	2274.96	2276.64	5037	1	1131.8	61.4	8	R.IAIPGLAGAGNSVLLVSNLNPER.V
HsFLAG-Control_HeLa_S1	5.7041	0.4789	2274.98	2276.64	5199.2	1	1263.9	63.6	5	R.IAIPGLAGAGNSVLLVSNLNPER.V
HsFLAG-Control_HeLa_S1	4.3313	0.2651	2275.77	2276.64	7096.1	1	845.9	31.8	3	R.IAIPGLAGAGNSVLLVSNLNPER.V
HsHeLa3_Ti_106.2844.284	4.27	0.3251	2276.09	2276.64	5081.2	1	663.6	52.3	3	R.IAIPGLAGAGNSVLLVSNLNPER.V
HsFLAG-Control_HeLa_S1	4.842	0.3544	2276.23	2276.64	7322.2	1	980.9	34.1	2	R.IAIPGLAGAGNSVLLVSNLNPER.V
HsFLAG-Control_293_Ti_2	5.1713	0.4578	2276.35	2276.64	5078.5	1	1058	61.4	6	R.IAIPGLAGAGNSVLLVSNLNPER.V
HsFLAG-Control_HeLa_NE	5.4593	0.3685	2276.4	2276.64	8307.3	1	1800	40.9	6	R.IAIPGLAGAGNSVLLVSNLNPER.V
HsHeLa3_Ti_105.3450.345	4.4179	0.3191	2276.54	2276.64	8470.3	1	1907	38.6	1	R.IAIPGLAGAGNSVLLVSNLNPER.V
HsFLAG-Control_HeLa_NE	4.9192	0.2565	2276.79	2276.64	7287.8	1	1538.5	40.9	4	R.IAIPGLAGAGNSVLLVSNLNPER.V
HsFLAG-Control_HeLa_NE	5.7103	0.4983	2279.21	2276.64	5363.6	1	1326.9	65.9	9	R.IAIPGLAGAGNSVLLVSNLNPER.V
HsFLAG-Control_HeLa_NE	5.8826	0.4616	2039.65	2040.37	9127.6	1	3092.6	52.9	12	R.VTPQSLFILFGVYGDVQR.V
HsGST-MOCK_Ti_406.336	5.5157	0.4752	2039.89	2040.37	9871	1	2122.8	64.7	11	R.VTPQSLFILFGVYGDVQR.V
HsHeLa3_Ti_105.4199.419	4.5749	0.3467	2041.14	2040.37	7456.8	1	1520.9	44.1	1	R.VTPQSLFILFGVYGDVQR.V
HsFLAG-Control_HeLa_NE	5.777	0.4778	2041.2	2040.37	9824.9	1	2275.2	67.6	11	R.VTPQSLFILFGVYGDVQR.V
HsHeLa3_Ti_106.2370.237	2.9403	0.2629	2578.94	2578.88	8241.9	1	432.9	34.8	1	K.ENALVQMADGNQAQLAMSHLNGHK.L
HsFLAG-MOCK_300mM_T	2.0774	0.1678	820.84	821.013	3876.8	3	258.6	75	4	K.LHGKPIR.I
HsFLAG-Control_HeLa_NE	1.9682	0.1179	991.56	992.126	6035.7	2	381	71.4	1	K.HQNVQLPR.E
HsFLAG-Control_HeLa_NE	1.9574	0.1291	991.58	992.126	6499.7	9	464.4	71.4	2	K.HQNVQLPR.E
HsFLAG-Control_HeLa_NE	2.7513	0.1339	992.25	992.126	5238	1	881.1	85.7	2	K.HQNVQLPR.E
HsFLAG-Control_HeLa_NE	2.816	0.1346	992.43	992.126	6125	1	884	85.7	7	K.HQNVQLPR.E

	HsHeLa3_Ti_106.1892.189	2.564	0.1768	992.74	992.126	5198.9		1	1066.3	92.9	1	K.HQNVQLPR.E
	HsFLAG-MOCK_300mM_T	3.7069	0.3227	2078.2	2078.25	6710.2		1	752.8	55.9	3	K.HQNVQLPREGQQEDQGLTK.D
	HsFLAG-Control_HeLa_NE	3.0439	0.3205	1059.33	1059.13	6276.8		2	614.7	75	10	K.DYGNSPLHR.F
	HsFLAG-Control_HeLa_NE	2.6686	0.187	2995.46	2996.35	5965.1		1	301.5	30.8	1	K.NFQNIFPPSATLHLSNIPPSVSEEDLK.V
	HsFLAG-MOCK_300mM_T	4.6391	0.154	2999.01	2996.35	3961.1		1	556.4	33.7	4	K.NFQNIFPPSATLHLSNIPPSVSEEDLK.V
	HsFLAG-Control_HeLa_NE	3.281	0.176	1107.3	1107.3	3933.9		2	722	80	3	K.VLFSSNGGVVK.G
	HsFLAG-Control_HeLa_NE	2.0293	0.2147	1107.67	1107.3	7132.6		6	444.1	60	1	K.VLFSSNGGVVK.G
gi|17921989|ref|N	33	503	0.538	448	49924	5.1	U		tubulin, alpha 1 [Homo sapiens]			
*	HsFLAG-Control_HeLa_S1	4.7739	0.4576	2070.76	2069.16	8343.4		1	1206.4	55.3	3	K.TIGGGDDSFTTFFCETGAGK.H
*	HsFLAG-Control_HeLa_S1	2.7348	0.0824	1717.1	1716.97	5027.2		1	1172.5	71.4	1	R.AVFVDLEPTVIDEIR.N
	HsFLAG-Control_HeLa_S1	4.2449	0.3005	2415.72	2416.66	8163.2		1	1212.2	36.2	4	R.QLFHPEQLITGKEDAANNYAR.G
	HsHeLa_Control-MG_Ti_10	3.4137	0.2652	2416.42	2416.66	7726.4		1	627.9	45	8	R.QLFHPEQLITGKEDAANNYAR.G
	HsGST-MOCK_Ti_103.173	4.1081	0.2897	2416.8	2416.66	6806.6		1	1048.6	36.2	1	R.QLFHPEQLITGKEDAANNYAR.G
	HsFLAG-Control_HeLa_NE	3.5321	0.3633	2417.37	2416.66	8286.1		1	502	42.5	3	R.QLFHPEQLITGKEDAANNYAR.G
	HsFLAG-Control_MG_293_	3.4903	0.1725	1719.53	1719.9	7713.5		1	803	61.5	17	R.NLDIERPTYTNLNR.L
	HsFLAG-Control_HeLa_S1	4.6066	0.4074	1488.47	1488.77	7506.5		1	1467.1	76.9	9	R.LISQIVSSITASLR.F
	HsFLAG-Control_HeLa_S1	4.684	0.43	1488.49	1488.77	7157.4		1	1312.2	73.1	22	R.LISQIVSSITASLR.F
	HsHeLa_Control-MG_Ti_20	5.0495	0.4454	1488.53	1488.77	8030.6		1	1907.4	80.8	39	R.LISQIVSSITASLR.F
	HsFLAG-Control_HeLa_S1	4.722	0.3946	1488.57	1488.77	8151.1		1	1172.8	69.2	9	R.LISQIVSSITASLR.F
	HsFLAG-Control_HeLa_S1	4.3035	0.346	1488.75	1488.77	5615.6		1	1324.7	55.8	2	R.LISQIVSSITASLR.F
	HsFLAG-Control_HeLa_S1	4.1471	0.2471	1489.29	1488.77	5256.5		3	867.3	50	2	R.LISQIVSSITASLR.F
	HsFLAG-Control_HeLa_NE	4.6049	0.3537	1489.3	1488.77	6361.1		1	1211.5	73.1	15	R.LISQIVSSITASLR.F
	HsFLAG-Control_HeLa_NE	4.3453	0.2295	1489.54	1488.77	5799.3		1	1231.8	53.8	2	R.LISQIVSSITASLR.F
	HsFLAG-Control_HeLa_S1	3.7596	0.3173	1490.02	1488.77	5380.1		1	894.9	50	1	R.LISQIVSSITASLR.F
	HsFLAG-Control_HeLa_NE	5.8208	0.383	2410.89	2410.69	6224.2		1	1491.8	62.5	149	R.FDGALNVDLTEFQTNLVPYPR.I
	HsFLAG-Control_HeLa_S1	3.7053	0.2052	1757.29	1758.07	4837.7		5	804.3	45	1	R.IHFPLATYAPVISAEK.A
	HsFLAG-Control_HeLa_NE	4.2732	0.3578	1757.6	1758.07	4681.9		1	893.2	70	13	R.IHFPLATYAPVISAEK.A
	HsHeLa_Control-MG_Ti_20	4.3621	0.4339	1757.74	1758.07	4584.4		1	1152	76.7	16	R.IHFPLATYAPVISAEK.A
	HsFLAG-Control_HeLa_S1	4.2526	0.2613	1757.75	1758.07	5170.2		2	1162.9	48.3	1	R.IHFPLATYAPVISAEK.A
	HsFLAG-Control_HeLa_S1	4.411	0.4766	1758.41	1758.07	4071.6		1	935.5	73.3	3	R.IHFPLATYAPVISAEK.A
	HsHeLa_Control-MG_Ti_10	4.4041	0.3426	2753.23	2752.04	7001.1		1	1357.7	52.2	2	K.AYHEQLSVAEITNACFEPANQMVK.C
	Hs293FLP-MG_Ti_103.214	3.0177	0.1953	1251.47	1250.43	4064.5		1	618.2	81.2	2	K.YMACCLLYR.G
*	HsFLAG-Control_HeLa_S1	2.5016	0.0892	985.51	986.156	6822.2		1	746.2	72.2	2	K.DVNAAIAAIK.T
	HsFLAG-Control_HeLa_S1	4.2609	0.3792	1742.64	1741.95	6595.1		1	848.5	61.5	13	K.RSIQFVDWCPTGFK.V
	HsHeLa_Control-MG_Ti_10	2.0279	0.2794	1584.51	1585.77	5859.1		2	301.2	41.7	1	R.SIQFVDWCPTGFK.V
	HsFLAG-Control_HeLa_S1	4.2773	0.4207	1585.41	1585.77	5673		1	1071.3	75	19	R.SIQFVDWCPTGFK.V
	HsHeLa_Control-MG_Ti_10	4.2534	0.4251	1587.43	1585.77	4819.9		1	915.9	75	18	R.SIQFVDWCPTGFK.V
	HsHeLa-FLAG-IP_S100_Ti_	4.1491	0.409	1825.53	1826.1	3764.8		1	755.9	64.7	121	K.VGINYQPPTVVPGGDLAK.V
	HsF-IP-293-MG_Ti_104.26	2.8488	0.3461	1865.28	1866.11	9656.2		1	1217.8	59.4	2	R.AVCMLSNTTAIAEAWAR.L
	HsGST-MOCK_Ti_404.302	2.6983	0.1597	2332.29	2331.52	9294.4		1	579.2	42.1	1	R.AFVHWYVGEGMEEGEFSEAR.E
	HsFLAG-Control_HeLa_S1	2.1109	0.2465	906.43	907.026	5999.8		4	545.2	78.6	1	R.EDMAALEK.D
gi|32189392|ref|N	12	37	0.535	198	21892	6	U		peroxiredoxin 2 isoform a [Homo sapiens]			
	Hs293FLP_Ti_305.1314.13	2.3118	0.3187	972.84	973.16	4399.8		1	585.8	75	3	R.IGKPAPDFK.A
	Hs293FLP-MG_Ti_202.185	2.1917	0.2778	978.39	979.121	6657.5		6	421.1	61.1	3	K.ATAVVDGAFK.E
*	HsHeLa_Control-MG_Ti_20	3.692	0.1258	2700.69	2701.02	6058.4		1	780.9	31.5	1	K.LGCEVLGVSVDSQFTHLAWINTPR.K
	Hs293FLP-MG_Ti_205.349	3.5756	0.3792	1863.67	1864.2	7361.9		1	1443.1	64.7	2	R.KEGGLGPLNIPLLADVTR.R
	HsHeLa_Control-MG_Ti_20	3.7201	0.2082	1864.11	1864.2	6037.1		9	895.9	39.7	2	R.KEGGLGPLNIPLLADVTR.R
	Hs293FLP-MG_Ti_205.347	4.6343	0.3016	1864.42	1864.2	5787.4		6	783.7	41.2	2	R.KEGGLGPLNIPLLADVTR.R
	HsHeLa_Control-MG_Ti_20	5.2909	0.4716	1864.53	1864.2	7147		1	1690.4	70.6	4	R.KEGGLGPLNIPLLADVTR.R

	Hs293FLP_Ti_305.3187.31	4.5309	0.4623	1864.74	1864.2	4444		1	1316.5	73.5	3	R.KEGGLGPLNIPLLADVTR.R
	Hs293FLP_Ti_305.3189.31	3.691	0.2002	1864.84	1864.2	5349.6		1	1193.3	45.6	1	R.KEGGLGPLNIPLLADVTR.R
	HsGST-MOCK_Ti_404.421	4.5025	0.3843	1735.53	1736.02	5533.7		1	845.3	65.6	4	K.EGGLGPLNIPLLADVTR.R
	Hs293FLP_TREX_Ti_102.1	3.0279	0.27	1212.5	1212.39	5952.5		1	1083.6	90	8	R.QITVNDLPVGR.S
	Hs293FLP-MG_Ti_204.219	4.5058	0.2759	3790.83	3791.09	10898.8		1	1109.9	25	4	R.LVQAFQYTDEHGEVCPAGWKPGSDTIKPNVDDSK.E
gi|5031753|ref|NI	30	337	0.526	449	49229	6.3	U	heterogeneous nuclear ribonucleoprotein H1 [Homo sapiens]				
*	HsHeLa3_Ti_103.1858.185	3.6518	0.3853	1505.66	1505.59	2651.7		1	462.4	79.2	6	R.GLPWSCSADEVQR.F
*	HsFLAG-Control_HeLa_NE	4.1456	0.1218	2108.07	2108.22	8088.5		1	1528.7	40.3	1	R.EGRPSGEAFVELESEDEVK.L
*	HsFLAG-Control_293_Ti_2	5.8437	0.3308	2108.65	2108.22	10863.7		1	1674.2	61.1	7	R.EGRPSGEAFVELESEDEVK.L
*	HsFLAG-Control_HeLa_NE	5.3875	0.3776	2108.7	2108.22	11194.7		1	1584.2	55.6	5	R.EGRPSGEAFVELESEDEVK.L
*	HsFLAG-Control_MG_293_	4.0869	0.2013	1335.29	1335.52	4933		2	1053.6	85	15	K.SNNVEMDWVLK.H
	Hs293FLP-MG_Ti_204.147	3.8795	0.4268	1685.48	1685.75	7488.8		1	1436.6	70	10	K.HTGPNSPDTANDGFVR.L
	HsFLAG-Control_293_Ti_2	4.52	0.5046	1685.48	1685.75	8106.6		1	2099.2	80	8	K.HTGPNSPDTANDGFVR.L
	HsFLAG-Control_HeLa_NE	4.3166	0.4328	1686.3	1685.75	6792.2		1	914.4	63.3	5	K.HTGPNSPDTANDGFVR.L
	HsFLAG-Control_293_Ti_2	4.3669	0.2323	1686.72	1685.75	7063.6		3	1191.3	45	1	K.HTGPNSPDTANDGFVR.L
	HsFLAG-MOCK_300mM_T	4.0472	0.1915	1686.88	1685.75	5906.1		2	1316.5	48.3	1	K.HTGPNSPDTANDGFVR.L
*	HsGST-MOCK_Ti_105.400	5.3273	0.3492	3753.5	3753.26	4854		1	708.1	28	12	R.GLPFGCSKEEIVQFFSGLEIVPNGITLPVDFQGR.S
*	Hs293FLP-MG_Ti_203.501	3.6462	0.3545	2904.96	2906.31	4536.8		1	382.1	36	9	K.EEIVQFFSGLEIVPNGITLPVDFQGR.S
*	Hs293FLP-MG_Ti_203.500	4.0783	0.278	2906.48	2906.31	7967.3		3	717.6	28	2	K.EEIVQFFSGLEIVPNGITLPVDFQGR.S
	HsFlag1P_Ti_102.3107.310	5.4581	0.4545	1841.95	1843	8129.4		1	2087.4	71.9	105	R.STGEAFVQFASQEIAEK.A
*	Hs293FLP-MG_Ti_202.253	4.7384	0.5245	2717.6	2718.68	9239.1		1	1322.3	46	10	R.GAYGGGYGGYDDYNGYNDGYGFGSDR.F
	HsFLAG-Control_293_Ti_2	3.8505	0.4656	1604.09	1602.68	9274.9		1	1651.1	79.2	9	R.DLNYCFSGMSDHR.Y
*	HsGST-MOCK_Ti_103.140	4.8165	0.4565	2099.34	2099.21	7000.7		1	867.5	50	2	R.YGDGGSTFQSTTGHCVHMR.G
	HsFLAG-Control_HeLa_S1	3.9094	0.2338	1996.83	1998.2	9892.6		2	1192.3	40.6	1	R.ATENDIYNFFSPLNPVR.V
	HsFLAG-Control_HeLa_NE	4.6608	0.3601	1997.35	1998.2	7568.7		1	1568.7	68.8	16	R.ATENDIYNFFSPLNPVR.V
	HsFLAG-Control_293_Ti_2	4.7208	0.3986	1997.49	1998.2	7549.3		1	1676.5	71.9	55	R.ATENDIYNFFSPLNPVR.V
	HsGST-MOCK_Ti_403.397	4.7263	0.4323	1997.5	1998.2	7501		1	1361.2	65.6	2	R.ATENDIYNFFSPLNPVR.V
	HsFLAG-Control_HeLa_S1	4.3947	0.4897	1997.59	1998.2	7565.5		1	1326.5	65.6	6	R.ATENDIYNFFSPLNPVR.V
	HsFLAG-Control_HeLa_NE	4.2241	0.188	1998.1	1998.2	8148.8		8	882.3	35.9	1	R.ATENDIYNFFSPLNPVR.V
	HsFLAG-Control_HeLa_NE	5.2012	0.4834	1998.25	1998.2	8235.9		1	1839.9	68.8	23	R.ATENDIYNFFSPLNPVR.V
	Hs293FLP-MG_Ti_202.411	4.5072	0.2946	1998.27	1998.2	7716.3		1	1486.3	46.9	2	R.ATENDIYNFFSPLNPVR.V
	HsFLAG-Control_HeLa_NE	4.903	0.1706	1998.31	1998.2	8396.7		1	1484.8	43.8	2	R.ATENDIYNFFSPLNPVR.V
	HsFLAG-Control_HeLa_NE	2.6268	0.1908	1092.55	1093.23	6937.7		1	767.6	72.2	2	R.VHIEIGPDGR.V
	HsFLAG-Control_HeLa_NE	3.4554	0.2844	1093.46	1093.23	5275.7		1	1166.4	83.3	16	R.VHIEIGPDGR.V
*	HsFLAG-Control_HeLa_NE	5.218	0.3047	2178.77	2179.36	6666.4		1	839.3	52.5	1	R.VTGEADVEFATHEDAVAAMSK.D
*	Hs293FLP-MG_Ti_204.237	3.7696	0.3407	2142.47	2143.32	9860.7		7	499.3	36.8	2	R.YVELFLNSTAGASGGAYEHR.Y
gi|4504253|ref|NI	6	10	0.524	143	15145	10.7	U	H2A histone family, member X [Homo sapiens]				
	Hs293FLP-MG_Ti_104.190	2.3447	0.1182	944.77	945.109	4092.1		5	353.2	68.8	1	R.AGLQFPVGR.V
	HsHeLa_Control-MG_Ti_10	2.6626	0.17	945.58	945.109	3921		2	699.4	81.2	1	R.AGLQFPVGR.V
	HsFLAG-Control_HeLa_NE	4.5014	0.4747	2916.07	2917.38	7823.6		1	640.8	32.1	1	R.VGAGAPVYLAAVLEYLTAEILELAGNAAR.D
	HsFLAG-Control_HeLa_NE	6.3703	0.4516	2916.71	2917.38	9322.9		1	2302	36.6	3	R.VGAGAPVYLAAVLEYLTAEILELAGNAAR.D
	HsHeLa_Control-MG_Ti_10	3.6354	0.3585	1693.91	1693.9	7274.3		1	861.3	65.4	1	R.HLQLAIRNDEELNK.L
	Hs283FLP_Ti_106.2811.28	4.7386	0.3289	2273.16	2272.78	5689.3		1	869.1	50	3	K.LLGGVTIAQGGVLPNIQAVLLPK.K
gi|29789090|ref|N	20	47	0.521	522	56085	8.8	U	RCC1-like [Homo sapiens]				
*	HsGST-MOCK_Ti_402.184	2.8898	0.207	1646.57	1646.71	6467.5		1	990.5	62.5	2	K.AAAAAWEEPSSGNGTAR.A
*	HsGST-MOCK_Ti_304.167	3.1528	0.3649	1479.5	1480.66	3588.5		1	531.3	60.7	2	K.AGGAAVVITEPEHTK.E
*	HsGST-MOCK_Ti_405.402	5.0574	0.4111	1774.54	1775.06	7618		1	1663	70	2	K.GQLLIFGATNWDLIGR.K
*	HsGST-MOCK_Ti_405.217	5.0756	0.4468	1930.86	1932.15	9333.3		1	1708.3	61.1	4	R.TVVSGSCAAHSLLITTEGK.L

*	HsGST-MOCK_Ti_102.180	4.4285	0.3943	1812.44	1812.04	8745.5		1	1634.9	62.5	2	R.LIEGLSHEVIVSAACGR.N
*	HsGST-MOCK_Ti_305.279	6.3428	0.5101	2036.16	2037.24	10365.5		1	3331.7	75	5	R.NHTLALTETGSVFAFGENK.M
*	HsGST-MOCK_Ti_304.295	3.4701	0.3277	2931.96	2931.35	3899.5		1	191.7	29.6	2	K.MGQLGLGNQTDAVPSPAQIMYNGQPITK.M
*	HsGST-MOCK_Ti_404.233	3.7365	0.372	2301.81	2301.4	7496		1	838.7	50	3	K.GNLYSFGCPEYGQLGHNSDGK.F
*	HsFlag1P_Ti_104.2075.207	3.7798	0.3097	1649.53	1649.81	6249.9		1	951	70.8	1	R.AQRIEYDCELVPR.R
*	HsGST-MOCK_Ti_402.222	3.1293	0.2058	1294.21	1294.41	5111.6		1	822.4	77.8	2	R.IEYDCELVPR.R
*	HsGST-MOCK_Ti_303.268	2.4102	0.3025	1405.97	1406.67	2740.4		4	219.1	54.2	1	K.DGQILPVPNVVVR.D
*	HsGST-MOCK_Ti_403.195	4.6763	0.3193	1727.77	1728.87	7949.8		1	1545.3	70	1	R.DVACGANHTLVLDSQK.R
*	HsGST-MOCK_Ti_104.190	4.2867	0.4079	1390.62	1389.56	6783.2		1	1525.4	86.4	2	K.RVFSWGFGGYGR.L
*	HsGST-MOCK_Ti_104.190	3.623	0.23	1391.17	1389.56	4849.7		1	1273.7	59.1	1	K.RVFSWGFGGYGR.L
*	HsGST-MOCK_Ti_404.299	3.1485	0.3256	1233.21	1233.37	5594.9		1	1233.3	90	2	R.VFSWGFGGYGR.L
*	HsGST-MOCK_Ti_103.121	2.4972	0.3418	1509.45	1510.71	4721.8		1	420.8	58.3	2	R.LGHAEQKDEMVPR.L
*	HsGST-MOCK_Ti_103.122	4.8519	0.4212	1509.72	1510.71	9446.1		1	1631.2	75	2	R.LGHAEQKDEMVPR.L
*	HsFLAG-MOCK_300mM_T	2.8123	0.2596	1512.67	1510.71	7010		3	568.2	54.2	1	R.LGHAEQKDEMVPR.L
*	HsGST-MOCK_Ti_105.240	4.4888	0.4242	3248.64	3248.57	6476.2		2	510.3	23.3	6	K.SSIIVAADESTISWGPSPTFGELGYGDHKPK.S
*	HsGST-MOCK_Ti_404.358	4.8221	0.4949	2395.08	2395.74	8174.8		1	946.3	47.6	4	K.TLDGIFSEQVAMGYSHSLVIAR.D
gi|4506669|ref|N	2	16	0.518	114	11514	4.3	U		ribosomal protein P1 isoform 1 [Homo sapiens]			
	HsFLAG-Control_293_Ti_1	3.9399	0.3506	1703.47	1703.98	3992.8		1	673.5	63.3	12	K.AAGVNVEPFWPGLFAK.A
	HsFLAG-Control_293_Ti_1	7.3279	0.4978	3812.24	3811.21	10758.7		1	2253.2	28.6	4	K.ALANVNIGSLICNVGAGGPAPAAGAAPAGGPAPSTAAAPAEEK.K
gi|4502599|ref|N	13	28	0.513	277	30375	8.3	U		carbonyl reductase 1 [Homo sapiens]			
*	HsGST-MOCK_Ti_303.230	3.8946	0.2466	1178.34	1178.37	6386.9		1	1462.3	90	2	R.LFSGDVVLTAR.D
	HsGST-MOCK_Ti_303.196	5.0904	0.2499	1654.31	1653.84	7891.5		1	1910.3	73.3	1	R.GQAAVQQLQAEGLSPR.F
	HsGST-MOCK_Ti_304.242	4.7586	0.2392	1600.73	1600.77	9739.2		1	2194.6	83.3	1	R.FHQLDIDDLQSIR.A
*	HsGST-MOCK_Ti_302.350	4.7012	0.2856	1780.53	1781.02	7479.8		1	1872.8	78.1	1	K.EYGGLDVLVNNAGIAFK.V
*	HsGST-MOCK_Ti_302.317	2.8075	0.0893	1300.42	1301.53	6252.2		9	599.8	60	1	R.DVCTELLPLIK.P
*	HsGST-MOCK_Ti_302.317	3.4093	0.1778	1301.07	1301.53	5216.7		2	1168.8	85	2	R.DVCTELLPLIK.P
*	HsGST-MOCK_Ti_305.296	3.7947	0.2278	1739.3	1740.02	5609.3		1	634.6	57.1	2	R.DVCTELLPLIKPQGR.V
*	HsGST-MOCK_Ti_303.241	4.063	0.3569	1191.31	1191.43	6108.7		1	1306.2	85	2	R.VVNVSSIMSVR.A
*	HsGST-MOCK_Ti_304.291	5.4083	0.4569	1996.51	1997.27	5587.2		1	2030.9	84.4	3	K.FRSETITEEELVGLMNK.F
*	HsGST-MOCK_Ti_302.297	4.3491	0.3224	1693.51	1693.91	7965.2		1	2063.3	78.6	2	R.SETITEEELVGLMNK.F
*	HsGST-MOCK_Ti_302.191	2.0357	0.124	1281.36	1282.4	2795.4		1	230.7	63.6	1	K.EGWPSSAYGVTK.I
*	HsGST-MOCK_Ti_303.335	5.8876	0.4098	3164.36	3166.47	6329.5		1	1417.8	33.6	8	K.SPEEGAETPVYLALLPPDAEGPHGQFVSEK.R
*	HsGST-MOCK_Ti_303.334	3.202	0.1586	3165.01	3166.47	3673.9		1	262.3	31	2	K.SPEEGAETPVYLALLPPDAEGPHGQFVSEK.R
gi|23111018|ref|N	94	361	0.511	852	94370	6.7	U		RNA binding motif protein 10 isoform 2 [Homo sapiens]			
	HsFlag1P_Ti_106.2224.222	2.5407	0.2286	1630.04	1629.7	7053.6		4	440.5	59.1	1	R.SRDHDYRDMDYR.S
	Hs293FLP_Ti_305.1079.10	2.0714	0.0834	1180.5	1181.3	4592		9	300.7	60	1	R.GQLQSHGVQAR.E
	Hs293FLP-MG_Ti_205.125	3.6294	0.3232	1180.54	1181.3	8588.5		1	1165.7	75	8	R.GQLQSHGVQAR.E
	HsHeLa_Control-MG_Ti_10	2.1742	0.0972	1180.87	1181.3	4327.4		5	317.3	60	1	R.GQLQSHGVQAR.E
	Hs293FLP_TREX_Ti_105.1	3.6954	0.3178	1181.18	1181.3	6944		1	1068.5	75	19	R.GQLQSHGVQAR.E
	HsFLAG-Control_MG_293_	3.6442	0.3241	1181.36	1181.3	6267.1		1	1113.3	85	2	R.GQLQSHGVQAR.E
	HsFLAG-Control_MG_293_	2.4	0.155	1181.45	1181.3	5409.5		6	363.8	60	1	R.GQLQSHGVQAR.E
	HsFLAG-Control_Hela_Ti_1	3.7211	0.2977	1182.21	1181.3	7236.5		1	1331.3	85	5	R.GQLQSHGVQAR.E
	HsFLAG-Control_HeLa_NE	4.4983	0.428	1725.08	1725.9	9222		1	1748.1	71.4	6	R.GFAFVEFSHLQDATR.W
	HsHeLa_Control-MG_Ti_20	5.1413	0.5023	1725.1	1725.9	7337.8		1	1979.5	82.1	5	R.GFAFVEFSHLQDATR.W
	HsHeLa_Control-MG_Ti_20	3.5406	0.2981	1726.86	1725.9	5898.5		1	1256.7	48.2	1	R.GFAFVEFSHLQDATR.W
	HsHeLa_Control-MG_Ti_10	3.7665	0.3034	1727.27	1725.9	5166.5		1	1323.2	50	1	R.GFAFVEFSHLQDATR.W
	HsHeLa_Control_Ti_104.33	3.5384	0.185	1727.47	1725.9	5135.4		1	1320	50	1	R.GFAFVEFSHLQDATR.W
	HsHeLa_Control_Ti_104.33	4.4451	0.446	1727.77	1725.9	5795.7		1	1557.3	78.6	5	R.GFAFVEFSHLQDATR.W

	Hs293FLP_Ti_304.2631.26	4.6098	0.3769	1727.85	1725.9	6756.5	1	2053	82.1	14	R.GFAFVEFSHLQDATR.W
	HsFlag1P_Ti_106.2548.254	5.4069	0.4044	1770.27	1770.02	9851.6	1	2367.9	78.6	9	R.WMEANQHSLNILGQK.V
	HsFLAG-MOCK_300mM_T	2.2163	0.2357	1288.63	1289.49	3618.1	3	353.9	65	1	K.VSMHYSDPKPK.I
	HsFlag1P_Ti_102.2178.217	2.5288	0.1476	1191.29	1192.28	6235.8	1	522.5	68.8	2	K.INEDWLCNK.C
	HsHeLa_Control-MG_Ti_10	2.5844	0.2116	1191.58	1192.28	5788.1	5	514.7	68.8	2	K.INEDWLCNK.C
	Hs293FLP-MG_Ti_102.206	2.5039	0.2577	1191.66	1192.28	6146.3	4	447.5	62.5	1	K.INEDWLCNK.C
	HsHeLa_Control-MG_Ti_10	3.3874	0.219	1192.72	1192.28	6003.4	1	1106.1	87.5	4	K.INEDWLCNK.C
	HsFLAG-Control_HeLa_NE	3.3236	0.2222	1193.33	1192.28	8126.2	1	1244.4	87.5	1	K.INEDWLCNK.C
	HsHeLa_Control-MG_Ti_10	4.0826	0.1948	1329.89	1329.5	4900.3	3	1121.7	77.3	4	K.SEAEQKLPLGTR.L
	HsHeLa_Control-MG_Ti_20	4.268	0.2497	1198.4	1198.37	5439.1	1	1362.7	95	11	R.LDQQTLPLGGR.E
	Hs293FLP-MG_Ti_202.410	3.9939	0.3174	4422.41	4422.89	6400.9	1	450.6	18.3	2	R.ELSQGLLPLPQPYQAQGVLASQALSQGSEPSSENANDTIILR.N
	HsHeLa_Control-MG_Ti_20	4.744	0.4219	2827.69	2829.2	7040	1	1139.3	46.2	2	R.NLNPHSTMDSILGALAPYAVLSSSNVR.V
	Hs293FLP-MG_Ti_205.408	4.6483	0.241	2827.95	2829.2	7557.1	1	1217.4	32.7	2	R.NLNPHSTMDSILGALAPYAVLSSSNVR.V
	HsHeLa_Control-MG_Ti_20	4.3762	0.3177	2828.64	2829.2	9567.3	1	1478.4	31.7	2	R.NLNPHSTMDSILGALAPYAVLSSSNVR.V
	Hs293FLP-MG_Ti_205.407	4.4509	0.338	2828.76	2829.2	6829.3	1	1296.6	48.1	1	R.NLNPHSTMDSILGALAPYAVLSSSNVR.V
	HsHeLa_Control-MG_Ti_10	3.6661	0.3442	2829.29	2829.2	5739.5	1	766.7	40.4	2	R.NLNPHSTMDSILGALAPYAVLSSSNVR.V
	Hs293FLP_Ti_306.3446.34	3.9379	0.2906	2829.35	2829.2	5898.9	1	721.8	40.4	2	R.NLNPHSTMDSILGALAPYAVLSSSNVR.V
	HsHeLa_Control-MG_Ti_10	4.3703	0.1372	2829.81	2829.2	6719	1	1090.2	30.8	1	R.NLNPHSTMDSILGALAPYAVLSSSNVR.V
	Hs293FLP_Ti_305.3753.37	4.3448	0.2356	2830	2829.2	6641.3	4	744.9	28.8	2	R.NLNPHSTMDSILGALAPYAVLSSSNVR.V
*	HsFLAG-Control_HeLa_NE	4.5891	0.294	3348.99	3348.95	7749.5	1	835.3	25.8	1	R.GFAFIQLSTIEAAQLLQILQALHPPLTIDGK.T
	HsHeLa_Control-MG_Ti_20	2.2886	0.2035	921.4	922.069	5470.9	9	408.5	71.4	7	K.TINVEFAK.G
	Hs293FLP-MG_Ti_202.201	2.7263	0.1106	922.33	922.069	2462.9	3	513.4	85.7	1	K.TINVEFAK.G
	Hs293FLP-MG_Ti_205.217	4.5107	0.2996	3533.36	3533.85	6108.9	2	464.7	21.5	1	K.GTKGPGITGTKGDPTGAGPEASLEPGADSVSMQAFSR.A
	HsF-IP-293-MG_Ti_102.21	5.6979	0.3628	2534.89	2535.7	4435.1	1	791.4	52	15	K.GDPTGAGPEASLEPGADSVSMQAFSR.A
	HsFlag1P_Ti_105.2566.256	8.1089	0.5995	3768.76	3770.12	8722.1	1	2327.2	33.1	27	R.AQPGAAPGIYQQSAEASSSQGTAANSQSYTIMSPAVLK.S
	Hs293FLP-MG_Ti_103.160	2.3072	0.2638	1515.64	1516.65	4750.8	1	419.4	61.5	2	R.TYVPALEQSADGHK.E
	Hs293FLP_TREX_Ti_103.1	3.631	0.3802	1516.44	1516.65	4525.3	1	903.2	80.8	4	R.TYVPALEQSADGHK.E
	Hs293FLP-MG_Ti_203.168	2.3773	0.2259	1516.6	1516.65	5973.5	1	317.8	50	2	R.TYVPALEQSADGHK.E
	Hs283FLP_Ti_103.1435.14	2.5233	0.2224	1516.62	1516.65	4188.9	1	464.4	65.4	1	R.TYVPALEQSADGHK.E
	HsHeLa_Control-MG_Ti_20	4.0518	0.3786	1517.43	1516.65	4765	1	782.5	73.1	6	R.TYVPALEQSADGHK.E
	Hs293FLP-MG_Ti_203.168	3.4167	0.2487	1517.45	1516.65	4200	1	546.1	65.4	2	R.TYVPALEQSADGHK.E
	Hs293FLP-MG_Ti_103.159	3.3858	0.3642	1517.82	1516.65	4231.1	1	747	76.9	2	R.TYVPALEQSADGHK.E
	HsHeLa_Control-MG_Ti_10	4.4337	0.4303	2186.84	2187.37	6324.5	1	968.6	57.5	3	R.TYVPALEQSADGHKETGAPSK.E
	Hs293FLP-MG_Ti_203.199	2.0984	0.1654	1148.47	1149.29	2716.5	2	191.1	72.2	1	K.NSFQPISSLR.D
	HsF-IP-293-MG_Ti_103.16	2.365	0.2641	1148.48	1149.29	2091.8	2	135.1	72.2	1	K.NSFQPISSLR.D
	Hs283FLP_Ti_103.1627.16	2.9629	0.2357	1149.47	1149.29	4091.4	3	674.4	83.3	3	K.NSFQPISSLR.D
	Hs293FLP-MG_Ti_203.199	2.7046	0.1925	1149.5	1149.29	4283.9	2	665.6	83.3	1	K.NSFQPISSLR.D
	HsF-IP-293-MG_Ti_103.16	2.6274	0.166	1149.51	1149.29	3712.3	6	532.3	77.8	1	K.NSFQPISSLR.D
	Hs283FLP_Ti_102.1766.17	2.3318	0.2714	1438.55	1439.56	2791.5	1	271.1	57.7	1	R.ESATADAGYAILEK.K
	HsHeLa_Control-MG_Ti_10	2.316	0.3256	1438.7	1439.56	3518	1	413.2	65.4	1	R.ESATADAGYAILEK.K
	Hs293FLP-MG_Ti_102.207	2.4671	0.2685	1438.74	1439.56	3187.7	1	338.2	61.5	2	R.ESATADAGYAILEK.K
	HsFLAG-Control_HeLa_NE	4.2382	0.3887	1438.91	1439.56	7071.8	1	2220.1	84.6	14	R.ESATADAGYAILEK.K
	HsF-IP-293-MG_Ti_102.17	4.35	0.3192	1439.56	1439.56	6814.5	1	2014.1	84.6	8	R.ESATADAGYAILEK.K
	HsHeLa_Control-MG_Ti_10	4.2312	0.3601	1439.78	1439.56	6549.5	1	1890.2	84.6	6	R.ESATADAGYAILEK.K
	Hs293FLP-MG_Ti_202.021	4.0079	0.3795	1441.63	1439.56	6912.8	1	1504	73.1	8	R.ESATADAGYAILEK.K
	HsHeLa_Control-MG_Ti_10	2.5786	0.0966	1214.14	1211.32	5412.3	2	491.2	70	1	K.LASDDRPSPPR.G

	HsF-IP-293-MG_Ti_106.184	2.4745	0.1137	1047.51	1048.19	4077		1	391.5	75	1	R.HQQLSGLHK.Q
	HsHeLa_Control-MG_Ti_10	2.4092	0.1628	1047.79	1048.19	4590		2	384.7	68.8	1	R.HQQLSGLHK.Q
	HsFLAG-Control_HeLa_NE	3.11	0.0924	1048.24	1048.19	6182.4		2	842.8	81.2	1	R.HQQLSGLHK.Q
	HsHeLa_Control-MG_Ti_10	3.0269	0.0993	1048.83	1048.19	5767		1	830	87.5	2	R.HQQLSGLHK.Q
	Hs293FLP-MG_Ti_205.181	4.0299	0.2007	1639.64	1639.81	9684.4		1	1669.7	73.1	5	R.RAHLSENELEALEK.N
	HsHeLa_Control-MG_Ti_20	2.7825	0.2137	1482.46	1483.62	4364.5		1	524.8	58.3	2	R.AHLSENELEALEK.N
	Hs293FLP-MG_Ti_203.192	3.0185	0.184	1482.55	1483.62	6558.5		1	832.2	62.5	2	R.AHLSENELEALEK.N
	Hs293FLP_Ti_303.1679.16	3.2309	0.2489	1482.74	1483.62	4590.3		1	575.5	58.3	1	R.AHLSENELEALEK.N
	HsHeLa_Control-MG_Ti_20	4.5638	0.392	1482.83	1483.62	5983		1	1394.1	87.5	1	R.AHLSENELEALEK.N
	HsFLAG-Control_HeLa_NE	4.4097	0.3893	1482.85	1483.62	5190.9		1	1433.6	87.5	10	R.AHLSENELEALEK.N
	HsF-IP-293-MG_Ti_104.161	4.1295	0.3485	1483.29	1483.62	5072.4		1	1215.8	83.3	13	R.AHLSENELEALEK.N
	Hs293FLP-MG_Ti_203.191	4.5868	0.4135	1483.59	1483.62	5865.6		1	1531.2	87.5	2	R.AHLSENELEALEK.N
	Hs283FLP_Ti_104.1561.15	3.0485	0.1979	1483.62	1483.62	5321.1		1	794.7	66.7	1	R.AHLSENELEALEK.N
	Hs283FLP_Ti_104.1553.15	3.1976	0.1039	1484.25	1483.62	5841		1	1053.8	83.3	1	R.AHLSENELEALEK.N
	HsHeLa_Control-MG_Ti_20	1.8126	0.082	1126.5	1127.28	3899.3		7	331.7	55.6	1	K.YGIPEPPEPK.R
	HsHeLa_Control-MG_Ti_10	5.1422	0.4216	1858.36	1857.03	5259.6		1	2001.7	78.1	5	R.KYGGISTASVDFEQPTR.D
	HsFlag1P_Ti_105.2252.225	3.8658	0.2669	2928.17	2929.13	7617.4		1	979	30.6	1	R.KYGGISTASVDFEQPTRDGLGSDNIGSR.M
	HsHeLa_Control-MG_Ti_20	4.949	0.4651	1729.63	1728.86	7850.2		1	1414.2	66.7	18	K.YGGISTASVDFEQPTR.D
	HsHeLa_Control-MG_Ti_10	3.6549	0.302	1091.59	1091.12	4011.7		1	771.8	80	8	R.DGLGSDNIGSR.M
	HsFlag1P_Ti_106.2481.248	1.9421	0.1137	964.4	965.217	6583.3		9	683.2	78.6	1	R.MLQAMGWK.E
	HsHeLa_Control-MG_Ti_20	3.5071	0.2445	1441.52	1441.67	7138.2		2	922.8	66.7	5	K.KQGIVTPIEAQTR.V
	HsFlag1P_Ti_104.1989.198	2.9007	0.1916	1312.69	1313.5	4627.4		1	905.9	86.4	5	K.QGIVTPIEAQTR.V
	HsFLAG-Control_HeLa_NE	2.3634	0.3301	1365.35	1366.42	6452.2		1	485.8	58.3	1	R.GSSYGVTSTESYK.E
	HsFLAG-Control_Hela_Ti_1	1.9639	0.2699	1365.46	1366.42	5462.4		1	384.5	54.2	1	R.GSSYGVTSTESYK.E
	HsF-IP-293-MG_Ti_102.139	2.4856	0.1599	1365.47	1366.42	5114.6		7	231.4	45.8	1	R.GSSYGVTSTESYK.E
	Hs283FLP_Ti_102.1346.13	2.5386	0.2461	1365.55	1366.42	4936.9		1	367.9	54.2	1	R.GSSYGVTSTESYK.E
	HsHeLa_Control_Ti_102.13	2.2511	0.1992	1365.6	1366.42	5313.6		1	413.7	54.2	1	R.GSSYGVTSTESYK.E
	HsHeLa_Control-MG_Ti_20	3.5419	0.3333	1366.19	1366.42	6111.3		1	1364.2	79.2	8	R.GSSYGVTSTESYK.E
	HsF-IP-293-MG_Ti_102.139	3.6824	0.3676	1366.37	1366.42	4805.4		1	1076.5	79.2	6	R.GSSYGVTSTESYK.E
	HsFLAG-Control_Hela_Ti_1	2.8624	0.2878	1366.45	1366.42	6229.7		1	878.7	66.7	2	R.GSSYGVTSTESYK.E
	Hs293FLP_TREX_Ti_102.1	2.8776	0.2978	1366.45	1366.42	5552.4		1	747.8	66.7	1	R.GSSYGVTSTESYK.E
	HsHelaFlag1P_Ti_102.1344	2.5134	0.3016	1367.41	1366.42	3939.1		2	358.8	50	2	R.GSSYGVTSTESYK.E
	HsHeLa_Control_Ti_102.13	2.8562	0.29	1368.53	1366.42	4229.4		1	562.3	62.5	2	R.GSSYGVTSTESYK.E
	HsFlag1P_Ti_105.1812.181	4.2098	0.5065	1974.1	1975.12	7301.3		1	778.5	50	4	R.GSSYGVTSTESYKETLHK.T
gi|5174525|ref|NI	136	566	0.507	2468	270618	4.8	U		microtubule-associated protein 1B isoform 1 [Homo sapiens]			
*	HsHeLa_Control-MG_Ti_20	6.0913	0.4531	2017.72	2017.38	6427.7		1	2433.7	84.4	3	K.FYLLVVVGEIVTEEHLR.R
*	Hs293FLP-MG_Ti_203.229	4.0032	0.2013	1056.35	1056.25	5961		1	1138.9	88.9	7	R.AIGNIELGIR.S
*	Hs293FLP-MG_Ti_202.350	4.9865	0.4022	1979.25	1979.12	5732.8		1	1404.5	76.7	8	R.SWDTNLIECNLDQELK.L
*	Hs293FLP-MG_Ti_203.160	1.8871	0.1262	988.49	989.116	4637.5		5	438.3	68.8	1	R.FSPEVPGQK.I
*	HsHeLa_Control-MG_Ti_20	4.7432	0.3926	2372.1	2373.62	5621.2		1	914.4	54.8	25	R.SDVLETVVLINPSDEAVSTEVR.L
*	Hs293FLP-MG_Ti_203.342	3.5416	0.1604	2373.38	2373.62	6283.2		2	679.6	32.1	1	R.SDVLETVVLINPSDEAVSTEVR.L
	Hs293FLP-MG_Ti_202.318	3.2766	0.3084	1653.22	1653.8	5091.7		1	1156	73.1	4	K.ASLTLFCPEEGDWK.N
	Hs293FLP-MG_Ti_205.226	3.5391	0.242	1942.27	1942.14	10707.4		1	964.5	56.7	2	K.NSNLDRHNLQDFINIK.L
	Hs293FLP-MG_Ti_204.232	3.3554	0.2167	1241.44	1242.42	5780.4		3	597.7	72.2	1	R.HNLQDFINIK.L
	HsHeLa_Control-MG_Ti_20	4.05	0.2699	1242.44	1242.42	7267.4		1	1343.2	83.3	3	R.HNLQDFINIK.L
	Hs293FLP-MG_Ti_204.232	4.1106	0.2474	1242.47	1242.42	7042.5		1	1459.4	88.9	2	R.HNLQDFINIK.L
	HsF-IP-293-MG_Ti_104.319	2.6792	0.1203	2171.1	2170.41	12460.9		3	673.8	40	2	R.GDSALFAVNGFNMLINGGSER.K
	Hs293FLP-MG_Ti_206.323	5.5237	0.4565	3044.02	3044.46	9958.3		1	2245.4	38.5	1	R.HLDRVDSILLTHIGDDNLPGINSMLQR.K
	HsHeLa_Control-MG_Ti_20	5.6005	0.3793	2082.98	2082.45	7399.5		1	1858.5	69.4	58	K.NLISPDLGVVFLNVPENLK.N

Hs293FLP-MG_Ti_203.427	3.5417	0.1097	2083.28	2082.45	6755.8	1	1284.7	41.7	1	K.NLISPDLGVVFLNVPENLK.N
Hs293FLP-MG_Ti_204.248	4.1818	0.4096	1872.11	1873.08	8665.5	1	1156.4	64.3	3	K.RSIEEACFTLQYLNK.L
Hs293FLP-MG_Ti_203.286	4.6785	0.4389	1716.63	1716.9	9676.1	1	1809.4	73.1	2	R.SIEEACFTLQYLNK.L
HsHeLa_Control-MG_Ti_20	4.9455	0.395	1531.36	1531.79	6385.7	1	1473.7	80.8	10	R.SVGNTIDPVILFQK.M
Hs293FLP-MG_Ti_202.329	4.0307	0.3855	1531.46	1531.79	6826.7	1	1107.4	69.2	2	R.SVGNTIDPVILFQK.M
Hs293FLP-MG_Ti_202.330	3.1329	0.3564	1531.58	1531.79	4917.5	1	516.8	57.7	1	R.SVGNTIDPVILFQK.M
HsHeLa_Control-MG_Ti_20	3.1108	0.4134	1531.67	1531.79	4271.8	1	348.1	53.8	2	R.SVGNTIDPVILFQK.M
HsHeLa_Control-MG_Ti_20	4.4383	0.4054	4081.77	4080.63	7622.1	1	897.1	25.7	1	K.DKAEFILPNGQEVDLPISYLTSVSSLIVWHPANPAEK.I
HsHeLa_Control-MG_Ti_20	4.3593	0.4006	3834.66	3837.36	3367.6	1	408.9	26.5	5	K.AEFILPNGQEVDLPISYLTSVSSLIVWHPANPAEK.I
HsHeLa_Control-MG_Ti_20	4.821	0.3361	2023.32	2023.29	3476	1	702.4	73.5	18	R.VLFPGNSTQYNILEGLEK.L
Hs293FLP-MG_Ti_202.210	2.8485	0.1502	1253.67	1254.47	6646.3	9	415.7	54.5	1	K.DLTGQVPTPVVK.Q
HsF-IP-293-MG_Ti_102.16	3.768	0.2506	1254.26	1254.47	4024.1	1	864	81.8	2	K.DLTGQVPTPVVK.Q
Hs293FLP-MG_Ti_202.210	4.0403	0.1835	1254.46	1254.47	3762.9	1	693.5	77.3	2	K.DLTGQVPTPVVK.Q
HsFLAG-Control_293_Ti_2	2.18	0.1697	1254.66	1254.47	7295.5	9	459.4	54.5	1	K.DLTGQVPTPVVK.Q
Hs293FLP_Ti_302.1728.17	3.74	0.3025	1255.47	1254.47	3770.5	7	582	72.7	1	K.DLTGQVPTPVVK.Q
Hs293FLP_TREX_Ti_106.2	3.2972	0.2917	1366.47	1366.64	3827.9	2	412.2	62.5	2	R.ESLKPAAKPLPSK.S
HsHeLa_Control-MG_Ti_20	2.5746	0.2498	909.25	909.117	7902.6	1	919.2	81.2	1	K.PAAKPLPSK.S
HsHeLa_Control-MG_Ti_20	3.2545	0.3064	1490.61	1491.73	3327.7	1	366.3	66.7	3	K.VNHVEKPPKVESK.E
Hs293FLP_Ti_306.2087.20	2.8338	0.2662	1490.81	1491.73	4430.9	2	341.8	58.3	1	K.VNHVEKPPKVESK.E
HsHeLa_Control-MG_Ti_20	3.6274	0.1524	1491.54	1491.73	6653.4	2	828.2	70.8	2	K.VNHVEKPPKVESK.E
HsF-IP-293-MG_Ti_106.17	3.1272	0.2627	1491.68	1491.73	8463.5	5	585.9	54.2	3	K.VNHVEKPPKVESK.E
Hs293FLP-MG_Ti_203.129	2.6916	0.1887	1325.58	1326.49	3042	1	288.3	63.6	1	K.EVPSKEEPSPVK.A
Hs293FLP-MG_Ti_203.129	2.6528	0.1342	1328.05	1326.49	4416.2	3	471	68.2	1	K.EVPSKEEPSPVK.A
Hs293FLP-MG_Ti_203.146	2.934	0.2135	1953.74	1954.19	6375.6	5	428.2	50	1	K.EVPSKEEPSPVKAEVAEK.Q
HsHeLa_Control-MG_Ti_20	2.8021	0.0894	854.01	853.096	3937.8	2	612.4	92.9	1	K.KPAALKPK.V
Hs293FLP-MG_Ti_203.463	5.5887	0.4507	2625.07	2626.04	10243	1	2409.9	48.3	2	K.AAEAVAAAVGTGATTAAVMAAAGIAAIGPAK.E
Hs293FLP-MG_Ti_204.435	4.8395	0.3771	2626.21	2626.04	10003.7	1	1484.9	31.7	1	K.AAEAVAAAVGTGATTAAVMAAAGIAAIGPAK.E
HsHeLa_Control-MG_Ti_20	5.2217	0.3419	1653.38	1652.8	7146.2	1	1959.7	84.6	10	K.DFEELKAEEVDVTK.D
HsHeLa_Control-MG_Ti_20	3.079	0.2328	1699.34	1699.9	3754.1	1	505.4	69.2	1	K.DIKPQLELIEDEEK.L
HsHeLa_Control-MG_Ti_20	3.6628	0.1883	1940.77	1941.23	5160.9	1	845	46.7	1	K.DIKPQLELIEDEEKLK.E
Hs293FLP-MG_Ti_203.258	4.176	0.2461	1941.43	1941.23	5727	2	709.6	43.3	2	K.DIKPQLELIEDEEKLK.E
Hs293FLP-MG_Ti_203.257	4.4982	0.3744	1941.68	1941.23	5397.5	1	988.5	70	2	K.DIKPQLELIEDEEKLK.E
HsHeLa_Control-MG_Ti_20	3.295	0.1517	1942.35	1941.23	7154.3	1	988.9	66.7	2	K.DIKPQLELIEDEEKLK.E
HsHeLa_Control-MG_Ti_20	4.6306	0.3585	3327.38	3328.78	6204.8	1	1002.6	31.5	5	K.DIKPQLELIEDEEKLKETEPVEAYVIQK.E
HsF-IP-293-MG_Ti_104.16	3.8506	0.3068	1647.39	1647.91	4259	1	1041.2	80.8	3	K.LKETEPVEAYVIQK.E
HsF-IP-293-MG_Ti_102.17	3.5296	0.4119	1405.74	1406.58	5875.1	1	1082.9	81.8	2	K.ETEPVEAYVIQK.E
Hs293FLP-MG_Ti_202.221	5.7341	0.4013	3346.71	3346.41	8442.8	1	1501.5	31.7	2	K.GPAESPDEGITTTEGEGECEQTPEELEPVEK.Q
Hs293FLP-MG_Ti_202.292	3.3729	0.3168	3139.91	3141.15	7229.9	1	491.7	35.2	1	K.QGVDDIEKFEDEGAGFEESSETGDYEEK.A
Hs293FLP-MG_Ti_202.291	5.7993	0.4486	3140.76	3141.15	9199.3	1	935.1	27.8	2	K.QGVDDIEKFEDEGAGFEESSETGDYEEK.A
Hs293FLP_Ti_302.1440.14	4.5337	0.365	2563.38	2562.54	3838.5	1	629.4	47.7	1	K.AETEEAEEPEEDGEEHVCVSASK.H
HsF-IP-293-MG_Ti_106.20	4.722	0.4651	2120.34	2120.19	8811.5	1	2259.8	72.2	4	K.HSPTEDEESAKAEADAYIR.E
HsF-IP-293-MG_Ti_102.18	5.8851	0.3014	1943.22	1942.09	10288.5	1	2354	63.9	13	K.AAEAGGAEEQYGFLTTPTK.Q
Hs293FLP-MG_Ti_202.276	3.5989	0.2187	2743.44	2744.85	10028	1	1087.7	30.4	1	R.DVMSDETNNEETESPSQEFVNITK.Y
Hs293FLP-MG_Ti_202.274	3.8077	0.2961	2744.39	2744.85	6520.2	1	500.6	39.1	2	R.DVMSDETNNEETESPSQEFVNITK.Y
Hs293FLP-MG_Ti_202.268	2.986	0.1182	2985.82	2985.19	7733.8	1	599	36.5	1	K.YESSLYSQEYSKPADVTPLNGFSEGSK.T
Hs293FLP-MG_Ti_203.229	4.9505	0.3241	3673.02	3673.88	10812.6	1	789.5	22.7	2	K.YESSLYSQEYSKPADVTPLNGFSEGSKTDATDGK.D
Hs293FLP_TREX_Ti_102.1	1.9175	0.1887	1022.32	1023.09	5618.7	1	564.5	72.2	1	K.DSISAVSSEK.V

HsF-IP-293-MG_Ti_102.08	2.5174	0.1978	1023.15	1023.09	5482.3	2	746.8	77.8	1	K.DSISAVSSEK.V
Hs293FLP-MG_Ti_204.176	1.8427	0.3414	1422.48	1423.61	7080.3	1	712.3	57.7	1	K.SPSLSPSPPSPLEK.T
HsF-IP-293-MG_Ti_104.15	3.7303	0.263	1423.54	1423.61	4139.4	1	493.8	61.5	4	K.SPSLSPSPPSPLEK.T
Hs293FLP_TREX_Ti_102.1	3.4788	0.1807	1349.18	1349.53	6035.6	1	760.2	68.2	11	R.SVNFSLTPNEIK.V
Hs293FLP-MG_Ti_202.241	3.5683	0.39	3124.34	3124.31	9301.5	1	514.9	32.1	4	K.VSAEAEVAPVSPEVTQEVVEEHCASPEDK.T
HsFLAG-Control_293_Ti_2	3.495	0.3285	2966.2	2967.17	6914.5	1	527.7	33.3	2	K.TLEVVSPSQSVTGSAGHTPYYQSPTDEK.S
HsHeLa_Control-MG_Ti_20	4.4453	0.3273	2712.06	2713.06	5024.1	1	829.1	34.4	2	K.SSHLPTEVIEKPPAVPVSFEFSDAK.D
Hs293FLP-MG_Ti_205.267	4.3935	0.2291	2712.17	2713.06	5795.1	1	1076.6	36.5	2	K.SSHLPTEVIEKPPAVPVSFEFSDAK.D
Hs293FLP-MG_Ti_205.269	4.515	0.4085	2712.59	2713.06	5512.5	1	725.6	43.8	1	K.SSHLPTEVIEKPPAVPVSFEFSDAK.D
HsHeLa_Control-MG_Ti_20	6.0498	0.4476	3356.64	3356.67	5200.7	1	1121.7	36.2	11	K.SSHLPTEVIEKPPAVPVSFEFSDAKDENER.A
HsHeLa_Control-MG_Ti_20	3.3428	0.2968	2136.83	2135.3	10066.9	1	913.5	50	1	K.PPAVPVSFEFSDAKDENER.A
Hs293FLP-MG_Ti_202.213	3.8772	0.2858	2014.56	2015.2	5451.6	1	694	55.6	9	R.ASVSPMDEPVPDSESPIEK.V
Hs293FLP-MG_Ti_205.324	5.394	0.4147	2779.37	2780.1	8648.2	1	1451.3	32	2	K.VLSPLRSPPLIGSESAYESFLSADDK.A
Hs293FLP-MG_Ti_202.331	5.847	0.549	2113.64	2114.27	7020.9	1	2692	78.9	10	R.SPPLIGSESAYESFLSADDK.A
HsHeLa_Control-MG_Ti_20	2.1642	0.1037	993.43	994.046	4636.2	5	449.2	62.5	1	R.GAESPFEEK.S
Hs293FLP-MG_Ti_202.252	4.1864	0.4797	2385.22	2385.56	6708.1	1	810.4	50	7	K.QGSPDQVSPVSEMTSTSLYQDK.Q
Hs293FLP_TREX_Ti_103.1	4.0883	0.4085	1712.5	1712.85	4292.2	1	660	67.9	15	K.STDFAPIKEDFGQEK.K
HsF-IP-293-MG_Ti_104.17	4.5971	0.5103	2076.43	2077.27	8146.4	1	1740.9	66.7	5	K.KTDDVEAMSSQPALALDER.K
Hs293FLP-MG_Ti_203.278	5.7718	0.3943	2054.19	2054.31	7791.5	1	2175.7	69.4	1	R.KLGDVSPTQIDVSQFGSFK.E
Hs293FLP-MG_Ti_204.246	3.8277	0.2788	2527.32	2527.79	8643.1	1	813.5	45.5	2	R.KLGDVSPTQIDVSQFGSFKEDTK.M
Hs293FLP-MG_Ti_202.314	4.1151	0.3444	1925.55	1926.13	5325	1	938.7	58.8	2	K.LGDVSPTQIDVSQFGSFK.E
Hs293FLP-MG_Ti_102.157	2.0067	0.1397	1153.66	1154.28	5215.5	1	434.9	65	1	K.MSISEGTVSDK.S
Hs293FLP-MG_Ti_202.357	3.9324	0.3685	2808.41	2809.01	9101.1	1	769.5	37.5	2	R.SEQSSMSIEFGQESPEQSLAMDFSR.Q
Hs293FLP_TREX_Ti_102.1	3.6887	0.3266	1905.24	1904.04	4150.9	1	350	44.1	10	R.ESSPLYSPTFSDSTSAVK.E
Hs293FLP_TREX_Ti_104.1	5.2703	0.4954	2409.58	2410.53	5646.5	1	1475.6	61.4	7	K.TATCHSSSSPPIDAASAEPYGFR.A
Hs293FLP-MG_Ti_204.188	4.8385	0.3866	2409.73	2410.53	5968.4	1	1099.7	54.5	10	K.TATCHSSSSPPIDAASAEPYGFR.A
Hs293FLP_Ti_303.1701.17	4.977	0.4275	2410.18	2410.53	5199.3	1	1348.1	61.4	2	K.TATCHSSSSPPIDAASAEPYGFR.A
Hs293FLP_TREX_Ti_104.1	4.3066	0.2017	2410.46	2410.53	7284.9	1	1500.9	38.6	2	K.TATCHSSSSPPIDAASAEPYGFR.A
Hs293FLP_Ti_303.1699.16	3.74	0.1558	2410.64	2410.53	6842.4	3	778.5	31.8	1	K.TATCHSSSSPPIDAASAEPYGFR.A
Hs293FLP-MG_Ti_206.293	4.9721	0.4186	1853.68	1854.14	10806.3	1	2606.2	73.3	4	R.ASVLFDTMQHHLALNR.D
Hs293FLP_TREX_Ti_103.1	4.7163	0.4524	1989.84	1991.12	7510.4	1	748.7	56.2	11	K.TPGDFSYAYQKPEETTR.S
Hs293FLP-MG_Ti_203.176	3.7782	0.2819	1991.75	1991.12	5230.6	1	814.8	42.2	1	K.TPGDFSYAYQKPEETTR.S
HsF-IP-293-MG_Ti_106.21	5.2283	0.3815	3740.92	3741.82	11204.4	1	1177.7	25.8	5	K.TPGDFSYAYQKPEETTRSPDEEDYDYESYEK.T
HsHeLa_Control-MG_Ti_20	5.1508	0.3791	1769.05	1769.73	7525.3	1	2038.4	80.8	5	R.SPDEEDYDYESYEK.T
Hs293FLP-MG_Ti_102.165	2.4642	0.3355	1281.57	1282.35	4644.9	1	396	60	2	R.TSDVGGYYYEK.I
HsF-IP-293-MG_Ti_102.14	3.4849	0.3758	1282.27	1282.35	3888.6	1	903.4	85	3	R.TSDVGGYYYEK.I
Hs293FLP-MG_Ti_102.165	3.0866	0.2944	1282.6	1282.35	3923.4	2	780.3	85	2	R.TSDVGGYYYEK.I
Hs293FLP-MG_Ti_204.182	2.9952	0.1974	2010.57	2011.2	7122	6	421.8	46.9	1	R.TSDVGGYYYEKIERTTK.S
Hs293FLP_TREX_Ti_102.1	2.7389	0.3828	1490.28	1491.55	6667.5	1	654.8	57.7	1	K.SPSDSGYSYETIGK.T
Hs293FLP-MG_Ti_202.189	2.8984	0.379	1490.54	1491.55	8672.3	1	600.4	53.8	1	K.SPSDSGYSYETIGK.T
Hs293FLP-MG_Ti_202.190	3.6735	0.336	1491.25	1491.55	7784.1	1	1273.3	69.2	3	K.SPSDSGYSYETIGK.T
HsHeLa_Control-MG_Ti_20	4.5721	0.4448	1491.45	1491.55	7917.8	1	1946.1	80.8	3	K.SPSDSGYSYETIGK.T
HsF-IP-293-MG_Ti_102.15	3.9816	0.4209	1491.48	1491.55	6657.4	1	1501.8	76.9	2	K.SPSDSGYSYETIGK.T
Hs293FLP_TREX_Ti_102.1	4.7213	0.3532	1659.26	1659.74	7644.7	1	2486.7	84.6	13	K.TPEDGDYSYEIIEK.T
HsHeLa_Control-MG_Ti_20	4.6301	0.2919	1575.33	1575.63	6294	1	1716.5	84.6	17	R.TPEEGGYSYDISEK.T
Hs293FLP_TREX_Ti_102.1	2.5508	0.3188	1544.36	1545.64	4845.3	1	645.3	65.4	1	K.TTSPPEVSGYSYEK.T
HsHeLa_Control-MG_Ti_20	3.7031	0.3492	1545.28	1545.64	4208.9	1	549.7	69.2	2	K.TTSPPEVSGYSYEK.T
Hs293FLP_TREX_Ti_102.1	3.0066	0.3474	1545.42	1545.64	4103.1	1	480.9	65.4	2	K.TTSPPEVSGYSYEK.T
Hs293FLP-MG_Ti_202.186	2.7061	0.3209	1545.44	1545.64	5787.4	1	408.1	50	4	K.TTSPPEVSGYSYEK.T

	HsHeLa_Control-MG_Ti_20	5.6851	0.4174	3551.2	3551.63	6920.6		1	679.7	25.8	2	R.RLLDDISNGYDDSEDGGHTLGDPSYSYETTEK.I
	HsF-IP-293-MG_Ti_105.18	4.7621	0.4589	3395.85	3395.44	6514.5		1	823.3	27.5	7	R.LLDDISNGYDDSEDGGHTLGDPSYSYETTEK.I
	Hs293FLP_TREX_Ti_102.1	4.3764	0.4478	1926.33	1927.03	4555.6		1	1014.3	71.9	16	K.ITSFPESEGYSYETSTK.T
	Hs293FLP-MG_Ti_203.153	3.3669	0.1597	2024.93	2025.1	9076.3		2	633.5	50	1	K.TTRTPDTSTYCYETAEK.I
	HsF-IP-293-MG_Ti_102.14	3.9483	0.4698	1666.43	1666.7	6574.9		1	1694.9	80.8	3	R.TPDTSTYCYETAEK.I
	HsF-IP-293-MG_Ti_102.17	4.9361	0.4454	2316.48	2316.4	5976.4		1	1354.5	60.5	11	R.TPQASTYSYETSDLCYTAEK.K
	Hs293FLP-MG_Ti_203.184	4.2093	0.407	2443.09	2444.58	10320.5		1	858.3	40	2	R.TPQASTYSYETSDLCYTAEKK.S
	HsF-IP-293-MG_Ti_105.15	4.8901	0.4566	2445.19	2444.58	7525.2		1	919.1	36.2	1	R.TPQASTYSYETSDLCYTAEKK.S
	Hs293FLP-MG_Ti_203.227	3.5932	0.3836	1716.22	1716.82	8488.2		1	1280	69.2	1	R.QDVDLCLVSSCEYK.H
	Hs293FLP-MG_Ti_202.466	2.6954	0.2596	3107.78	3109.33	9301.4		1	441.3	28.8	1	K.TELSPSFINPNPLEWFASEEPTEESEK.P
	Hs293FLP-MG_Ti_203.413	5.5844	0.4315	4450.21	4451.84	7054		1	724.6	21.3	8	K.TELSPSFINPNPLEWFASEEPTEESEKPLTQSGGAPPPPGGK.Q
	Hs293FLP_TREX_Ti_105.1	3.8535	0.3753	1361.31	1361.54	4427.3		1	840.6	71.4	3	K.PLTQSGGAPPPPGGK.Q
	HsHeLa_Control-MG_Ti_20	2.0067	0.0984	898.47	899.078	3837.7		2	363.3	75	1	K.SKPLAASPK.P
	HsHeLa_Control-MG_Ti_20	2.5809	0.3154	1364.56	1365.66	3800.9		1	301.9	53.8	2	K.SKPLAASPKPAGLK.E
	Hs293FLP_TREX_Ti_106.2	3.0003	0.3193	1365.57	1365.66	5166.3		1	575.4	61.5	2	K.SKPLAASPKPAGLK.E
	HsHeLa_Control-MG_Ti_20	2.6033	0.3402	1142.9	1143.33	2834.4		1	366.9	70	1	K.AAKPTTTPEVK.A
	HsHeLa_Control-MG_Ti_20	3.748	0.3775	2628.67	2629.94	3952.9		1	263.6	39.1	5	K.SSAVPPGLPVYLDLCYIPNHSNSK.N
	HsHeLa_Control-MG_Ti_20	2.7448	0.2087	997.4	998.123	3870.1		7	426.9	78.6	4	K.NVDVEFFK.R
	HsFLAG-Control_293_Ti_2	5.5766	0.4756	1928.51	1929.01	7628.4		1	1703.4	64.7	12	R.SSYYVVSGNDPAAEEPSR.A
	Hs293FLP-MG_Ti_203.370	3.754	0.2574	2940.38	2939.21	6067		1	515.3	25	1	R.SSYYVVSGNDPAAEEPSRAVLDALLEGK.A
	Hs293FLP-MG_Ti_202.296	3.7575	0.1962	1028.41	1029.22	3886.9		1	1049	88.9	5	R.AVLDALLEGK.A
	Hs293FLP-MG_Ti_202.298	2.4687	0.2016	1028.5	1029.22	10995		1	852.2	66.7	2	R.AVLDALLEGK.A
	HsHeLa_Control-MG_Ti_20	2.2589	0.1799	1028.6	1029.22	3518.2		3	411.9	66.7	1	R.AVLDALLEGK.A
	HsF-IP-293-MG_Ti_102.22	3.7058	0.2483	1029.29	1029.22	3671.5		1	979.6	88.9	4	R.AVLDALLEGK.A
	HsHeLa_Control-MG_Ti_20	3.7959	0.1662	1029.34	1029.22	4447.9		1	924.2	83.3	8	R.AVLDALLEGK.A
	Hs293FLP_Ti_302.2467.24	2.5858	0.1814	1030.04	1029.22	8634.6		7	826.8	66.7	3	R.AVLDALLEGK.A
gi|4503545|ref|N	6	16	0.506	154	16832	5.2	U	eukaryotic translation initiation factor 5A [Homo sapiens]				
	HsHeLa_Control_Ti_106.33	3.471	0.3788	1298.82	1299.56	6719.6		1	1188.7	72.7	1	K.VHLVGIDIFTGK.K
	HsHeLa_Control-MG_Ti_20	3.616	0.2903	1299.28	1299.56	5463.8		1	1286.8	81.8	4	K.VHLVGIDIFTGK.K
	HsGST-MOCK_Ti_304.193	2.8938	0.3003	2160.75	2162.39	8537.7		1	736.8	50	1	K.KYEDICPSTHNMDVPNIK.R
*	HsHeLa_Control-MG_Ti_20	5.8242	0.44	2739.29	2738.03	10171.3		1	2137	38	1	K.RNDFQLIGIQDGYLSLLQDSGEVR.E
*	HsFLAG-Control_HeLa_NE	4.4789	0.3178	2580.7	2581.84	8733.2		1	1390.7	50	3	R.NDFQLIGIQDGYLSLLQDSGEVR.E
	HsGST-MOCK_Ti_306.049	5.0622	0.4083	2627.07	2627.97	9107.5		1	1264.5	47.8	6	K.YDCGEEILITVLSAMTEEAAVAIK.A
gi|5032161|ref|N	5	14	0.5	112	12473	4.8	U	elongin C [Homo sapiens]				
*	Hs293FLP-MG_Ti_302.144	4.0127	0.3926	1549.33	1548.67	5498.3		1	1881.6	88.5	2	K.TYGGCEGPDAMYVK.L
	Hs293FLP-MG_Ti_306.238	2.748	0.0986	1344.52	1345.54	4997.1		6	461.5	59.1	1	K.LISSDGHEFIVK.R
	Hs293FLP-MG_Ti_306.238	3.7505	0.2283	1346.65	1345.54	4658.4		1	1040.7	86.4	3	K.LISSDGHEFIVK.R
	Hs293FLP-MG_Ti_303.119	2.8484	0.3758	1057.4	1057.19	3442.6		1	286.7	72.2	6	R.EHALTSGTIK.A
*	Hs293FLP-MG_Ti_304.202	2.6788	0.1928	2211.65	2212.4	8966.2		1	558.9	42.1	2	K.AMLSGPGQFAENETNEVNFR.E
gi|47604944|ref|	72	366	0.498	929	103709	8.2	U	SCY1-like 2 protein [Homo sapiens]				
*	HsFLAG-Control_293_Ti_2	4.9069	0.3367	1620.5	1618.85	7829		1	1626.2	70	5	K.VTADVTSAVMGNPVTR.E
*	HsFLAG-Control_293_Ti_1	2.2989	0.2942	1209.33	1211.37	5203		1	451.6	63.6	2	R.HIASGGNGLAWK.I
*	HsFLAG-Control_293_Ti_1	2.9682	0.3056	1210.14	1211.37	3256.3		1	491.6	77.3	1	R.HIASGGNGLAWK.I
*	HsFLAG-Control_MG_293_	2.9148	0.3301	1210.41	1211.37	5788.6		1	596.9	63.6	2	R.HIASGGNGLAWK.I
*	HsFLAG-Control_293_Ti_2	2.6718	0.2917	1210.56	1211.37	6059.4		1	529.1	59.1	2	R.HIASGGNGLAWK.I
*	HsFLAG-Control_MG_293_	3.9553	0.3135	1211.21	1211.37	3408.1		1	768.8	86.4	2	R.HIASGGNGLAWK.I
*	HsFLAG-Control_293_Ti_2	3.9323	0.3689	1211.23	1211.37	3362.3		1	870.6	90.9	2	R.HIASGGNGLAWK.I
*	HsFLAG-Control_293_Ti_2	3.1781	0.2539	1181.51	1182.36	2547.4		1	296.3	77.8	6	K.QEVAVFVFDK.K

*	HsFLAG-Control_MG_293_	2.7212	0.2046	1184.31	1182.36	5132.5	2	542.7	77.8	1	K.QEVAVFVFDK.K
*	HsFLAG-Control_293_Ti_1	2.9327	0.0983	958.61	958.109	7246.6	1	1163.8	100	3	K.RGVQQLTR.L
*	HsFLAG-Control_293_Ti_2	3.0473	0.2505	1421.62	1422.62	5246.1	1	389.7	59.1	1	R.LLTVQHPLEESR.D
*	HsFLAG-Control_MG_293_	2.8435	0.2088	1421.69	1422.62	7139.4	1	458.7	54.5	1	R.LLTVQHPLEESR.D
*	HsFLAG-Control_293_Ti_1	3.214	0.1093	1421.91	1422.62	9295.1	1	1525.5	81.8	5	R.LLTVQHPLEESR.D
*	HsFLAG-Control_293_Ti_2	4.0626	0.1563	1422.23	1422.62	6331.3	1	1099	77.3	5	R.LLTVQHPLEESR.D
*	HsFLAG-Control_293_Ti_1	2.5241	0.1416	1422.4	1422.62	6276	3	348.4	59.1	1	R.LLTVQHPLEESR.D
*	HsFLAG-Control_HeLa_S1	3.7144	0.1882	1422.44	1422.62	6300.4	1	1146.4	81.8	4	R.LLTVQHPLEESR.D
*	HsFLAG-Control_MG_293_	3.4146	0.2872	1422.57	1422.62	5514.9	1	900.4	77.3	3	R.LLTVQHPLEESR.D
*	HsFLAG-Control_293_Ti_1	5.8458	0.4206	3676.59	3677.08	5975.4	1	1494.1	35.2	17	R.DCLAFCTEPVFASLANVLGNWENLPSPISPDIK.D
*	HsFLAG-Control_HeLa_S1	4.9234	0.4197	1964.43	1965.26	7453.7	1	1580.3	67.6	3	K.YGLLQVSEGLSFLHSSVK.M
*	Hs293FLP-MG_Ti_205.343	5.1611	0.4239	1964.48	1965.26	8186.3	1	2133	70.6	2	K.YGLLQVSEGLSFLHSSVK.M
*	HsFLAG-Control_HeLa_S1	4.6333	0.4082	1964.53	1965.26	7103.2	1	1216.6	61.8	4	K.YGLLQVSEGLSFLHSSVK.M
*	HsFLAG-Control_HeLa_S1	5.029	0.3389	1964.77	1965.26	6120.7	1	1737.6	47.1	2	K.YGLLQVSEGLSFLHSSVK.M
*	HsFLAG-Control_HeLa_NE	4.4733	0.3584	1964.96	1965.26	6146.9	1	1011.3	61.8	5	K.YGLLQVSEGLSFLHSSVK.M
*	HsFLAG-Control_293_Ti_1	5.0528	0.3764	1965.16	1965.26	7206.8	1	1887.8	70.6	7	K.YGLLQVSEGLSFLHSSVK.M
*	Hs293FLP-MG_Ti_205.342	4.9663	0.3401	1965.23	1965.26	7982.1	1	2011.8	48.5	2	K.YGLLQVSEGLSFLHSSVK.M
*	HsFLAG-Control_293_Ti_1	4.5834	0.2898	1965.43	1965.26	7490.8	1	1840	47.1	2	K.YGLLQVSEGLSFLHSSVK.M
*	HsFLAG-Control_HeLa_S1	4.3734	0.323	1965.66	1965.26	6463.9	1	1626.2	47.1	1	K.YGLLQVSEGLSFLHSSVK.M
*	HsFLAG-Control_HeLa_NE	4.6112	0.3219	1966.24	1965.26	5968.5	1	2433.7	54.4	2	K.YGLLQVSEGLSFLHSSVK.M
*	HsFLAG-Control_MG_293_	3.7807	0.2918	1693.41	1694	7215.5	1	984	64.3	2	K.MVHGNITPENIILNK.S
*	HsFLAG-Control_293_Ti_2	5.0947	0.4652	2173.06	2174.35	7482.1	1	1297.8	61.1	7	K.IMGFDFCVSSTNPSEQEPK.F
*	HsFLAG-Control_MG_293_	2.773	0.1036	1031.65	1032.23	2950.1	1	430.3	87.5	2	K.GKPIFEVNK.Q
*	HsFLAG-Control_HeLa_S1	3.571	0.4378	1679.41	1679.96	4900.3	1	572.5	65.4	4	K.GKPIFEVNKQDIYK.S
*	HsFLAG-Control_293_Ti_1	3.0123	0.3486	1501.72	1502.67	4416.6	1	382.6	57.7	2	R.LGSSSLTNIPEEVR.E
*	HsFLAG-Control_MG_293_	4.3809	0.2803	1502.53	1502.67	5739.3	1	932.2	69.2	2	R.LGSSSLTNIPEEVR.E
*	Hs293FLP-MG_Ti_202.230	4.1022	0.2556	1502.55	1502.67	4951.3	2	621.9	61.5	11	R.LGSSSLTNIPEEVR.E
*	HsFLAG-Control_MG_293_	2.8066	0.2249	1502.6	1502.67	5294.7	5	205.7	42.3	1	R.LGSSSLTNIPEEVR.E
*	HsFLAG-Control_HeLa_S1	3.9151	0.3262	1502.65	1502.67	4401.9	3	603.2	65.4	12	R.LGSSSLTNIPEEVR.E
*	HsFlag1P_Ti_106.2564.256	3.2467	0.3095	1995.55	1996.23	4557.5	1	391.4	47.1	1	R.LGSSSLTNIPEEVREHVK.L
*	HsFLAG-Control_293_Ti_2	4.6159	0.3978	2013.99	2013.36	6152.1	1	998.7	61.8	6	K.LLLNVTPTVRPDADQMTK.I
*	HsFLAG-Control_HeLa_S1	5.612	0.3618	2492.6	2493.82	7203.3	1	1457.9	60	62	K.IPFFDDVGAVTLQYFDTLFQR.D
*	Hs293FLP-MG_Ti_206.033	4.0923	0.3309	2493.66	2493.82	8317.6	1	1282.2	37.5	1	K.IPFFDDVGAVTLQYFDTLFQR.D
*	HsFLAG-Control_293_Ti_2	2.5292	0.131	1225.62	1226.55	4627.4	1	594.6	70	1	K.LILPELGPVFK.Q
*	HsFLAG-Control_HeLa_NE	3.2306	0.1516	1226.24	1226.55	3497.1	2	606.8	80	14	K.LILPELGPVFK.Q
*	HsFLAG-Control_293_Ti_2	3.0342	0.0981	1226.37	1226.55	3747.1	2	622.9	75	3	K.LILPELGPVFK.Q
*	HsFLAG-Control_293_Ti_1	4.0799	0.2539	1712.65	1712.09	8347.2	1	1259.9	76.9	17	K.QQEPIQILLIFLQK.M
*	HsFLAG-Control_293_Ti_2	2.2744	0.276	1078.34	1079.3	3350.7	7	184.3	68.8	1	K.NSVLPMVYR.A
*	HsFLAG-Control_293_Ti_1	4.0347	0.2956	1320.62	1320.46	8134.3	1	1844.6	81.8	19	K.NACLQTSSLAVR.V
*	HsFLAG-Control_293_Ti_2	2.0402	0.082	989.42	990.154	8212.4	4	691.6	75	1	R.VNSLVCLGK.I
*	HsFLAG-Control_MG_293_	3.2934	0.2019	989.72	990.154	6488.5	1	1081.1	87.5	3	R.VNSLVCLGK.I
*	HsFLAG-Control_293_Ti_1	4.8206	0.3504	2060.7	2060.44	4624.2	1	787.2	65.6	5	K.WFVLDDILPFLQQIPSK.E
*	HsFLAG-Control_293_Ti_2	3.5473	0.3124	1404.44	1404.75	4644.2	1	514.6	62.5	3	K.EPAVLMGILGIYK.C
*	HsFLAG-Control_293_Ti_2	2.8762	0.2868	1404.48	1404.75	6457.7	1	1008.9	75	2	K.EPAVLMGILGIYK.C
*	HsFLAG-Control_HeLa_S1	4.7458	0.1919	3081.35	3078.63	11161.1	1	1683	30.8	3	K.VLPHLIPLSIENNLNLNQFNSFISVIK.E
*	HsFLAG-Control_MG_293_	4.7465	0.2621	1525.45	1525.76	7681.6	1	1289.2	77.3	7	K.LEQLHIMQEQQK.S
*	HsFLAG-Control_293_Ti_2	4.5077	0.3448	1697.34	1695.9	7030.5	1	1209.5	67.9	1	K.SLDIGNQMNVSEEMK.V
*	HsFLAG-Control_MG_293_	2.9244	0.1884	1229.29	1230.36	8814.3	3	618.1	60	1	K.VTNIGNQQIDK.V
*	HsFLAG-Control_293_Ti_2	2.7167	0.1805	1229.4	1230.36	6552.5	9	427.9	60	1	K.VTNIGNQQIDK.V

*	HsFLAG-Control_293_Ti_1	2.7929	0.1144	1229.53	1230.36	6635.7	9	416.4	60	1	K.VTNIGNQQIDK.V
*	HsHeLa3_Ti_103.1327.132	2.6273	0.2166	1229.61	1230.36	5896.2	1	487.1	65	1	K.VTNIGNQQIDK.V
*	HsFLAG-Control_293_Ti_2	4.0082	0.12	1230.24	1230.36	4879.4	1	1073.2	90	1	K.VTNIGNQQIDK.V
*	HsFLAG-Control_293_Ti_1	4.0577	0.1353	1230.46	1230.36	4674.9	1	1045.2	90	5	K.VTNIGNQQIDK.V
*	HsFLAG-Control_HeLa_NE	4.1508	0.1812	1230.63	1230.36	4329.3	1	1027.1	90	12	K.VTNIGNQQIDK.V
*	HsFLAG-Control_293_Ti_1	4.8666	0.478	1908.16	1909.06	6667.6	1	1496.3	70.6	3	K.VFNNIGADLLTGSESENK.E
*	Hs293FLP-MG_Ti_203.267	4.3044	0.3734	2692.72	2693.88	8887.3	1	719.8	37.5	24	K.VFNNIGADLLTGSESENKEDGLQNK.H
*	HsFlag1P_Ti_102.2748.274	5.0897	0.3924	2692.74	2693.88	8641	1	985.8	43.8	4	K.VFNNIGADLLTGSESENKEDGLQNK.H
*	HsFLAG-Control_HeLa_S1	3.8716	0.392	2692.76	2693.88	8169	1	611.7	37.5	3	K.VFNNIGADLLTGSESENKEDGLQNK.H
*	HsFLAG-Control_HeLa_NE	4.3497	0.2556	2694.87	2693.88	4398.9	1	634.3	31.2	1	K.VFNNIGADLLTGSESENKEDGLQNK.H
*	HsFLAG-Control_HeLa_S1	3.7416	0.1581	2695.29	2693.88	3661.9	1	463	31.2	1	K.VFNNIGADLLTGSESENKEDGLQNK.H
*	HsFlag1P_Ti_106.2100.210	4.5819	0.1492	1414.4	1414.65	9689.4	1	1786.2	81.8	1	K.LAKEQEQAQKLK.S
*	HsFLAG-Control_293_Ti_1	3.4152	0.3815	1858.05	1859.18	5704.5	1	445.2	50	8	K.SQQPLKPQVHTPVATVK.Q
*	HsFLAG-Control_293_Ti_2	5.9749	0.4437	2357.58	2357.65	8798.3	1	1918.1	59.5	12	K.DLTDTLMDNMSSLTSLSVSTPK.S
*	HsFLAG-Control_293_Ti_2	3.265	0.3017	2294.94	2295.7	4233	1	446.4	43.2	1	K.MTLGTPPTLPNFNALSVPPAGAK.Q
gi|24307971|ref|N	69	330	0.498	464	54003	6.8	U	serine/threonine kinase 38 like [Homo sapiens]			
*	HsHeLa_Control_Ti_105.36	4.5352	0.3458	2119.73	2120.37	6657.8	1	1396.5	65.6	8	K.LTLENFYSNLILQHEER.E
*	HsHeLa_Control-MG_Ti_10	4.6058	0.4289	2120.26	2120.37	7104.2	1	1625.8	68.8	10	K.LTLENFYSNLILQHEER.E
*	HsHeLa_Control-MG_Ti_20	4.6795	0.2392	2120.48	2120.37	4735.5	1	797.4	43.8	3	K.LTLENFYSNLILQHEER.E
*	HsFLAG-Control_HeLa_NE	4.0023	0.1453	2120.7	2120.37	6494.2	1	1090.1	45.3	1	K.LTLENFYSNLILQHEER.E
*	Hs293FLP-MG_Ti_203.362	4.5047	0.4095	2120.76	2120.37	9482.2	1	1607.3	62.5	6	K.LTLENFYSNLILQHEER.E
*	Hs293FLP_Ti_303.3155.31	3.867	0.2941	2121.15	2120.37	4415.1	1	807.1	43.8	1	K.LTLENFYSNLILQHEER.E
*	Hs293FLP_Ti_303.3153.31	4.426	0.3666	2122.54	2120.37	6430.5	1	981.9	56.2	7	K.LTLENFYSNLILQHEER.E
*	HsF-IP-293-MG_Ti_105.16	4.5688	0.5195	1820.14	1821.01	9184.8	1	2557.6	80	4	K.KLEVAMEEEGLADEEK.K
*	HsFlag1P_Ti_104.2542.254	4.3493	0.3267	1393.89	1394.57	6858	1	1722.6	86.4	2	R.TRLGLDDFESLK.V
*	HsHeLa_Control-MG_Ti_20	2.2071	0.1872	1136.45	1137.28	5475.6	7	469.1	66.7	1	R.LGLDDFESLK.V
*	Hs283FLP_Ti_102.2387.23	2.6124	0.1468	1136.51	1137.28	6595.6	1	650	72.2	2	R.LGLDDFESLK.V
*	HsF-IP-293-MG_Ti_102.23	3.1966	0.1292	1137.45	1137.28	4745.1	4	1061.7	88.9	8	R.LGLDDFESLK.V
*	HsHeLa_Control-MG_Ti_20	3.5567	0.0911	1137.49	1137.28	6585	4	1135.6	88.9	2	R.LGLDDFESLK.V
*	HsFLAG-Control_HeLa_NE	3.3633	0.1906	1137.68	1137.28	6078.1	5	1197.1	88.9	10	R.LGLDDFESLK.V
	HsHeLa_Control-MG_Ti_10	2.3171	0.1532	1065.57	1066.22	6077.8	6	529.4	71.4	3	K.MFYSFQDK.R
*	HsFLAG-MOCK_300mM_T	3.5567	0.1127	3494	3491.88	8099.1	7	426	19	1	K.DTLTEEETQFYISETVLAIDAIHQLGFIHR.D
*	HsFLAG-Control_HeLa_NE	3.2661	0.2602	1355.56	1355.57	3733.2	1	534.5	77.3	15	R.DIKPDNLLLDAK.G
	HsFLAG-Control_293_Ti_2	2.6151	0.2965	1210.33	1211.37	5258.2	1	695.6	70	4	K.LSDFGLCTGLK.K
	HsFLAG-Control_HeLa_NE	2.5471	0.2723	1210.38	1211.37	5294.4	1	605	65	5	K.LSDFGLCTGLK.K
	HsHeLa_Control-MG_Ti_20	2.5733	0.2852	1210.38	1211.37	4203.2	1	377.7	55	2	K.LSDFGLCTGLK.K
	HsFLAG-Control_MG_293_	2.5821	0.3547	1210.39	1211.37	5238.7	1	636.4	65	4	K.LSDFGLCTGLK.K
	Hs293FLP_TREX_Ti_102.2	2.6622	0.2892	1210.4	1211.37	4466	1	478.7	60	2	K.LSDFGLCTGLK.K
	Hs293FLP-MG_Ti_202.251	2.3237	0.2827	1210.45	1211.37	4990	1	490.7	60	1	K.LSDFGLCTGLK.K
	HsFLAG-MOCK_300mM_T	2.6108	0.361	1210.47	1211.37	4601.5	1	551.2	65	3	K.LSDFGLCTGLK.K
	HsF-IP-293-MG_Ti_102.19	2.4689	0.2527	1210.49	1211.37	4535	1	547.2	65	2	K.LSDFGLCTGLK.K
	HsHeLa-FLAG-IP_S100_Ti_	1.8467	0.1459	1210.53	1211.37	4890.3	1	392	55	1	K.LSDFGLCTGLK.K
	Hs283FLP_Ti_102.2003.20	2.6768	0.2557	1210.55	1211.37	4679.7	1	568.8	65	2	K.LSDFGLCTGLK.K
	HsFLAG-Control_HeLa_NE	2.5274	0.3029	1210.58	1211.37	5048.5	1	631.1	70	2	K.LSDFGLCTGLK.K
	HsFLAG-Control_HeLa_S1	2.3076	0.2541	1210.58	1211.37	5353.8	2	480.4	60	2	K.LSDFGLCTGLK.K
	HsFLAG-Control_Hela_Ti_1	2.1004	0.2798	1210.61	1211.37	5239.4	4	310.3	50	2	K.LSDFGLCTGLK.K
	HsHeLa_Control_Ti_103.23	2.6092	0.2765	1210.62	1211.37	4162.2	1	422.2	60	2	K.LSDFGLCTGLK.K
	HsFLAG-MOCK_150mM_T	2.5559	0.2977	1210.63	1211.37	4371.3	1	557.2	65	2	K.LSDFGLCTGLK.K
	Hs293FLP_Ti_302.2103.21	2.4897	0.2237	1210.7	1211.37	4081.1	1	469.5	60	2	K.LSDFGLCTGLK.K

	HsHeLa_Control-MG_Ti_10	2.4806	0.2699	1210.72	1211.37	3999.7		1	436.9	60	2	K.LSDFGLCTGLK.K
	Hs293FLP-MG_Ti_102.243	2.2777	0.1812	1210.73	1211.37	4149.3		2	375.8	55	2	K.LSDFGLCTGLK.K
	HsFLAG-Control_293_Ti_2	4.0226	0.2724	1211.17	1211.37	6036.8		1	1564.9	90	3	K.LSDFGLCTGLK.K
	HsFLAG-Control_HeLa_NE	3.8264	0.3062	1211.23	1211.37	5545		2	1300	85	9	K.LSDFGLCTGLK.K
	HsFLAG-Control_HeLa_NE	3.9803	0.2422	1211.24	1211.37	6010.2		1	1532.1	90	6	K.LSDFGLCTGLK.K
	Hs293FLP_TREX_Ti_102.2	3.8489	0.3113	1211.25	1211.37	5383.6		1	1329.4	85	4	K.LSDFGLCTGLK.K
	HsFLAG-Control_HeLa_S1	4.022	0.2854	1211.26	1211.37	5874		2	1516.2	90	11	K.LSDFGLCTGLK.K
	HsHeLa-FLAG-IP_S100_Ti_	4.1443	0.3235	1211.29	1211.37	5663.3		1	1567.1	90	52	K.LSDFGLCTGLK.K
	HsF-IP-293-MG_Ti_102.19	3.8997	0.3475	1211.31	1211.37	5359.9		1	1521.9	90	4	K.LSDFGLCTGLK.K
	Hs293FLP-MG_Ti_202.252	4.1153	0.3165	1211.32	1211.37	6077.1		1	1604.4	90	1	K.LSDFGLCTGLK.K
	HsFLAG-Control_HeLa_NE	4.0494	0.2091	1211.32	1211.37	5901.1		1	1581.2	90	2	K.LSDFGLCTGLK.K
	HsFLAG-MOCK_150mM_T	3.9522	0.2989	1211.44	1211.37	5985.5		1	1555.7	90	2	K.LSDFGLCTGLK.K
	HsHeLa_Control-MG_Ti_20	3.9398	0.2841	1211.46	1211.37	7189.5		1	1564.6	85	2	K.LSDFGLCTGLK.K
	Hs283FLP_Ti_102.2001.20	4.0562	0.3185	1211.48	1211.37	5413.7		1	1513.2	90	2	K.LSDFGLCTGLK.K
	HsFlag1P_Ti_103.2474.247	2.3605	0.2426	1211.55	1211.37	5138.1		1	478.4	60	3	K.LSDFGLCTGLK.K
	HsHeLa_Control-MG_Ti_10	3.9558	0.3415	1211.65	1211.37	5209.5		1	1430.3	90	2	K.LSDFGLCTGLK.K
	HsHeLa_Control_Ti_103.23	3.7085	0.2509	1212.02	1211.37	5631.6		1	1225.4	85	2	K.LSDFGLCTGLK.K
	HsFlag1P_Ti_102.2452.245	3.9867	0.2505	1212.23	1211.37	5494		1	1425.2	90	6	K.LSDFGLCTGLK.K
	HsFLAG-MOCK_300mM_T	3.9448	0.2963	1212.46	1211.37	5598.4		1	1438.9	90	3	K.LSDFGLCTGLK.K
	HsFLAG-Control_MG_293_	3.8678	0.3049	1212.47	1211.37	6343.4		1	1641.9	90	5	K.LSDFGLCTGLK.K
	Hs293FLP-MG_Ti_102.242	3.5428	0.1193	1212.59	1211.37	5107.3		1	1225.1	85	3	K.LSDFGLCTGLK.K
	Hs293FLP_Ti_302.2102.21	3.8678	0.244	1212.73	1211.37	5175.9		1	1388.9	90	4	K.LSDFGLCTGLK.K
	HsFLAG-MOCK_300mM_T	2.772	0.2874	1338.65	1339.54	5388.3		1	426.2	59.1	1	K.LSDFGLCTGLKK.A
	HsFlag1P_Ti_106.2458.245	2.8721	0.312	1338.78	1339.54	5464		1	449.3	59.1	1	K.LSDFGLCTGLKK.A
	HsFlag1P_Ti_106.2456.245	3.7584	0.3281	1339.14	1339.54	6523.9		1	1077.5	81.8	6	K.LSDFGLCTGLKK.A
	HsFLAG-MOCK_300mM_T	3.1443	0.2011	1339.66	1339.54	6422.2		1	903.1	77.3	7	K.LSDFGLCTGLKK.A
	HsFlag1P_Ti_106.2201.220	3.0143	0.24	1079.47	1080.19	7686.1		3	798.5	78.6	1	K.AHRTEFYR.N
*	HsF-IP-293-MG_Ti_106.214	4.7908	0.5162	2078.48	2079.25	3977.5		1	741.4	64.7	17	R.NLTHNPPSDFSFQNMNSK.R
*	HsF-IP-293-MG_Ti_102.237	2.8437	0.2186	1585.45	1585.84	3317.3		1	453.4	61.5	2	K.ETLVFPPEVPISEK.A
*	HsFLAG-MOCK_300mM_T	3.5404	0.2999	1046.31	1046.17	7664.1		2	1246.9	83.3	9	R.IGNSGVEEIK.G
*	HsHeLa_Control-MG_Ti_20	4.8318	0.2766	2756.02	2754.03	11037.6		1	1437.1	32.6	3	R.IGNSGVEEIKGHPFFEGVDWEHIR.E
*	HsHeLa_Control-MG_Ti_20	4.8305	0.4663	1726.45	1726.89	4941.5		1	899.9	73.1	5	K.GHPFFEGVDWEHIR.E
*	HsFLAG-Control_HeLa_NE	3.4702	0.221	1237.41	1237.49	6128.6		1	1005.8	80	13	R.ERPAAIPIEIK.S
*	HsFLAG-Control_HeLa_NE	4.6684	0.1504	3301.48	3301.46	7496.8		2	533	24.1	6	K.SIDDTSNFDDFPESDILQPVPNTTEPDYK.S
*	HsFlag1P_Ti_106.2704.270	4.3558	0.3136	1564.46	1564.78	5857.8		1	1325.4	81.8	5	K.SKDWVFLNYTYK.R
*	Hs293FLP-MG_Ti_205.151	3.0237	0.0912	1007.01	1007.14	7222.4		1	1414.3	100	2	K.RFEGLTQR.G
gi|20127479|ref|N	101	380	0.496	930	103533	6	U	RNA binding motif protein 10 isoform 1 [Homo sapiens]				
	HsFlag1P_Ti_106.2224.222	2.5407	0.2286	1630.04	1629.7	7053.6		4	440.5	59.1	1	R.SRDHDYRDMDYR.S
*	HsHeLa_Control-MG_Ti_10	5.4866	0.4749	3799.26	3799.69	8647.1		1	777.1	22.7	2	R.EYGSQEGKHDYDDSSEEQSAEDSYEASPGSETQR.R
*	HsHeLa_Control_Ti_102.15	5.2572	0.4648	2920.44	2920.8	6919		1	1367.5	50	2	K.HDYDDSSEEQSAEDSYEASPGSETQR.R
*	HsHeLa_Control_Ti_102.13	3.6239	0.0891	2904.02	2904.75	5289.3		1	578.1	45.5	1	R.DQDYRTEQGEEEEEEEDEEEEEK.A
*	Hs283FLP_Ti_102.1363.13	4.3744	0.2995	2904.23	2904.75	8935.9		1	1686.4	36.4	1	R.DQDYRTEQGEEEEEEEDEEEEEK.A
*	HsHeLa_Control-MG_Ti_10	4.4496	0.1763	2904.4	2904.75	5703.6		1	806.1	50	1	R.DQDYRTEQGEEEEEEEDEEEEEK.A
*	Hs293FLP_Ti_302.1375.13	3.7909	0.1445	2904.85	2904.75	6122.9		1	796.4	47.7	1	R.DQDYRTEQGEEEEEEEDEEEEEK.A
*	HsHeLa_Control_Ti_102.14	5.7004	0.3293	2905.24	2904.75	8060.5		1	2058.5	40.9	1	R.DQDYRTEQGEEEEEEEDEEEEEK.A
*	Hs293FLP-MG_Ti_201.040	5.7663	0.3236	2226.88	2227.08	9662.6		1	2252.8	67.6	11	R.TEQGEEEEEEEDEEEEEK.A
	Hs293FLP_Ti_305.1079.10	2.0714	0.0834	1180.5	1181.3	4592		9	300.7	60	1	R.GQLQSHGVQAR.E
	Hs293FLP-MG_Ti_205.125	3.6294	0.3232	1180.54	1181.3	8588.5		1	1165.7	75	8	R.GQLQSHGVQAR.E

HsHeLa_Control-MG_Ti_10	2.1742	0.0972	1180.87	1181.3	4327.4	5	317.3	60	1	R.GQLQSHGVQAR.E
Hs293FLP_TREX_Ti_105.1	3.6954	0.3178	1181.18	1181.3	6944	1	1068.5	75	19	R.GQLQSHGVQAR.E
HsFLAG-Control_MG_293_	3.6442	0.3241	1181.36	1181.3	6267.1	1	1113.3	85	2	R.GQLQSHGVQAR.E
HsFLAG-Control_MG_293_	2.4	0.155	1181.45	1181.3	5409.5	6	363.8	60	1	R.GQLQSHGVQAR.E
HsFLAG-Control_Hela_Ti_1	3.7211	0.2977	1182.21	1181.3	7236.5	1	1331.3	85	5	R.GQLQSHGVQAR.E
HsFLAG-Control_HeLa_NE	4.4983	0.428	1725.08	1725.9	9222	1	1748.1	71.4	6	R.GFAFVEFSHLQDATR.W
HsHeLa_Control-MG_Ti_20	5.1413	0.5023	1725.1	1725.9	7337.8	1	1979.5	82.1	5	R.GFAFVEFSHLQDATR.W
HsHeLa_Control-MG_Ti_20	3.5406	0.2981	1726.86	1725.9	5898.5	1	1256.7	48.2	1	R.GFAFVEFSHLQDATR.W
HsHeLa_Control-MG_Ti_10	3.7665	0.3034	1727.27	1725.9	5166.5	1	1323.2	50	1	R.GFAFVEFSHLQDATR.W
HsHeLa_Control_Ti_104.33	3.5384	0.185	1727.47	1725.9	5135.4	1	1320	50	1	R.GFAFVEFSHLQDATR.W
HsHeLa_Control_Ti_104.33	4.4451	0.446	1727.77	1725.9	5795.7	1	1557.3	78.6	5	R.GFAFVEFSHLQDATR.W
Hs293FLP_Ti_304.2631.26	4.6098	0.3769	1727.85	1725.9	6756.5	1	2053	82.1	14	R.GFAFVEFSHLQDATR.W
HsFlag1P_Ti_106.2548.254	5.4069	0.4044	1770.27	1770.02	9851.6	1	2367.9	78.6	9	R.WMEANQHSLNILGQK.V
HsFLAG-MOCK_300mM_T	2.2163	0.2357	1288.63	1289.49	3618.1	3	353.9	65	1	K.VSMHYSDPKPK.I
HsFlag1P_Ti_102.2178.217	2.5288	0.1476	1191.29	1192.28	6235.8	1	522.5	68.8	2	K.INEDWLCNK.C
HsHeLa_Control-MG_Ti_10	2.5844	0.2116	1191.58	1192.28	5788.1	5	514.7	68.8	2	K.INEDWLCNK.C
Hs293FLP-MG_Ti_102.206	2.5039	0.2577	1191.66	1192.28	6146.3	4	447.5	62.5	1	K.INEDWLCNK.C
HsHeLa_Control-MG_Ti_10	3.3874	0.219	1192.72	1192.28	6003.4	1	1106.1	87.5	4	K.INEDWLCNK.C
HsFLAG-Control_HeLa_NE	3.3236	0.2222	1193.33	1192.28	8126.2	1	1244.4	87.5	1	K.INEDWLCNK.C
HsHeLa_Control-MG_Ti_10	4.0826	0.1948	1329.89	1329.5	4900.3	3	1121.7	77.3	4	K.SEAEQKLPLGTR.L
HsHeLa_Control-MG_Ti_20	4.268	0.2497	1198.4	1198.37	5439.1	1	1362.7	95	11	R.LDQQTLPLGGR.E
Hs293FLP-MG_Ti_202.410	3.9939	0.3174	4422.41	4422.89	6400.9	1	450.6	18.3	2	R.ELSQGLLPLPQPYQAQGVLASQALSQGSEPSSENANDTIILR.N
HsHeLa_Control-MG_Ti_20	4.744	0.4219	2827.69	2829.2	7040	1	1139.3	46.2	2	R.NLNPHSTMDSILGALAPYAVLSSSNVR.V
Hs293FLP-MG_Ti_205.408	4.6483	0.241	2827.95	2829.2	7557.1	1	1217.4	32.7	2	R.NLNPHSTMDSILGALAPYAVLSSSNVR.V
HsHeLa_Control-MG_Ti_20	4.3762	0.3177	2828.64	2829.2	9567.3	1	1478.4	31.7	2	R.NLNPHSTMDSILGALAPYAVLSSSNVR.V
Hs293FLP-MG_Ti_205.407	4.4509	0.338	2828.76	2829.2	6829.3	1	1296.6	48.1	1	R.NLNPHSTMDSILGALAPYAVLSSSNVR.V
HsHeLa_Control-MG_Ti_10	3.6661	0.3442	2829.29	2829.2	5739.5	1	766.7	40.4	2	R.NLNPHSTMDSILGALAPYAVLSSSNVR.V
Hs293FLP_Ti_306.3446.34	3.9379	0.2906	2829.35	2829.2	5898.9	1	721.8	40.4	2	R.NLNPHSTMDSILGALAPYAVLSSSNVR.V
HsHeLa_Control-MG_Ti_10	4.3703	0.1372	2829.81	2829.2	6719	1	1090.2	30.8	1	R.NLNPHSTMDSILGALAPYAVLSSSNVR.V
Hs293FLP_Ti_305.3753.37	4.3448	0.2356	2830	2829.2	6641.3	4	744.9	28.8	2	R.NLNPHSTMDSILGALAPYAVLSSSNVR.V
HsHeLa_Control-MG_Ti_20	2.2886	0.2035	921.4	922.069	5470.9	9	408.5	71.4	7	K.TINVEFAK.G
Hs293FLP-MG_Ti_202.201	2.7263	0.1106	922.33	922.069	2462.9	3	513.4	85.7	1	K.TINVEFAK.G
Hs293FLP-MG_Ti_205.217	4.5107	0.2996	3533.36	3533.85	6108.9	2	464.7	21.5	1	K.GTKGPGITGTKGDPTGAGPEASLEPGADSVSMQAFSR.A
HsF-IP-293-MG_Ti_102.21	5.6979	0.3628	2534.89	2535.7	4435.1	1	791.4	52	15	K.GDPTGAGPEASLEPGADSVSMQAFSR.A
HsFlag1P_Ti_105.2566.256	8.1089	0.5995	3768.76	3770.12	8722.1	1	2327.2	33.1	27	R.AQPGAAPGIYQQSAEASSSQGTAANSQSYTIMSPAVLK.S
Hs293FLP-MG_Ti_103.160	2.3072	0.2638	1515.64	1516.65	4750.8	1	419.4	61.5	2	R.TYVPALEQSADGHK.E
Hs293FLP_TREX_Ti_103.1	3.631	0.3802	1516.44	1516.65	4525.3	1	903.2	80.8	4	R.TYVPALEQSADGHK.E
Hs293FLP-MG_Ti_203.168	2.3773	0.2259	1516.6	1516.65	5973.5	1	317.8	50	2	R.TYVPALEQSADGHK.E
Hs283FLP_Ti_103.1435.14	2.5233	0.2224	1516.62	1516.65	4188.9	1	464.4	65.4	1	R.TYVPALEQSADGHK.E
HsHeLa_Control-MG_Ti_20	4.0518	0.3786	1517.43	1516.65	4765	1	782.5	73.1	6	R.TYVPALEQSADGHK.E
Hs293FLP-MG_Ti_203.168	3.4167	0.2487	1517.45	1516.65	4200	1	546.1	65.4	2	R.TYVPALEQSADGHK.E
Hs293FLP-MG_Ti_103.159	3.3858	0.3642	1517.82	1516.65	4231.1	1	747	76.9	2	R.TYVPALEQSADGHK.E
HsHeLa_Control-MG_Ti_10	4.4337	0.4303	2186.84	2187.37	6324.5	1	968.6	57.5	3	R.TYVPALEQSADGHKETGAPSK.E
Hs293FLP-MG_Ti_203.199	2.0984	0.1654	1148.47	1149.29	2716.5	2	191.1	72.2	1	K.NSFQPISSLR.D
HsF-IP-293-MG_Ti_103.168	2.365	0.2641	1148.48	1149.29	2091.8	2	135.1	72.2	1	K.NSFQPISSLR.D
Hs283FLP_Ti_103.1627.16	2.9629	0.2357	1149.47	1149.29	4091.4	3	674.4	83.3	3	K.NSFQPISSLR.D

Hs293FLP-MG_Ti_203.199	2.7046	0.1925	1149.5	1149.29	4283.9		2	665.6	83.3	1	K.NSFQPISSLR.D
HsF-IP-293-MG_Ti_103.16	2.6274	0.166	1149.51	1149.29	3712.3		6	532.3	77.8	1	K.NSFQPISSLR.D
Hs283FLP_Ti_102.1766.17	2.3318	0.2714	1438.55	1439.56	2791.5		1	271.1	57.7	1	R.ESATADAGYAILEK.K
HsHeLa_Control-MG_Ti_10	2.316	0.3256	1438.7	1439.56	3518		1	413.2	65.4	1	R.ESATADAGYAILEK.K
Hs293FLP-MG_Ti_102.207	2.4671	0.2685	1438.74	1439.56	3187.7		1	338.2	61.5	2	R.ESATADAGYAILEK.K
HsFLAG-Control_HeLa_NE	4.2382	0.3887	1438.91	1439.56	7071.8		1	2220.1	84.6	14	R.ESATADAGYAILEK.K
HsF-IP-293-MG_Ti_102.17	4.35	0.3192	1439.56	1439.56	6814.5		1	2014.1	84.6	8	R.ESATADAGYAILEK.K
HsHeLa_Control-MG_Ti_10	4.2312	0.3601	1439.78	1439.56	6549.5		1	1890.2	84.6	6	R.ESATADAGYAILEK.K
Hs293FLP-MG_Ti_202.021	4.0079	0.3795	1441.63	1439.56	6912.8		1	1504	73.1	8	R.ESATADAGYAILEK.K
HsHeLa_Control-MG_Ti_10	2.5786	0.0966	1214.14	1211.32	5412.3		2	491.2	70	1	K.LASDDRPSPPR.G
HsF-IP-293-MG_Ti_106.18	2.4745	0.1137	1047.51	1048.19	4077		1	391.5	75	1	R.HQQLSGLHK.Q
HsHeLa_Control-MG_Ti_10	2.4092	0.1628	1047.79	1048.19	4590		2	384.7	68.8	1	R.HQQLSGLHK.Q
HsFLAG-Control_HeLa_NE	3.11	0.0924	1048.24	1048.19	6182.4		2	842.8	81.2	1	R.HQQLSGLHK.Q
HsHeLa_Control-MG_Ti_10	3.0269	0.0993	1048.83	1048.19	5767		1	830	87.5	2	R.HQQLSGLHK.Q
Hs293FLP-MG_Ti_205.181	4.0299	0.2007	1639.64	1639.81	9684.4		1	1669.7	73.1	5	R.RAHLSENELEALEK.N
HsHeLa_Control-MG_Ti_20	2.7825	0.2137	1482.46	1483.62	4364.5		1	524.8	58.3	2	R.AHLSENELEALEK.N
Hs293FLP-MG_Ti_203.192	3.0185	0.184	1482.55	1483.62	6558.5		1	832.2	62.5	2	R.AHLSENELEALEK.N
Hs293FLP_Ti_303.1679.16	3.2309	0.2489	1482.74	1483.62	4590.3		1	575.5	58.3	1	R.AHLSENELEALEK.N
HsHeLa_Control-MG_Ti_20	4.5638	0.392	1482.83	1483.62	5983		1	1394.1	87.5	1	R.AHLSENELEALEK.N
HsFLAG-Control_HeLa_NE	4.4097	0.3893	1482.85	1483.62	5190.9		1	1433.6	87.5	10	R.AHLSENELEALEK.N
HsF-IP-293-MG_Ti_104.16	4.1295	0.3485	1483.29	1483.62	5072.4		1	1215.8	83.3	13	R.AHLSENELEALEK.N
Hs293FLP-MG_Ti_203.191	4.5868	0.4135	1483.59	1483.62	5865.6		1	1531.2	87.5	2	R.AHLSENELEALEK.N
Hs283FLP_Ti_104.1561.15	3.0485	0.1979	1483.62	1483.62	5321.1		1	794.7	66.7	1	R.AHLSENELEALEK.N
Hs283FLP_Ti_104.1553.15	3.1976	0.1039	1484.25	1483.62	5841		1	1053.8	83.3	1	R.AHLSENELEALEK.N
HsHeLa_Control-MG_Ti_20	1.8126	0.082	1126.5	1127.28	3899.3		7	331.7	55.6	1	K.YGIPEPPEPK.R
HsHeLa_Control-MG_Ti_10	5.1422	0.4216	1858.36	1857.03	5259.6		1	2001.7	78.1	5	R.KYGGISTASVDFEQPTR.D
HsFlag1P_Ti_105.2252.225	3.8658	0.2669	2928.17	2929.13	7617.4		1	979	30.6	1	R.KYGGISTASVDFEQPTRDGLGSDNIGSR.M
HsHeLa_Control-MG_Ti_20	4.949	0.4651	1729.63	1728.86	7850.2		1	1414.2	66.7	18	K.YGGISTASVDFEQPTR.D
HsHeLa_Control-MG_Ti_10	3.6549	0.302	1091.59	1091.12	4011.7		1	771.8	80	8	R.DGLGSDNIGSR.M
HsFlag1P_Ti_106.2481.248	1.9421	0.1137	964.4	965.217	6583.3		9	683.2	78.6	1	R.MLQAMGWK.E
HsHeLa_Control-MG_Ti_20	3.5071	0.2445	1441.52	1441.67	7138.2		2	922.8	66.7	5	K.KQGIVTPIEAQTR.V
HsFlag1P_Ti_104.1989.198	2.9007	0.1916	1312.69	1313.5	4627.4		1	905.9	86.4	5	K.QGIVTPIEAQTR.V
HsFLAG-Control_HeLa_NE	2.3634	0.3301	1365.35	1366.42	6452.2		1	485.8	58.3	1	R.GSSYGVTSTESYK.E
HsFLAG-Control_Hela_Ti_1	1.9639	0.2699	1365.46	1366.42	5462.4		1	384.5	54.2	1	R.GSSYGVTSTESYK.E
HsF-IP-293-MG_Ti_102.13	2.4856	0.1599	1365.47	1366.42	5114.6		7	231.4	45.8	1	R.GSSYGVTSTESYK.E
Hs283FLP_Ti_102.1346.13	2.5386	0.2461	1365.55	1366.42	4936.9		1	367.9	54.2	1	R.GSSYGVTSTESYK.E
HsHeLa_Control_Ti_102.13	2.2511	0.1992	1365.6	1366.42	5313.6		1	413.7	54.2	1	R.GSSYGVTSTESYK.E
HsHeLa_Control-MG_Ti_20	3.5419	0.3333	1366.19	1366.42	6111.3		1	1364.2	79.2	8	R.GSSYGVTSTESYK.E
HsF-IP-293-MG_Ti_102.13	3.6824	0.3676	1366.37	1366.42	4805.4		1	1076.5	79.2	6	R.GSSYGVTSTESYK.E
HsFLAG-Control_Hela_Ti_1	2.8624	0.2878	1366.45	1366.42	6229.7		1	878.7	66.7	2	R.GSSYGVTSTESYK.E
Hs293FLP_TREX_Ti_102.1	2.8776	0.2978	1366.45	1366.42	5552.4		1	747.8	66.7	1	R.GSSYGVTSTESYK.E
HsHelaFlag1P_Ti_102.134	2.5134	0.3016	1367.41	1366.42	3939.1		2	358.8	50	2	R.GSSYGVTSTESYK.E
HsHeLa_Control_Ti_102.13	2.8562	0.29	1368.53	1366.42	4229.4		1	562.3	62.5	2	R.GSSYGVTSTESYK.E
HsFlag1P_Ti_105.1812.181	4.2098	0.5065	1974.1	1975.12	7301.3		1	778.5	50	4	R.GSSYGVTSTESYKETLHK.T
gi|21626466|ref|	50	189	0.492	847	94623	6.3 U		matrin 3 [Homo sapiens]			
gi|62750354|ref|	50	189	0.492	847	94623	6.3 U		matrin 3 [Homo sapiens]			
HsFLAG-Control_HeLa_NE	2.7045	0.1913	1040.27	1040.12	6703.4		2	1063.3	87.5	4	K.SFQQSSLSR.D
HsHeLa3_Ti_103.4678.467	2.7763	0.2188	2372.97	2372.74	8352.7		1	431.7	33.3	1	R.DLSAAGIGLLAAATQSLSMPASLGR.M
HsHeLa3_Ti_103.4659.465	5.4666	0.4164	2373.68	2372.74	6627.4		1	1162.6	35.4	2	R.DLSAAGIGLLAAATQSLSMPASLGR.M

HsFLAG-MOCK_300mM_T	4.9348	0.3569	4205.54	4206.65	6896.5	1	764.4	22.5	2	R.LASLMNLGMSSSLNQQGAHSALSSASTSSHNLQSIFNIGSR.G
HsFLAG-Control_HeLa_NE	3.1146	0.2376	1092.91	1092.24	4479.7	1	586.4	77.8	4	R.GPLPLSSQHR.G
HsFLAG-MOCK_300mM_T	5.8236	0.3016	2870	2867.15	8033	1	1978.6	36.1	3	R.GPLPLSSQHRGDADQASNILASFGLSAR.D
HsFLAG-Control_HeLa_NE	5.9665	0.414	1794.59	1793.93	7621.5	1	1856.5	70.6	18	R.GDADQASNILASFGLSAR.D
HsFLAG-Control_HeLa_NE	4.2488	0.2124	1481.01	1480.57	8784.5	1	1375.1	77.3	3	R.DLDELSRYPEDK.I
HsFLAG-Control_HeLa_NE	4.4869	0.1992	3081.59	3082.52	7448.9	1	881	29	3	R.DLDELSRYPEDKITPENLPQILLQLK.R
HsFLAG-Control_HeLa_NE	3.1688	0.1607	1620.43	1620.97	4256.1	1	564.5	69.2	10	K.ITPENLPQILLQLK.R
HsFLAG-Control_HeLa_NE	3.254	0.1807	1366.07	1366.47	7409.3	1	834.5	68.2	1	R.RTEEGPTLSYGR.D
HsFLAG-Control_HeLa_NE	3.5052	0.2862	1210.28	1210.29	6300.8	1	1674.3	90	12	R.TEEGPTLSYGR.D
HsFLAG-Control_HeLa_NE	4.7108	0.2587	2363.46	2363.46	7509.9	1	1480.2	43.8	2	R.DSFDDRGPSLNPVLDYDHGSR.S
HsFLAG-Control_HeLa_NE	3.8331	0.3735	1627.69	1627.75	4710.9	1	643.8	64.3	4	R.GPSLNPVLDYDHGSR.S
HsFLAG-MOCK_300mM_T	4.2044	0.3972	2929.02	2927.98	5947.3	1	582.1	29.5	1	R.CRDDSFFGETSHNYHKFDSEYER.M
HsFLAG-MOCK_300mM_T	3.197	0.2557	1198.75	1198.39	5476.3	1	810.9	75	2	R.MGRGPGPLQER.S
HsHeLa3_Ti_106.2202.220	5.239	0.4421	1998.13	1998.18	8477.2	1	1847.9	68.8	5	K.GYPHLCSICDLPVHSNK.E
HsHeLa3_Ti_106.1926.192	3.2418	0.4125	1509.68	1509.58	5716.3	1	728.5	70.8	2	K.EWSQHINGASHSR.R
HsFLAG-Control_HeLa_NE	2.1549	0.1797	1324.73	1325.43	3828.8	7	144.7	46.2	1	R.GNLGAGNGNLQGPR.H
HsFLAG-Control_HeLa_NE	3.2401	0.3705	1324.91	1325.43	9351.1	1	1091.2	65.4	4	R.GNLGAGNGNLQGPR.H
HsFLAG-Control_HeLa_NE	3.3749	0.4203	1325.26	1325.43	9941.4	1	1568.3	73.1	3	R.GNLGAGNGNLQGPR.H
HsFLAG-MOCK_300mM_T	1.8975	0.1429	1144.68	1145.37	4957.8	1	500.4	62.5	1	R.VVHIMDFQR.G
HsHeLa3_Ti_106.2188.218	2.5793	0.3219	1145.87	1145.37	4264	2	924.9	87.5	2	R.VVHIMDFQR.G
HsFLAG-Control_HeLa_NE	5.1828	0.3867	2438.84	2439.9	5033.7	1	651.6	52.5	4	R.YQLLQLVEPFGVISNHLILNK.I
HsHeLa3_Ti_106.3174.317	4.7847	0.3334	2439.53	2439.9	4434.5	1	725.3	57.5	2	R.YQLLQLVEPFGVISNHLILNK.I
HsFLAG-Control_HeLa_NE	4.8382	0.3174	2440.38	2439.9	6700.3	1	755.6	32.5	2	R.YQLLQLVEPFGVISNHLILNK.I
HsFLAG-MOCK_300mM_T	4.4277	0.3504	2440.97	2439.9	3716.4	1	645.2	60	2	R.YQLLQLVEPFGVISNHLILNK.I
HsFLAG-MOCK_300mM_T	4.1433	0.2313	2441.37	2439.9	5767.5	1	775.3	36.2	3	R.YQLLQLVEPFGVISNHLILNK.I
HsHeLa3_Ti_106.3175.317	4.2146	0.2672	2442.35	2439.9	5570.8	1	772.9	35	1	R.YQLLQLVEPFGVISNHLILNK.I
HsFLAG-Control_HeLa_NE	4.8231	0.3059	2037.7	2038.31	5095.3	1	800.4	61.1	4	R.VIHLSNLPHSGYSDSAVLK.L
HsGST-MOCK_Ti_104.163	3.6396	0.3401	2037.8	2038.31	6117.7	1	1123.1	41.7	1	R.VIHLSNLPHSGYSDSAVLK.L
HsHeLa3_Ti_106.2174.217	5.1147	0.3317	2038.05	2038.31	4735.7	1	1143.4	69.4	2	R.VIHLSNLPHSGYSDSAVLK.L
HsFLAG-Control_HeLa_NE	3.852	0.2592	2038.29	2038.31	7449.1	1	711.6	33.3	2	R.VIHLSNLPHSGYSDSAVLK.L
HsFLAG-MOCK_300mM_T	5.465	0.351	2039.39	2038.31	4801.2	1	1077.5	69.4	6	R.VIHLSNLPHSGYSDSAVLK.L
HsHeLa3_Ti_106.2191.219	3.5847	0.2824	2039.59	2038.31	5497.2	1	656	36.1	1	R.VIHLSNLPHSGYSDSAVLK.L
HsFLAG-MOCK_300mM_T	3.4657	0.301	2442.39	2442.55	5794.6	1	408.4	42.9	1	K.KSKTDGSQKTESSTEGKEQEEK.S
HsFLAG-Control_HeLa_NE	4.2771	0.3663	1916.76	1916.05	9544.1	2	1222.9	56.2	8	K.IEELDQENEAALENGIK.N
HsFLAG-Control_HeLa_NE	4.7778	0.3404	4044.26	4045.1	6046.5	1	806.9	26.4	2	K.IEELDQENEAALENGIKNEENTEPGAESSENADDPNK.D
HsHeLa3_Ti_102.0813.081	3.8301	0.2046	2148.3	2148.07	3355	1	458.7	55.3	3	K.NEENTEPGAESSENADDPNK.D
HsGST-MOCK_Ti_402.208	4.1158	0.4151	2777.9	2778.73	9302.9	1	1244	47.8	1	K.DTSENADGQSDENKDDYTIPDEYR.I
HsFLAG-Control_HeLa_NE	3.7166	0.2737	2778.37	2778.73	6765	1	764	30.4	1	K.DTSENADGQSDENKDDYTIPDEYR.I
HsFlag1P_Ti_106.2761.276	4.2086	0.3428	1969.83	1970.32	4303.6	1	637.3	58.8	18	R.IGPYQPNVPVGIDYVIPK.T
HsFLAG-Control_HeLa_NE	4.4376	0.3049	1970.24	1970.32	6972.6	1	1693.7	47.1	1	R.IGPYQPNVPVGIDYVIPK.T
HsFLAG-Control_HeLa_NE	4.6731	0.3271	1972.03	1970.32	4294.9	1	819.2	64.7	22	R.IGPYQPNVPVGIDYVIPK.T
HsHeLa3_Ti_103.2062.206	3.2572	0.3673	1574.56	1574.74	6239.6	1	433.7	54.2	3	K.LCSLFYTNEEVAK.N
HsFLAG-Control_HeLa_NE	3.0936	0.0991	1574.64	1574.74	5894.8	1	611.4	62.5	2	K.LCSLFYTNEEVAK.N
HsGST-MOCK_Ti_105.123	3.0794	0.3567	1472.43	1472.57	6396.3	1	611.5	63.6	4	K.NTHCSSLPHYQK.L
HsHeLa3_Ti_106.1922.192	3.1028	0.4483	1472.63	1472.57	6470.9	1	1046.4	77.3	1	K.NTHCSSLPHYQK.L
HsFLAG-MOCK_300mM_T	3.1818	0.32	1472.63	1472.57	5075.7	1	497.4	68.2	1	K.NTHCSSLPHYQK.L
HsFLAG-MOCK_300mM_T	3.303	0.3136	1715.05	1713.9	5624.7	1	768.2	65.4	1	K.NTHCSSLPHYQKLK.K

gi|74136883|ref|N	80	431	0.49	825	90585	6	U	heterogeneous nuclear ribonucleoprotein U isoform a [Homo sapiens]				
	HsHeLa_Control-MG_Ti_10	3.3075	0.1768	1075.64	1075.25	5672.7		8	1041.8	87.5	5	K.VSELKEELK.K
	Hs293FLP-MG_Ti_204.137	3.4889	0.1285	1204.81	1203.42	8856		2	1642.3	88.9	10	K.VSELKEELKK.R
	HsF-IP-293-MG_Ti_105.178	4.4598	0.3869	3127.32	3128.31	6481		1	1022.5	29.8	5	R.LQAALDDEEAGGRPAMEPGNGSLDLGGDSAGR.S
	HsFLAG-Control_HeLa_NE	3.7425	0.3796	1716.91	1715.95	5707.3		1	782.8	52.9	25	K.SSGPTSLFAVTVAPPGAR.Q
*	HsHeLa_Control-MG_Ti_20	4.2753	0.3828	1667.43	1667.78	4910.5		1	629.8	57.9	2	K.KAEGGGGGGRPGAPAAGDGK.T
*	HsHeLa_Control-MG_Ti_10	3.9062	0.3406	2153.67	2154.3	4711.3		1	466.3	45.7	2	K.KAEGGGGGGRPGAPAAGDGKTEQK.G
*	HsHeLa_Control-MG_Ti_10	3.3363	0.3618	2025.77	2026.13	4687.9		2	333.4	38.6	2	K.AEGGGGGGRPGAPAAGDGKTEQK.G
	Hs293FLP_TREX_Ti_102.1	2.8767	0.2358	1291.35	1292.39	6870.2		2	645.9	66.7	2	R.GYFEYIEENK.Y
	Hs293FLP-MG_Ti_202.246	3.04	0.1985	1291.43	1292.39	11084.1		9	768.7	61.1	1	R.GYFEYIEENK.Y
	Hs293FLP-MG_Ti_102.236	2.5721	0.3291	1291.43	1292.39	7214.4		9	457.2	55.6	2	R.GYFEYIEENK.Y
	HsHeLa_Control-MG_Ti_20	2.749	0.1121	1291.44	1292.39	7730.2		4	713.8	66.7	2	R.GYFEYIEENK.Y
	Hs283FLP_Ti_102.1985.19	3.1821	0.2169	1291.48	1292.39	6858.4		6	567.6	66.7	2	R.GYFEYIEENK.Y
	HsHeLa_Control_Ti_102.21	3.0385	0.2029	1291.55	1292.39	7051.6		2	631.3	66.7	1	R.GYFEYIEENK.Y
	HsHeLa_Control-MG_Ti_10	2.9665	0.3189	1291.57	1292.39	5600.2		8	406.3	61.1	2	R.GYFEYIEENK.Y
	HsHeLa3_Ti_103.2074.207	2.7078	0.1868	1291.6	1292.39	6982.5		8	537.7	61.1	1	R.GYFEYIEENK.Y
	Hs293FLP_Ti_302.2063.20	3.0591	0.2034	1291.63	1292.39	6423.6		4	564	66.7	2	R.GYFEYIEENK.Y
	Hs293FLP_TREX_Ti_102.1	4.127	0.3764	1291.84	1292.39	7930.9		1	1378.8	83.3	4	R.GYFEYIEENK.Y
	HsF-IP-293_Ti_102.1815.18	3.9319	0.3396	1292.11	1292.39	8835.8		1	1491	83.3	4	R.GYFEYIEENK.Y
	Hs293FLP-MG_Ti_202.246	4.216	0.3211	1292.4	1292.39	7891.5		1	1276.2	83.3	1	R.GYFEYIEENK.Y
	HsHeLa_Control_Ti_102.21	4.119	0.3647	1292.41	1292.39	7406.4		1	1411.9	83.3	3	R.GYFEYIEENK.Y
	Hs293FLP-MG_Ti_102.236	4.2724	0.2835	1292.59	1292.39	7393.2		1	1321.7	83.3	3	R.GYFEYIEENK.Y
	HsF-IP-293-MG_Ti_102.195	4.1818	0.3727	1293.23	1292.39	7184.8		1	1355	83.3	5	R.GYFEYIEENK.Y
	HsHeLa3_Ti_102.2177.217	3.7851	0.3449	1293.45	1292.39	7620.7		1	1359.3	83.3	1	R.GYFEYIEENK.Y
	HsHeLa_Control-MG_Ti_10	4.1738	0.3325	1293.82	1292.39	7642.6		1	1411	83.3	3	R.GYFEYIEENK.Y
	Hs283FLP_Ti_102.1978.19	4.2509	0.3298	1294.07	1292.39	7551.1		1	1363.6	83.3	3	R.GYFEYIEENK.Y
	Hs293FLP-MG_Ti_205.214	2.8502	0.2793	1698.44	1698.83	10672.4		1	1051.1	66.7	1	R.GYFEYIEENKYSR.A
	Hs293FLP-MG_Ti_204.294	5.4064	0.388	3639.06	3637.78	6667		1	756.2	28.4	23	K.SPQPPVEEEDEHFDDTVVCLDTYNCDLHFK.I
	HsHeLa3_Ti_106.3246.324	4.9886	0.3563	2033.7	2032.32	9191.6		1	2219.1	63.9	3	R.LSASSLTMESFAFLWAGGR.A
	Hs293FLP-MG_Ti_202.181	1.9633	0.1137	996.52	997.096	3370.9		9	362.7	71.4	1	K.DIDIHEVR.I
	Hs293FLP-MG_Ti_103.151	2.9258	0.0852	997.58	997.096	5546.9		3	943.1	85.7	2	K.DIDIHEVR.I
	HsHeLa_Control-MG_Ti_20	6.4821	0.486	4331.3	4331.41	11204.4		1	1389.6	26.4	16	K.TCNCETEDYGEKFDENDVITCFANFESDEVELSYAK.N
	Hs293FLP-MG_Ti_205.405	4.5498	0.4245	2843.75	2843.98	9317.3		1	834.6	30.4	1	K.FDENDVITCFANFESDEVELSYAK.N
	HsHeLa_Control-MG_Ti_20	4.8945	0.3959	2844.27	2843.98	10254.7		1	1234	45.7	24	K.FDENDVITCFANFESDEVELSYAK.N
	Hs293FLP-MG_Ti_202.200	3.3884	0.2424	1049.12	1049.17	7509.3		1	1133.1	88.9	2	K.NGQDLGVAFK.I
	Hs293FLP-MG_Ti_202.200	2.3829	0.2893	1049.52	1049.17	4569.3		5	244.1	61.1	2	K.NGQDLGVAFK.I
	HsHeLa_Control-MG_Ti_10	3.1491	0.2973	1049.57	1049.17	6408.2		1	967.3	83.3	4	K.NGQDLGVAFK.I
	HsGST-MOCK_Ti_106.239	3.563	0.3934	2416.03	2415.69	8091.6		1	1450.8	38.2	1	R.PLFPHVLCHNCAVEFNFGQK.E
	HsHeLa_Control-MG_Ti_20	2.7708	0.1698	2724.52	2726.06	4328		1	410	45.2	1	K.EKPYFPIPEEYTFIQNVPLEDR.V
	Hs293FLP-MG_Ti_203.367	2.7874	0.1797	2726.08	2726.06	5002.8		1	421.7	42.9	1	K.EKPYFPIPEEYTFIQNVPLEDR.V
	Hs293FLP-MG_Ti_205.339	5.1679	0.3486	2726.46	2726.06	7800		1	1035	36.9	5	K.EKPYFPIPEEYTFIQNVPLEDR.V
	HsHeLa_Control-MG_Ti_20	5.7	0.2332	2727.21	2726.06	6750.4		1	1538.3	42.9	12	K.EKPYFPIPEEYTFIQNVPLEDR.V
	HsFLAG-Control_HeLa_NE	5.1043	0.2648	2727.6	2726.06	8757.3		1	1221	36.9	9	K.EKPYFPIPEEYTFIQNVPLEDR.V
	HsHeLa_Control_Ti_103.36	4.9563	0.4235	2468.94	2468.77	4345.2		1	847	57.9	27	K.PYFPIPEEYTFIQNVPLEDR.V
	HsHeLa_Control-MG_Ti_10	5.0575	0.3561	1705.89	1706.04	5749.2		1	1884	80	10	K.KDCEVVMMIGLPGAGK.T
	HsHeLa3_Ti_103.2868.286	3.0346	0.3574	1577.64	1577.86	6662.1		1	774.6	57.1	3	K.DCEVVMMIGLPGAGK.T
	HsHeLa3_Ti_103.2866.286	4.0198	0.2727	1578.57	1577.86	6284.8		1	1534.2	71.4	4	K.DCEVVMMIGLPGAGK.T
	HsHeLa3_Ti_103.2174.217	3.7587	0.2331	1383.4	1383.6	4609.5		1	1426.1	86.4	14	K.YNILGTNTIMDK.M

	Hs293FLP-MG_Ti_103.173	2.0434	0.1715	783.81	784.022	7243.9		2	725.3	83.3	3	K.MMVAGFK.K
	Hs283FLP_Ti_103.1494.14	2.2845	0.1199	819.65	819.979	4092.1		3	450.5	83.3	3	K.FIEIAAR.K
	HsGST-MOCK_Ti_102.159	5.0237	0.3539	1804.62	1805	4413.9		1	1134	80	13	K.RNFILDQTNVSAAAQR.R
	HsFLAG-Control_HeLa_NE	5.1378	0.3582	1648.42	1648.82	7710.9		1	3208.1	89.3	21	R.NFILDQTNVSAAAQR.R
	HsHeLa_Control-MG_Ti_10	3.257	0.2808	1130.67	1130.32	4873.4		1	1226.8	93.8	9	K.MCLFAGFQR.K
	HsHeLa_Control-MG_Ti_10	2.012	0.1156	772.82	772.929	5737.5		9	555.7	75	2	K.AVVVCPK.D
	Hs293FLP_Ti_303.1293.12	3.2142	0.2915	1423.61	1423.57	5262.4		1	968.1	77.3	4	K.AVVVCPKDEDYK.Q
	HsHeLa_Control-MG_Ti_20	4.1405	0.3942	1763.63	1764.03	7697.4		1	1140.1	63.3	2	K.KAEVEGKDLPEHAVLK.M
	Hs293FLP-MG_Ti_205.156	5.0793	0.4086	1763.67	1764.03	8951.3		1	1563	66.7	1	K.KAEVEGKDLPEHAVLK.M
	Hs293FLP-MG_Ti_205.156	5.3414	0.2418	1764.14	1764.03	6585		1	2048.6	56.7	1	K.KAEVEGKDLPEHAVLK.M
	HsHeLa_Control-MG_Ti_20	3.5373	0.1138	1764.4	1764.03	7882.8		2	1083.4	41.7	1	K.KAEVEGKDLPEHAVLK.M
	HsHeLa_Control-MG_Ti_20	2.0396	0.2094	1021.4	1022.19	4556.9		3	405.4	62.5	1	K.DLPEHAVLK.M
	Hs293FLP-MG_Ti_205.426	4.2451	0.431	2603.19	2603.85	5708.4		1	720.6	34.5	3	K.GNFTLPEVAECFDEITYVELQK.E
	Hs283FLP_Ti_106.2919.29	4.9586	0.5231	2603.41	2603.85	6185.4		1	1380.9	59.5	26	K.GNFTLPEVAECFDEITYVELQK.E
	HsHeLa_Control-MG_Ti_20	3.8181	0.3042	3187.83	3189.47	6842.7		1	651	38.5	10	K.GNFTLPEVAECFDEITYVELQKEEAQK.L
	HsHeLa_Control-MG_Ti_10	2.7595	0.1518	1266.64	1267.42	6576.1		7	560.5	61.1	2	K.LLEQYKEESK.K
	Hs283FLP_Ti_103.1263.12	3.1573	0.1517	1266.64	1267.42	6508.3		2	674	72.2	1	K.LLEQYKEESK.K
	HsHeLa_Control-MG_Ti_20	3.4914	0.2436	1267.33	1267.42	7614.3		1	1334.4	88.9	4	K.LLEQYKEESK.K
	Hs293FLP-MG_Ti_203.149	3.5304	0.2609	1267.49	1267.42	7320.6		2	1238.7	83.3	2	K.LLEQYKEESK.K
	Hs293FLP-MG_Ti_203.149	2.8656	0.1645	1267.53	1267.42	7519.5		2	611.1	66.7	1	K.LLEQYKEESK.K
	Hs293FLP-MG_Ti_103.138	3.9008	0.1988	1267.91	1267.42	6796.9		2	1237.3	88.9	10	K.LLEQYKEESK.K
	Hs293FLP_TREX_Ti_104.1	4.1162	0.2288	1395.55	1395.6	9590		1	1407.2	80	8	K.LLEQYKEESKK.A
	Hs293FLP-MG_Ti_104.215	4.7149	0.396	2212.95	2213.33	8653		1	1118.6	55.9	15	K.NQSQGYNQWQQGQFWGQK.P
	HsF-IP-293-MG_Ti_103.19	5.1759	0.3691	2213.35	2213.33	9114.5		1	2530.1	47.1	3	K.NQSQGYNQWQQGQFWGQK.P
	HsF-IP-293-MG_Ti_103.19	4.7816	0.3407	2214.27	2213.33	10143.6		1	1627.2	61.8	14	K.NQSQGYNQWQQGQFWGQK.P
	HsHeLa3_Ti_106.2052.205	1.9245	0.3063	1465.52	1466.56	6109.5		3	308.2	50	1	K.PWSQHYHQGYY.-
	HsHeLa_Control-MG_Ti_10	2.9373	0.4155	1465.55	1466.56	5204.7		1	563.8	65	1	K.PWSQHYHQGYY.-
	Hs283FLP_Ti_106.1960.19	2.7555	0.3079	1465.61	1466.56	5258.6		1	547.7	65	1	K.PWSQHYHQGYY.-
	Hs293FLP_Ti_306.2339.23	2.2248	0.3076	1465.81	1466.56	4624.2		1	385.1	55	1	K.PWSQHYHQGYY.-
	Hs283FLP_Ti_106.1961.19	3.5593	0.3783	1466.53	1466.56	6642.4		1	863.3	75	1	K.PWSQHYHQGYY.-
	HsHeLa_Control-MG_Ti_10	3.5408	0.3313	1466.72	1466.56	7113.1		1	879.4	70	2	K.PWSQHYHQGYY.-
	HsHeLa3_Ti_106.2040.204	3.0972	0.2061	1466.97	1466.56	7988.7		1	1240.7	80	2	K.PWSQHYHQGYY.-
	Hs293FLP_Ti_306.2338.23	3.258	0.2866	1467.49	1466.56	6890		1	756.5	70	3	K.PWSQHYHQGYY.-
gi|33286418|ref|	24	84	0.49	531	57937	7.8	U	pyruvate kinase 3 isoform 1 [Homo sapiens]				
	HsFLAG-Control_293_Ti_2	2.3982	0.1991	1359.56	1360.52	3229.2		6	121.5	54.2	1	R.NTGIICTIGPASR.S
	HsFLAG-Control_MG_293_	4.0255	0.423	1360.02	1360.52	8653.2		1	1697.2	79.2	7	R.NTGIICTIGPASR.S
	Hs293FLP_TREX_Ti_103.1	4.3777	0.379	1360.53	1360.52	7199.6		1	1466.6	79.2	7	R.NTGIICTIGPASR.S
	HsHeLa_Control-MG_Ti_10	4.3449	0.3785	1886.31	1885.05	7791.9		1	1114.8	60	2	R.LNFSHGTHEYHAETIK.N
	Hs293FLP-MG_Ti_203.329	3.5234	0.3518	2466.02	2466.79	7016.6		1	744.4	30.7	1	R.TATESFASDPILYRPVAVALDTK.G
	HsHeLa_Control_Ti_103.31	3.7761	0.3277	2466.48	2466.79	3598.2		1	341.2	40.9	3	R.TATESFASDPILYRPVAVALDTK.G
	HsHeLa_Control-MG_Ti_20	3.591	0.2193	2467.5	2466.79	7178.6		1	983.8	33	1	R.TATESFASDPILYRPVAVALDTK.G
	Hs293FLP_Ti_303.2873.28	3.4613	0.3052	2467.89	2466.79	3557		1	313.2	40.9	2	R.TATESFASDPILYRPVAVALDTK.G
	HsFLAG-Control_Hela_Ti_1	3.0361	0.2205	990.83	991.086	3929.7		1	749.9	83.3	1	K.GSGTAEVELK.K
	HsHeLa_Control-MG_Ti_10	3.9352	0.2636	1469.43	1469.6	5656.1		1	976.5	80	1	K.CDENILWLDYK.N
	HsHeLa_Control-MG_Ti_10	2.4999	0.3242	1462.77	1463.71	5926.6		1	659.3	58.3	1	K.IYVDDGLISLQVK.Q
	HsFLAG-Control_HeLa_S1	4.1166	0.2629	1463.77	1463.71	10472.4		2	2258.6	83.3	4	K.IYVDDGLISLQVK.Q
	HsHeLa_Control-MG_Ti_10	4.6588	0.3686	1463.85	1463.71	7271.8		1	2519.5	91.7	2	K.IYVDDGLISLQVK.Q
	Hs293FLP-MG_Ti_202.304	4.9547	0.3263	1780.64	1780.93	7725		1	1531.4	64.7	7	K.GADFLVTEVENGGSLGSK.K
	HsHeLa_Control-MG_Ti_10	5.3421	0.443	1766.03	1766.05	4302.5		1	930.4	67.6	12	K.KGVNLPGAAVDLPAVSEK.D

	HsFLAG-Control_HeLa_S1	5.4174	0.4441	1639.21	1637.87	4697.5		1	1201.1	78.1	5	K.GVNLPGAAVDLPAVSEK.D
	HsHeLa3_Ti_105.4487.448	2.5804	0.4226	1860.64	1861.12	7324.9		1	784.8	56.7	1	K.FGVEQDVDMVFASFIR.K
	HsHeLa3_Ti_102.1989.198	2.5626	0.1797	1142.65	1142.29	4023		1	464	65	1	R.GDLGIEIPAEK.V
	HsHeLa3_Ti_106.2763.276	3.1805	0.434	1879.44	1878.26	5230.1		1	927.6	62.5	1	R.AGKPVICATQMLESMIK.K
	HsHeLa3_Ti_103.3842.384	4.8198	0.3904	3498.36	3496.79	5418.8		1	707.5	26.5	2	R.AEGSDVANAVLDGADCIMLSGETAKGDYPLEAVR.M
*	HsHeLa_Control-MG_Ti_20	4.1018	0.4534	1932.66	1933.17	7261.9		1	1326.4	70	1	R.EAEAAIYHLQLFEELR.R
*	HsFLAG-Control_Hela_Ti_1	5.151	0.4713	2175.79	2176.43	5558		1	1212.3	61.9	17	R.LAPITSDPTEATAVGAVEASFK.C
	HsFLAG-Control_293_Ti_2	1.848	0.0898	840.43	841.041	3488.3		2	200.6	64.3	1	R.APIIAVTR.N
	HsFLAG-Control_HeLa_S1	4.3487	0.3263	1644.51	1643.75	6866		1	1542.4	76.9	3	K.DPVQEAWAEDVDLR.V
gi|4506701|ref|N	6	11	0.49	143	15808	10.5	U		ribosomal protein S23 [Homo sapiens]			
*	Hs293FLP_Ti_305.1221.12	2.0585	0.1282	810.68	810.972	4541.7		1	471.6	71.4	2	K.AHLGTALK.A
*	HsHeLa_Control-MG_Ti_20	2.5683	0.192	1056.52	1057.15	3933.5		1	451.8	65	2	K.ANPFGGASHAK.G
	HsGST-MOCK_Ti_405.401	4.5054	0.2742	3128.42	3126.46	9924.3		1	1001.1	28.7	1	K.KITAFVPNDGCLNFIEENDEVLVAGFGR.K
	HsGST-MOCK_Ti_105.136	3.6945	0.3876	1207.78	1206.39	5559.8		1	1091.6	81.8	4	R.KGHAVGDIPGVR.F
	HsHeLa_Control-MG_Ti_20	2.9965	0.2963	1078.39	1078.22	4712.1		1	581.2	70	1	K.GHAVGDIPGVR.F
	HsFLAG-Control_MG_293_	2.6733	0.1319	1190.58	1191.46	8571.5		8	676	65	1	K.VANVSLLALYK.G
gi|5031635|ref|N	9	30	0.488	166	18502	8.1	U		cofilin 1 (non-muscle) [Homo sapiens]			
*	Hs293FLP_TREX_Ti_104.2	2.7828	0.2517	1183.2	1182.33	5858.8		1	856.6	77.8	3	K.AVLFCLSEDK.K
*	Hs293FLP_TREX_Ti_104.1	3.0748	0.3602	1311.32	1310.5	7320.5		1	853.2	70	1	K.AVLFCLSEDKK.N
*	HsFLAG-Control_HeLa_NE	1.9629	0.1058	915.62	916.062	5822		7	425.8	71.4	1	K.NIILEEGK.E
*	HsFLAG-MOCK_300mM_T	5.4778	0.2892	3065.53	3064.46	11813.5		1	1228.2	26.9	3	K.NIILEEGKEILVGDVGQTVDDPYATFVK.M
*	HsFLAG-Control_HeLa_S1	5.7222	0.4867	2167.17	2167.42	6948.5		1	1966.3	68.4	11	K.EILVGDVGQTVDDPYATFVK.M
	HsHeLa_Control-MG_Ti_20	2.0894	0.2159	1337.29	1338.46	6860.2		1	421.3	55	2	R.YALYDATYETK.E
	HsHeLa_Control_Ti_102.17	3.658	0.2187	1338.44	1338.46	5164.4		1	1292.9	90	1	R.YALYDATYETK.E
	HsHeLa_Control-MG_Ti_20	5.4254	0.3379	1990.65	1991.34	7681.4		1	2123	75	5	K.KEDLVFIFWAPESAPLK.S
*	HsFLAG-Control_Hela_Ti_1	4.2464	0.2505	1341.09	1341.59	4564.9		1	964.5	73.1	3	K.LGGSAVISLEGKPL.-
gi|20270371|ref|N	31	255	0.486	245	28048	7.2	U		hypothetical protein LOC134147 [Homo sapiens]			
*	HsFLAG-Control_HeLa_NE	2.2226	0.0979	981.59	982.125	4547.5		2	385.7	71.4	2	R.EVQVEHIK.A
*	HsFLAG-MOCK_300mM_T	4.8983	0.413	1970.96	1971.31	5103.5		1	1232.4	68.8	22	K.AVIVIQDIFGWQLPNTR.Y
*	HsFLAG-Control_HeLa_S1	5.1553	0.2805	1971	1971.31	6854.5		1	1928.2	51.6	1	K.AVIVIQDIFGWQLPNTR.Y
*	HsFLAG-Control_HeLa_S1	5.3027	0.3622	1972.02	1971.31	6306		1	1485	71.9	61	K.AVIVIQDIFGWQLPNTR.Y
*	HsFLAG-Control_HeLa_S1	3.3402	0.203	993.1	993.191	4979		1	1136.9	88.9	8	R.AGVSVYGIVK.D
*	HsFlag1P_Ti_105.3227.322	5.6314	0.4223	2071.17	2071.34	9233.8		1	2059.9	63.9	8	R.AGVSVYGIVKDSEDIYNLK.N
*	HsHeLa-FLAG-IP_S100_Ti_	2.6938	0.1985	1096.33	1097.17	5282		2	581.5	75	1	K.DSEDIYNLK.N
*	HsFLAG-Control_HeLa_S1	2.3984	0.1589	1096.47	1097.17	7609.8		3	736.5	75	1	K.DSEDIYNLK.N
*	HsFLAG-Control_HeLa_S1	2.9119	0.2764	1096.49	1097.17	7648.4		1	773.2	75	2	K.DSEDIYNLK.N
*	HsHeLa_Control_Ti_102.16	2.8039	0.2064	1096.6	1097.17	5450.4		4	584.2	75	3	K.DSEDIYNLK.N
*	HsFLAG-Control_HeLa_S1	2.6686	0.2266	1096.63	1097.17	6510.5		8	716.9	75	1	K.DSEDIYNLK.N
*	HsFLAG-Control_HeLa_S1	3.6667	0.2277	1096.68	1097.17	5893.3		4	890.4	81.2	1	K.DSEDIYNLK.N
*	HsHeLa-FLAG-IP_S100_Ti_	3.0325	0.265	1097.04	1097.17	5973.2		2	854.1	81.2	2	K.DSEDIYNLK.N
*	HsFLAG-Control_HeLa_NE	2.8827	0.1964	1097.2	1097.17	6500.1		1	873	81.2	2	K.DSEDIYNLK.N
*	HsFLAG-Control_HeLa_S1	3.3657	0.2899	1097.29	1097.17	5465.6		2	913.6	81.2	2	K.DSEDIYNLK.N
*	HsFLAG-Control_HeLa_S1	5.6934	0.3708	1932.81	1931.28	5575.4		1	1607.2	75	86	K.NPTLFIFAENDVVIPLK.D
*	HsFLAG-Control_HeLa_S1	5.5231	0.3683	2816.4	2816.31	5945.4		1	1325.6	36.5	8	K.NPTLFIFAENDVVIPLKDVSLLTQK.L
*	HsHeLa_Control-MG_Ti_20	2.6136	0.1982	903.46	904.051	4029.7		3	414.6	78.6	10	K.DVSLLTQK.L
*	HsFLAG-MOCK_300mM_T	3.54	0.2833	1576.49	1575.81	9405.2		1	1117.2	72.7	1	K.LKEHCKVEYQIK.T
*	HsHeLa_Control-MG_Ti_20	2.0966	0.2532	1373.52	1374.5	3234.8		2	119.8	40.9	1	K.TFSGQTHGFVHR.K
*	HsFLAG-Control_HeLa_NE	2.303	0.2285	1373.66	1374.5	6172.5		3	317.8	54.5	1	K.TFSGQTHGFVHR.K

*	HsFLAG-Control_HeLa_S1	2.5667	0.3678	1373.77	1374.5	5823.9	1	369	59.1	2	K.TFSGQTHGFVHR.K
*	HsFLAG-Control_HeLa_S1	3.9357	0.5195	1373.86	1374.5	9952.6	1	1942.9	81.8	9	K.TFSGQTHGFVHR.K
*	HsFLAG-Control_HeLa_NE	3.7551	0.4253	1374.48	1374.5	8585.3	1	1171.5	68.2	6	K.TFSGQTHGFVHR.K
*	HsFLAG-Control_HeLa_S1	2.8387	0.2571	1374.65	1374.5	5625.5	1	367.2	59.1	1	K.TFSGQTHGFVHR.K
*	HsFLAG-Control_HeLa_S1	3.6607	0.4101	1374.84	1374.5	8604.2	1	1167.1	68.2	2	K.TFSGQTHGFVHR.K
*	Hs293FLP_Ti_306.2258.22	3.3587	0.3911	1376.61	1374.5	6858.4	1	1024.1	72.7	1	K.TFSGQTHGFVHR.K
*	HsFLAG-Control_Hela_Ti_1	3.8805	0.2527	2050.91	2051.19	4996	1	406.6	50	5	R.KREDCSPADKPYIDEAR.R
*	HsHeLa_Control-MG_Ti_20	4.1386	0.2636	2051.4	2051.19	5797.2	4	1223.3	48.4	2	R.KREDCSPADKPYIDEAR.R
*	HsFLAG-Control_HeLa_S1	3.3092	0.3123	1767.3	1766.83	6502.7	1	935.1	64.3	1	R.EDCSPADKPYIDEAR.R
*	HsHeLa_Control-MG_Ti_20	3.3368	0.1183	1186.22	1186.4	6408.5	7	881.1	81.2	2	R.RNLIEWLNK.Y
gi|4503471|ref|NI	57	295	0.485	462	50141	9	U	eukaryotic translation elongation factor 1 alpha 1 [Homo sapiens]			
	HsGST-MOCK_Ti_105.161	5.0627	0.3697	1589.75	1589.84	7575.5	1	2410.8	82.1	28	K.THINIVVIGHVDSGK.S
	HsHeLa_Control-MG_Ti_20	2.1168	0.0805	1120.6	1121.28	4071.8	2	445.4	66.7	1	K.STTTGHLIYK.C
	HsFLAG-Control_HeLa_NE	3.2571	0.3469	1121.08	1121.28	8100.5	1	1088.6	72.2	19	K.STTTGHLIYK.C
	HsFLAG-Control_293_Ti_2	3.0545	0.334	1121.22	1121.28	8815.4	1	1167	77.8	9	K.STTTGHLIYK.C
	HsFLAG-Control_MG_293_	3.8503	0.3494	1405.35	1405.6	6125.7	1	986	72.7	62	K.YYVTIIDAPGHR.D
*	HsFLAG-MOCK_300mM_T	3.9997	0.3257	1909.83	1909.2	4709.1	1	633.2	60	1	K.YYVTIIDAPGHRDFIK.N
	HsGST-MOCK_Ti_102.404	3.739	0.3542	2910.16	2911.26	7190.7	1	546.8	32.1	2	K.NMITGTSQADCAVLIVAAGVGEFEAGISK.N
	HsGST-MOCK_Ti_303.534	4.7274	0.3861	2912.77	2911.26	8229.7	1	1623.9	33	4	K.NMITGTSQADCAVLIVAAGVGEFEAGISK.N
	HsGST-MOCK_Ti_405.245	2.884	0.275	1314.28	1315.56	3797.5	1	422.1	63.6	2	R.EHALLAYTLGVK.Q
	Hs293FLP-MG_Ti_204.231	3.1474	0.3715	1314.52	1315.56	6113	1	627.9	63.6	1	R.EHALLAYTLGVK.Q
	HsFLAG-Control_HeLa_NE	3.8894	0.3764	1314.54	1315.56	7099.1	1	843.2	68.2	1	R.EHALLAYTLGVK.Q
	HsFLAG-Control_HeLa_S1	3.3633	0.3249	1314.54	1315.56	6442.6	1	682.8	63.6	1	R.EHALLAYTLGVK.Q
	HsHeLa3_Ti_105.2226.222	3.7276	0.3842	1314.65	1315.56	5432.8	1	771	68.2	6	R.EHALLAYTLGVK.Q
	HsGST-MOCK_Ti_405.244	3.0462	0.2235	1314.83	1315.56	6532.9	2	861.4	72.7	2	R.EHALLAYTLGVK.Q
	HsHeLa_Control-MG_Ti_10	3.4703	0.3478	1314.83	1315.56	5679.7	1	655	63.6	2	R.EHALLAYTLGVK.Q
	HsFLAG-Control_HeLa_S1	4.0957	0.3505	1315.1	1315.56	6796.4	1	1542.9	86.4	7	R.EHALLAYTLGVK.Q
	HsFLAG-Control_HeLa_S1	3.3605	0.3219	1315.28	1315.56	7637	1	1057.6	72.7	3	R.EHALLAYTLGVK.Q
	HsGST-MOCK_Ti_305.236	3.3426	0.261	1315.47	1315.56	3468.6	1	431.4	68.2	3	R.EHALLAYTLGVK.Q
	HsGST-MOCK_Ti_305.236	3.4506	0.2703	1315.48	1315.56	5538.1	1	959.1	81.8	7	R.EHALLAYTLGVK.Q
	HsFLAG-Control_HeLa_NE	3.1986	0.3053	1315.53	1315.56	6457.5	2	1086.8	77.3	2	R.EHALLAYTLGVK.Q
	HsFLAG-Control_HeLa_S1	3.6587	0.3109	1315.58	1315.56	6360.4	2	555.9	59.1	3	R.EHALLAYTLGVK.Q
	HsHeLa3_Ti_105.2218.221	3.3286	0.2525	1316.68	1315.56	6114.4	2	1130.5	81.8	2	R.EHALLAYTLGVK.Q
	HsHeLa_Control-MG_Ti_10	3.3203	0.2631	1316.86	1315.56	6340.9	1	1163.7	81.8	6	R.EHALLAYTLGVK.Q
	HsGST-MOCK_Ti_102.183	2.8304	0.2663	1317.2	1315.56	6447.2	1	1041.9	77.3	1	R.EHALLAYTLGVK.Q
*	HsGST-MOCK_Ti_102.024	5.5659	0.4436	3696.32	3698.21	6354	1	1315.9	32	7	K.KIGYNPDTVAFVPISGWNGDNMLEPSANMPWFK.G
	HsGST-MOCK_Ti_102.288	4.727	0.4142	2785.5	2785.09	5899.5	1	490.2	28	2	R.KDGNASGTTLLEALDCILPPTRPTDK.P
	HsF-IP-293-MG_Ti_106.26	3.9296	0.1716	2655.77	2656.92	6529.7	3	445.9	35.4	3	K.DGNASGTTLLEALDCILPPTRPTDK.P
	Hs293FLP-MG_Ti_203.417	3.8732	0.2516	2655.81	2656.92	7487.7	1	495.8	35.4	1	K.DGNASGTTLLEALDCILPPTRPTDK.P
	HsHeLa_Control-MG_Ti_20	4.4261	0.341	2656.31	2656.92	5408.6	1	773.3	33.3	2	K.DGNASGTTLLEALDCILPPTRPTDK.P
	Hs283FLP_Ti_106.2780.27	3.9835	0.2415	2656.91	2656.92	6341.3	1	544.5	39.6	3	K.DGNASGTTLLEALDCILPPTRPTDK.P
	HsHeLa3_Ti_104.3859.385	3.7273	0.2886	2656.97	2656.92	7063.1	1	502.4	37.5	11	K.DGNASGTTLLEALDCILPPTRPTDK.P
	HsFLAG-Control_293_Ti_1	3.9548	0.2565	2657.21	2656.92	4899.5	2	421	28.1	1	K.DGNASGTTLLEALDCILPPTRPTDK.P
	HsGST-MOCK_Ti_404.425	4.0974	0.2737	2657.25	2656.92	5198.4	1	593.3	30.2	2	K.DGNASGTTLLEALDCILPPTRPTDK.P
	HsHeLa3_Ti_103.4042.404	4.9245	0.3211	2657.5	2656.92	4177.2	1	533	33.3	2	K.DGNASGTTLLEALDCILPPTRPTDK.P
	HsHeLa_Control-MG_Ti_20	4.2834	0.3028	2657.7	2656.92	6635.7	2	574.6	39.6	5	K.DGNASGTTLLEALDCILPPTRPTDK.P
	Hs293FLP-MG_Ti_203.416	4.1604	0.3362	2657.77	2656.92	5933.7	1	778.9	32.3	1	K.DGNASGTTLLEALDCILPPTRPTDK.P
	HsF-IP-293-MG_Ti_106.26	4.4562	0.204	2658.01	2656.92	4518.3	1	714.8	35.4	1	K.DGNASGTTLLEALDCILPPTRPTDK.P
	HsGST-MOCK_Ti_303.412	4.7498	0.2542	2658.05	2656.92	6564.7	1	447.9	35.4	5	K.DGNASGTTLLEALDCILPPTRPTDK.P

*	HsFLAG-Control_HeLa_S1	4.7477	0.256	3025.02	3023.38	9881.3		4	606	22.2	3	K.DGNASGTTLLEALDCILPPTRPTDKPLR.L
*	HsHeLa_Control-MG_Ti_20	4.4221	0.2834	3978.86	3980.52	9399.8		6	465.8	17.9	2	K.DGNASGTTLLEALDCILPPTRPTDKPLRLPLQDVYK.I
	Hs293FLP-MG_Ti_204.174	1.8645	0.2129	1025.5	1026.22	4916.9		7	205.7	55	1	K.IGGIGTVPVGR.V
	Hs293FLP-MG_Ti_304.147	1.8582	0.2752	1025.51	1026.22	4087.8		7	177.1	55	1	K.IGGIGTVPVGR.V
	HsFLAG-Control_Hela_Ti_1	1.9211	0.1678	1025.52	1026.22	5051.1		4	266.3	60	1	K.IGGIGTVPVGR.V
	HsFLAG-Control_293_Ti_2	2.1086	0.236	1025.57	1026.22	5224.8		4	263.8	60	2	K.IGGIGTVPVGR.V
	HsFLAG-Control_293_Ti_2	3.6738	0.3122	1026.38	1026.22	5169		4	914.7	85	3	K.IGGIGTVPVGR.V
	HsFLAG-Control_MG_293_	3.7743	0.2639	1026.42	1026.22	5236.3		5	894.4	80	1	K.IGGIGTVPVGR.V
	HsFLAG-Control_HeLa_S1	3.4654	0.1423	1026.43	1026.22	4798.2		8	804.6	80	13	K.IGGIGTVPVGR.V
	HsHeLa3_Ti_105.1615.161	3.0073	0.2554	1027.39	1026.22	4582.7		6	778.6	80	1	K.IGGIGTVPVGR.V
*	HsFLAG-MOCK_300mM_T	4.8307	0.3105	3525.45	3524.2	5667		1	437.5	22.8	2	K.IGGIGTVPVGRVETGVLKPGMVVTFAPVNVTTEVK.S
	HsGST-MOCK_Ti_406.291	4.7347	0.3369	2516.71	2517	4730.5		1	514.8	45.7	26	R.VETGVLKPGMVVTFAPVNVTTEVK.S
	HsHeLa3_Ti_104.2667.266	4.7234	0.2826	1789.14	1790.13	5522.4		1	922.6	62.5	6	K.PGMVVTFAPVNVTTEVK.S
	HsHeLa3_Ti_102.1954.195	2.5375	0.2376	1259.61	1260.45	5698.3		2	538.9	58.3	2	K.SGDAAIVDMVPGK.P
*	HsGST-MOCK_Ti_404.343	4.9192	0.4679	2995.81	2997.37	6706.2		1	755.6	28.7	2	K.SGDAAIVDMVPGKPMCVESFSDYPPLGR.F
*	HsHeLa3_Ti_104.3113.311	3.5765	0.4775	2996.87	2997.37	4418.1		1	505.4	38.9	3	K.SGDAAIVDMVPGKPMCVESFSDYPPLGR.F
*	HsGST-MOCK_Ti_303.340	3.3785	0.3745	2997.1	2997.37	6139.8		1	307.8	29.6	2	K.SGDAAIVDMVPGKPMCVESFSDYPPLGR.F
*	HsHeLa3_Ti_103.3290.329	4.2001	0.1736	2999.22	2997.37	6238.1		1	883	29.6	2	K.SGDAAIVDMVPGKPMCVESFSDYPPLGR.F
	HsFLAG-Control_293_Ti_1	2.1166	0.1645	914.48	915.121	2775.6		1	178.6	75	1	R.QTVAVGVIK.A
gi|4507261|ref|N	1	3	0.484	62	7304	8.5	U	statherin isoform a [Homo sapiens]				
*	HsFLAG-Control_293_Ti_2	4.9182	0.3385	3646.4	3646.01	5973.4		2	504.2	25	3	R.FGYGYGPYQPVPEQPLYPQPYQPQYQQYTF.-
gi|9506651|ref|N	7	81	0.483	234	26093	6.2	U	potassium channel tetramerisation domain containing 5 [Homo sapiens]				
*	HsFLAG-Control_MG_293_	3.5665	0.296	1145.31	1145.27	6203		1	1452.4	83.3	7	R.GGIGAGLGGGLCR.R
*	HsFLAG-Control_293_Ti_2	4.2281	0.3229	1660.49	1659.85	8676.1		1	1208.3	56.2	8	R.CSAGLGALAQRPGSVSK.W
*	HsFLAG-Control_293_Ti_2	3.1586	0.2587	1343.36	1342.54	5285		1	550.7	68.2	3	R.LNVGGTYFLTTR.Q
*	HsFLAG-Control_293_Ti_2	3.1912	0.387	1555.38	1555.77	6536.1		1	986.3	70.8	3	R.DPTYFGPVLNYLR.H
*	HsFlag1P_Ti_105.4312.431	6.2354	0.4145	2383.01	2384.64	8771.6		1	2004.5	60	45	K.DLAEEGVLEEAEFYNITSLIK.L
	HsFLAG-Control_293_Ti_2	5.2966	0.4718	2499.55	2500.76	8109.8		1	1506.2	57.5	3	R.VLQCQEEELTQMVSTMSDGWK.F
*	HsFLAG-Control_HeLa_NE	3.5971	0.4414	1760.14	1760.86	5335		1	624.1	60	12	K.ELHNTPYGTASEPSEK.A
gi|14141166|ref|	18	106	0.481	362	38222	6.8	U	poly(rC)-binding protein 2 isoform b [Homo sapiens]				
gi|14141168|ref|	18	106	0.475	366	38651	6.8	U	poly(rC)-binding protein 2 isoform a [Homo sapiens]				
	HsFLAG-MOCK_300mM_T	3.7768	0.4013	1482.96	1482.83	6028.7		1	1195.7	76.9	2	R.LLMHGKEVGSIIGK.K
	HsFLAG-Control_HeLa_NE	4.0721	0.1996	1289.32	1289.35	6636.7		1	1467.5	85	25	R.INISEGNCPER.I
	HsHeLa3_Ti_105.2595.259	2.8512	0.1912	1358.64	1359.65	7780.8		8	655.7	58.3	1	R.IITLAGPTNAIFK.A
	HsFLAG-Control_293_Ti_1	2.2998	0.1553	1358.72	1359.65	8425		4	529.7	54.2	1	R.IITLAGPTNAIFK.A
	HsFLAG-MOCK_300mM_T	3.6084	0.3079	1359.24	1359.65	4255.9		1	744.8	75	15	R.IITLAGPTNAIFK.A
	HsFLAG-Control_HeLa_NE	3.9964	0.2824	1359.54	1359.65	4776.6		1	907.8	79.2	7	R.IITLAGPTNAIFK.A
	HsFLAG-Control_HeLa_S1	2.9877	0.2325	1359.66	1359.65	7669.2		1	843.1	62.5	2	R.IITLAGPTNAIFK.A
	HsFLAG-Control_HeLa_NE	3.2645	0.2955	1359.71	1359.65	7897.5		1	896.6	66.7	1	R.IITLAGPTNAIFK.A
	HsFLAG-Control_HeLa_NE	3.9073	0.2638	1359.81	1359.65	5197.3		1	1021.2	79.2	7	R.IITLAGPTNAIFK.A
	HsFLAG-Control_293_Ti_2	3.3617	0.202	1360.12	1359.65	6340.4		1	824.2	66.7	7	R.IITLAGPTNAIFK.A
	HsHeLa_Control_Ti_105.31	2.9389	0.1942	1361.02	1359.65	4237		1	713.7	75	1	R.IITLAGPTNAIFK.A
	HsFLAG-MOCK_300mM_T	4.3252	0.2965	3353.65	3353.83	6029.2		1	997.7	29.2	3	K.AFAMIIDKLEEDISSSMTNSTAASRPPVTLR.L
	HsHeLa3_Ti_104.1799.180	3.2137	0.3342	1431.5	1429.67	4003.3		1	487.1	65.4	3	R.LVVPASQCGSLIGK.G
	HsGST-MOCK_Ti_402.221	4.9595	0.4065	2090.84	2091.26	6640.2		1	1123.5	57.9	9	R.ESTGAQVQVAGDMLPNSTER.A
	HsFLAG-Control_HeLa_NE	3.5682	0.3328	1713.61	1714.02	3516.5		1	629.9	70	14	R.AITIAGIPQSIIECVK.Q
	HsFLAG-Control_HeLa_S1	4.0863	0.2965	2431.88	2430.77	4417.4		1	458.6	31.8	1	K.GVTIPYRPKPSSSPVIFAGGQDR.Y
	HsHeLa3_Ti_103.1363.136	3.1173	0.2554	1159.84	1159.24	4475.6		1	832	80	4	K.IANPVEGSTDR.Q

	HsFLAG-Control_HeLa_S1	5.1229	0.464	2206.92	2206.55	6455.7		1	899.6	52.5	3	R.QVTITGSAASISLAQYLINVR.L
gi|11136628|ref|N	16	71	0.48	225	24764	4.7	U	eukaryotic translation elongation factor 1 beta 2 [Homo sapiens]				
gi|4503477|ref|N	16	71	0.48	225	24764	4.7	U	eukaryotic translation elongation factor 1 beta 2 [Homo sapiens]				
	HsGST-MOCK_Ti_303.306	5.634	0.4033	1604.36	1604.8	7386.7		1	2350.2	85.7	15	K.SPAGLQVLNDYLADK.S
	HsFLAG-Control_MG_293_	2.0266	0.1299	726.64	726.938	3702.4		1	463.1	83.3	3	K.KPALVAK.S
	HsGST-MOCK_Ti_404.354	6.0939	0.1355	2849.27	2851.16	5904.8		1	886.6	34.8	6	K.SSILLDVKPWDDETDMAKLEECVR.S
	HsGST-MOCK_Ti_303.348	3.7755	0.1478	2851.07	2851.16	7026.4		1	613.2	41.3	1	K.SSILLDVKPWDDETDMAKLEECVR.S
	HsGST-MOCK_Ti_302.251	5.09	0.236	1996.66	1995.13	8875.4		1	2571.4	80	2	K.PWDDETDMAKLEECVR.S
	HsGST-MOCK_Ti_303.224	3.1548	0.2948	1347.39	1348.5	4834.9		1	348.9	50	3	R.SIQADGLVWGSSK.L
	HsGST-MOCK_Ti_403.240	4.552	0.4393	1348.09	1348.5	5859.7		1	1463.5	83.3	4	R.SIQADGLVWGSSK.L
	HsGST-MOCK_Ti_304.187	1.8821	0.2503	945.42	946.178	3098.6		4	332.3	68.8	1	K.LVPVGYGIK.K
	HsGST-MOCK_Ti_304.189	2.9994	0.3378	1474.47	1475.65	4272.6		2	535	63.6	3	K.KLQIQCVVEDDK.V
	HsGST-MOCK_Ti_404.199	4.8653	0.3375	1474.84	1475.65	7647.6		1	2151.3	90.9	5	K.KLQIQCVVEDDK.V
	HsGST-MOCK_Ti_101.077	4.8945	0.3341	1475.3	1475.65	7192.3		1	1660.3	86.4	2	K.KLQIQCVVEDDK.V
	HsGST-MOCK_Ti_304.023	5.9751	0.5591	4493.24	4494.99	8950.3		1	1459.1	25.7	6	K.LQIQCVVEDDKVGTDMLEEQITAFEDYVQSMDVAAFNKI.-
	HsGST-MOCK_Ti_302.545	4.9342	0.453	3053.77	3053.38	7726.2		1	1034	42.3	3	K.VGTDMLEEQITAFEDYVQSMDVAAFNK.I
	HsGST-MOCK_Ti_303.570	5.3471	0.4711	3054	3053.38	7194.5		1	1032.1	31.7	3	K.VGTDMLEEQITAFEDYVQSMDVAAFNK.I
	HsGST-MOCK_Ti_305.006	5.5284	0.4282	3165.29	3166.54	6653.4		1	1467.3	36.1	3	K.VGTDMLEEQITAFEDYVQSMDVAAFNKI.-
	HsGST-MOCK_Ti_303.008	4.8588	0.4737	3165.49	3166.54	7011.9		1	780.2	38.9	11	K.VGTDMLEEQITAFEDYVQSMDVAAFNKI.-
gi|4826898|ref|N	6	11	0.479	140	15054	8.3	U	profilin 1 [Homo sapiens]				
*	HsFLAG-Control_293_Ti_2	4.6381	0.3605	1646.1	1644.95	5749.6		1	820.7	60	1	K.TFVNITPAEVGVLVGK.D
*	Hs293FLP_TREX_Ti_106.2	5.139	0.414	1742.56	1742.93	6561.5		1	1705	80	3	K.DRSSFYVNGLTLGGQK.C
*	Hs293FLP_TREX_Ti_103.2	4.4816	0.4099	1471.45	1471.65	6303.7		1	1382.7	76.9	4	R.SSFYVNGLTLGGQK.C
*	Hs293FLP_TREX_Ti_104.1	3.5899	0.3914	1724.58	1724.91	4470		1	448.2	56.2	1	K.STGGAPTFNVTVTKTDK.T
*	HsHeLa3_Ti_104.2177.217	2.5574	0.2319	874.76	875.158	8094.3		2	713.9	71.4	1	K.TLVLLMGK.E
*	Hs293FLP_TREX_Ti_104.1	1.9463	0.184	1023.46	1024.17	2502.5		7	153.1	55.6	1	K.EGVHGGLINK.K
gi|62414289|ref|N	21	223	0.476	466	53652	5.1	U	vimentin [Homo sapiens]				
*	HsHeLa-FLAG-IP_S100_Ti_	4.461	0.2322	1429.43	1429.57	6542.7		1	1672.2	80.8	8	R.SLYASSPGGVYATR.S
*	HsHeLa-FLAG-IP_S100_Ti_	6.0232	0.481	2127.72	2127.36	8683.4		1	2603.5	72.2	56	R.LLQDSVDFSLADAINTEFK.N
*	HsHeLa-FLAG-IP_S100_Ti_	2.7269	0.1253	871.14	870.981	3016.7		3	725.4	100	2	R.FANYIDK.V
*	HsHeLa-FLAG-IP_S100_Ti_	3.935	0.1468	1170.43	1170.44	5070.1		1	1168.4	88.9	18	K.ILLAELEQLK.G
*	HsFlag1P_Ti_106.2638.263	2.9915	0.182	1540.18	1540.84	10157.7		2	837.7	57.7	1	K.ILLAELEQLKGQGK.S
*	HsHeLa-FLAG-IP_S100_Ti_	3.6077	0.2183	1256.06	1255.39	5756.6		1	1136.1	83.3	9	R.LGDLYEEEMR.E
*	HsHeLa-FLAG-IP_S100_Ti_	3.7179	0.2051	1217.25	1217.32	6174.2		1	1242.3	88.9	6	R.RQVDQLTNDK.A
*	HsHeLa-FLAG-IP_S100_Ti_	2.9394	0.2377	1076.88	1077.2	6080.9		8	770.8	81.2	2	R.DNLAEDIMR.L
*	HsFLAG-Control_HeLa_S1	3.3434	0.2942	1325.75	1324.39	8302.5		1	1217.5	80	8	R.EEAENTLQSFR.Q
*	HsFLAG-Control_HeLa_S1	3.1421	0.2626	1088.98	1089.15	5302.3		1	837.6	83.3	7	R.QDVDNASLAR.L
*	HsFLAG-Control_HeLa_S1	3.7411	0.248	1535.14	1534.79	9285		1	1292.5	70.8	5	R.KVESLQEEIAFLK.K
	HsFLAG-Control_HeLa_S1	2.5514	0.1421	1309.34	1310.41	5869.4		1	439.7	66.7	1	K.NLQEAEEWYK.S
	HsHeLa-FLAG-IP_S100_Ti_	3.9546	0.1201	1310.13	1310.41	6762.9		3	1198.2	83.3	13	K.NLQEAEEWYK.S
	HsFLAG-Control_HeLa_S1	3.4526	0.0868	1310.27	1310.41	6168.1		1	1134	83.3	3	K.NLQEAEEWYK.S
*	HsHeLa-FLAG-IP_S100_Ti_	4.3357	0.2135	1093.95	1094.17	6197.5		1	1509.1	94.4	6	K.FADLSEAANR.N
*	HsHeLa-FLAG-IP_S100_Ti_	3.7295	0.2714	1491.22	1491.65	5760		1	694.7	70.8	26	R.QVQSLTCEVDALK.G
*	HsHeLa-FLAG-IP_S100_Ti_	5.8107	0.4715	2186.94	2188.33	8128.1		1	2201.4	69.4	19	R.EMEENFAVEAANYQDTIGR.L
	HsHeLa-FLAG-IP_S100_Ti_	2.8382	0.1203	932.36	933.006	3007.7		7	641.4	92.9	1	K.LLEGEESR.I
*	HsFLAG-Control_HeLa_S1	3.2663	0.1628	1571.88	1571.86	4780		1	675.6	65.4	13	R.ISLPLPNFSSLNLR.E
*	HsFLAG-Control_HeLa_S1	3.4999	0.2712	1669.73	1669.83	4759.9		1	578.9	60.7	11	R.ETNLDSLPLVDTHSK.R
*	HsFLAG-Control_HeLa_S1	3.4606	0.2526	1838.2	1837.85	8947.6		1	1088.1	60	8	R.DGQVINETSQHHDDLE.-

gi|29294624|ref|N	8	48	0.475	118	13527	9.9	U	small nuclear ribonucleoprotein polypeptide D2 [Homo sapiens]				
gi|4759158|ref|NI	8	48	0.475	118	13527	9.9	U	small nuclear ribonucleoprotein polypeptide D2 [Homo sapiens]				
	HsHeLa_Control-MG_Ti_20	3.9346	0.3147	2164.02	2164.38	9913.2		2	1395.7	38.9	1	K.REEEEFNTGPLSVLTQSVK.N
	Hs293FLP-MG_Ti_203.315	4.4264	0.2982	2164.57	2164.38	9045.8		1	1438.5	38.9	1	K.REEEEFNTGPLSVLTQSVK.N
	HsF-IP-293-MG_Ti_106.243	3.707	0.2306	2165.99	2164.38	11547.5		1	1379.1	52.8	9	K.REEEEFNTGPLSVLTQSVK.N
	HsF-IP-293_Ti_202.0174.01	4.2379	0.4554	2006.59	2008.19	6443.9		1	716.5	52.9	19	R.EEEEFNTGPLSVLTQSVK.N
	HsFLAG-Control_Hela_Ti_1	2.8197	0.2817	1232.37	1232.35	6582.5		2	658.5	72.2	1	K.NNTQVLINCR.N
	HsHeLa3_Ti_105.1559.155	3.3352	0.3013	1245.36	1244.42	7642.1		1	942.6	72.2	1	R.HCNMVLENVK.E
	Hs283FLP_Ti_102.1831.18	2.8572	0.0875	1329.18	1329.6	4649.7		2	757.6	72.2	4	K.DRYISKMFLR.G
	HsF-IP-293-MG_Ti_103.122	2.4795	0.1107	712.45	712.867	3804.6		7	424.9	75	12	R.NPLIAGK.-
gi|10863927|ref|N	11	36	0.461	165	18012	7.8	U	peptidylprolyl isomerase A isoform 1 [Homo sapiens]				
gi|89058333|ref|X	11	36	0.342	222	24517	7.4	U	PREDICTED: similar to peptidylprolyl isomerase A isoform 1 [Homo sapiens]				
gi|89058151|ref|X	11	36	0.342	222	24517	7.4	U	PREDICTED: similar to peptidylprolyl isomerase A isoform 1 [Homo sapiens]				
	Hs293FLP_TREX_Ti_105.2	2.1541	0.151	1055.28	1056.2	8290.5		3	582.3	68.8	2	R.VSFELFADK.V
	HsHeLa3_Ti_103.2434.243	2.5598	0.2327	1055.73	1056.2	8561		1	990.3	75	2	R.VSFELFADK.V
	Hs293FLP_TREX_Ti_104.2	3.1958	0.1307	1056.23	1056.2	3545.6		2	775.3	87.5	2	R.VSFELFADK.V
	HsHeLa3_Ti_103.2431.243	3.1848	0.1273	1056.99	1056.2	4330.5		1	923.6	87.5	3	R.VSFELFADK.V
	HsFlag1P_Ti_105.2688.268	3.7239	0.2131	1381.39	1380.63	6124.7		1	1064.6	77.3	3	R.VSFELFADKVPK.T
	Hs293FLP_Ti_303.2326.23	4.7457	0.4024	1833.59	1833.05	5532.2		1	1136.4	71.4	12	K.SIYGEKFEDENFILK.H
	HsFLAG-Control_HeLa_NE	3.0165	0.0863	1156.01	1155.29	3596.6		7	683.1	87.5	5	K.FEDENFILK.H
	HsHeLa3_Ti_106.2531.253	2.8541	0.1606	2793.81	2793.09	7093.5		1	670.5	38.5	1	K.HTGPGILSMANAGPNTNGSQFFICTAK.T
	HsHeLa3_Ti_102.2319.231	1.9789	0.3177	1278.76	1279.47	2429.2		2	135.6	60	1	K.EGMNIVEAMER.F
	HsHeLa3_Ti_103.1678.167	2.6585	0.1596	1247.65	1248.39	4897.8		1	486.1	65	2	K.KITIADCGQLE.-
	HsHeLa3_Ti_103.1688.168	3.5669	0.2195	1248.57	1248.39	5702.4		1	964.8	75	3	K.KITIADCGQLE.-
gi|4503117|ref|NI	6	18	0.459	98	11140	7.6	U	cystatin B [Homo sapiens]				
*	HsGST-MOCK_Ti_403.231	4.1033	0.3264	1327.36	1327.52	6810.5		1	1763.9	90.9	3	K.SQVVAGTNYFIK.V
*	HsGST-MOCK_Ti_305.204	4.3874	0.3823	1424.75	1423.57	5805.8		1	1332.4	86.4	4	K.VHVGDEDFVHLR.V
*	Hs293FLP-MG_Ti_206.268	5.1887	0.416	2458.64	2459.76	7826.9		1	1633	60	5	R.VFQSLPHENKPLTLSNYQTNK.A
*	HsGST-MOCK_Ti_104.159	4.1621	0.3439	2458.7	2459.76	3869.9		1	529.7	35	1	R.VFQSLPHENKPLTLSNYQTNK.A
*	HsHeLa_Control-MG_Ti_20	4.0992	0.36	2459.4	2459.76	4332.3		1	833.2	41.2	2	R.VFQSLPHENKPLTLSNYQTNK.A
*	HsHeLa_Control-MG_Ti_20	5.2511	0.3882	2459.44	2459.76	8357.3		1	1660.4	57.5	3	R.VFQSLPHENKPLTLSNYQTNK.A
gi|4504517|ref|NI	6	57	0.449	205	22783	6.4	U	heat shock 27kDa protein 1 [Homo sapiens]				
*	HsFLAG-Control_HeLa_NE	4.144	0.2464	1164.72	1164.35	7284.6		1	1694.1	94.4	10	R.LFDQAFGLPR.L
*	HsFLAG-Control_HeLa_S1	5.6318	0.5139	4095.03	4095.61	7340.2		1	1264.2	27.7	2	R.LPEEWSQWLGGSSWPGYVRPLPPAAIESPAVAAPAYSR.A
*	HsHeLa_Control-MG_Ti_10	4.7682	0.4144	1785.96	1785.01	7050		1	1281.8	66.7	17	R.VSLDVNHFAPDELTVK.T
*	HsFLAG-Control_HeLa_S1	3.5619	0.2437	1147.11	1147.31	5508.1		1	980.8	80	1	K.TKDGVVEITGK.H
*	HsFLAG-Control_HeLa_NE	2.6002	0.2355	917.65	918.035	6402		1	681.6	75	5	K.DGVVEITGK.H
*	HsFLAG-Control_HeLa_S1	3.66	0.3224	1907.13	1907.13	5046.9		1	381.8	50	22	K.LATQSNEITIPVTFESR.A
gi|4885165|ref|NI	4	15	0.449	98	11006	5.5	U	cystatin A [Homo sapiens]				
*	HsFLAG-Control_293_Ti_2	4.6179	0.3953	1644.28	1644.82	7184.5		1	1579.2	76.9	5	K.TNETYGKLEAVQYK.T
*	HsFLAG-Control_Hela_Ti_1	3.953	0.3048	1357.27	1357.55	6677.7		1	1688.1	86.4	1	K.TQVVAGTNYYIK.V
*	HsFLAG-Control_Hela_Ti_1	2.477	0.1487	1357.44	1357.55	6324.8		2	419.3	59.1	1	K.TQVVAGTNYYIK.V
*	HsFLAG-Control_HeLa_S1	3.9093	0.5003	1976.25	1977.18	3839.6		1	413.5	55.9	8	K.SLPGQNEDLVLTGYQVDK.N
gi|34098946|ref|N	10	28	0.448	324	35924	9.9	U	nuclease sensitive element binding protein 1 [Homo sapiens]				
	Hs293FLP_TREX_Ti_104.1	4.6707	0.3218	1745.58	1745.93	7523.4		1	1699.8	75	4	R.NDTKEDVFVHQTAIK.K
	HsHeLa_Control-MG_Ti_10	3.2281	0.3251	1875.08	1874.1	8473.9		1	1219.1	60	1	R.NDTKEDVFVHQTAIKK.N
	HsHeLa_Control_Ti_102.21	4.3285	0.3574	1796.81	1796.88	4791		1	826.4	62.5	11	R.SVGDGETVEFDVVEGEK.G
*	HsFLAG-MOCK_300mM_T	3.6248	0.1333	1696.96	1696.86	5052.5		1	1372.3	63.9	4	K.GAEAANVTGPGGVPVQGSK.Y

*	Hs293FLP_TREX_Ti_102.0	3.5023	0.2744	1690	1689.69	9441.2		1	1136.7	69.2	2	R.NYQQNYQNSESGEK.N
*	HsHeLa_Control-MG_Ti_10	3.6852	0.3588	3258.58	3259.26	7773.5		1	1101.6	29.5	2	R.NYQQNYQNSESGEKNEGSESAPEGQAQQR.R
*	Hs293FLP_Ti_305.1594.15	3.6679	0.3186	3225.81	3225.48	5449.1		1	402.7	25.9	1	R.RPQYSNPPVQGEVMEGADNQGAGEQGRPVR.Q
*	HsFLAG-Control_MG_293_	3.5119	0.1741	1265.97	1266.4	7349.2		6	622.3	70	1	R.RPENPKPQDGK.E
*	HsHeLa_Control-MG_Ti_10	2.6819	0.2502	1624.65	1624.79	6991.7		1	680.8	61.5	1	R.RPENPKPQDGKETK.A
*	Hs293FLP_TREX_Ti_101.0	2.9319	0.2638	1899.5	1898.89	3481.4		1	497.4	52.6	1	K.AADPPAENSSAPEAEQGGAE.-
gi|39930523|ref|N	10	45	0.446	381	41037	5	U	hypothetical protein LOC144097 [Homo sapiens]				
*	HsFLAG-Control_HeLa_NE	3.5594	0.2499	2122.45	2122.26	5016.1		1	676.8	36.8	1	K.TPPPRPSPLEAGSDGCEEPK.Q
*	Hs293FLP-MG_Ti_205.155	2.7509	0.1808	2123.35	2122.26	9271.2		1	492.1	42.1	2	K.TPPPRPSPLEAGSDGCEEPK.Q
*	HsHeLa_Control-MG_Ti_10	5.3968	0.4873	2070.26	2069.28	6208.3		1	1235.4	64.7	5	R.SHILEQHPHTLDLSPSEK.S
*	HsF-IP-293-MG_Ti_106.28	4.7378	0.2521	2000.86	2001.25	6919.3		1	2628	73.5	12	K.SNILEAWSEGVALLQDVR.A
*	HsFlag1P_Ti_105.3226.322	4.8866	0.2977	2223.8	2224.58	8349.8		1	944.4	47.4	3	R.MPAEIVVLLDSEDNPSLPKR.S
*	HsFLAG-Control_HeLa_NE	4.6533	0.4181	1861	1860.16	5963.8		1	731.3	55.9	16	R.GLRPLELPAVPATEPGNK.K
*	HsHeLa_Control_Ti_102.22	3.1104	0.2893	2650.06	2650.82	5128.4		1	386.5	41.7	2	K.NLDPDPEPPSPDSPTETFAAPAEVR.H
*	HsFLAG-Control_HeLa_NE	3.4066	0.0907	1200.68	1199.31	4779.5		1	1303.2	90	1	K.DREVAEGGLPR.A
*	HsFLAG-Control_HeLa_S1	2.8146	0.201	1276.26	1276.44	7104.8		1	999.2	75	2	R.AESPSPAPPPGLR.G
*	Hs293FLP-MG_Ti_204.223	4.1652	0.2434	2776.7	2777.02	10900.3		3	803	26	1	K.RVGAGDTSDWPTVLSESSTTVAGKPEK.G
gi|5730065|ref|N	19	122	0.445	247	28152	6	U	spindlin [Homo sapiens]				
*	HsFLAG-Control_HeLa_S1	2.5524	0.1523	1325.71	1326.5	4833.5		1	343	58.3	3	R.SSVGPSKPVSQPR.R
*	HsFLAG-Control_HeLa_S1	3.0744	0.2231	1326.44	1326.5	3809.5		1	445.3	62.5	9	R.SSVGPSKPVSQPR.R
*	HsFLAG-Control_HeLa_NE	2.7414	0.1165	1326.73	1326.5	4846.4		1	301.8	54.2	2	R.SSVGPSKPVSQPR.R
*	HsHeLa-FLAG-IP_S100_Ti_	2.8836	0.2659	1326.84	1326.5	3917.3		1	420.7	62.5	3	R.SSVGPSKPVSQPR.R
*	HsFLAG-Control_HeLa_NE	4.2609	0.2746	1857.68	1857.2	3271.9		1	643.8	68.8	43	K.GTVLDQVPVNPSLYLIK.Y
*	HsFLAG-Control_HeLa_S1	5.5151	0.4336	1694.69	1693.82	8717.1		1	2522.1	88.5	9	K.YDGFDCVYGLELNK.D
*	HsFLAG-Control_HeLa_NE	3.7966	0.4115	2094.79	2094.21	7482.3		1	721.1	50	8	K.YDGFDCVYGLELNKDER.V
*	HsFLAG-Control_HeLa_S1	3.7772	0.1609	1098.99	1099.27	5421.4		1	1539.3	94.4	3	R.VSALEVLPDR.V
*	HsFlag1P_Ti_103.2093.20	4.4117	0.382	1371.51	1372.58	7864.1		1	2387.5	87.5	6	R.ISDAHLADTMIGK.A
	HsHeLa_Control-MG_Ti_10	4.0915	0.3401	1777.54	1777.04	6757.4		1	1720	76.9	1	K.DPVLYMYQLLDDYK.E
	HsFlag1P_Ti_106.3196.31	5.5281	0.375	2346.24	2347.65	10130.9		1	2660	66.7	4	K.DPVLYMYQLLDDYKEGDLR.I
	HsFLAG-Control_HeLa_S1	4.5343	0.3515	2347.02	2347.65	4881.8		1	856.9	38.9	1	K.DPVLYMYQLLDDYKEGDLR.I
	HsF-IP-293-MG_Ti_106.27	5.0438	0.2755	2347.34	2347.65	9931.9		1	2671.7	66.7	2	K.DPVLYMYQLLDDYKEGDLR.I
	HsFLAG-Control_HeLa_NE	2.7657	0.1821	854.29	854.037	3938.9		1	651.2	91.7	2	K.PSVYFIK.F
	HsFLAG-Control_HeLa_NE	4.0442	0.3492	1789.83	1789.98	4977.2		1	817.4	46.2	1	K.FDDDFHIYVYDLVK.T
	HsFLAG-Control_HeLa_S1	3.9146	0.3163	1790.12	1789.98	4844.5		1	1279.7	55.8	3	K.FDDDFHIYVYDLVK.T
	HsFLAG-Control_HeLa_NE	4.7853	0.4088	1790.36	1789.98	8202.8		1	2020.3	80.8	5	K.FDDDFHIYVYDLVK.T
	HsFLAG-Control_HeLa_S1	5.8606	0.4583	1790.46	1789.98	8612.6		1	2552	84.6	10	K.FDDDFHIYVYDLVK.T
	HsFLAG-Control_HeLa_S1	4.7497	0.4247	1791.38	1789.98	8548.6		1	1784.2	76.9	7	K.FDDDFHIYVYDLVK.T
gi|4504445|ref|N	12	43	0.441	320	34196	9.2	U	heterogeneous nuclear ribonucleoprotein A1 isoform a [Homo sapiens]				
	HsHeLa3_Ti_105.3090.309	4.5282	0.3687	1785.58	1785.99	6082.7		2	1780.4	76.7	9	K.LFIGGLSFETTDESLR.S
	HsHeLa3_Ti_105.2447.244	3.5625	0.3412	2522.75	2522.76	8940.5		1	486.1	37.5	3	R.SHFEQWGTLTDCVVMRDPNTK.R
	HsHeLa3_Ti_104.3921.392	4.7467	0.4889	2150.92	2149.38	6734.3		1	1128.1	57.9	2	R.GFGFVTYATVEEVDAAMNAR.P
	HsHeLa3_Ti_106.2811.281	2.9572	0.358	2510.83	2511.81	7747.7		1	557.5	36.4	1	R.GFGFVTYATVEEVDAAMNARPHK.V
	HsHeLa3_Ti_103.0754.075	2.9209	0.2546	1166.16	1166.19	5370.5		1	597.6	81.2	2	K.EDTEEHHLR.D
	HsHeLa3_Ti_105.2479.247	3.8073	0.2837	1219.53	1219.44	6699.7		2	1625	88.9	3	K.IEVIEIMTDR.G
	HsHeLa3_Ti_105.2430.243	4.4011	0.3524	1859.16	1856.99	8999.6		1	1872.5	48.3	2	K.RGFAFVTFDDHDSVDK.I
	HsHeLa3_Ti_103.2474.247	3.6882	0.1837	1703.05	1700.8	4900.1		1	751.7	64.3	3	R.GFAFVTFDDHDSVDK.I
	HsHeLa3_Ti_106.1843.184	3.5117	0.3068	1486.8	1486.55	7334.6		1	1683.9	86.4	3	K.YHTVNGHNCEVR.K
	HsHeLa3_Ti_103.1590.159	3.791	0.3621	1376.88	1376.47	5034.1		1	785.5	69.2	2	R.SSGPYGGGGQYFAK.P
	Hs293FLP_TREX_Ti_105.1	4.0307	0.3919	1629.49	1629.77	7357.3		1	1190.7	66.7	9	R.SSGPYGGGGQYFAKPR.N

	HsHeLa3_Ti_103.1150.115	4.8554	0.4695	1695.06	1695.66	6014.4		1	1222.4	64.7	4	R.NQGGYGGSSSSSSYGSGR.R
gi|16507237|ref|N	23	196	0.431	654	72333	5.2	U	heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa) [Homo sapiens]				
	HsHeLa_Control-MG_Ti_10	3.4607	0.2799	1567.62	1567.74	4879.5		1	759.3	69.2	10	R.ITPSYVAFTPEGER.L
	HsFLAG-Control_HeLa_NE	4.4809	0.4059	1678.36	1678.8	5144.1		1	1285.4	78.6	13	K.NQLTSNPENTVFDAK.R
	HsGST-MOCK_Ti_302.184	3.5871	0.2384	1430.92	1431.55	4722.9		1	948.6	77.3	1	R.TWNDPSVQQDIK.F
	HsFLAG-MOCK_300mM_T	4.0908	0.2379	1735.37	1734.01	4901.4		1	1002.7	70	1	K.KTKPYIQVDIGGGQTK.T
	HsHeLa_Control-MG_Ti_10	3.604	0.3826	1537.55	1537.81	4462		1	1221.7	84.6	4	K.TFAPEEISAMVLTK.M
	HsHeLa_Control-MG_Ti_20	4.5532	0.2999	2016.65	2017.3	5160.4		1	995	67.6	3	K.KVTHAVVTVPAYFNDAQR.Q
	HsHeLa3_Ti_106.2239.223	3.1075	0.2958	1889.76	1889.12	4775.1		1	677.5	62.5	1	K.VTHAVVTVPAYFNDAQR.Q
	HsHeLa_Control-MG_Ti_20	5.5061	0.3911	1661.88	1660.91	4282.5		1	1591.7	86.7	75	R.IINEPTAAAIAYGLDK.R
	HsGST-MOCK_Ti_404.258	4.3238	0.4122	1816.51	1817.1	7746.6		1	1218.8	65.6	4	R.IINEPTAAAIAYGLDKR.E
	HsHeLa_Control-MG_Ti_20	2.8374	0.16	1154.61	1154.27	6652.3		1	746.9	77.8	5	K.RALSSQHQAR.I
	HsFLAG-Control_HeLa_NE	4.5787	0.4475	2165.87	2166.3	6386.8		1	2002.9	76.5	5	R.IEIESFYEGEDFSETLTR.A
	HsHeLa_Control-MG_Ti_10	3.6824	0.3009	1513.9	1513.75	5270.9		1	859.3	72.7	2	R.AKFEELNMDLFR.S
	HsHeLa_Control-MG_Ti_20	5.2951	0.3175	1589.73	1589.79	9908		1	2657.9	78.6	8	K.KSDIDEIVLVGGSTR.I
	HsHeLa_Control-MG_Ti_10	5.2164	0.435	1839.48	1838.02	6885.8		1	1962.2	78.1	11	K.SQIFSTASDNQPTVTIK.V
	HsHeLa_Control-MG_Ti_20	3.0232	0.1851	1192.44	1192.36	7161		4	972.2	77.8	5	K.VYEGERPLTK.D
	HsHeLa_Control-MG_Ti_20	3.9198	0.4359	1934.78	1935.19	6040.8		1	1490.3	70.6	7	K.DNHLLGTFDLTGIPPAPR.G
	HsHeLa_Control-MG_Ti_20	2.7247	0.0837	1075.23	1075.17	7406.4		3	1089.1	87.5	1	K.ITITNDQNR.L
	HsHeLa_Control-MG_Ti_10	3.6831	0.1824	1318.13	1317.44	4961.8		5	1216.9	90	3	R.NELESYAYSLK.N
	HsGST-MOCK_Ti_102.210	4.7365	0.5019	2532.2	2532.72	8513.4		1	1319.3	55	3	K.AVEEKIEWLESHQDADIEDFK.A
	HsHeLa_Control-MG_Ti_20	5.0625	0.4038	1975.83	1976.11	9296.7		1	2667	80	6	K.IEWLESHQDADIEDFK.A
	HsFLAG-MOCK_300mM_T	4.1686	0.3084	1656.02	1654.99	7985.2		1	1570.6	73.1	2	K.KKELEEIVQPIISK.L
	HsHeLa_Control-MG_Ti_20	4.2721	0.2365	1398.4	1398.64	7233.7		1	1246	77.3	4	K.ELEEIVQPIISK.L
	HsFLAG-Control_HeLa_NE	4.9602	0.515	2176.45	2177.28	8025.7		1	974.4	50	22	K.LYGSAGPPPTGEEDTAEKDEL.-
gi|20149594|ref|N	53	253	0.427	724	83264	5	U	heat shock 90kDa protein 1, beta [Homo sapiens]				
	HsFLAG-Control_HeLa_S1	3.2249	0.2813	1275.53	1276.39	5305.9		2	360.7	59.1	1	R.ELISNASDALDK.I
	HsHeLa3_Ti_102.1735.173	2.3869	0.3371	1275.7	1276.39	3254.4		1	203.8	59.1	1	R.ELISNASDALDK.I
	HsFLAG-Control_HeLa_NE	3.9623	0.3066	1276.13	1276.39	6399.8		1	1082.8	77.3	9	R.ELISNASDALDK.I
	HsFLAG-Control_HeLa_S1	3.9813	0.2935	1276.45	1276.39	6438.2		1	1279.8	81.8	5	R.ELISNASDALDK.I
	HsFLAG-Control_HeLa_S1	3.5279	0.3649	1545.79	1545.73	8298.4		1	1425.9	73.1	2	R.ELISNASDALDKIR.Y
	HsFLAG-Control_HeLa_NE	4.3103	0.339	1809.78	1810.01	3724.2		1	845	73.3	7	K.IRYESLTDPSKLDSGK.E
	HsFLAG-Control_HeLa_S1	2.678	0.2106	1039.44	1040.12	6287.3		3	663.1	75	4	R.YESLTDPSK.L
	HsFLAG-Control_HeLa_NE	2.7149	0.2011	1039.45	1040.12	6815.8		1	815.2	81.2	4	R.YESLTDPSK.L
	HsFLAG-Control_HeLa_NE	3.4808	0.2474	1040.52	1040.12	3725.7		4	589.2	87.5	2	R.YESLTDPSK.L
	HsFLAG-Control_HeLa_NE	3.3925	0.3111	1542.17	1540.67	6161.9		1	885.9	69.2	3	R.YESLTDPSKLDSGK.E
	HsFLAG-Control_HeLa_NE	4.4034	0.1007	1243.05	1243.45	5205.6		1	1215	86.4	20	K.ADLINNLGTIAK.S
	HsFLAG-Control_HeLa_S1	5.634	0.452	2257.72	2257.29	8942.2		1	2330.1	65.8	16	K.HNDDEQYAWESSAGGSFTVR.A
	HsFLAG-Control_HeLa_S1	3.3042	0.2832	1312.18	1312.33	6777.7		1	777.6	77.8	15	K.EDQTEYLEER.R
	HsFLAG-Control_HeLa_S1	3.5901	0.1509	1151.58	1152.25	8718.8		6	968.9	75	4	K.YIDQEELNK.T
*	HsFLAG-Control_HeLa_S1	5.789	0.4676	1847.93	1848.92	7437.7		1	1906.9	82.1	55	R.NPDDITQEEYGEFYK.S
	HsFLAG-Control_HeLa_NE	4.7198	0.3685	1528.53	1528.66	7778.9		1	1591.3	79.2	15	K.SLTNDWEDHLAVK.H
	HsFLAG-Control_HeLa_S1	3.1275	0.2534	1349.94	1349.49	5003.1		1	677	75	4	K.HFSVEGQLEFR.A
*	HsFLAG-Control_HeLa_NE	3.3786	0.1271	1237.49	1237.4	6036.8		3	1275.4	88.9	2	R.RAPFDLFENK.K
*	HsFLAG-Control_HeLa_S1	3.3884	0.178	1365.24	1365.58	8028.5		9	1119.5	75	1	R.RAPFDLFENKK.K
	Hs293FLP_TREX_Ti_104.1	2.2479	0.1466	1020.64	1020.17	5697.7		6	461.6	71.4	1	K.KFYEAFSK.N
*	HsFLAG-Control_HeLa_S1	2.191	0.2143	1141.7	1142.21	5626.3		1	407	66.7	2	K.LGIHEDSTNR.R
*	HsFLAG-Control_HeLa_NE	2.6341	0.3242	1141.71	1142.21	5894.3		1	503.1	66.7	1	K.LGIHEDSTNR.R
*	HsFLAG-Control_HeLa_NE	3.1679	0.3528	1142.22	1142.21	6405.5		1	903.6	83.3	2	K.LGIHEDSTNR.R

*	HsFLAG-Control_HeLa_S1	3.0058	0.3562	1142.84	1142.21	5931.7	1	1053.2	88.9	4	K.LGIHEDSTNR.R
	HsFLAG-Control_HeLa_NE	2.5769	0.1754	1160.35	1161.3	7541.9	1	863.9	72.2	3	K.SIYYITGESK.E
	HsFLAG-Control_HeLa_S1	2.5148	0.221	1160.47	1161.3	6813.7	1	754.9	72.2	1	K.SIYYITGESK.E
	HsFLAG-Control_HeLa_S1	2.3138	0.1998	1160.52	1161.3	6133.2	1	537.6	66.7	2	K.SIYYITGESK.E
	HsFLAG-Control_HeLa_NE	2.084	0.0823	1160.54	1161.3	9000.5	5	555.8	55.6	1	K.SIYYITGESK.E
	HsFLAG-Control_HeLa_S1	2.6506	0.2133	1160.58	1161.3	7847.6	1	879.2	72.2	1	K.SIYYITGESK.E
	HsFLAG-Control_HeLa_S1	2.9858	0.1922	1160.7	1161.3	8757.7	1	1028	72.2	2	K.SIYYITGESK.E
	HsFLAG-Control_HeLa_S1	3.2439	0.2195	1161.09	1161.3	4948	1	1060.4	83.3	2	K.SIYYITGESK.E
	HsFLAG-Control_HeLa_S1	2.7454	0.2521	1161.11	1161.3	5562.6	1	811.9	77.8	1	K.SIYYITGESK.E
	HsFLAG-Control_HeLa_S1	3.1987	0.2268	1161.16	1161.3	6138.1	1	1075.3	77.8	2	K.SIYYITGESK.E
	HsFLAG-Control_HeLa_NE	3.2065	0.2692	1161.17	1161.3	4925.4	1	949.4	83.3	2	K.SIYYITGESK.E
	HsFLAG-Control_HeLa_S1	3.2209	0.2532	1161.46	1161.3	4530.4	1	961.4	83.3	2	K.SIYYITGESK.E
	HsFLAG-Control_HeLa_S1	2.625	0.2281	1161.56	1161.3	7341.6	1	676.9	66.7	2	K.SIYYITGESK.E
	HsFLAG-Control_HeLa_NE	2.7698	0.2498	1161.93	1161.3	4283.3	1	897.3	83.3	1	K.SIYYITGESK.E
	HsFLAG-Control_HeLa_S1	2.9252	0.1111	1163.49	1161.3	4686.9	1	848.7	77.8	1	K.SIYYITGESK.E
	HsFLAG-Control_HeLa_S1	3.0728	0.3189	1251.13	1250.35	8877.3	1	1052.9	75	5	K.EQVANSAFVER.V
	HsHeLa3_Ti_103.3231.323	3.1593	0.4305	2449.84	2449.74	4448.7	1	226.5	34.2	1	R.GFEVVYMTEPIDEYCVQQLK.E
	HsFLAG-Control_HeLa_S1	2.5834	0.3358	1416.47	1417.47	3338.4	1	318	63.6	2	K.EGLELPEDEEEK.K
	HsFLAG-Control_HeLa_NE	2.8612	0.171	1417.26	1417.47	2994.8	7	388	68.2	6	K.EGLELPEDEEEK.K
	HsFLAG-Control_HeLa_S1	2.6126	0.0994	1010.16	1010.14	3542.1	5	518.3	85.7	1	K.AKFENLCK.L
*	HsHeLa3_Ti_103.2956.295	2.7087	0.286	2433.38	2433.67	6914.6	2	351.7	32.5	1	R.LVSSPCCIVTSTYGWTANMER.I
*	HsFLAG-MOCK_300mM_T	4.1596	0.2568	1912.31	1912.2	6388.9	3	1328.9	70	1	K.KHLEINPDHPIVETLR.Q
*	HsFLAG-Control_HeLa_S1	4.1255	0.1738	1783.09	1784.03	7228.6	1	1746.9	78.6	3	K.HLEINPDHPIVETLR.Q
*	HsFLAG-Control_HeLa_NE	4.4675	0.2901	1783.71	1784.03	6328.2	1	1390.7	75	11	K.HLEINPDHPIVETLR.Q
*	HsFLAG-Control_HeLa_S1	3.5668	0.2018	1784.68	1784.03	6557.3	2	1094.2	44.6	1	K.HLEINPDHPIVETLR.Q
*	HsFLAG-MOCK_300mM_T	3.683	0.2081	3290.72	3288.73	6480.2	1	1160.1	30.2	1	K.AVKDLVVLLFETALLSSGFSLEDPQTHSNR.I
*	HsFLAG-Control_HeLa_S1	5.8762	0.3863	2989.72	2990.34	9786.5	1	2002.2	35.6	4	K.DLVVLLFETALLSSGFSLEDPQTHSNR.I
*	HsFLAG-Control_HeLa_S1	4.6037	0.4103	2990.16	2990.34	6256.4	1	767.9	40.4	4	K.DLVVLLFETALLSSGFSLEDPQTHSNR.I
*	HsFLAG-Control_HeLa_NE	5.1025	0.4334	2990.62	2990.34	7851.1	1	1532.4	33.7	2	K.DLVVLLFETALLSSGFSLEDPQTHSNR.I
*	HsFLAG-Control_HeLa_S1	4.556	0.29	3534.29	3534.72	6727.8	1	621	25	7	K.LGLGIDEDEVAAEEPNAAVPDEIPPLEGDEDASR.M
gi|4506625|ref|N	20	51	0.426	148	16561	11	U	ribosomal protein L27a [Homo sapiens]			
*	HsHeLa_Control-MG_Ti_10	2.0269	0.2256	943.53	944	4085.8	3	300.2	68.8	1	R.GHVSHGHGR.I
*	HsHeLa_Control-MG_Ti_20	2.7813	0.2337	943.79	944	5133.3	1	991.6	87.5	1	R.GHVSHGHGR.I
	HsHeLa_Control-MG_Ti_20	3.7612	0.3273	1586.23	1586.79	7246.6	1	934.2	66.7	2	R.INFDKYHPGYFGK.V
	Hs293FLP_TREX_Ti_105.1	4.2859	0.2959	1579.51	1579.72	7288.4	1	1527.2	79.2	14	K.RNQSFCPTVNLDK.L
	Hs293FLP-MG_Ti_202.208	3.3477	0.1714	1422.94	1423.53	6221.8	1	1091.2	77.3	3	R.NQSFCPTVNLDK.L
	HsHeLa_Control-MG_Ti_20	4.5425	0.3747	2637.79	2637.92	6614.4	1	1247.8	39.3	1	R.NQSFCPTVNLDKLWTLVSEQTR.V
	HsHeLa_Control-MG_Ti_10	2.4712	0.3148	1232.69	1233.41	3612.1	1	184.9	66.7	1	K.LWTLVSEQTR.V
	Hs293FLP_Ti_302.2094.20	2.3419	0.233	1232.77	1233.41	3467.3	1	230.8	72.2	1	K.LWTLVSEQTR.V
	HsGST-MOCK_Ti_403.250	3.3623	0.2492	1233.32	1233.41	6497.9	1	985.2	83.3	4	K.LWTLVSEQTR.V
	HsHeLa_Control-MG_Ti_20	3.3591	0.1513	1233.5	1233.41	6031.9	1	975.7	83.3	7	K.LWTLVSEQTR.V
	HsHeLa_Control_Ti_103.23	2.8413	0.185	1233.54	1233.41	7322.7	1	1095.5	83.3	1	K.LWTLVSEQTR.V
	HsHeLa_Control-MG_Ti_20	3.358	0.2335	1354.58	1354.59	7382.3	2	1014.4	70.8	1	K.NKTGAAPIIDVVR.S
	Hs293FLP_TREX_Ti_102.1	2.5364	0.2295	1111.44	1112.32	4427	3	277.2	60	2	K.TGAAPIIDVVR.S
	Hs293FLP-MG_Ti_202.230	1.8274	0.186	1111.57	1112.32	5165.5	8	239.4	55	1	K.TGAAPIIDVVR.S
	Hs293FLP-MG_Ti_202.230	4.0214	0.2665	1112.31	1112.32	3097.7	1	862	95	3	K.TGAAPIIDVVR.S
	Hs293FLP-MG_Ti_102.221	2.9264	0.2592	1112.4	1112.32	3747	3	788.6	85	1	K.TGAAPIIDVVR.S
	Hs293FLP-MG_Ti_102.222	2.4207	0.3054	1112.92	1112.32	4216.9	4	262.7	60	1	K.TGAAPIIDVVR.S
	HsHeLa_Control-MG_Ti_20	3.3483	0.2642	1114.07	1112.32	3934.6	2	762.3	90	3	K.TGAAPIIDVVR.S

	Hs293FLP_TREX_Ti_102.1	3.0671	0.2844	1114.38	1112.32	3329.7		2	787.7	90	1	K.TGAAPIIDVVR.S
	Hs293FLP-MG_Ti_204.242	3.656	0.3221	1710.64	1710.97	7981.4		1	1109	63.3	2	K.TGAAPIIDVVRSGYYK.V
gi|4506769|ref|N	4	6	0.426	101	11457	6.8	U	S100 calcium-binding protein A7 [Homo sapiens]				
	HsFLAG-Control_293_Ti_1	2.1402	0.2399	1442.41	1442.53	4824		1	287.9	59.1	1	K.ENFPNFLSACDK.K
*	HsFLAG-Control_MG_293_	2.5991	0.1554	1257.36	1257.39	7390.8		8	794.6	70	1	K.GTNYLADVFEK.K
*	HsFLAG-Control_Hela_Ti_1	5.1539	0.4344	2312.75	2313.61	10264.6		1	1519.3	55.3	3	K.KIDFSEFLSLLGDIATDYHK.Q
*	HsFLAG-MOCK_300mM_T	5.0005	0.3437	2314.36	2313.61	5667.1		1	1055.7	40.8	1	K.KIDFSEFLSLLGDIATDYHK.Q
gi|7706337|ref|N	5	8	0.424	177	20198	4.8	U	coatomer protein complex, subunit zeta 1 [Homo sapiens]				
*	HsFLAG-MOCK_300mM_T	3.5959	0.2533	1674.57	1674.94	7679.9		1	1420.6	67.9	1	K.AILILDNDGDRLFAK.Y
*	HsFLAG-MOCK_300mM_T	3.965	0.3389	3609.82	3608.1	6219.2		1	652.5	25	1	R.ALLENMEGLFLAVDEIVDGGVILESDPQQVVHR.V
*	HsFLAG-Control_HeLa_S1	3.9879	0.2953	2469.63	2469.8	7809.9		4	652	28.4	1	R.VALRGEDVPLTEQTVSQVLQSAK.E
*	HsFLAG-MOCK_300mM_T	4.0796	0.3561	2970.07	2968.38	7202.8		1	963.8	30.8	1	R.VALRGEDVPLTEQTVSQVLQSAKEQIK.W
*	HsFLAG-Control_HeLa_S1	4.8599	0.4759	2029.98	2030.24	5546.1		1	1128.4	66.7	4	R.GEDVPLTEQTVSQVLQSAK.E
gi|17986258|ref|N	6	18	0.424	151	16930	4.7	U	smooth muscle and non-muscle myosin alkali light chain isoform 1 [Homo sapiens]				
gi|17986264|ref|N	6	18	0.408	157	17557	4.6	U	smooth muscle and non-muscle myosin alkali light chain isoform 3 [Homo sapiens]				
gi|17986262|ref|N	6	18	0.552	116	12939	4.9	U	smooth muscle and non-muscle myosin alkali light chain isoform 4 [Homo sapiens]				
gi|17986260|ref|N	6	18	0.552	116	12970	4.7	U	smooth muscle and non-muscle myosin alkali light chain isoform 2 [Homo sapiens]				
	HsFLAG-MOCK_150mM_T	3.9347	0.3169	1355.23	1355.53	4693.6		1	1052.5	79.2	5	R.ALGQNPTNAEVLK.V
	HsFLAG-MOCK_300mM_T	2.8889	0.2903	1431.99	1431.65	5480.3		1	695.5	66.7	1	K.VLGNPKSDEMNVK.V
	HsFLAG-MOCK_150mM_T	3.7269	0.3471	1888.68	1889.26	4645		1	996.1	66.7	1	K.VLDFEHFLPMLQTVAK.N
	HsFLAG-Control_HeLa_NE	4.1888	0.4122	1545.31	1545.6	8559.4		1	1553.4	75	8	K.DQGTYEDYVEGLR.V
	HsHeLa_Control-MG_Ti_10	2.7952	0.2864	995.92	996.195	5082.8		2	789.5	75	1	R.HVLVTLGEK.M
	HsFLAG-MOCK_150mM_T	3.0925	0.2235	996.3	996.195	3156.8		6	737.7	93.8	2	R.HVLVTLGEK.M
gi|6678271|ref|N	11	34	0.423	414	44740	6.2	U	TAR DNA binding protein [Homo sapiens]				
*	HsFLAG-Control_HeLa_NE	3.5922	0.2004	3878.98	3877.13	8708.6		3	426.4	18.6	1	R.VTEDENDEPIEIPSEDDGTVLLSTVTAQFPGACGLR.Y
*	HsHeLa3_Ti_106.1956.195	3.0358	0.3403	1311.67	1311.47	5737.9		1	559.3	66.7	2	R.YRNPVSQCMR.G
*	HsFLAG-Control_HeLa_NE	4.0612	0.2213	2625.49	2626.03	9140.9		6	656.8	27.2	1	R.LVEGILHAPDAGWGNLVYVVNYPK.D
*	HsHeLa3_Ti_105.3511.351	4.8758	0.3716	2627	2626.03	4184		1	786.7	52.2	3	R.LVEGILHAPDAGWGNLVYVVNYPK.D
*	HsHeLa3_Ti_103.3411.341	4.3562	0.368	1342.77	1342.62	6778.8		1	1604.2	81.8	4	K.TSDLIVLGLPWK.T
*	HsHeLa3_Ti_102.1495.149	2.5122	0.0933	1145.48	1145.25	4300.7		2	688.7	75	1	R.FTEYETQVK.V
*	HsGST-MOCK_Ti_103.415	5.6939	0.4638	3702.85	3704.08	9339.2		1	1343	30.2	2	R.CTEDMTEDELREFFSQYGDVMDVFIPKPFR.A
*	HsHeLa3_Ti_105.4090.409	2.9484	0.2666	2324.77	2323.67	8860.2		1	724.5	44.4	1	R.EFFSQYGDVMDVFIPKPFR.A
*	HsHeLa3_Ti_106.3274.327	4.5157	0.4575	2673.96	2673.99	6529.5		1	897	47.8	1	R.AFAFVTFADDQIAQSLCGEDLIIK.G
*	HsHeLa3_Ti_105.1515.151	2.8922	0.2159	1254.47	1252.41	5236.5		1	1010.5	77.3	1	K.GISVHISNAEPK.H
*	HsFLAG-Control_HeLa_NE	4.8408	0.3829	1728.77	1727.79	7798.1		1	1941.1	70.6	17	R.FGGNPGGFGNQGGFGNSR.G
gi|40807496|ref|N	57	281	0.421	1048	116954	6.7	U	OTU domain containing 4 protein isoform 1 [Homo sapiens]				
	HsHeLa_Control-MG_Ti_10	2.7398	0.1852	1064.55	1064.26	4932.8		1	965.6	92.9	1	-.MACIHYLR.E
	Hs283FLP_Ti_105.2811.28	4.5662	0.3562	1711.28	1709.89	4837.9		1	1506	88.5	1	K.FEAFIEGSFEEYLK.R
	HsHeLa_Control-MG_Ti_20	5.5435	0.3195	2852.31	2853.16	8571.7		1	1906.7	38	4	R.KDFIIYREPNVSPSQVTENNFPEK.V
	Hs293FLP-MG_Ti_203.265	4.5094	0.4619	2723.61	2724.99	10002.6		1	1185.9	47.7	2	K.DFIIYREPNVSPSQVTENNFPEK.V
	Hs293FLP-MG_Ti_203.264	5.5313	0.3917	2724.75	2724.99	6590.2		1	1206.4	37.5	2	K.DFIIYREPNVSPSQVTENNFPEK.V
	Hs283FLP_Ti_106.2255.22	4.4146	0.3525	2725.34	2724.99	8994.2		1	989.3	47.7	3	K.DFIIYREPNVSPSQVTENNFPEK.V
	Hs283FLP_Ti_106.2259.22	4.9365	0.2948	2727.63	2724.99	6145		1	1259	39.8	3	K.DFIIYREPNVSPSQVTENNFPEK.V
	HsHeLa-FLAG-IP_S100_Ti_	2.8022	0.3616	1917.32	1917.04	5104		1	275.1	40.6	1	R.EPNVSPSQVTENNFPEK.V
	HsHeLa_Control-MG_Ti_20	4.6751	0.4264	2152.54	2153.45	9288.9		1	1796.3	64.7	6	K.VLLCFSNGNHYDIVYPIK.Y
	Hs293FLP-MG_Ti_202.423	4.7272	0.3424	2065.57	2065.31	8056.4		1	1709.5	65.6	15	K.ESSAMCQSLLYELLYEK.V
*	Hs283FLP_Ti_104.1659.16	4.6078	0.4296	1974.74	1975.21	5963		1	649.9	50	12	K.TAAAAADVNGFKPLSGNELK.N
*	HsF-IP-293-MG_Ti_102.14	3.198	0.1344	1261.25	1260.35	5382.1		1	868.8	77.3	2	K.NNGNSTSLPLSR.K

*	Hs283FLP_Ti_102.2330.23	3.2622	0.1388	1194.39	1194.37	3228.1	1	637.7	87.5	5	R.NVEYEIWLK.S
*	Hs293FLP-MG_Ti_203.228	3.4103	0.4081	1784.36	1785.95	6312.2	1	614.4	63.3	1	K.RDYSIAAGLQYEVGDK.C
*	HsHeLa_Control-MG_Ti_10	4.4468	0.371	2466.01	2466.75	6090.6	1	835	47.7	3	K.FLNADVQGIHSENGPVLVEELGK.K
*	Hs293FLP-MG_Ti_203.288	4.5276	0.393	2466.48	2466.75	8750.5	1	1457.6	52.3	2	K.FLNADVQGIHSENGPVLVEELGK.K
*	Hs293FLP-MG_Ti_203.289	5.22	0.38	2466.65	2466.75	4542.9	1	1475.8	45.5	2	K.FLNADVQGIHSENGPVLVEELGK.K
*	HsHeLa_Control-MG_Ti_20	5.4819	0.449	2467.15	2466.75	4855.5	1	1533.6	45.5	2	K.FLNADVQGIHSENGPVLVEELGK.K
*	HsHeLa_Control-MG_Ti_10	4.9153	0.3775	2594.35	2594.93	6537.4	1	989.1	50	2	K.FLNADVQGIHSENGPVLVEELGKK.H
*	Hs293FLP_Ti_304.2311.23	5.222	0.4767	2594.57	2594.93	5237.6	1	1164.6	38	7	K.FLNADVQGIHSENGPVLVEELGKK.H
*	Hs293FLP_TREX_Ti_105.1	4.1628	0.3551	1839.34	1838.93	5477.2	1	1079.9	73.3	5	K.KPSTSGQNFHSDVDYR.G
*	Hs283FLP_Ti_105.1333.13	3.5743	0.2821	1839.8	1838.93	4188.4	2	831.3	48.3	1	K.KPSTSGQNFHSDVDYR.G
*	Hs283FLP_Ti_105.1325.13	4.677	0.4081	1839.96	1838.93	5729.2	1	1153.5	73.3	8	K.KPSTSGQNFHSDVDYR.G
*	HsHeLa_Control-MG_Ti_20	3.1878	0.3513	1603.27	1603.65	2553	1	328.7	64.3	3	R.QHAFSSHSSGSQSQK.F
*	HsHeLa_Control-MG_Ti_20	2.7293	0.1852	1391.28	1391.44	5615.2	5	660.6	70	1	R.ERVEDFDHTSR.E
*	HsHeLa_Control-MG_Ti_10	2.9839	0.3008	1107.62	1106.14	5918.6	2	919.3	87.5	2	R.VEDFDHTSR.E
*	Hs293FLP_TREX_Ti_102.1	3.5379	0.282	1428.46	1428.5	6344.6	1	985.7	77.3	13	R.ESNYFGLSPEER.R
*	HsHeLa_Control-MG_Ti_20	6.4409	0.4332	3913.69	3913.17	7268.7	1	1473.7	30.9	15	R.LLYEIQNRDEQAFPALSSSSVNQSASQSSNPCVQR.K
*	Hs293FLP-MG_Ti_202.222	4.135	0.4617	2882.1	2882.98	8362.9	1	1282.6	46.2	3	R.DEQAFPALSSSSVNQSASQSSNPCVQR.K
*	Hs293FLP-MG_Ti_204.115	3.0374	0.2495	1236.47	1237.32	5705.2	4	528.3	65	5	K.DSIHGHSQLDK.R
*	HsHeLa_Control-MG_Ti_20	2.244	0.358	1236.47	1237.32	3578.2	1	244.5	55	1	K.DSIHGHSQLDK.R
*	Hs293FLP-MG_Ti_204.117	3.2737	0.2817	1237.16	1237.32	6010.5	8	709.9	70	3	K.DSIHGHSQLDK.R
*	HsHeLa_Control-MG_Ti_10	2.7689	0.2173	1237.65	1237.32	5595.5	3	678.4	70	1	K.DSIHGHSQLDK.R
*	HsHeLa_Control-MG_Ti_20	2.758	0.1907	1237.73	1237.32	5559.4	6	587.9	70	2	K.DSIHGHSQLDK.R
*	HsHeLa_Control-MG_Ti_10	3.0561	0.3165	1237.73	1237.32	4442.5	1	482.8	70	1	K.DSIHGHSQLDK.R
*	HsFLAG-Control_HeLa_NE	5.2543	0.3451	1615.31	1615.74	8101.8	1	2628.9	88.5	12	K.RPEPSTLENITDDK.Y
*	Hs293FLP-MG_Ti_204.183	5.9717	0.4364	2536.41	2536.76	9013.4	1	1676.4	39.8	2	K.RPEPSTLENITDDKYATVSSPSK.S
*	Hs283FLP_Ti_105.1737.17	3.7477	0.2837	2131.85	2132.38	3646.9	1	452.9	58.3	7	R.AIVPPYSLCQTGEDLPKDK.N
*	Hs283FLP_Ti_105.2415.24	1.8529	0.1275	971.55	972.175	3919.5	3	355.4	78.6	1	R.FFFNLGVK.A
*	Hs293FLP-MG_Ti_202.379	3.0321	0.3044	2669.77	2670.97	7062.4	1	244.1	32.6	1	R.QNIVLPSDEKGELDLSLENLDLSK.D
*	Hs283FLP_Ti_106.2488.24	3.3996	0.2764	2671.93	2670.97	8215.5	1	533.5	37	3	R.QNIVLPSDEKGELDLSLENLDLSK.D
*	HsF-IP-293-MG_Ti_106.24	4.0771	0.3918	2672.9	2670.97	4988.7	1	375.8	28.3	2	R.QNIVLPSDEKGELDLSLENLDLSK.D
*	Hs283FLP_Ti_102.2661.26	5.1598	0.359	1545.82	1546.72	6886.4	1	1555.9	76.9	17	K.GELDLSLENLDLSK.D
*	Hs293FLP-MG_Ti_202.209	5.3644	0.4781	1669.36	1669.71	6162.9	1	1799.6	85.7	22	K.DCGSVSTVDEFPEAR.G
*	Hs293FLP-MG_Ti_205.147	5.5247	0.3896	2117.81	2119.26	5280.2	1	1054	63.2	5	R.GEHVHSLPEASVSSKPDEGR.T
*	HsHeLa_Control-MG_Ti_20	5.1877	0.4334	2118.94	2119.26	7729.3	1	2098.4	48.7	1	R.GEHVHSLPEASVSSKPDEGR.T
*	HsHeLa_Control-MG_Ti_20	4.5442	0.3672	2119.44	2119.26	7039.7	1	1046.8	60.5	1	R.GEHVHSLPEASVSSKPDEGR.T
*	Hs293FLP-MG_Ti_205.147	5.2588	0.2662	2119.58	2119.26	7562.5	1	1852.4	46.1	1	R.GEHVHSLPEASVSSKPDEGR.T
*	HsHeLa_Control-MG_Ti_20	3.9833	0.3479	3036.37	3037.19	7259.6	1	671.5	26.9	1	R.GEHVHSLPEASVSSKPDEGRTEQSSQTR.K
*	HsHeLa_Control-MG_Ti_20	2.9412	0.2894	1567.59	1568.81	5351.9	1	911.4	63.3	1	R.KADTALASIPPVAEGK.A
*	HsFlag1P_Ti_105.2013.201	5.0761	0.4361	1568.44	1568.81	5418.4	1	1711.8	80	8	R.KADTALASIPPVAEGK.A
*	Hs293FLP_Ti_303.1635.16	3.0745	0.3587	1568.7	1568.81	5263	1	910.2	63.3	1	R.KADTALASIPPVAEGK.A
*	Hs293FLP_Ti_303.1627.16	4.7038	0.3812	1568.75	1568.81	4376.1	1	1459	80	13	R.KADTALASIPPVAEGK.A
*	Hs283FLP_Ti_104.1517.15	5.0318	0.4162	1568.87	1568.81	4516.6	1	1258.2	76.7	7	R.KADTALASIPPVAEGK.A
*	HsF-IP-293-MG_Ti_102.14	4.8903	0.3991	1546.65	1546.63	5001.1	1	1214.4	76.7	31	K.TAADVVSPGANSVDSR.V
*	HsHeLa_Control-MG_Ti_10	4.7565	0.4098	2360.24	2359.51	6237.1	1	936.9	55.3	1	R.VQRPKEESSEDENEVSNILR.S
*	HsHeLa_Control-MG_Ti_20	3.4331	0.2524	1311.92	1311.36	8510.2	1	1055.3	77.8	3	R.SRDEGYQYHR.N
gi|50053795|ref|	49	329	0.421	611	69151	5.7	U	eukaryotic translation initiation factor 4B [Homo sapiens]			
*	Hs283FLP_Ti_104.2507.25	5.7692	0.5059	2278.14	2277.45	6944.4	1	1351.5	56.8	15	K.TISLTDFLAEDGGTGGGSTYVSK.P
*	HsHeLa_Control-MG_Ti_20	5.6496	0.4064	3226.89	3226.26	7621.2	1	1217	31.5	7	K.PVSWADETDDLEGDVSTTWHSNDDDVYR.A

*	HsHeLa_Control-MG_Ti_20	5.8178	0.4607	2340.32	2342.61	6469.7		1	1400.1	62.5	7	K.SPPYTAFLGNLPYDVTEESIK.E
*	HsF-IP-293_Ti_205.3410.34	5.233	0.4817	2340.73	2342.61	5356.4		1	1027	60	37	K.SPPYTAFLGNLPYDVTEESIK.E
*	HsF-IP-293-MG_Ti_102.344	4.8066	0.4031	2340.83	2342.61	5223.8		1	996.1	60	24	K.SPPYTAFLGNLPYDVTEESIK.E
*	HsFLAG-Control_HeLa_NE	4.6212	0.4063	2341.66	2342.61	6614.1		1	842.5	50	23	K.SPPYTAFLGNLPYDVTEESIK.E
*	HsF-IP-293-MG_Ti_102.324	5.7263	0.3338	2342.06	2342.61	5372.1		1	1277.9	43.8	2	K.SPPYTAFLGNLPYDVTEESIK.E
*	Hs293FLP-MG_Ti_202.406	3.9763	0.279	2342.09	2342.61	6538.7		1	642.7	45	5	K.SPPYTAFLGNLPYDVTEESIK.E
*	Hs293FLP-MG_Ti_202.413	5.3127	0.2303	2342.14	2342.61	7799.7		1	1510.1	40	1	K.SPPYTAFLGNLPYDVTEESIK.E
*	Hs283FLP_Ti_102.3301.33	4.2878	0.187	2342.59	2342.61	5413.1		6	869.2	38.8	1	K.SPPYTAFLGNLPYDVTEESIK.E
*	HsGST-MOCK_Ti_403.407	2.9562	0.3052	2342.6	2342.61	6920.3		1	675.5	47.5	2	K.SPPYTAFLGNLPYDVTEESIK.E
*	HsHeLa_Control-MG_Ti_20	4.2741	0.2694	2342.76	2342.61	6315.9		1	1209	41.2	1	K.SPPYTAFLGNLPYDVTEESIK.E
*	HsHeLa_Control-MG_Ti_10	3.5693	0.2058	2343.23	2342.61	4874.3		3	542.4	32.5	1	K.SPPYTAFLGNLPYDVTEESIK.E
*	HsHeLa_Control-MG_Ti_20	3.738	0.3532	2920.82	2922.26	5277.5		1	379.1	37.5	4	K.SPPYTAFLGNLPYDVTEESIKEFFR.G
*	HsHeLa_Control-MG_Ti_20	4.5319	0.3365	2921.76	2922.26	8031.1		2	642.2	26	5	K.SPPYTAFLGNLPYDVTEESIKEFFR.G
*	HsHeLa_Control-MG_Ti_10	4.1955	0.2616	2922.72	2922.26	5147.4		1	694.3	33.3	4	K.SPPYTAFLGNLPYDVTEESIKEFFR.G
*	Hs283FLP_Ti_103.1448.14	2.9941	0.1446	830.34	829.975	4592		1	925.1	85.7	2	R.GLNISAVR.L
*	Hs283FLP_Ti_103.1450.14	1.9013	0.1525	830.63	829.975	3624.1		5	212.7	71.4	1	R.GLNISAVR.L
*	HsF-IP-293-MG_Ti_106.295	3.7623	0.2783	2947.08	2948.17	9360.1		1	912.8	28.8	1	K.GFGYAEFEDLDSLLSALSLNEESLGNR.R
*	Hs293FLP-MG_Ti_205.487	5.6655	0.4802	2947.56	2948.17	12358.5		1	2678.3	37.5	4	K.GFGYAEFEDLDSLLSALSLNEESLGNR.R
*	HsF-IP-293_Ti_206.3102.31	5.1124	0.4269	2947.89	2948.17	7201.5		1	1037.6	44.2	12	K.GFGYAEFEDLDSLLSALSLNEESLGNR.R
*	Hs293FLP-MG_Ti_205.486	5.5193	0.4976	2947.9	2948.17	7586.4		1	1325.9	48.1	13	K.GFGYAEFEDLDSLLSALSLNEESLGNR.R
*	HsF-IP-293-MG_Ti_106.295	5.8379	0.3712	2948.17	2948.17	7100.4		1	1202.8	46.2	20	K.GFGYAEFEDLDSLLSALSLNEESLGNR.R
*	HsHeLa_Control-MG_Ti_20	5.3347	0.4353	2948.3	2948.17	8936.1		1	1235.7	44.2	26	K.GFGYAEFEDLDSLLSALSLNEESLGNR.R
*	HsHeLa_Control-MG_Ti_20	6.7576	0.4246	2949	2948.17	9140.7		1	1553.7	35.6	4	K.GFGYAEFEDLDSLLSALSLNEESLGNR.R
*	Hs283FLP_Ti_105.4083.40	6.9287	0.4098	2949.43	2948.17	9028.5		1	1919.1	35.6	7	K.GFGYAEFEDLDSLLSALSLNEESLGNR.R
*	Hs293FLP-MG_Ti_205.464	4.225	0.3772	3103.85	3104.36	6326.1		2	621.5	24.1	7	K.GFGYAEFEDLDSLLSALSLNEESLGNRR.I
*	HsHeLa_Control-MG_Ti_20	1.9277	0.218	1357.47	1358.49	3621.4		7	206.2	45.5	1	R.IRVDVADQAQDK.D
*	Hs293FLP_TREX_Ti_103.1	4.3476	0.2835	1358.54	1358.49	5398.8		1	1432.5	86.4	15	R.IRVDVADQAQDK.D
*	HsHeLa_Control-MG_Ti_10	4.2372	0.3066	1359.75	1358.49	5345.4		1	1433.2	86.4	4	R.IRVDVADQAQDK.D
*	HsHeLa_Control-MG_Ti_10	3.0468	0.2241	1509.87	1509.53	3998.1		2	694.6	77.3	2	R.NRDSDKTDTDWR.A
*	HsHeLa_Control-MG_Ti_10	2.3967	0.3049	1239.59	1239.24	3773		1	325.2	55.6	1	R.DSDKTDTDWR.A
*	HsHeLa_Control-MG_Ti_20	3.7084	0.2757	1610.56	1608.71	4292.4		1	690.7	69.2	13	R.ARPATDSFDDYPPR.R
*	HsHeLa_Control-MG_Ti_20	2.728	0.2542	914.35	914.012	5469.5		1	933.2	100	2	R.RAFGSGYR.R
*	HsHeLa_Control-MG_Ti_20	2.5395	0.2107	1531.5	1532.74	4073.1		8	232	46.7	2	R.AASIFGGAKPVDTAAR.E
*	HsHeLa_Control-MG_Ti_20	4.3197	0.3449	1532.07	1532.74	7292.4		2	926.6	63.3	13	R.AASIFGGAKPVDTAAR.E
*	HsFLAG-Control_HeLa_S1	3.8316	0.2185	1533.4	1532.74	7185.3		4	679.6	53.3	10	R.AASIFGGAKPVDTAAR.E
*	HsFlag1P_Ti_106.1958.195	3.3734	0.0988	1300.44	1300.5	9340		1	1180.4	77.8	1	R.LQKEQEKLQR.Q
*	HsF-IP-293-MG_Ti_102.128	3.1447	0.1388	1049.16	1048.14	4157.5		4	595	81.2	5	K.SLENETLNK.E
*	HsHeLa_Control-MG_Ti_20	5.7495	0.4263	3220.02	3220.48	7338.1		1	1240.3	32.4	9	K.SLENETLNKEEDCHSPTSKPPKPDQPLK.V
*	HsHeLa_Control-MG_Ti_20	3.879	0.3358	2190.58	2191.37	7318.1		1	614.8	52.8	4	K.EEDCHSPTSKPPKPDQPLK.V
*	HsF-IP-293-MG_Ti_106.184	2.9151	0.1527	2190.62	2191.37	7768.7		2	363	38.9	1	K.EEDCHSPTSKPPKPDQPLK.V
*	Hs293FLP-MG_Ti_205.139	2.8528	0.2023	2190.68	2191.37	8939.4		3	526.2	44.4	1	K.EEDCHSPTSKPPKPDQPLK.V
*	HsF-IP-293-MG_Ti_106.183	4.1344	0.2635	2190.98	2191.37	9671.7		1	991.7	33.3	1	K.EEDCHSPTSKPPKPDQPLK.V
*	HsHeLa_Control-MG_Ti_20	3.5284	0.1394	2191.7	2191.37	9469.2		2	1119.2	37.5	1	K.EEDCHSPTSKPPKPDQPLK.V
*	HsHeLa_Control-MG_Ti_10	3.5459	0.2349	2192.67	2191.37	8330.2		1	1072.6	36.1	1	K.EEDCHSPTSKPPKPDQPLK.V
*	HsHeLa_Control-MG_Ti_20	2.7585	0.2571	1295.25	1295.4	3804		7	430.7	62.5	2	K.VAPAQPSEEGPGR.K
*	HsHeLa_Control-MG_Ti_20	3.7948	0.1945	1446.2	1446.62	8756.5		1	1746.9	79.2	2	R.KDENKVDGMNAPK.G
*	HsHeLa-FLAG-IP_S100_Ti_	5.8837	0.4864	2076.24	2077.03	7955		1	1379.5	61.1	2	K.YAALSVDGEDENEGEDYAE.-
gi|4506671|ref|NI	5	14	0.417	115	11665	4.5	U		ribosomal protein P2 [Homo sapiens]			
	HsFLAG-Control_293_Ti_1	3.6283	0.2844	1869.45	1870.11	10083.1		1	1600.3	58.3	4	R.YVASYLLAALGGNSSPSAK.D

*	Hs293FLP_TREX_Ti_106.2	4.9181	0.3805	1901.62	1902.11	8949	1	1601.3	65.6	2	K.KILDSVGIEADDDRLNK.V
*	Hs293FLP_TREX_Ti_106.2	5.0486	0.3724	1902.41	1902.11	5535	1	1646.1	53.1	1	K.KILDSVGIEADDDRLNK.V
*	Hs293FLP_TREX_Ti_104.1	4.7723	0.3584	1772.74	1773.94	6348.3	1	1432.9	73.3	6	K.ILDSVGIEADDDRLNK.V
*	HsFLAG-Control_HeLa_NE	3.4757	0.1721	1259.29	1257.43	7985.5	1	1421.5	81.8	1	K.NIEDVIAQGIGK.L
gi|11386157|ref|N	4	6	0.411	146	16185	6.9	U	cytidine deaminase [Homo sapiens]			
*	HsGST-MOCK_Ti_104.178	3.6255	0.2543	2618.9	2616.92	10064.6	1	959.7	31	1	K.RPACTLKPECVQQLLVCSQEAK.K
*	HsHeLa_Control-MG_Ti_10	3.938	0.3859	2325.24	2325.55	4513.4	1	1144.4	60	2	K.SAYCPYSHFPVGAALLTQEGR.I
*	HsHeLa_Control-MG_Ti_10	3.8298	0.2113	2326.8	2325.55	7491.1	6	798.4	31.2	1	K.SAYCPYSHFPVGAALLTQEGR.I
*	HsHeLa_Control-MG_Ti_10	4.1741	0.4166	1999.83	1998.1	5805.2	1	848.1	59.4	2	K.GCNIENACYPLGICAER.T
gi|38201714|ref|N	11	50	0.408	326	36092	9.2	U	ELAV-like 1 [Homo sapiens]			
*	HsGST-MOCK_Ti_303.325	4.6197	0.4296	2162.45	2163.45	4938.9	1	524.9	55.9	4	R.TNLIVNYLPQNMTQDELR.S
*	HsFLAG-Control_HeLa_NE	2.8571	0.2381	1353.62	1354.5	6877.2	1	594.7	58.3	2	R.SLFSSIGEVESAK.L
*	HsHeLa3_Ti_103.2380.238	3.8203	0.111	1354.67	1354.5	5191.5	1	1358.7	83.3	2	R.SLFSSIGEVESAK.L
*	HsFLAG-Control_HeLa_NE	4.1273	0.356	1355.1	1354.5	5530.6	1	1448.4	87.5	11	R.SLFSSIGEVESAK.L
*	HsHeLa3_Ti_106.2359.235	3.3085	0.3442	1783.86	1784.02	7597.3	2	837.6	53.1	2	K.VAGHSLGYGFVNYVTAK.D
*	HsFLAG-Control_HeLa_NE	2.8005	0.1551	1336.21	1336.53	5824.5	5	905.9	72.7	2	K.VSYARPSSEVIK.D
*	HsFLAG-Control_HeLa_NE	4.3168	0.2589	1220.44	1219.38	8941.3	1	2057	90	8	K.DANLYISGLPR.T
*	HsFLAG-Control_HeLa_NE	3.8937	0.3256	1190.48	1189.35	6751.5	1	1289.7	85	5	R.VLVDQTTGLSR.G
*	HsGST-MOCK_Ti_104.160	5.1227	0.2868	2769.13	2770.03	4336.6	1	604.8	31	2	K.RSEAEEAITSFNGHKPPGSSEPITVK.F
*	HsFLAG-Control_HeLa_NE	4.7549	0.322	1569.16	1569.8	8282.6	1	1550.3	73.1	10	K.NVALLSQLYHSPAR.R
*	HsFLAG-MOCK_300mM_T	3.1125	0.177	1234.9	1234.36	5255.9	1	743.3	70	2	R.FGGPVHHQAQR.F
gi|17933772|ref|N	4	39	0.408	103	11801	6.8	U	S100 calcium binding protein A16 [Homo sapiens]			
*	HsFlag1P_Ti_103.3159.315	3.0832	0.2595	1294.61	1295.57	6419.6	1	724.1	70	2	K.AVIVLVENFYK.Y
*	HsHeLa_Control-MG_Ti_20	4.3422	0.3002	1296.29	1295.57	6899.7	1	1394.8	80	12	K.AVIVLVENFYK.Y
*	HsHeLa_Control-MG_Ti_20	4.0196	0.3002	1366.25	1366.48	8749.4	1	1914.2	86.4	7	K.LIQNLDANHDGR.I
*	HsHeLa_Control-MG_Ti_20	6.2635	0.3721	2083.35	2082.4	7819.3	1	1720.2	63.9	18	R.ISFDEYWTLIGGITGPIAK.L
gi|4504255|ref|N	4	9	0.406	128	13553	10.6	U	H2A histone family, member Z [Homo sapiens]			
	Hs293FLP-MG_Ti_104.190	2.3447	0.1182	944.77	945.109	4092.1	5	353.2	68.8	1	R.AGLQFPVGR.I
	HsHeLa_Control-MG_Ti_10	2.6626	0.17	945.58	945.109	3921	2	699.4	81.2	1	R.AGLQFPVGR.I
	HsFLAG-Control_HeLa_NE	6.262	0.4089	2896.59	2897.3	10111.4	1	2090.8	33.9	5	R.VGATAAVYSAAILEYLTAEVLELAGNASK.D
	HsGST-MOCK_Ti_105.150	4.106	0.3691	1371.5	1371.63	5944	1	1177.2	73.1	2	K.ATIAGGGVIPHIHK.S
gi|52632383|ref|N	15	42	0.404	589	64133	8.2	U	heterogeneous nuclear ribonucleoprotein L isoform a [Homo sapiens]			
*	HsFLAG-Control_HeLa_NE	3.4832	0.2697	1077.4	1077.27	4737.5	1	847.4	88.9	5	K.TPASPVVHIR.G
*	HsGST-MOCK_Ti_305.060	3.9791	0.403	3088.4	3089.61	7363	1	796.4	28.6	1	R.GLIDGVVEADLVEALQEFGPISYVVVMPK.K
*	HsGST-MOCK_Ti_306.057	3.8237	0.3292	3091.03	3089.61	7557.4	1	670.7	33.9	2	R.GLIDGVVEADLVEALQEFGPISYVVVMPK.K
	HsFLAG-Control_HeLa_NE	4.5273	0.2853	3868.89	3870.41	8281.9	1	640.4	21.2	1	R.SVNSVLLFTILNPIYSITTDVLYTICNPCGPVQR.I
	HsFLAG-MOCK_300mM_T	3.263	0.3709	1731.3	1730.85	5455.1	1	705.4	53.3	1	K.ASLNGADIYSGCCTLK.I
	HsFLAG-Control_HeLa_NE	3.9114	0.4111	2734.86	2735.75	6787.8	1	769	43.8	3	K.NDQDTWDYTNPNLSGQGDPGSNPNK.R
	HsFLAG-MOCK_150mM_T	5.1825	0.3722	1589.66	1589.8	5629.3	1	1644.3	87.5	11	R.VFNVFCLYGNVEK.V
	HsHeLa3_Ti_104.2032.203	3.2022	0.3524	1870.18	1869.12	7314.6	1	651	50	2	K.SKPGAAMVEMADGYAVDR.A
	HsHeLa3_Ti_106.2255.225	3.0603	0.3915	1636.59	1635.88	5630	1	707.6	65.4	1	R.AITHLNNNFMFGQK.L
	HsFLAG-Control_HeLa_NE	4.1363	0.337	2188.29	2189.37	5534	1	807.1	52.6	2	K.QPAIMPGQSYGLEDGSCSYK.D
	HsHeLa_Control-MG_Ti_20	6.4121	0.421	3775.45	3775.18	10892.9	1	1561.7	27.4	4	R.IQHPSNVLHFFNAPLEVTEENFFEICDELGVK.R
	HsHeLa3_Ti_103.1980.198	2.3341	0.33	1222.65	1223.33	8016.8	3	545.2	55	2	R.SSSGLLEWESK.S
	HsFLAG-Control_HeLa_NE	3.0914	0.288	1224.37	1223.33	6900.4	1	904.4	70	2	R.SSSGLLEWESK.S
	HsFLAG-MOCK_300mM_T	4.3559	0.3246	3072.51	3072.42	5977.2	1	746.6	29.8	1	R.SSSGLLEWESKSDALETLGFLNHYQMK.N
	HsHeLa3_Ti_104.2912.291	3.8858	0.3268	1869.39	1868.11	5633.8	1	707.5	60	4	K.SDALETLGFLNHYQMK.N
gi|14043072|ref|N	9	18	0.402	353	37430	8.9	U	heterogeneous nuclear ribonucleoprotein A2/B1 isoform B1 [Homo sapiens]			
gi|4504447|ref|N	9	18	0.416	341	36006	8.6	U	heterogeneous nuclear ribonucleoprotein A2/B1 isoform A2 [Homo sapiens]			

	HsHeLa3_Ti_105.3159.315	4.553	0.3655	1800.75	1800.02	5947.5		1	1544	73.3	2	K.LFIGGLSFETTEESLR.N
	HsHeLa3_Ti_103.1642.164	2.7474	0.191	1087.61	1088.16	4587.5		2	353.3	71.4	2	R.NYYEQWGK.L
	HsHeLa_Control-MG_Ti_20	3.3233	0.223	1339.58	1339.49	5135.1		1	854.6	79.2	1	R.EESGKPGAHVTVK.K
	HsHeLa3_Ti_103.2483.248	2.7629	0.3388	1697.8	1696.81	6087.8		1	658.5	53.6	1	R.GFGFVTFDDHDPVDK.I
	HsGST-MOCK_Ti_104.117	3.0895	0.2491	1412.34	1411.52	8280.6		1	1218.3	72.7	1	K.YHTINGHNAEVR.K
	HsHeLa3_Ti_103.1612.161	2.7018	0.2095	1015.43	1014.04	4520.8		1	1088.8	77.8	1	R.GGNFGFGDSR.G
	HsHeLa_Control-MG_Ti_20	2.8652	0.2294	1377.98	1378.45	7120.5		1	656.1	57.1	4	R.GGGGNFGPGPGSNFR.G
	HsHeLa3_Ti_103.1934.193	5.1977	0.4321	2495.67	2496.53	7494.7		1	959.8	40.7	2	R.GFGDGYNGYGGGPGGGNFGGSPGYGGGR.G
	HsHeLa3_Ti_104.1560.156	5.3917	0.5792	2191.57	2191.26	6203		1	1267.6	56.2	4	R.NMGGPYGGGNYGPGGSGGSGGYGGR.S
gi|7657532|ref|N	10	26	0.4	90	10180	5.5	U	S100 calcium-binding protein A6 [Homo sapiens]				
*	HsHeLa_Control-MG_Ti_10	2.0948	0.0927	915.77	916.022	3257.9		7	364.7	64.3	2	K.LQDAEIAR.L
*	HsFLAG-Control_HeLa_NE	4.157	0.2398	3188.81	3189.59	6247.8		1	666.2	25.9	1	R.NKDQEVNFQEYVTFLGALALIYNEALKG.-
*	HsHeLa_Control-MG_Ti_20	4.0177	0.4028	3189.64	3189.59	8712.7		1	778.3	37	2	R.NKDQEVNFQEYVTFLGALALIYNEALKG.-
*	HsFLAG-Control_Hela_Ti_1	5.0855	0.3347	2890.28	2890.26	9206.3		1	1377.9	45.8	1	K.DQEVNFQEYVTFLGALALIYNEALK.G
*	HsHeLa_Control-MG_Ti_20	5.3663	0.4812	2945.85	2947.31	8724.6		1	1127.8	42	6	K.DQEVNFQEYVTFLGALALIYNEALKG.-
*	HsFLAG-Control_HeLa_S1	4.4149	0.3394	2946.32	2947.31	7422.5		1	992.4	44	5	K.DQEVNFQEYVTFLGALALIYNEALKG.-
*	HsFLAG-Control_Hela_Ti_1	4.0052	0.3411	2947.06	2947.31	6771.5		1	780.1	40	5	K.DQEVNFQEYVTFLGALALIYNEALKG.-
*	HsFLAG-Control_Hela_Ti_1	3.5091	0.1953	2948.46	2947.31	6824.5		5	447.4	24	1	K.DQEVNFQEYVTFLGALALIYNEALKG.-
*	HsFLAG-Control_HeLa_S1	4.4613	0.2475	2948.8	2947.31	9283.6		2	917.3	29	2	K.DQEVNFQEYVTFLGALALIYNEALKG.-
*	HsHeLa_Control-MG_Ti_20	4.1594	0.3854	2948.82	2947.31	6116.8		3	416.3	24	1	K.DQEVNFQEYVTFLGALALIYNEALKG.-
gi|40254869|ref|N	21	100	0.397	499	55442	5.8	U	pre-mRNA processing factor 31 homolog [Homo sapiens]				
*	HsFlag1P_Ti_106.3130.313	4.837	0.2662	2390.6	2391.73	10149.5		1	736.9	42.5	6	R.VIVDANNLTVEIENELNIIHK.F
*	Hs293FLP-MG_Ti_206.341	3.5674	0.2577	2390.65	2391.73	9502.5		2	621.8	40	2	R.VIVDANNLTVEIENELNIIHK.F
*	HsHeLa_Control-MG_Ti_20	3.8113	0.1109	2391.73	2391.73	2695.8		2	491.6	37.5	1	R.VIVDANNLTVEIENELNIIHK.F
*	Hs293FLP_Ti_304.3534.35	4.5854	0.4048	2035.11	2033.34	5554.1		1	808.6	62.5	17	K.RFPELESLVPNALDYIR.T
*	Hs293FLP-MG_Ti_203.437	3.6057	0.3179	1878.01	1877.15	4757.8		1	596.4	63.3	1	R.FPELESLVPNALDYIR.T
*	HsHeLa3_Ti_105.3704.370	4.2583	0.3256	1905.81	1906.29	3216.3		1	839.8	61.1	6	R.MSFIAPNLSIIIGASTAAK.I
*	HsFlag1P_Ti_106.2501.250	2.7714	0.2981	1260.52	1261.52	5000.2		1	347.6	54.2	4	K.IMGVAGGLTNLSK.M
*	HsF-IP-293-MG_Ti_103.18	3.8308	0.3479	1260.71	1261.52	4891.2		1	1327.1	87.5	2	K.IMGVAGGLTNLSK.M
*	HsF-IP-293-MG_Ti_104.20	4.0638	0.2999	1476.45	1475.77	7362.5		1	964.6	66.7	2	K.MPACNIMLLGAQR.K
*	HsHeLa_Control-MG_Ti_20	4.8656	0.3537	3516.8	3517.96	7984.3		1	927.9	26.6	1	R.KTLSGFSSTSVLPHTGYIYHSDIVQSLPPDLR.R
*	Hs293FLP-MG_Ti_206.310	6.0708	0.4877	3388.91	3389.79	7537.6		1	1423.4	31.7	9	K.TLSGFSSTSVLPHTGYIYHSDIVQSLPPDLR.R
*	HsHeLa_Control-MG_Ti_10	2.2422	0.1934	1235.49	1236.28	5945.1		1	460.2	55	1	R.VDSFHESTEGK.V
*	HsHeLa_Control-MG_Ti_10	3.7165	0.3967	1236.78	1236.28	6635.7		1	1165.7	85	5	R.VDSFHESTEGK.V
*	Hs293FLP-MG_Ti_203.179	3.2931	0.2223	1351.69	1351.5	7035.9		1	966.6	75	7	K.VGYELKDEIER.K
*	HsFlag1P_Ti_106.3038.303	3.6883	0.3446	2672.63	2673.91	10537.8		1	1208.8	45.7	1	R.MSFGEIEEDAYQEDLGFSLGHLGK.S
*	Hs293FLP-MG_Ti_202.369	4.7723	0.342	2602.66	2603.89	9164.8		1	1177.9	32	1	R.SSGTASSVAFTPLQGLEIVNPQAAEK.K
*	Hs293FLP-MG_Ti_202.368	4.0686	0.3967	2602.71	2603.89	5873.1		1	568.1	40	3	R.SSGTASSVAFTPLQGLEIVNPQAAEK.K
*	HsHeLa_Control-MG_Ti_20	5.4629	0.3499	2604.23	2603.89	6335.6		1	726	42	27	R.SSGTASSVAFTPLQGLEIVNPQAAEK.K
*	HsF-IP-293-MG_Ti_102.28	4.3067	0.3113	2604.84	2603.89	9656.6		1	894.7	27	1	R.SSGTASSVAFTPLQGLEIVNPQAAEK.K
*	HsFlag1P_Ti_106.2820.282	3.9399	0.3129	2730.7	2732.06	5958.3		1	648.2	27.9	2	R.SSGTASSVAFTPLQGLEIVNPQAAEKK.V
*	HsFlag1P_Ti_103.3027.303	2.4395	0.0968	1222.44	1223.43	9422.8		2	569.9	61.1	1	K.YFSSMAEFLK.V
gi|23065552|ref|N	12	34	0.396	225	26560	5.5	U	glutathione S-transferase M3 [Homo sapiens]				
*	HsGST-MOCK_Ti_302.259	2.8339	0.2629	1587.45	1588.75	6604.8		1	577.6	58.3	2	R.LLLEFTDTSYEEK.R
*	HsGST-MOCK_Ti_302.259	4.996	0.3194	1587.88	1588.75	7966.9		1	2126.7	87.5	4	R.LLLEFTDTSYEEK.R
*	HsGST-MOCK_Ti_306.353	5.1627	0.3343	2008.09	2009.35	7000.3		1	1749.7	71.9	5	K.FKLDLDFPNLPYLLDGK.N
*	HsGST-MOCK_Ti_305.440	4.1504	0.2147	2008.52	2009.35	6210.4		1	1447.8	48.4	2	K.FKLDLDFPNLPYLLDGK.N
*	HsGST-MOCK_Ti_305.313	3.7789	0.3255	1747.97	1749.04	3285.2		1	772.8	76.9	3	K.IRVDIIENQVMDFR.T
*	HsGST-MOCK_Ti_302.263	3.9817	0.2208	1479.72	1479.69	8275.8		1	2074.2	81.8	1	R.VDIIENQVMDFR.T

*	HsGST-MOCK_Ti_303.241	2.34	0.1086	971.33	972.088	5780.8		4	602.4	78.6	2	K.FSWFAGEK.L
*	HsGST-MOCK_Ti_302.492	4.4458	0.3609	1972.62	1974.22	7996.5		1	1758.8	51.7	1	K.LTFVDFLTYDILDQNR.I
*	HsGST-MOCK_Ti_303.506	5.2859	0.3785	1973.45	1974.22	11972.2		1	2992.3	76.7	8	K.LTFVDFLTYDILDQNR.I
*	HsGST-MOCK_Ti_303.221	1.9342	0.1427	1135.43	1136.26	2727.6		9	235.4	75	1	K.CLDEFPNLK.A
*	HsGST-MOCK_Ti_303.205	4.4065	0.333	1443.97	1444.59	7713.7		1	1754.4	81.8	3	K.IAAYLQSDQFCK.M
*	HsGST-MOCK_Ti_303.203	3.3042	0.298	1443.99	1444.59	5782.4		1	633.8	68.2	2	K.IAAYLQSDQFCK.M
gi|4758638|ref|NI	10	59	0.393	224	25035	6.4	U	peroxiredoxin 6 [Homo sapiens]				
*	Hs293FLP_Ti_306.3302.33	5.8201	0.4931	2032.03	2032.27	6707.5		1	1944.8	75	1	R.FHDFLGDSWGILFSHPR.D
*	HsHeLa_Control-MG_Ti_20	6.6002	0.5203	2032.05	2032.27	8665.1		1	2976	81.2	5	R.FHDFLGDSWGILFSHPR.D
*	HsHeLa_Control-MG_Ti_20	4.3749	0.2671	2032.1	2032.27	6063.5		1	1044.1	43.8	1	R.FHDFLGDSWGILFSHPR.D
*	HsHeLa_Control-MG_Ti_20	3.278	0.2092	1396.6	1396.51	6491.9		2	652.5	68.2	6	R.DFTPVCTTELGR.A
*	HsHeLa_Control-MG_Ti_20	4.659	0.4499	1899.74	1898.17	7341.9		1	1645.9	71.9	6	K.LIALSIDSVEDHLAWSK.D
*	HsFLAG-Control_HeLa_NE	3.6344	0.3086	1583.3	1583.62	7486.2		1	922.4	66.7	7	K.DINAYNCEEPTEK.L
*	HsHeLa_Control-MG_Ti_10	3.1344	0.1706	2650.18	2650.87	5651.7		4	334.5	35.7	1	K.DINAYNCEEPTEKLPFPIIDDR.N
*	HsFLAG-Control_293_Ti_2	3.3854	0.2231	1085.86	1086.28	4655.2		1	1018.9	93.8	22	K.LPFPIIDDR.N
*	HsFLAG-Control_Hela_Ti_1	2.6125	0.2628	1008.56	1008.21	6069.5		3	696.8	75	8	R.VVFVFGPDK.K
*	HsFLAG-Control_MG_293_	2.7943	0.1423	1193.03	1192.4	4202.6		1	463.7	70	2	K.LSILYPATTGR.N
gi|30795231|ref|	6	10	0.392	227	22693	4.6	U	brain abundant, membrane attached signal protein 1 [Homo sapiens]				
*	HsHeLa3_Ti_102.1065.106	3.1136	0.2415	1428.65	1428.5	6575.6		1	1095.1	69.2	2	K.ESEPQAAAEPAEAK.E
*	HsHeLa3_Ti_103.1230.123	4.3073	0.3355	1776.69	1776.9	3679.2		2	567.1	58.3	2	K.APEQEQAAPGPAAGGEAPK.A
*	HsHeLa3_Ti_103.1395.139	3.1435	0.1884	2636.65	2637.77	4690.3		1	310.9	33.3	1	K.AAEAAAAPAESAAPAAGEEPSKEEGEPK.K
*	HsHeLa3_Ti_104.0951.095	4.3061	0.297	1413.66	1413.57	4110.8		1	974.6	80.8	2	K.KTEAPAAPAAQETK.S
*	HsHeLa3_Ti_102.1161.116	1.9824	0.3301	1386.83	1387.49	3334.3		2	200.6	50	1	K.ETPAATEAPSSTPK.A
*	HsHeLa3_Ti_102.1133.113	3.0187	0.2926	1387.63	1387.49	4414.8		5	499.4	61.5	2	K.ETPAATEAPSSTPK.A
gi|30410792|ref|	6	43	0.389	239	27402	5.7	U	proteasome activator subunit 2 [Homo sapiens]				
*	HsFLAG-Control_HeLa_NE	4.6085	0.2171	1688.55	1687.85	6900.8		1	1434.3	83.3	6	R.QNLFQEAEEFLYR.F
*	HsFLAG-Control_HeLa_S1	6.7549	0.3018	2532.63	2532.9	9795.3		1	2914	66.7	19	K.IIYLNQLLQEDSLNVADLTSLR.A
*	HsFLAG-Control_HeLa_S1	4.1824	0.2375	1809.95	1810.27	8165.1		1	843.7	53.3	4	K.VLSLLALVKPEVWTLK.E
*	HsFLAG-Control_HeLa_S1	4.2115	0.2798	1535.44	1535.65	8645.6		1	1612.6	76.9	2	K.IEDGNDFGVAIQEK.V
*	HsFLAG-Control_HeLa_S1	3.98	0.3578	1354.42	1353.56	5463.1		1	1087	77.3	4	K.TKVEAFQTTISK.Y
*	HsFLAG-Control_HeLa_S1	5.1172	0.4601	1900.52	1899.15	6348.9		1	1609.3	73.3	8	R.AFYAELYHIISSNLEK.I
gi|11415030|ref|	5	14	0.388	103	11367	11.4	U	H4 histone family, member E [Homo sapiens]				
gi|89066445|ref|	5	14	0.388	103	11367	11.4	U	PREDICTED: similar to germinal histone H4 gene isoform 4 [Homo sapiens]				
gi|89066443|ref|	5	14	0.388	103	11367	11.4	U	PREDICTED: similar to germinal histone H4 gene isoform 3 [Homo sapiens]				
gi|89066441|ref|	5	14	0.388	103	11367	11.4	U	PREDICTED: similar to germinal histone H4 gene isoform 2 [Homo sapiens]				
gi|89066439|ref|	5	14	0.388	103	11367	11.4	U	PREDICTED: similar to germinal histone H4 gene isoform 1 [Homo sapiens]				
gi|4504323|ref|NI	5	14	0.388	103	11367	11.4	U	histone 2, H4 [Homo sapiens]				
gi|4504321|ref|NI	5	14	0.388	103	11367	11.4	U	H4 histone family, member M [Homo sapiens]				
gi|4504317|ref|NI	5	14	0.388	103	11367	11.4	U	H4 histone family, member K [Homo sapiens]				
gi|4504315|ref|NI	5	14	0.388	103	11367	11.4	U	H4 histone family, member J [Homo sapiens]				
gi|4504313|ref|NI	5	14	0.388	103	11367	11.4	U	H4 histone family, member I [Homo sapiens]				
gi|4504311|ref|NI	5	14	0.388	103	11367	11.4	U	H4 histone family, member H [Homo sapiens]				
gi|4504309|ref|NI	5	14	0.388	103	11367	11.4	U	H4 histone family, member G [Homo sapiens]				
gi|4504307|ref|NI	5	14	0.388	103	11367	11.4	U	H4 histone family, member D [Homo sapiens]				
gi|4504305|ref|NI	5	14	0.388	103	11367	11.4	U	H4 histone family, member C [Homo sapiens]				
gi|4504303|ref|NI	5	14	0.388	103	11367	11.4	U	H4 histone family, member B [Homo sapiens]				
gi|4504301|ref|NI	5	14	0.388	103	11367	11.4	U	H4 histone family, member A [Homo sapiens]				
gi|28173560|ref|	5	14	0.388	103	11367	11.4	U	histone H4 [Homo sapiens]				
	HsF-IP-293_Ti_204.1623.1	3.2717	0.1446	1325.85	1326.54	6521.7		4	896.4	72.7	6	R.DNIQGITKPAIR.R

	Hs293FLP_TREX_Ti_104.1	3.5105	0.2807	1338.43	1337.52	5787.5		1	897.9	80	1	K.RISGLIYEETR.G
	Hs293FLP-MG_Ti_102.201	3.8695	0.171	1181.77	1181.33	4482.4		4	961.8	88.9	3	R.ISGLIYEETR.G
	Hs293FLP-MG_Ti_102.114	3.1154	0.2712	1134.03	1135.22	3841.8		1	703.3	83.3	3	R.DAVTYTEHAK.R
	HsGST-MOCK_Ti_402.232	1.8862	0.1231	714.31	714.796	3574.9		7	264.9	66.7	1	R.TLYGFGG.-
gi|4502969|ref|N	6	14	0.387	271	30037	5.5	U		catechol-O-methyltransferase isoform MB-COMT [Homo sapiens]			
gi|6466450|ref|N	6	14	0.475	221	24449	5.3	U		catechol-O-methyltransferase isoform S-COMT [Homo sapiens]			
	HsHeLa_Control-MG_Ti_20	6.2596	0.429	3178.7	3179.48	10975.8		1	2298	36.1	2	R.ILNHVLQHAEPGNAQSVLEAIDTYCEQK.E
	Hs293FLP-MG_Ti_202.305	4.036	0.384	1828.09	1829.07	6225.6		1	802.7	60	2	R.LITIEINPDCAAITQR.M
	HsFLAG-Control_HeLa_S1	4.3422	0.3282	1681.99	1682.01	4932.4		1	855.6	63.3	4	K.VTLVVGASQDIIPQLK.K
	Hs293FLP-MG_Ti_202.401	4.0895	0.3638	1804.9	1806.08	7538		1	1688.4	78.6	3	R.YLPDTLLLEECGLLR.K
	Hs293FLP-MG_Ti_204.330	4.2665	0.2214	2335.47	2336.66	8618.4		1	1317.9	36.9	2	K.GTVLLADNVICPGAPDFLAHVR.G
	HsHeLa-FLAG-IP_S100_Ti_	1.8273	0.1729	888.22	888.993	2751.5		7	188	64.3	1	R.EVVDGLEK.A
gi|53829365|ref|N	7	23	0.384	263	28527	5.3	U		potassium channel tetramerisation domain containing 2 [Homo sapiens]			
	HsFLAG-Control_MG_293_	4.6879	0.3807	1754.52	1754.98	4931.4		1	843.4	61.8	6	R.PAAAVAQPLEPGPGPPER.A
	HsFLAG-Control_MG_293_	3.7058	0.224	1754.95	1754.98	5872.9		2	1114.3	42.6	1	R.PAAAVAQPLEPGPGPPER.A
	HsFLAG-Control_293_Ti_2	3.7157	0.2647	1328.38	1328.51	6697.8		1	949.1	72.7	2	R.LNVGGTYFVTTR.Q
	HsFLAG-Control_293_Ti_2	3.4701	0.3739	1569.49	1569.8	6856.6		1	1172.7	75	1	R.DPTYFGPILNYLR.H
	HsFLAG-Control_293_Ti_2	5.6566	0.3954	2385.36	2382.63	10826		1	1909.5	55	9	K.ELAEEGVLEEAEFYNIASLVR.L
	HsFLAG-Control_293_Ti_2	5.2966	0.4718	2499.55	2500.76	8109.8		1	1506.2	57.5	3	R.VLQCQEEELTQMVSTMSDGWK.F
*	HsFLAG-Control_293_Ti_2	2.5914	0.2248	1744.57	1744.9	11877.6		2	674.9	46.7	1	R.ELNNSTNGIVIEPSEK.A
gi|18375623|ref|N	20	74	0.383	428	48991	5.7	U		HLA-B associated transcript 1 [Homo sapiens]			
gi|4758112|ref|N	20	74	0.383	428	48991	5.7	U		HLA-B associated transcript 1 [Homo sapiens]			
	HsFLAG-Control_HeLa_NE	2.9102	0.2152	1296.6	1297.41	4190.9		1	218.6	54.5	2	K.GSYVSIHSSGFR.D
	HsFLAG-Control_HeLa_NE	3.3999	0.3467	1297.35	1297.41	6239.4		1	1014.2	72.7	2	K.GSYVSIHSSGFR.D
	HsFLAG-Control_HeLa_NE	3.1536	0.356	1297.62	1297.41	5696.1		1	730.8	68.2	3	K.GSYVSIHSSGFR.D
	HsFLAG-MOCK_300mM_T	5.1172	0.3001	3653.38	3654.03	4854.3		1	730.6	28.2	2	R.AIVDCGFEHPSEVQHECIPQAILGMDVLCQAK.S
	HsFLAG-Control_HeLa_NE	2.6266	0.1728	1137.6	1138.4	7730.1		2	726	70	2	K.VAVFFGGLSIK.K
	HsFLAG-Control_HeLa_NE	3.3902	0.3183	1138.55	1138.4	5384.7		1	977.9	85	1	K.VAVFFGGLSIK.K
	HsFLAG-MOCK_300mM_T	3.4773	0.2859	1436.68	1435.64	5678.4		1	1005	75	2	K.KNCPHIVVGTPGR.I
	HsFLAG-MOCK_300mM_T	3.4991	0.3177	1308.04	1307.46	5987.5		1	1276.7	81.8	2	K.NCPHIVVGTPGR.I
	HsFLAG-MOCK_300mM_T	2.8673	0.2384	1176.53	1177.27	4683		1	715.7	75	2	K.HFILDECDK.M
	HsFLAG-MOCK_300mM_T	2.9461	0.1885	1177.45	1177.27	3721.6		6	751.1	81.2	1	K.HFILDECDK.M
	HsFLAG-Control_HeLa_NE	3.4418	0.3925	1463.16	1463.72	5746.5		1	821.1	72.7	4	K.LTLHGLQQYYVK.L
	HsFLAG-Control_HeLa_NE	3.6145	0.3768	1464	1463.72	6104.4		1	861.3	72.7	2	K.LTLHGLQQYYVK.L
	HsFLAG-Control_HeLa_S1	2.7595	0.1186	2277.94	2278.67	9889.4		1	685.4	42.1	1	R.CIALAQLLVEQNFPAIAIHR.G
	HsFLAG-MOCK_300mM_T	4.3223	0.3571	2279.93	2278.67	3959.7		1	967.1	44.7	1	R.CIALAQLLVEQNFPAIAIHR.G
	HsFLAG-Control_HeLa_NE	5.0318	0.336	2280.39	2278.67	5361.7		1	1206.4	43.4	2	R.CIALAQLLVEQNFPAIAIHR.G
	HsFLAG-Control_HeLa_NE	3.7388	0.3438	1260.68	1260.53	7837.1		1	1712.5	90	1	R.RILVATNLFGR.G
	HsFLAG-Control_HeLa_S1	3.8361	0.2249	1104.14	1104.34	5719.5		1	1117.8	83.3	14	R.ILVATNLFGR.G
	HsFLAG-Control_HeLa_NE	4.782	0.4338	1480.11	1480.62	6927.2		1	1731.5	80.8	16	K.GLAITFVSDENDAK.I
	HsFLAG-Control_HeLa_NE	4.2776	0.2765	3551.8	3552.87	10571.7		1	645.6	22.4	5	K.ILNDVQDRFEVNISELPDEIDISSYIEQTR.-
	HsFLAG-Control_HeLa_NE	4.6289	0.3115	2596.92	2598.82	4850.5		1	746.4	52.4	9	R.FEVNISELPDEIDISSYIEQTR.-
gi|4507555|ref|N	19	69	0.379	694	75492	7.7	U		thymopoietin isoform alpha [Homo sapiens]			
	Hs283FLP_Ti_102.1671.16	4.8223	0.4195	1699.67	1698.87	4311.7		1	785.6	70	4	K.SELVANNVTLPAGEQR.K
	HsFLAG-Control_HeLa_NE	4.0695	0.272	1826.55	1827.05	5640.8		2	506.9	50	2	K.SELVANNVTLPAGEQRK.D
	HsFLAG-Control_HeLa_NE	3.2736	0.338	1720.37	1719.98	8982.6		1	793.9	57.7	1	K.DVYVQLYLQHLTAR.N
	HsFLAG-Control_HeLa_NE	3.6445	0.3427	1252.35	1252.42	6377.2		1	1343.9	77.3	13	R.NRPPLPAGTNSK.G
	HsFLAG-Control_HeLa_NE	4.3441	0.3386	2571.7	2571.72	6972.6		1	1615.3	37	2	K.GPPDFSSDEEREPTPVLGSGAAAAGR.S
	HsFLAG-Control_HeLa_NE	4.949	0.2151	2689.91	2689.89	9766.4		1	905.9	38.6	4	R.QEDKDDLDVTELTNEDLLDQLVK.Y

	HsF-IP-293_Ti_203.3434.34	3.5692	0.1968	2190.44	2189.38	6699.7		1	659.9	47.2	1	K.DDLDVTELTNEDLLDQLVK.Y
	HsFLAG-Control_HeLa_NE	3.2365	0.2587	1331.53	1331.51	4823.4		1	929.4	70.8	5	K.YGVNPGPIVGTTR.K
	HsFLAG-Control_HeLa_NE	3.1144	0.2369	1650.66	1648.77	5132.5		1	918.7	73.3	5	R.SSTPLPTISSSAENTR.Q
*	HsFLAG-Control_HeLa_NE	2.9906	0.2659	1705.48	1705.96	5283.9		1	641.5	60	1	K.GDLPREPLVATNLPGR.G
*	HsFLAG-Control_HeLa_NE	3.2559	0.2952	1285.58	1286.38	7274.7		1	765.7	63.6	1	R.SHISDQSPLSSK.R
*	HsFLAG-Control_HeLa_NE	3.529	0.2761	1286.39	1286.38	5930.4		1	1044.2	77.3	2	R.SHISDQSPLSSK.R
*	HsFLAG-Control_HeLa_NE	4.0345	0.3	1286.53	1286.38	5353.3		1	1152.8	81.8	4	R.SHISDQSPLSSK.R
*	HsFLAG-Control_HeLa_NE	3.9276	0.3073	2140.49	2140.4	4508.4		2	459.2	47.4	8	K.ALEESESSQLISPPLAQAIR.D
*	HsFLAG-Control_HeLa_NE	4.1363	0.2945	1433.02	1431.55	10147		1	1980.3	85	2	K.VIEEEWQQVDR.Q
*	HsFLAG-Control_HeLa_NE	4.4482	0.3332	3895.34	3894.21	7603.1		1	688.3	22.9	1	K.VDDEILGFISEATPLGGIQAASTESCNQQLDLALCR.A
*	HsFLAG-Control_HeLa_NE	5.7224	0.3664	2035.09	2035.31	9000.2		1	2352.9	68.4	7	R.AYEAAASALQIATHTAFVAK.A
*	HsFLAG-Control_HeLa_NE	3.1321	0.2947	1067.58	1068.26	6136.8		1	918.5	77.8	4	R.THQALGILSK.T
*	HsFLAG-Control_HeLa_NE	4.5537	0.4999	1954	1954.06	7665.9		1	1113.1	59.4	2	K.TYDAASYICEAAFDEVK.M
gi|4506773|ref|N	3	10	0.377	114	13242	6.1	U	S100 calcium-binding protein A9 [Homo sapiens]				
*	HsFLAG-Control_Hela_Ti_1	4.1882	0.3665	1807.61	1808.04	7655.4		1	823.2	60.7	8	R.NIETIINTFHQYSVK.L
*	HsFLAG-Control_293_Ti_2	2.9402	0.1742	1456.21	1456.6	4445		1	490.4	66.7	1	K.LGHPDTLNQGEFK.E
*	HsFLAG-Control_MG_293_	3.4238	0.1828	1745.47	1743.93	8157.7		1	924.3	57.1	1	K.VIEHIMEDLDTNADK.Q
gi|10835063|ref|N	5	22	0.374	294	32575	4.8	U	nucleophosmin 1 isoform 1 [Homo sapiens]				
gi|40353734|ref|N	5	22	0.415	265	29465	4.6	U	nucleophosmin 1 isoform 2 [Homo sapiens]				
	Hs293FLP_TREX_Ti_102.1	3.4085	0.2927	1569.34	1569.63	7824.4		1	716.8	62.5	2	K.VDNDENEHQLSLR.T
	HsGST-MOCK_Ti_102.259	5.905	0.5076	2930.39	2931.29	11478		1	1757.1	29.6	2	R.TVSLGAGAKDELHIVEAEAMNYEGSPIK.V
	HsGST-MOCK_Ti_305.385	4.675	0.4054	2227.52	2228.66	7439.5		1	1475	60	11	K.MSVQPTVSLGGFEITPPVVLR.L
	HsFLAG-MOCK_300mM_T	6.1708	0.5274	3952.6	3952.6	8486.1		1	1313.2	28	1	K.VKLAADEDDDDDDEEDDDEDDDDDDFDDEEAEEK.A
	HsGST-MOCK_Ti_302.369	4.1804	0.3153	1820.34	1821.02	6548.5		1	1826.2	73.1	6	R.MTDQEAIQDLWQWR.K
gi|4827040|ref|N	120	448	0.371	955	108694	10.2	U	thyroid hormone receptor associated protein 3 [Homo sapiens]				
*	Hs293FLP-MG_Ti_205.143	3.7609	0.1168	3659.29	3659.77	8130.5		1	652.3	22.1	1	K.KSSSKDSRPSQAAGDNQGDEVKEQTFSGGTSQDTK.A
*	HsF-IP-293-MG_Ti_102.07	2.9695	0.2666	1773.88	1774.8	6813.9		1	651.4	56.2	1	K.DSRPSQAAGDNQGDEVK.E
*	Hs293FLP-MG_Ti_103.137	4.9164	0.2795	3142.56	3142.19	7606.1		3	767.1	26.7	3	K.DSRPSQAAGDNQGDEVKEQTFSGGTSQDTK.A
*	HsFLAG-Control_HeLa_NE	3.0702	0.3885	1386.27	1386.42	6300		1	855	70.8	7	K.EQTFSGGTSQDTK.A
*	HsFlag1P_Ti_103.1977.197	4.6199	0.3877	2055.29	2056.15	3379.4		1	715.7	63.2	5	K.ASESSKPWPDATYGTGSASR.A
*	HsHeLa_Control-MG_Ti_20	4.97	0.2366	2055.73	2056.15	4045.4		1	847.3	60.5	14	K.ASESSKPWPDATYGTGSASR.A
*	HsFLAG-Control_HeLa_NE	4.2094	0.4155	2057.39	2056.15	7243.9		1	1136.4	38.2	2	K.ASESSKPWPDATYGTGSASR.A
*	HsHeLa_Control-MG_Ti_20	1.946	0.2152	1016.44	1017.13	2203.9		1	134.3	66.7	1	R.ASAVSELSPR.E
*	Hs283FLP_Ti_102.1379.13	3.7861	0.2807	1017.5	1017.13	4929.5		2	1073.5	83.3	9	R.ASAVSELSPR.E
*	HsHeLa_Control-MG_Ti_10	3.4624	0.2811	1018.63	1017.13	4818.6		1	1129	88.9	1	R.ASAVSELSPR.E
*	Hs293FLP_TREX_Ti_103.1	2.3934	0.2462	984.5	985.172	3988.1		3	176.6	62.5	2	K.SPLQSVVVR.R
*	HsFlag1P_Ti_106.2356.235	2.5306	0.275	984.56	985.172	3364.2		1	207.7	68.8	2	K.SPLQSVVVR.R
*	HsHeLa_Control-MG_Ti_20	1.9429	0.2428	984.57	985.172	2231.4		1	122	68.8	1	K.SPLQSVVVR.R
*	HsFLAG-Control_HeLa_NE	2.4094	0.225	984.6	985.172	3987.9		2	233	68.8	3	K.SPLQSVVVR.R
*	Hs283FLP_Ti_103.1474.14	2.3896	0.2298	984.61	985.172	3211.9		1	198.7	68.8	1	K.SPLQSVVVR.R
*	HsFlag1P_Ti_106.2358.235	3.1465	0.2033	984.64	985.172	5792.3		2	1055.5	87.5	1	K.SPLQSVVVR.R
*	HsF-IP-293-MG_Ti_103.15	2.5373	0.2418	984.66	985.172	3726.6		1	210.1	68.8	2	K.SPLQSVVVR.R
*	Hs293FLP_Ti_303.1538.15	2.1818	0.2618	984.67	985.172	4103.4		1	206.1	68.8	1	K.SPLQSVVVR.R
*	Hs293FLP-MG_Ti_103.167	2.1788	0.2826	984.74	985.172	3013.2		1	229.2	75	2	K.SPLQSVVVR.R
*	HsFLAG-Control_HeLa_NE	3.2559	0.1604	985.38	985.172	5474.1		1	1091	93.8	3	K.SPLQSVVVR.R
*	Hs293FLP_TREX_Ti_103.1	3.3204	0.1629	985.47	985.172	5503		1	1164	93.8	1	K.SPLQSVVVR.R

*	HsF-IP-293_Ti_103.1526.15	3.0542	0.1222	985.47	985.172	5491.4	2	1078.7	93.8	2	K.SPLQSVVVR.R
*	Hs293FLP-MG_Ti_203.177	3.1764	0.1803	985.49	985.172	6746.6	1	1302.3	93.8	4	K.SPLQSVVVR.R
*	Hs283FLP_Ti_103.1479.14	3.1023	0.2232	985.61	985.172	5503.3	2	962.8	87.5	2	K.SPLQSVVVR.R
*	Hs293FLP_Ti_303.1539.15	3.2348	0.1981	985.7	985.172	4988.3	1	913.2	87.5	1	K.SPLQSVVVR.R
*	HsF-IP-293-MG_Ti_103.154	3.1306	0.1428	986.41	985.172	5725.4	1	1152.1	93.8	2	K.SPLQSVVVR.R
*	HsF-IP-293-MG_Ti_103.134	5.1043	0.2947	2606.63	2607.7	4160.7	1	678.9	34.6	2	K.SPPSTGSTYGSSQKEESAASGGAAYTK.R
*	Hs293FLP-MG_Ti_203.146	4.4203	0.3726	2606.65	2607.7	8642.3	1	1058.3	42.3	2	K.SPPSTGSTYGSSQKEESAASGGAAYTK.R
*	Hs283FLP_Ti_103.1248.12	4.7703	0.4509	2606.91	2607.7	9659.8	1	1185.6	40.4	2	K.SPPSTGSTYGSSQKEESAASGGAAYTK.R
*	Hs293FLP_Ti_303.1269.12	4.5834	0.4868	2607.07	2607.7	8514.6	1	1158.2	44.2	2	K.SPPSTGSTYGSSQKEESAASGGAAYTK.R
*	HsFLAG-Control_HeLa_NE	4.8012	0.4453	2607.19	2607.7	5365.2	2	477.9	27.9	2	K.SPPSTGSTYGSSQKEESAASGGAAYTK.R
*	HsHeLa_Control-MG_Ti_20	3.9977	0.3955	2607.3	2607.7	5098.8	1	748.7	30.8	2	K.SPPSTGSTYGSSQKEESAASGGAAYTK.R
*	HsF-IP-293-MG_Ti_103.134	4.5348	0.388	2607.47	2607.7	7718.5	1	1192.5	46.2	1	K.SPPSTGSTYGSSQKEESAASGGAAYTK.R
*	Hs293FLP-MG_Ti_103.134	4.412	0.4574	2607.6	2607.7	7393.9	1	986.2	42.3	2	K.SPPSTGSTYGSSQKEESAASGGAAYTK.R
*	Hs283FLP_Ti_103.1250.12	3.8978	0.3742	2607.78	2607.7	3622.2	5	282.7	25	1	K.SPPSTGSTYGSSQKEESAASGGAAYTK.R
*	HsHeLa_Control-MG_Ti_20	5.5219	0.4757	2607.92	2607.7	9583.9	1	1415.3	46.2	4	K.SPPSTGSTYGSSQKEESAASGGAAYTK.R
*	Hs293FLP-MG_Ti_103.135	3.7523	0.2478	2608.07	2607.7	3556.6	1	328.3	25	2	K.SPPSTGSTYGSSQKEESAASGGAAYTK.R
*	Hs293FLP_Ti_303.1270.12	4.1387	0.2962	2608.44	2607.7	3612	4	289.1	25	1	K.SPPSTGSTYGSSQKEESAASGGAAYTK.R
*	Hs293FLP-MG_Ti_205.144	4.1703	0.2905	2763.11	2763.89	5640	1	546	25.9	3	K.SPPSTGSTYGSSQKEESAASGGAAYTKR.Y
*	HsHeLa_Control-MG_Ti_10	3.8506	0.2921	1495.81	1495.63	7214.7	1	1428.6	81.8	5	K.RYLEEQKTENGK.D
*	HsF-IP-293_Ti_102.1258.12	2.393	0.3398	1140.33	1141.18	5646.6	5	401.8	54.5	2	K.GSFSDTGLGDGK.M
*	HsF-IP-293-MG_Ti_102.144	2.3555	0.2746	1140.35	1141.18	5017.4	1	511.6	63.6	2	K.GSFSDTGLGDGK.M
*	Hs293FLP-MG_Ti_202.179	2.4046	0.2176	1140.4	1141.18	6674.1	1	679.5	68.2	2	K.GSFSDTGLGDGK.M
*	HsFLAG-Control_HeLa_NE	2.4659	0.3559	1140.4	1141.18	6925.8	1	519.2	59.1	1	K.GSFSDTGLGDGK.M
*	Hs283FLP_Ti_102.1405.14	1.8518	0.1935	1140.4	1141.18	5592.3	4	304.5	50	1	K.GSFSDTGLGDGK.M
*	Hs293FLP-MG_Ti_102.158	2.4192	0.3102	1140.46	1141.18	5799.9	1	594.3	59.1	2	K.GSFSDTGLGDGK.M
*	HsHeLa_Control-MG_Ti_20	2.5461	0.3045	1140.46	1141.18	4608.2	1	638	68.2	2	K.GSFSDTGLGDGK.M
*	HsHeLa_Control-MG_Ti_10	2.1526	0.3859	1140.6	1141.18	4611.9	1	436.3	59.1	2	K.GSFSDTGLGDGK.M
*	HsHeLa_Control_Ti_102.14	2.401	0.4198	1140.68	1141.18	5359.9	1	500.8	59.1	2	K.GSFSDTGLGDGK.M
*	HsF-IP-293_Ti_102.1254.12	3.384	0.3968	1141.23	1141.18	6825.5	1	1625.6	81.8	2	K.GSFSDTGLGDGK.M
*	HsHeLa_Control-MG_Ti_20	3.2799	0.3722	1141.26	1141.18	7319.4	1	1661.8	81.8	1	K.GSFSDTGLGDGK.M
*	Hs293FLP-MG_Ti_202.180	3.4632	0.377	1141.28	1141.18	7331.7	1	1430.3	77.3	2	K.GSFSDTGLGDGK.M
*	Hs283FLP_Ti_102.1406.14	3.3013	0.3908	1141.34	1141.18	6868.3	1	1471	77.3	1	K.GSFSDTGLGDGK.M
*	HsFLAG-Control_HeLa_NE	3.4528	0.2892	1141.35	1141.18	7711	1	1791.8	81.8	4	K.GSFSDTGLGDGK.M
*	HsF-IP-293-MG_Ti_102.144	3.5747	0.4187	1141.38	1141.18	7372.9	1	1690.8	81.8	2	K.GSFSDTGLGDGK.M
*	HsFLAG-Control_HeLa_NE	3.4815	0.3596	1141.51	1141.18	7188.9	1	1508.3	77.3	2	K.GSFSDTGLGDGK.M
*	HsHeLa_Control-MG_Ti_10	3.3025	0.3392	1141.62	1141.18	7365.5	1	1771.5	81.8	2	K.GSFSDTGLGDGK.M
*	Hs293FLP-MG_Ti_102.159	3.2562	0.3371	1141.7	1141.18	5636.1	1	1339.4	77.3	1	K.GSFSDTGLGDGK.M
*	Hs293FLP-MG_Ti_205.169	4.0054	0.2693	1930.73	1931.13	6809.9	1	638.6	53.3	1	K.GRKESEFDDEPKFMSK.V
*	HsHeLa_Control-MG_Ti_20	3.3029	0.1991	1223.54	1224.27	5939.6	1	870.5	83.3	2	R.KESEFDDEPK.F
*	Hs293FLP-MG_Ti_205.195	2.4881	0.3918	1488.57	1489.71	4080.7	1	360.4	53.8	2	K.SGKWEGLVYAPPGK.E
*	HsHeLa_Control-MG_Ti_10	2.8142	0.3144	1488.76	1489.71	2987.3	5	226.7	50	2	K.SGKWEGLVYAPPGK.E
*	Hs293FLP_Ti_304.1830.18	2.2295	0.2839	1488.8	1489.71	3346.8	1	245.6	50	1	K.SGKWEGLVYAPPGK.E
*	HsFLAG-Control_HeLa_NE	4.2603	0.3251	1489.1	1489.71	6806.1	1	1293.9	73.1	3	K.SGKWEGLVYAPPGK.E
*	HsHeLa_Control-MG_Ti_20	4.3519	0.3911	1489.31	1489.71	4937.3	1	1382.2	80.8	12	K.SGKWEGLVYAPPGK.E
*	Hs293FLP-MG_Ti_205.195	4.2534	0.3865	1489.51	1489.71	6979.1	1	1526.6	76.9	3	K.SGKWEGLVYAPPGK.E
*	Hs293FLP_Ti_304.1817.18	4.1541	0.4478	1489.9	1489.71	5156.8	1	1257.2	76.9	8	K.SGKWEGLVYAPPGK.E
*	Hs293FLP-MG_Ti_206.268	4.402	0.3444	1746.66	1747	7099.2	1	1426.4	66.7	2	K.SGKWEGLVYAPPGKEK.Q
*	HsHeLa_Control-MG_Ti_10	3.5939	0.1956	1747.55	1747	3860.8	3	529.5	41.7	1	K.SGKWEGLVYAPPGKEK.Q
*	HsHeLa_Control-MG_Ti_10	3.9319	0.3213	1748.92	1747	6968.1	1	971.2	60	2	K.SGKWEGLVYAPPGKEK.Q

*	Hs293FLP-MG_Ti_202.241	4.0325	0.3477	1217.42	1217.41	6535.7	1	1778.1	95	13	K.WEGLVYAPPGK.E
*	HsHeLa_Control-MG_Ti_20	4.0589	0.3418	1217.49	1217.41	7101.1	1	1577	85	9	K.WEGLVYAPPGK.E
*	Hs283FLP_Ti_103.1823.18	2.0666	0.1293	1217.61	1217.41	5574.2	1	501.7	60	1	K.WEGLVYAPPGK.E
*	HsHeLa_Control-MG_Ti_10	3.4182	0.3386	1475.86	1474.7	5230.3	3	929.2	75	2	K.WEGLVYAPPGKEK.Q
*	Hs293FLP-MG_Ti_203.168	4.7046	0.3563	1623.52	1623.71	7328.3	1	1757.2	83.3	20	R.KTEELEEESFPER.S
*	HsFLAG-Control_HeLa_NE	4.6299	0.3112	1495.34	1495.54	10530.9	1	1936.8	77.3	58	K.TEELEEESFPER.S
*	HsF-IP-293_Ti_106.1937.1	2.6606	0.102	999.29	999.158	3868	4	519.3	85.7	1	K.NFRVTAYK.A
*	Hs293FLP-MG_Ti_204.144	2.0305	0.2452	1090.56	1091.25	6051.4	7	450.9	60	1	K.LGAKGDFPTGK.S
*	Hs293FLP-MG_Ti_204.145	3.1458	0.3011	1091.22	1091.25	5951.8	1	1040.6	85	2	K.LGAKGDFPTGK.S
*	HsHeLa_Control_Ti_102.17	2.8932	0.3313	1201.47	1199.28	5515.1	1	1384.6	94.4	1	R.MDSFDEDLAR.P
*	HsF-IP-293-MG_Ti_106.22	2.7979	0.1897	2150.67	2151.36	3733.1	2	251.1	44.4	1	R.MDSFDEDLARPSGLLAQER.K
*	HsF-IP-293-MG_Ti_106.22	4.0949	0.3171	2151.56	2151.36	5477	1	1087.4	41.7	6	R.MDSFDEDLARPSGLLAQER.K
*	HsF-IP-293-MG_Ti_103.13	3.4607	0.1258	972.37	971.101	5690.3	1	1309.4	93.8	3	R.PSGLLAQER.K
*	HsFlag1P_Ti_106.2220.222	4.0761	0.3326	1629.99	1630.8	7756.5	1	1114.5	70.8	1	R.DLVHSNKKEQEFR.S
*	HsFLAG-Control_HeLa_NE	3.5187	0.331	1529.63	1530.68	6130.7	1	395.3	54.2	2	R.SIFQHIQSAQSQR.S
*	HsFLAG-Control_HeLa_NE	3.3859	0.313	1529.66	1530.68	6290.4	1	535.7	62.5	2	R.SIFQHIQSAQSQR.S
*	HsHeLa_Control-MG_Ti_10	3.3067	0.2927	1529.79	1530.68	5053.1	1	418.6	62.5	2	R.SIFQHIQSAQSQR.S
*	Hs283FLP_Ti_106.2008.20	3.289	0.4105	1529.8	1530.68	5115.2	1	397.4	58.3	2	R.SIFQHIQSAQSQR.S
*	HsHeLa_Control_Ti_106.27	3.2527	0.2828	1529.91	1530.68	5331.4	1	395.9	58.3	2	R.SIFQHIQSAQSQR.S
*	Hs293FLP_TREX_Ti_106.2	4.3389	0.39	1529.97	1530.68	7088.8	1	1499.1	79.2	5	R.SIFQHIQSAQSQR.S
*	Hs293FLP_Ti_306.2395.23	3.2702	0.3318	1530.03	1530.68	4760.5	1	363.1	58.3	4	R.SIFQHIQSAQSQR.S
*	HsF-IP-293_Ti_106.2026.2	4.2995	0.3884	1530.38	1530.68	7268.7	1	1281	75	11	R.SIFQHIQSAQSQR.S
*	Hs293FLP-MG_Ti_206.262	3.8863	0.2627	1530.54	1530.68	9279.7	1	1781.6	79.2	2	R.SIFQHIQSAQSQR.S
*	HsF-IP-293-MG_Ti_106.20	3.4929	0.2971	1530.58	1530.68	5005.7	1	363.9	58.3	2	R.SIFQHIQSAQSQR.S
*	Hs293FLP-MG_Ti_206.263	3.469	0.3495	1530.62	1530.68	5569.5	1	293.9	50	3	R.SIFQHIQSAQSQR.S
*	HsF-IP-293-MG_Ti_106.20	4.1803	0.2958	1530.64	1530.68	7144	1	1594.4	83.3	3	R.SIFQHIQSAQSQR.S
*	HsFLAG-Control_HeLa_NE	3.8996	0.22	1530.67	1530.68	7639.2	1	1176.8	70.8	3	R.SIFQHIQSAQSQR.S
*	HsHeLa_Control_Ti_106.27	3.8887	0.3332	1530.85	1530.68	6685.3	1	1333.8	79.2	2	R.SIFQHIQSAQSQR.S
*	Hs293FLP-MG_Ti_206.262	3.835	0.284	1531.07	1530.68	2934.2	1	805.2	62.5	1	R.SIFQHIQSAQSQR.S
*	HsFLAG-Control_HeLa_NE	3.8648	0.3106	1531.09	1530.68	8072.2	1	1373.1	75	3	R.SIFQHIQSAQSQR.S
*	Hs293FLP_Ti_306.2394.23	3.7315	0.3348	1531.61	1530.68	6987.5	1	1077.2	70.8	2	R.SIFQHIQSAQSQR.S
*	HsHeLa_Control-MG_Ti_10	3.4903	0.419	1625.99	1625.76	6884.7	1	990.1	73.1	5	K.EHHFGSSGMTLHER.F
*	Hs293FLP-MG_Ti_205.184	3.5693	0.197	1192.25	1192.36	6197.5	1	959.9	83.3	6	R.RIDISPSTFR.K
*	Hs293FLP_Ti_305.0975.09	2.5917	0.2493	1037.28	1038.17	5884.2	1	952.7	81.2	1	K.HGLAHDEMK.S
*	HsF-IP-293-MG_Ti_105.07	1.8778	0.2606	1037.36	1038.17	3435.5	3	283.2	62.5	1	K.HGLAHDEMK.S
*	HsHeLa_Control-MG_Ti_20	2.0917	0.2729	1037.36	1038.17	3158	7	183.9	56.2	1	K.HGLAHDEMK.S
*	HsHeLa_Control-MG_Ti_10	2.0047	0.1973	1037.43	1038.17	4067	1	322.5	56.2	1	K.HGLAHDEMK.S
*	Hs293FLP-MG_Ti_205.128	3.0616	0.2865	1037.97	1038.17	7908	1	1151.9	81.2	2	K.HGLAHDEMK.S
*	HsHeLa_Control-MG_Ti_10	3.3271	0.323	1039.43	1038.17	7061.7	1	1318	87.5	1	K.HGLAHDEMK.S
*	Hs293FLP-MG_Ti_203.159	3.327	0.2023	1121.39	1121.24	5083.1	1	1056.4	87.5	19	K.YKDDPVDLR.L
*	Hs293FLP-MG_Ti_104.148	5.1026	0.362	2381.08	2381.38	7869.3	1	989	52.6	22	K.AEEYTEETEEREESTTGFDK.S
*	HsHeLa_Control-MG_Ti_20	2.7496	0.2304	1849.51	1849.95	4433	8	338.5	53.8	1	K.RNREEEWDPEYTPK.S
*	Hs293FLP-MG_Ti_203.174	3.387	0.2196	1693.66	1693.77	4095.3	1	662.5	75	2	R.NREEEWDPEYTPK.S
	HsF-IP-293_Ti_102.1526.1	3.5091	0.2765	1422.83	1423.48	4814.6	1	767.9	80	7	R.EEEWDPEYTPK.S
*	HsHeLa_Control-MG_Ti_20	2.9838	0.1236	1111.36	1110.21	4792.9	1	1016.1	92.9	2	K.KYYLHDDR.E
*	HsHeLa_Control-MG_Ti_10	3.931	0.2925	1812.77	1812.89	6539	1	877.9	67.9	5	K.KYYLHDDREGEGSDK.W
*	Hs293FLP_Ti_303.1193.11	4.3255	0.422	1684.77	1684.72	9564.7	1	1560.3	73.1	14	K.YYLHDDREGEGSDK.W
*	HsHeLa_Control_Ti_102.14	5.4707	0.4387	2000.65	2000.94	5744.7	1	1243.2	67.6	6	K.FSGEEGEIEDDESGTENR.E
*	HsHeLa_Control_Ti_102.14	4.5626	0.4085	2386.93	2387.34	6536.5	1	628.6	45	4	K.FSGEEGEIEDDESGTENREEK.D

*	HsFLAG-Control_HeLa_NE	4.5681	0.303	3285.07	3286.27	6109.8		1	584.8	26.8	1	K.FSGEEGEIEDDESGTENREEKDNIQPTTE.-
gi|4503571|ref|NI	14	44	0.371	434	47169	7.4	U		enolase 1 [Homo sapiens]			
*	HsFLAG-Control_MG_293_	2.634	0.1939	1406.61	1407.56	8800.8		1	689	54.2	2	R.GNPTVEVDLFTSK.G
*	Hs293FLP_TREX_Ti_105.2	3.3026	0.2212	1407.3	1407.56	4235.1		2	568.8	66.7	2	R.GNPTVEVDLFTSK.G
	HsHeLa3_Ti_103.2746.274	4.6445	0.3922	1807.02	1806.03	3246.1		1	666.5	70.6	4	R.AAVPSGASTGIYEALELR.D
*	HsFLAG-Control_Hela_Ti_1	1.9043	0.1313	899.5	900.106	6729.3		5	587.8	68.8	1	K.TIAPALVSK.K
*	Hs293FLP_TREX_Ti_104.1	4.0197	0.2032	1445.11	1445.66	7653.7		1	1036.7	77.3	2	K.KLNVTEQEKIDK.L
*	HsHeLa3_Ti_105.3739.373	4.1285	0.1425	1911.19	1909.32	5761.3		5	1231.9	46.9	1	K.LAMQEFMILPVGAANFR.E
*	HsHeLa3_Ti_105.3734.373	3.9726	0.2495	1912.01	1909.32	5364.6		1	676.9	59.4	1	K.LAMQEFMILPVGAANFR.E
*	HsFLAG-Control_293_Ti_2	3.677	0.1949	1144.28	1144.32	7822.9		1	1284.6	83.3	7	R.IGAEVYHNLK.N
*	HsFLAG-Control_293_Ti_2	4.8602	0.4265	1963.37	1962.08	7963.5		1	1833.8	66.7	7	K.DATNVGDEGGFAPNILENK.E
*	HsHeLa3_Ti_102.2637.263	2.107	0.2947	1426.53	1426.61	10923.1		4	636	50	1	R.YISPDQLADLYK.S
*	HsHeLa3_Ti_102.2606.260	2.8566	0.2164	1426.7	1426.61	3227.1		1	550.9	72.7	1	R.YISPDQLADLYK.S
*	HsHeLa3_Ti_102.3841.384	5.5501	0.3811	2511.01	2511.66	5992.6		1	1752.4	67.5	10	K.DYPVVSIEDPFDQDDWGAWQK.F
	HsHeLa3_Ti_105.4294.429	4.94	0.5174	2356.24	2354.58	6378.9		1	1105.2	52.4	4	R.SGETEDTFIADLVVGLCTGQIK.T
*	Hs293FLP_TREX_Ti_102.1	1.9797	0.1482	904.37	904.993	5724.7		2	503.1	71.4	1	R.IEEELGSK.A
gi|4885379|ref|NI	31	68	0.37	219	21865	11	U		H1 histone family, member 4 [Homo sapiens]			
	Hs293FLP_TREX_Ti_106.2	4.2447	0.2855	1483.62	1483.75	6765.2		1	1180.6	76.9	2	K.RKASGPPVSELITK.A
	Hs293FLP_TREX_Ti_105.1	3.0697	0.3063	1326.44	1327.56	5625.4		1	525.1	54.2	2	R.KASGPPVSELITK.A
	HsFLAG-MOCK_300mM_T	4.3832	0.346	1327.6	1327.56	7311.6		1	1540.1	79.2	4	R.KASGPPVSELITK.A
	Hs293FLP_TREX_Ti_105.1	4.5528	0.2867	1327.6	1327.56	6535		1	1711.1	83.3	3	R.KASGPPVSELITK.A
	Hs293FLP_TREX_Ti_105.1	4.1842	0.2215	1327.89	1327.56	4082.6		1	1092.6	58.3	2	R.KASGPPVSELITK.A
	Hs293FLP-MG_Ti_302.158	2.2832	0.2134	1198.39	1199.39	5448.6		5	377.6	59.1	1	K.ASGPPVSELITK.A
	HsHeLa3_Ti_103.1780.178	2.1262	0.1215	1198.67	1199.39	7333.6		3	598.9	59.1	1	K.ASGPPVSELITK.A
	HsFLAG-MOCK_300mM_T	3.2152	0.232	1198.92	1199.39	6681.5		1	820.6	72.7	7	K.ASGPPVSELITK.A
	HsGST-MOCK_Ti_303.200	2.7091	0.2074	1199.13	1199.39	6241.3		1	738.8	72.7	1	K.ASGPPVSELITK.A
	Hs293FLP_TREX_Ti_106.2	4.5743	0.2973	1658.55	1658.94	11004.9		1	2292.6	71.9	2	K.AVAASKERSGVSLAALK.K
	Hs293FLP_TREX_Ti_106.2	4.2131	0.1736	1786.63	1787.11	8881.8		2	1187.9	58.8	1	K.AVAASKERSGVSLAALKK.A
	Hs293FLP_TREX_Ti_106.2	3.0895	0.171	1259.61	1259.49	4520.5		3	723	77.3	1	K.ERSGVSLAALKK.A
	Hs293FLP_TREX_Ti_102.1	3.0132	0.1626	846.13	846.015	3355.5		2	954.3	93.8	2	R.SGVSLAALK.K
	HsFLAG-MOCK_300mM_T	3.4949	0.1712	974.56	974.189	4235.3		2	983.5	94.4	2	R.SGVSLAALKK.A
	HsFLAG-MOCK_300mM_T	3.3324	0.347	1235.45	1236.41	7986.8		1	1354.2	72.7	1	K.KALAAAGYDVEK.N
	Hs293FLP_TREX_Ti_103.1	3.8244	0.3765	1235.5	1236.41	5633.7		1	876.3	72.7	2	K.KALAAAGYDVEK.N
	Hs293FLP_TREX_Ti_103.1	4.2764	0.2988	1236.31	1236.41	8294.8		1	2277.5	90.9	5	K.KALAAAGYDVEK.N
	Hs293FLP-MG_Ti_302.133	2.9735	0.2799	1107.49	1108.24	9558.8		1	1210.9	70	4	K.ALAAAGYDVEK.N
	HsHeLa3_Ti_102.1555.155	2.8055	0.3679	1107.57	1108.24	8392.9		2	806	65	1	K.ALAAAGYDVEK.N
	Hs293FLP_TREX_Ti_102.1	3.2612	0.3612	1107.6	1108.24	9082.9		1	1240	70	4	K.ALAAAGYDVEK.N
	Hs293FLP_TREX_Ti_102.1	3.37	0.2203	1108.28	1108.24	5059.1		1	1168.4	85	2	K.ALAAAGYDVEK.N
	HsHeLa3_Ti_102.1562.156	3.2598	0.2416	1108.48	1108.24	4781.3		1	1268.8	90	1	K.ALAAAGYDVEK.N
	HsGST-MOCK_Ti_402.186	3.2664	0.1912	1109.14	1108.24	6550.6		1	1106.2	80	2	K.ALAAAGYDVEK.N
	Hs293FLP_TREX_Ti_103.1	4.3703	0.3994	1579.29	1579.71	6540.5		1	1574.4	75	2	K.ALAAAGYDVEKNNSR.I
	Hs293FLP_TREX_Ti_105.1	3.0205	0.2991	1260.42	1261.51	5067.2		1	605.7	68.2	1	K.SLVSKGTLVQTK.G
	Hs293FLP_TREX_Ti_105.1	3.7512	0.3731	1261.67	1261.51	5381.4		1	1225.2	86.4	1	K.SLVSKGTLVQTK.G
	Hs293FLP_TREX_Ti_106.2	4.968	0.4135	2055.48	2054.35	10342.6		1	1603	57.5	1	K.SLVSKGTLVQTKGTGASGSFK.L
	Hs293FLP_TREX_Ti_105.1	4.0346	0.3258	1539.48	1539.73	6063.8		1	1084	70	4	K.GTLVQTKGTGASGSFK.L
	Hs293FLP_TREX_Ti_105.1	3.2555	0.1904	1167.28	1167.31	8367.3		1	1260.1	72.7	2	K.GTGASGSFKLNK.K
	Hs293FLP_TREX_Ti_106.2	3.5403	0.2379	1295.64	1295.48	8182.4		9	845	62.5	2	K.GTGASGSFKLNKK.A
*	HsGST-MOCK_Ti_102.066	2.2499	0.1004	784.55	784.934	3732.6		3	296.6	62.5	2	K.KPAAAAGAK.K
gi|5902102|ref|NI	18	209	0.37	119	13282	11.6	U		small nuclear ribonucleoprotein D1 polypeptide 16kDa [Homo sapiens]			

*	HsFLAG-Control_293_Ti_1	2.5471	0.1761	1269.74	1270.47	6835		2	623.4	70	1	K.LSHETVTIELK.N
*	Hs283FLP_Ti_105.1486.14	2.5422	0.2211	1270.63	1270.47	4912		1	787.9	80	1	K.LSHETVTIELK.N
*	Hs293FLP-MG_Ti_204.204	4.3126	0.2488	1555.39	1555.78	7087.7		1	1602.8	56.2	1	K.NREPVQLETLSIR.G
*	HsFLAG-Control_MG_293_	3.8284	0.3156	1555.47	1555.78	8824.5		1	1225.2	70.8	27	K.NREPVQLETLSIR.G
*	HsHeLa3_Ti_105.1958.195	3.9255	0.3656	1555.84	1555.78	6140.3		1	1179.7	79.2	6	K.NREPVQLETLSIR.G
*	Hs293FLP_Ti_304.1881.18	4.6008	0.2855	1556.2	1555.78	6212		1	1354.7	52.1	2	K.NREPVQLETLSIR.G
*	Hs283FLP_Ti_105.1699.16	4.0616	0.3743	1556.26	1555.78	6424		1	1156.1	79.2	7	K.NREPVQLETLSIR.G
*	HsFLAG-Control_293_Ti_2	4.1111	0.3386	1556.45	1555.78	7330.4		1	1448.1	79.2	9	K.NREPVQLETLSIR.G
*	HsHeLa_Control-MG_Ti_10	4.6141	0.293	1556.85	1555.78	7111.6		1	1524.5	54.2	1	K.NREPVQLETLSIR.G
*	Hs293FLP-MG_Ti_203.514	4.7048	0.4281	2287.77	2288.69	4543.1		1	972.8	63.2	9	R.YFILPDSLPLDTLLVDVEPK.V
*	HsF-IP-293_Ti_204.4677.4	4.7171	0.4051	2287.82	2288.69	4154.4		1	1007.4	68.4	78	R.YFILPDSLPLDTLLVDVEPK.V
*	Hs293FLP-MG_Ti_202.534	5.5985	0.3502	2288.33	2288.69	7056.1		1	1445.5	42.1	2	R.YFILPDSLPLDTLLVDVEPK.V
*	HsFLAG-Control_293_Ti_2	5.2219	0.3592	2288.35	2288.69	6619.3		2	984.2	36.8	2	R.YFILPDSLPLDTLLVDVEPK.V
*	HsHeLa_Control-MG_Ti_20	4.9572	0.3738	2288.36	2288.69	7166.5		1	1260.7	39.5	2	R.YFILPDSLPLDTLLVDVEPK.V
*	HsF-IP-293-MG_Ti_102.46	4.9436	0.4529	2288.65	2288.69	4384.5		1	709.1	57.9	15	R.YFILPDSLPLDTLLVDVEPK.V
*	HsFLAG-Control_HeLa_S1	4.9066	0.3861	2288.67	2288.69	4787.2		1	891.6	63.2	38	R.YFILPDSLPLDTLLVDVEPK.V
*	HsF-IP-293-MG_Ti_102.43	3.945	0.3364	2289.02	2288.69	8285.5		3	991.9	35.5	1	R.YFILPDSLPLDTLLVDVEPK.V
*	HsGST-MOCK_Ti_403.533	5.2978	0.4457	2289.04	2288.69	5334.1		1	1220.6	68.4	7	R.YFILPDSLPLDTLLVDVEPK.V
gi|4506681|ref|N	5	17	0.367	158	18431	10.3	U	ribosomal protein S11 [Homo sapiens]				
*	HsGST-MOCK_Ti_103.115	3.3044	0.2115	1231.7	1230.45	6754.4		1	1276.4	85	3	K.RVLLGETGKEK.L
*	HsGST-MOCK_Ti_402.189	2.605	0.2842	1138.77	1139.25	7203.5		1	881.9	83.3	1	K.EAIEGTYIDK.K
*	HsGST-MOCK_Ti_104.149	3.3523	0.2202	1136.59	1136.3	7148.1		1	1154.1	92.9	2	R.RDYLHYIR.K
*	HsGST-MOCK_Ti_406.254	3.2736	0.1953	1349.19	1348.53	5290.6		2	565.1	65	1	K.NMSVHLSPCFR.D
*	Hs293FLP-MG_Ti_203.262	4.5515	0.4632	1986.4	1987.23	6809.1		1	965.1	58.8	10	R.DVQIGDIVTVGECRPLSK.T
gi|4505417|ref|N	4	27	0.364	231	25953	6.3	U	NAD(P)H dehydrogenase, quinone 2 [Homo sapiens]				
*	HsHeLa_Control-MG_Ti_20	4.2992	0.4118	2583.79	2585.79	5564.3		1	923.9	52.3	6	K.DITGTLSNPEVFNYGVETHEAYK.Q
*	HsHeLa_Control-MG_Ti_20	5.4137	0.3586	2498.1	2497.98	7484.2		1	1609.2	55	11	R.EADLVIFQFPLYWFSVPAILK.G
*	HsHeLa_Control-MG_Ti_20	5.381	0.3994	2434.49	2433.73	3806.6		1	736	57.1	7	R.VLCQGFAFDIPGFYDSGLLQGK.L
*	HsHeLa_Control-MG_Ti_20	4.1052	0.4013	1986.45	1987.22	5555.4		1	1116.7	67.6	3	K.VLAPQISFAPEIASEEER.K
gi|14211889|ref|	7	21	0.364	99	11250	4.9	U	dpy-30-like protein [Homo sapiens]				
	HsGST-MOCK_Ti_304.005	4.5309	0.3482	2125.76	2126.59	4492.3		1	987.5	65.8	2	R.AYLDQTVVPILLQGLAVLAK.E
	HsFLAG-Control_HeLa_NE	4.5554	0.3746	2125.8	2126.59	3974.2		1	587.8	55.3	4	R.AYLDQTVVPILLQGLAVLAK.E
	HsHeLa3_Ti_104.0027.002	6.2807	0.3965	2126.46	2126.59	7790.5		1	2195.2	48.7	4	R.AYLDQTVVPILLQGLAVLAK.E
	HsFLAG-Control_HeLa_NE	5.7461	0.3563	2126.8	2126.59	8982.6		1	2224.4	44.7	4	R.AYLDQTVVPILLQGLAVLAK.E
	HsHeLa3_Ti_104.0014.001	4.041	0.3103	2127.02	2126.59	3512.7		1	505.9	55.3	3	R.AYLDQTVVPILLQGLAVLAK.E
*	HsFLAG-MOCK_300mM_T	4.643	0.1872	1889.55	1888.22	6998.1		1	1702.4	48.3	2	K.ERPPNPIEFLASYLLK.N
*	HsHeLa3_Ti_106.3420.342	3.7671	0.3853	1889.7	1888.22	6501.8		1	575	50	2	K.ERPPNPIEFLASYLLK.N
gi|15431293|ref|	9	20	0.363	204	24146	11.6	U	ribosomal protein L15 [Homo sapiens]				
gi|88998872|ref|	9	20	0.363	204	24174	11.6	U	PREDICTED: similar to ribosomal protein L15 isoform 6 [Homo sapiens]				
gi|88998870|ref|	9	20	0.363	204	24174	11.6	U	PREDICTED: similar to ribosomal protein L15 isoform 5 [Homo sapiens]				
gi|88998868|ref|	9	20	0.363	204	24174	11.6	U	PREDICTED: similar to ribosomal protein L15 isoform 4 [Homo sapiens]				
gi|88998866|ref|	9	20	0.363	204	24174	11.6	U	PREDICTED: similar to ribosomal protein L15 isoform 3 [Homo sapiens]				
gi|88998864|ref|	9	20	0.363	204	24174	11.6	U	PREDICTED: similar to ribosomal protein L15 isoform 1 [Homo sapiens]				
gi|88992466|ref|	9	20	0.363	204	24174	11.6	U	PREDICTED: similar to ribosomal protein L15 isoform 5 [Homo sapiens]				
gi|88992463|ref|	9	20	0.363	204	24174	11.6	U	PREDICTED: similar to ribosomal protein L15 isoform 4 [Homo sapiens]				
gi|88992460|ref|	9	20	0.363	204	24174	11.6	U	PREDICTED: similar to ribosomal protein L15 isoform 3 [Homo sapiens]				
gi|88992455|ref|	9	20	0.363	204	24174	11.6	U	PREDICTED: similar to ribosomal protein L15 isoform 1 [Homo sapiens]				
	Hs293FLP_TREX_Ti_106.2	4.4638	0.4114	1706.58	1706.95	5016.1		1	684.4	60	2	K.GATYGKPVHHGVNQLK.F
	Hs293FLP_TREX_Ti_106.2	2.7548	0.2742	1128.42	1129.31	4058.8		2	467.5	72.2	1	K.PVHHGVNQLK.F

	Hs293FLP_TREX_Ti_102.1	3.2226	0.1131	1019.35	1019.1	5655.2		1	975.4	87.5	4	R.SLQSVAEER.A
	Hs293FLP_TREX_Ti_102.1	4.6107	0.3627	1661.4	1661.81	5142.6		1	1037.3	73.1	3	R.VLNSYWVGEDSTYK.F
	HsHeLa_Control-MG_Ti_10	3.6586	0.2761	1506.91	1505.8	6236.2		1	1175.1	72.7	4	K.FFEVILIDPFHK.A
	Hs293FLP_TREX_Ti_104.1	3.3	0.2305	1259.38	1259.41	5834		1	902	77.8	2	R.RNPDTQWITK.P
	Hs293FLP_TREX_Ti_106.2	3.544	0.3343	1720.53	1720.97	5980.7		1	845.3	69.2	1	R.RNPDTQWITKPVHK.H
	Hs293FLP_TREX_Ti_106.2	3.5201	0.3645	1564.6	1564.78	7642.3		1	805.9	62.5	1	R.NPDTQWITKPVHK.H
	Hs293FLP_TREX_Ti_106.2	2.8404	0.25	1011.44	1012.12	4749.1		2	368.4	75	2	K.FHHTIGGSR.R
gi|4885375|ref|N	31	68	0.362	213	21365	10.9	U		H1 histone family, member 2 [Homo sapiens]			
*	Hs293FLP_TREX_Ti_106.2	4.0392	0.4308	1865.9	1867.16	10474.1		1	1062.3	52.8	2	K.AGGTPRKASGPPVSELITK.A
*	Hs293FLP_TREX_Ti_106.2	4.9301	0.4712	1867.35	1867.16	7196.7		1	1479.3	44.4	2	K.AGGTPRKASGPPVSELITK.A
	Hs293FLP_TREX_Ti_105.1	3.0697	0.3063	1326.44	1327.56	5625.4		1	525.1	54.2	2	R.KASGPPVSELITK.A
	HsFLAG-MOCK_300mM_T	4.3832	0.346	1327.6	1327.56	7311.6		1	1540.1	79.2	4	R.KASGPPVSELITK.A
	Hs293FLP_TREX_Ti_105.1	4.5528	0.2867	1327.6	1327.56	6535		1	1711.1	83.3	3	R.KASGPPVSELITK.A
	Hs293FLP_TREX_Ti_105.1	4.1842	0.2215	1327.89	1327.56	4082.6		1	1092.6	58.3	2	R.KASGPPVSELITK.A
	Hs293FLP-MG_Ti_302.158	2.2832	0.2134	1198.39	1199.39	5448.6		5	377.6	59.1	1	K.ASGPPVSELITK.A
	HsHeLa3_Ti_103.1780.178	2.1262	0.1215	1198.67	1199.39	7333.6		3	598.9	59.1	1	K.ASGPPVSELITK.A
	HsFLAG-MOCK_300mM_T	3.2152	0.232	1198.92	1199.39	6681.5		1	820.6	72.7	7	K.ASGPPVSELITK.A
	HsGST-MOCK_Ti_303.200	2.7091	0.2074	1199.13	1199.39	6241.3		1	738.8	72.7	1	K.ASGPPVSELITK.A
	Hs293FLP_TREX_Ti_106.2	4.5743	0.2973	1658.55	1658.94	11004.9		1	2292.6	71.9	2	K.AVAASKERSGVSLAALK.K
	Hs293FLP_TREX_Ti_106.2	4.2131	0.1736	1786.63	1787.11	8881.8		2	1187.9	58.8	1	K.AVAASKERSGVSLAALKK.A
	Hs293FLP_TREX_Ti_106.2	3.0895	0.171	1259.61	1259.49	4520.5		3	723	77.3	1	K.ERSGVSLAALKK.A
	Hs293FLP_TREX_Ti_102.1	3.0132	0.1626	846.13	846.015	3355.5		2	954.3	93.8	2	R.SGVSLAALK.K
	HsFLAG-MOCK_300mM_T	3.4949	0.1712	974.56	974.189	4235.3		2	983.5	94.4	2	R.SGVSLAALKK.A
	HsFLAG-MOCK_300mM_T	3.3324	0.347	1235.45	1236.41	7986.8		1	1354.2	72.7	1	K.KALAAAGYDVEK.N
	Hs293FLP_TREX_Ti_103.1	3.8244	0.3765	1235.5	1236.41	5633.7		1	876.3	72.7	2	K.KALAAAGYDVEK.N
	Hs293FLP_TREX_Ti_103.1	4.2764	0.2988	1236.31	1236.41	8294.8		1	2277.5	90.9	5	K.KALAAAGYDVEK.N
	Hs293FLP-MG_Ti_302.133	2.9735	0.2799	1107.49	1108.24	9558.8		1	1210.9	70	4	K.ALAAAGYDVEK.N
	HsHeLa3_Ti_102.1555.155	2.8055	0.3679	1107.57	1108.24	8392.9		2	806	65	1	K.ALAAAGYDVEK.N
	Hs293FLP_TREX_Ti_102.1	3.2612	0.3612	1107.6	1108.24	9082.9		1	1240	70	4	K.ALAAAGYDVEK.N
	Hs293FLP_TREX_Ti_102.1	3.37	0.2203	1108.28	1108.24	5059.1		1	1168.4	85	2	K.ALAAAGYDVEK.N
	HsHeLa3_Ti_102.1562.156	3.2598	0.2416	1108.48	1108.24	4781.3		1	1268.8	90	1	K.ALAAAGYDVEK.N
	HsGST-MOCK_Ti_402.186	3.2664	0.1912	1109.14	1108.24	6550.6		1	1106.2	80	2	K.ALAAAGYDVEK.N
	Hs293FLP_TREX_Ti_103.1	4.3703	0.3994	1579.29	1579.71	6540.5		1	1574.4	75	2	K.ALAAAGYDVEKNNSR.I
	Hs293FLP_TREX_Ti_105.1	3.0205	0.2991	1260.42	1261.51	5067.2		1	605.7	68.2	1	K.SLVSKGTLVQTK.G
	Hs293FLP_TREX_Ti_105.1	3.7512	0.3731	1261.67	1261.51	5381.4		1	1225.2	86.4	1	K.SLVSKGTLVQTK.G
	Hs293FLP_TREX_Ti_106.2	4.968	0.4135	2055.48	2054.35	10342.6		1	1603	57.5	1	K.SLVSKGTLVQTKGTGASGSFK.L
	Hs293FLP_TREX_Ti_105.1	4.0346	0.3258	1539.48	1539.73	6063.8		1	1084	70	4	K.GTLVQTKGTGASGSFK.L
	Hs293FLP_TREX_Ti_105.1	3.2555	0.1904	1167.28	1167.31	8367.3		1	1260.1	72.7	2	K.GTGASGSFKLNK.K
	Hs293FLP_TREX_Ti_106.2	3.5403	0.2379	1295.64	1295.48	8182.4		9	845	62.5	2	K.GTGASGSFKLNKK.A
gi|5729730|ref|N	12	60	0.361	504	56770	5.9	U		apoptosis inhibitor 5 [Homo sapiens]			
*	HsFLAG-Control_HeLa_NE	5.1207	0.4493	1744.59	1744.9	7396.2		1	2044.2	80	12	R.NYGILADATEQVGQHK.D
*	HsFLAG-Control_HeLa_NE	3.9787	0.195	1221.28	1221.4	6518		2	1344.7	80	7	K.DAYQVILDGVK.G
*	HsFLAG-Control_HeLa_NE	3.9989	0.2818	1472.09	1472.64	4050		1	842.6	79.2	6	K.ELPQFATGENLPR.V
*	HsFLAG-Control_HeLa_NE	5.9578	0.3983	3207.5	3207.65	8503.7		1	1410.1	30.4	5	R.VADILTQLLQTDDSAEFNLVNNALLSIFK.M
*	HsFLAG-Control_HeLa_NE	5.3931	0.4178	1905.66	1904.17	9473.8		1	2185.1	70.6	13	K.GTLGGLFSQILQGEDIVR.E
*	HsFLAG-Control_HeLa_NE	4.0427	0.148	1291.43	1290.45	5967.6		1	1180.1	85	4	K.EVEELILTESK.K
*	HsFLAG-Control_HeLa_NE	3.3972	0.1957	1419.43	1418.63	7019.2		1	1088.9	81.8	1	K.EVEELILTESKK.V
*	HsFLAG-MOCK_300mM_T	3.7438	0.3101	3892.23	3890.19	6736.3		1	815.7	25	1	R.QQLVELVAEQADLEQTFNPSDPDCVDRLLQCTR.Q
*	HsFLAG-Control_HeLa_NE	3.7828	0.172	1142.47	1142.38	7690.7		1	1308.1	88.9	5	K.ITNNINVLIK.D

*	HsFLAG-Control_HeLa_NE	2.8992	0.173	1217.54	1217.41	4572.3		1	645.8	72.2	1	K.DLFHIPPSYK.S
*	HsFLAG-MOCK_300mM_T	3.0866	0.2359	2030.91	2029.39	3858.6		1	357.7	47.1	1	K.STVTLSWKPVQKVEIGQK.R
*	HsFLAG-Control_HeLa_NE	3.5192	0.3605	1464.64	1464.53	5064.4		1	910.3	81.8	4	K.YSSNLGNFNYER.S
gi|4506185|ref|N	5	11	0.36	261	29484	7.7	U	proteasome alpha 4 subunit [Homo sapiens]				
*	HsFLAG-Control_293_Ti_2	4.6652	0.3363	2594.29	2594.82	7165.4		1	700.3	41.3	2	K.LNEDMACSVAGITSDANVLTNELR.L
*	HsHeLa_Control-MG_Ti_20	4.8627	0.2987	2696.06	2696.05	5770.6		1	926.8	52.4	2	R.YLLQYQEPIPCEQLVTALCDIK.Q
*	HsHeLa_Control-MG_Ti_10	4.3827	0.4818	2205.89	2205.35	4395.1		1	1197.7	72.2	3	K.HYGFQLYQSDPSGNYGGWK.A
*	HsFLAG-Control_293_Ti_2	3.3765	0.2719	1609.32	1608.82	7031.7		1	818.6	56.7	1	K.ATCIGNNSAAAVSMLK.Q
*	HsFLAG-Control_MG_293_	2.9645	0.1698	1432.37	1431.67	6075.5		3	641.1	58.3	3	K.LSAEKVEIATLTR.E
gi|7705696|ref|N	9	27	0.36	172	19206	5.4	U	endoplasmic reticulum thioredoxin superfamily member, 18 kDa [Homo sapiens]				
*	Hs293FLP_Ti_306.2459.24	3.5281	0.3229	1125.62	1125.24	5669.9		1	1107.2	87.5	4	K.GFGDHIHWR.T
*	Hs293FLP_Ti_304.2619.26	4.1859	0.3719	1552.49	1550.9	3021.6		1	563.1	71.4	5	K.EAAASGLPLMVIIHK.S
*	Hs293FLP_Ti_302.2294.22	2.1774	0.1985	989.92	990.188	3286.2		3	501.1	75	1	R.ILFLDPSGK.V
*	HsFLAG-MOCK_300mM_T	2.9818	0.2823	2682.07	2683.04	4778.9		1	487.9	43.5	2	R.ILFLDPSGKVHPEIINENGNPSYK.Y
*	Hs293FLP_Ti_305.2338.23	3.2088	0.2388	2682.08	2683.04	5246.6		1	512.3	43.5	2	R.ILFLDPSGKVHPEIINENGNPSYK.Y
*	Hs293FLP-MG_Ti_205.259	4.0189	0.2096	2682.89	2683.04	5481.3		1	649.8	31.5	1	R.ILFLDPSGKVHPEIINENGNPSYK.Y
*	HsHeLa_Control-MG_Ti_10	4.7688	0.2098	2685.75	2683.04	4832.8		1	721.9	34.8	3	R.ILFLDPSGKVHPEIINENGNPSYK.Y
*	HsHeLa_Control-MG_Ti_20	4.2752	0.4686	1710.67	1711.87	3639.8		1	985.5	82.1	8	K.VHPEIINENGNPSYK.Y
*	Hs293FLP-MG_Ti_203.299	3.2298	0.3328	1649.63	1649.9	10870.4		1	1769	73.1	1	K.YFYVSAEQVVQGMK.E
gi|7661958|ref|N	74	346	0.354	920	106122	10	U	BCL2-associated transcription factor 1 [Homo sapiens]				
	Hs293FLP-MG_Ti_103.116	4.2686	0.2971	1442.85	1442.57	4496.5		2	911.5	75	9	K.KAEGEPQEESPLK.S
	HsF-IP-293-MG_Ti_105.15	4.2602	0.2754	2608.4	2609.68	4613.8		1	427	42.9	3	K.SQEEPKDTFEHDPSESIDEFNK.S
	Hs293FLP-MG_Ti_306.237	3.692	0.4131	2608.41	2609.68	4254.9		1	519.8	47.6	1	K.SQEEPKDTFEHDPSESIDEFNK.S
	Hs293FLP-MG_Ti_203.190	4.7394	0.2621	2608.75	2609.68	7028.8		1	1057.3	36.9	1	K.SQEEPKDTFEHDPSESIDEFNK.S
	Hs293FLP-MG_Ti_203.190	4.0194	0.4754	2608.86	2609.68	4719.7		1	683.3	52.4	2	K.SQEEPKDTFEHDPSESIDEFNK.S
	Hs283FLP_Ti_105.1581.15	4.0195	0.3453	2608.88	2609.68	4522.5		1	351.3	40.5	5	K.SQEEPKDTFEHDPSESIDEFNK.S
	HsFLAG-Control_HeLa_NE	3.8143	0.3422	2608.92	2609.68	5472.9		1	396.8	40.5	1	K.SQEEPKDTFEHDPSESIDEFNK.S
	HsF-IP-293-MG_Ti_105.18	4.8778	0.3121	2609.15	2609.68	5020.4		1	769.3	35.7	5	K.SQEEPKDTFEHDPSESIDEFNK.S
	HsHeLa_Control_Ti_103.20	3.6894	0.2965	2609.65	2609.68	4258.9		1	715.4	39.3	1	K.SQEEPKDTFEHDPSESIDEFNK.S
	HsFLAG-Control_HeLa_NE	4.4793	0.2928	2609.78	2609.68	5503.5		1	994.4	39.3	2	K.SQEEPKDTFEHDPSESIDEFNK.S
	Hs283FLP_Ti_104.2388.23	4.4679	0.2976	2609.93	2609.68	4879.3		1	929.9	39.3	4	K.SQEEPKDTFEHDPSESIDEFNK.S
	Hs293FLP-MG_Ti_105.200	3.5827	0.2809	2610.54	2609.68	4295.5		1	410.6	42.9	4	K.SQEEPKDTFEHDPSESIDEFNK.S
	Hs293FLP-MG_Ti_105.200	3.8551	0.2815	2611.6	2609.68	4440.2		1	544.1	34.5	1	K.SQEEPKDTFEHDPSESIDEFNK.S
	HsHeLa_Control_Ti_103.21	3.6537	0.3622	2612.16	2609.68	4472.1		1	539.3	47.6	4	K.SQEEPKDTFEHDPSESIDEFNK.S
	HsFLAG-Control_HeLa_NE	5.0441	0.3677	1910.23	1910.95	5038.6		1	1211.9	73.3	5	K.DTFEHDPSESIDEFNK.S
	Hs293FLP-MG_Ti_202.289	4.8623	0.4437	2081.58	2082.19	4344.8		1	1036	63.2	16	K.SSATSGDIWPGLSAYDNSPR.S
	HsHeLa_Control-MG_Ti_20	3.6063	0.4059	1843.57	1842.93	6122.5		1	906.8	63.3	2	K.NTPSQHSHSIQHSPER.S
	Hs293FLP_Ti_306.2264.22	3.4083	0.2608	1721.99	1720.89	6373.3		1	727.9	57.1	4	R.YSPSQNSPIHHIPSR.R
	Hs283FLP_Ti_102.1419.14	2.3846	0.4217	1501.45	1502.53	6003.2		1	511.6	53.8	1	R.SSFYPDGGDQETAK.T
	HsHeLa_Control_Ti_102.14	2.3205	0.185	1501.61	1502.53	5733		3	363.9	46.2	2	R.SSFYPDGGDQETAK.T
	Hs293FLP-MG_Ti_102.160	2.0577	0.285	1501.68	1502.53	5072.4		3	309.8	42.3	2	R.SSFYPDGGDQETAK.T
	HsF-IP-293_Ti_102.1268.1	3.085	0.2893	1502.22	1502.53	2840.5		1	554.7	76.9	1	R.SSFYPDGGDQETAK.T
	HsF-IP-293-MG_Ti_102.14	2.4381	0.266	1502.35	1502.53	5606.8		1	399.1	50	2	R.SSFYPDGGDQETAK.T
	HsF-IP-293-MG_Ti_102.14	3.0554	0.2523	1502.37	1502.53	2747.5		1	404.6	65.4	2	R.SSFYPDGGDQETAK.T
	HsHeLa_Control-MG_Ti_10	2.3845	0.2616	1502.55	1502.53	5796.6		1	489.2	53.8	1	R.SSFYPDGGDQETAK.T
	Hs293FLP-MG_Ti_102.161	2.7868	0.2594	1502.6	1502.53	2467.8		1	354.4	65.4	1	R.SSFYPDGGDQETAK.T
	Hs283FLP_Ti_102.1417.14	2.6933	0.235	1502.68	1502.53	2778.5		1	458.9	69.2	2	R.SSFYPDGGDQETAK.T
	HsFLAG-Control_HeLa_NE	3.0327	0.3137	1503	1502.53	3285.7		1	495.9	69.2	4	R.SSFYPDGGDQETAK.T
	Hs293FLP-MG_Ti_202.172	3.7527	0.499	1788.52	1788.87	5741.7		1	1215.2	71.9	1	R.SSFYPDGGDQETAKTGK.F

	HsF-IP-293-MG_Ti_106.22	5.3436	0.3611	2245.89	2246.31	5886.4		1	1606.5	69.4	10	K.GRAEGEWEDQEALDYFSDK.E
	Hs293FLP-MG_Ti_105.253	4.6412	0.468	2033.75	2033.07	7949.2		1	2032.6	75	10	R.AEGEWEDQEALDYFSDK.E
	Hs283FLP_Ti_102.1357.13	5.838	0.4935	1922.53	1922.82	6981.6		1	2089.5	80	22	K.FNDSEGDDTEETEDYR.Q
	HsHeLa_Control-MG_Ti_20	4.1149	0.4	1776.87	1777.89	7495.1		1	1082.7	66.7	6	K.SFATASHRNTEEEGLK.Y
*	HsHeLa_Control-MG_Ti_20	4.4539	0.3954	1708.44	1708.95	8859.1		1	1827.5	67.9	6	K.LKETGYVVERPSTTK.D
*	HsHeLa_Control-MG_Ti_20	3.8031	0.4708	1951.61	1952.22	7662.2		1	822.2	59.4	2	K.LKETGYVVERPSTTKDK.H
	Hs293FLP_Ti_303.1251.12	2.0747	0.0942	1466.85	1467.62	2740		1	222.5	54.2	1	K.ETGYVVERPSTTK.D
	HsFLAG-Control_HeLa_NE	4.0119	0.3318	1467.43	1467.62	7006.1		1	904.1	70.8	20	K.ETGYVVERPSTTK.D
	Hs293FLP-MG_Ti_203.146	2.5808	0.1428	1467.49	1467.62	3517		1	306.8	58.3	2	K.ETGYVVERPSTTK.D
	Hs293FLP-MG_Ti_303.121	3.8984	0.3154	1467.56	1467.62	5823		1	926.4	75	4	K.ETGYVVERPSTTK.D
	HsFLAG-Control_293_Ti_2	3.0228	0.2083	1467.57	1467.62	8359.9		1	553.9	58.3	2	K.ETGYVVERPSTTK.D
	HsHeLa_Control-MG_Ti_20	3.6018	0.2921	1710.03	1710.88	6504.2		1	707.8	60.7	1	K.ETGYVVERPSTTKDK.H
	HsHeLa_Control-MG_Ti_20	3.4975	0.2166	1573.57	1573.83	7924.3		1	1333	75	2	K.LKDLFDYSPPLHK.N
	HsFLAG-Control_HeLa_NE	2.2798	0.1683	1332.18	1332.5	5588.9		8	369	55	1	K.DLFDYSPPLHK.N
	Hs283FLP_Ti_105.1871.18	3.4646	0.2425	1332.32	1332.5	6364.4		2	1002	75	11	K.DLFDYSPPLHK.N
	HsHeLa_Control_Ti_103.23	2.8874	0.2104	1332.55	1332.5	5500.6		1	944.3	75	2	K.DLFDYSPPLHK.N
	HsHeLa_Control-MG_Ti_10	3.3112	0.0852	1222.98	1222.34	6714.1		4	787.4	72.2	11	K.STFREESPLR.I
	HsFlag1P_Ti_106.2169.216	4.0871	0.3181	1369.95	1370.57	7811		1	1066	72.7	10	K.MIASDSHRPEVK.L
	HsFlag1P_Ti_106.2364.236	3.6088	0.3892	1812.35	1813.08	5930.8		1	790.6	65.6	14	K.MAPVPLDDSNRPASLTK.D
	Hs283FLP_Ti_106.2095.20	3.1316	0.2854	1439.69	1439.7	5682.1		1	896.3	75	11	K.DRLLASTLVHSVK.K
	HsF-IP-293-MG_Ti_105.16	2.4818	0.2632	1167.54	1168.42	4506.2		1	365.5	60	3	R.LLASTLVHSVK.K
	HsFLAG-Control_HeLa_NE	2.5169	0.3168	1167.62	1168.42	5843.7		1	497.1	65	1	R.LLASTLVHSVK.K
	HsFLAG-Control_MG_293_	2.1901	0.222	1167.65	1168.42	5958.2		9	371.3	55	1	R.LLASTLVHSVK.K
	HsFLAG-Control_HeLa_NE	2.68	0.2024	1167.67	1168.42	5487.1		4	425.6	60	2	R.LLASTLVHSVK.K
	Hs283FLP_Ti_106.2063.20	2.3436	0.2039	1167.67	1168.42	4435.6		3	465	70	2	R.LLASTLVHSVK.K
	HsHeLa_Control-MG_Ti_10	2.281	0.1774	1167.72	1168.42	4403.9		7	321	55	1	R.LLASTLVHSVK.K
	HsF-IP-293-MG_Ti_105.17	3.7119	0.3023	1167.77	1168.42	5656.8		1	1443.5	90	9	R.LLASTLVHSVK.K
	HsFLAG-Control_HeLa_NE	3.5225	0.2403	1168.4	1168.42	5524		1	1141.3	85	2	R.LLASTLVHSVK.K
	HsFLAG-Control_HeLa_NE	3.4651	0.2726	1168.41	1168.42	5303.9		1	1092.6	85	2	R.LLASTLVHSVK.K
	HsHeLa_Control_Ti_106.28	3.1839	0.2792	1168.53	1168.42	5034.1		1	1106.1	85	2	R.LLASTLVHSVK.K
	Hs283FLP_Ti_106.2060.20	3.5571	0.2799	1168.53	1168.42	5104.5		1	852	75	7	R.LLASTLVHSVK.K
	HsHeLa_Control-MG_Ti_10	3.4683	0.2555	1168.55	1168.42	4937.9		1	1048.5	85	8	R.LLASTLVHSVK.K
	HsHeLa_Control_Ti_106.28	3.8897	0.3442	1297.34	1296.6	7805.9		1	1502.1	77.3	1	R.LLASTLVHSVKK.E
	Hs293FLP_Ti_306.3180.31	4.2947	0.3775	2049.47	2049.34	9191.7		1	977.1	50	3	K.STSESFIQHIVSLVHHVK.E
	Hs293FLP-MG_Ti_206.326	4.6544	0.4146	2049.64	2049.34	10764.5		1	1393.5	55.9	2	K.STSESFIQHIVSLVHHVK.E
	Hs293FLP-MG_Ti_206.326	3.8436	0.3622	2049.97	2049.34	5190.3		1	983.8	44.1	1	K.STSESFIQHIVSLVHHVK.E
	Hs293FLP_Ti_306.3178.31	3.9343	0.3553	2050.54	2049.34	4792.1		1	768.2	39.7	2	K.STSESFIQHIVSLVHHVK.E
*	HsF-IP-293-MG_Ti_102.12	2.982	0.1898	993.39	993.123	6805.8		3	1325.6	87.5	7	K.SAAMTLNER.F
	Hs293FLP-MG_Ti_205.173	3.7302	0.2231	1158.39	1158.34	5834		1	1464.2	94.4	5	R.RIDISPSTLR.K
*	HsFlag1P_Ti_105.1870.187	3.7664	0.3621	1805.64	1804.95	4761.8		1	687.9	69.2	3	K.RPKEEEWDPEYTPK.S
	HsF-IP-293_Ti_102.1526.1	3.5091	0.2765	1422.83	1423.48	4814.6		1	767.9	80	7	K.EEEWDPEYTPK.S
*	Hs293FLP-MG_Ti_205.215	3.2776	0.3433	2143.63	2144.31	9684.1		1	704.8	50	2	K.KYFLHDDRDDGVDYWAK.R
*	Hs283FLP_Ti_106.2196.21	4.5978	0.4075	2015.99	2016.13	6664.5		1	1084.4	63.3	15	K.YFLHDDRDDGVDYWAK.R
	HsHeLa_Control-MG_Ti_10	5.7904	0.3491	2358.89	2359.39	6813.3		1	1730.2	63.2	13	K.YQGDGIVEDEEETMENNEEK.K
	HsF-IP-293-MG_Ti_103.17	4.0181	0.3086	2486.6	2487.57	9684.8		1	872.7	45	8	K.YQGDGIVEDEEETMENNEEKK.D
gi|40254816|ref|	38	221	0.35	732	84674	5	U	heat shock protein 90kDa alpha (cytosolic), class A member 1 isoform 2 [Homo sapiens]				
	HsFLAG-Control_HeLa_S1	2.4492	0.1648	1291.51	1292.39	4628.6		1	302.8	59.1	1	R.ELISNSSDALDK.I
	HsFLAG-Control_HeLa_S1	3.2785	0.2502	1292.15	1292.39	6546.2		1	726.9	68.2	10	R.ELISNSSDALDK.I
	HsFLAG-Control_HeLa_S1	3.3867	0.2554	1292.42	1292.39	5189		5	656.4	68.2	3	R.ELISNSSDALDK.I

	HsFLAG-Control_HeLa_S1(	3.2975	0.1427	1192.37	1191.42	7693.8		3	1304.4	88.9	6	K.ELHINLIPNK.Q
*	HsFLAG-Control_HeLa_S1(	3.4575	0.2103	1591.54	1590.82	5913.8		2	662.3	62.5	2	K.ELHINLIPNKQDR.T
	HsFLAG-Control_HeLa_NE	4.4034	0.1007	1243.05	1243.45	5205.6		1	1215	86.4	20	K.ADLINNLGTIAK.S
	HsFLAG-Control_HeLa_S1(	5.634	0.452	2257.72	2257.29	8942.2		1	2330.1	65.8	16	K.HNDDEQYAWESSAGGSFTVR.T
	HsFLAG-Control_HeLa_S1(	3.3042	0.2832	1312.18	1312.33	6777.7		1	777.6	77.8	15	K.EDQTEYLEER.R
	HsFLAG-Control_HeLa_S1(	3.9401	0.3021	1779.66	1780.08	5732.9		1	1407.9	51.8	1	K.HSQFIGYPITLFVEK.E
	HsFLAG-Control_HeLa_S1(	4.6022	0.3566	1780.14	1780.08	7627		1	1659.1	75	6	K.HSQFIGYPITLFVEK.E
	HsFLAG-Control_HeLa_S1(	5.013	0.4458	1780.42	1780.08	6666.5		1	1717.5	82.1	8	K.HSQFIGYPITLFVEK.E
	HsFLAG-Control_HeLa_S1(	3.5901	0.1509	1151.58	1152.25	8718.8		6	968.9	75	4	K.YIDQEELNK.T
	HsFLAG-Control_HeLa_S1(	5.4991	0.3687	1834.65	1834.89	6758.2		1	2036.9	85.7	32	R.NPDDITNEEYGEFYK.S
	HsFLAG-Control_HeLa_NE	4.7198	0.3685	1528.53	1528.66	7778.9		1	1591.3	79.2	15	K.SLTNDWEDHLAVK.H
	HsFLAG-Control_HeLa_S1(	3.1275	0.2534	1349.94	1349.49	5003.1		1	677	75	4	K.HFSVEGQLEFR.A
	HsFLAG-Control_HeLa_NE	3.7466	0.2381	1264.71	1265.41	6070.2		1	1041.7	83.3	10	R.RAPFDLFENR.K
	HsFLAG-Control_HeLa_NE	2.4384	0.1143	948.48	949.051	8413.3		8	681.8	75	1	K.FYEQFSK.N
	HsFLAG-Control_HeLa_S1(	2.5696	0.1448	1168.59	1169.24	5147.3		2	436.5	66.7	3	K.LGIHEDSQNR.K
	HsFLAG-Control_HeLa_NE	2.8368	0.2315	1169.2	1169.24	6356.4		7	602.8	66.7	3	K.LGIHEDSQNR.K
	HsFLAG-Control_HeLa_S1(	2.8613	0.2441	1169.35	1169.24	6648.7		1	820.8	72.2	5	K.LGIHEDSQNR.K
	HsFLAG-Control_HeLa_NE	2.6665	0.1841	1297.57	1297.41	8151.2		1	940.5	70	1	K.LGIHEDSQNRK.K
	HsFLAG-Control_HeLa_S1(	3.73	0.4072	1551.39	1551.71	7872.1		1	1334.4	73.1	1	R.YYTSASGDEMVSLK.D
	HsFLAG-Control_HeLa_NE	3.403	0.3361	1224.51	1225.39	6426		2	721.8	66.7	5	K.HIYYITGETK.D
	HsFLAG-Control_HeLa_S1(	3.2831	0.3573	1224.53	1225.39	6930.1		1	843.9	72.2	6	K.HIYYITGETK.D
	Hs283FLP_Ti_105.1393.13	3.1232	0.3785	1224.58	1225.39	5786.9		1	754.6	72.2	2	K.HIYYITGETK.D
	HsFLAG-Control_HeLa_S1(	3.2689	0.4124	1224.59	1225.39	6192.5		1	931.4	77.8	1	K.HIYYITGETK.D
	HsFLAG-Control_HeLa_S1(	3.3338	0.3832	1224.82	1225.39	3650.2		1	668.6	77.8	1	K.HIYYITGETK.D
	HsFLAG-Control_HeLa_NE	3.3596	0.3489	1225.24	1225.39	3715.7		1	927.2	88.9	4	K.HIYYITGETK.D
	HsFLAG-Control_HeLa_S1(	3.247	0.3207	1225.56	1225.39	3672.2		1	869.1	88.9	1	K.HIYYITGETK.D
	HsFLAG-Control_HeLa_S1(	3.7466	0.3254	1236.22	1236.33	7080.7		2	1140	80	13	K.DQVANSAFVER.L
	HsFLAG-Control_HeLa_S1(	2.5834	0.3358	1416.47	1417.47	3338.4		1	318	63.6	2	K.EGLELPEDEEEK.K
	HsFLAG-Control_HeLa_NE	2.8612	0.171	1417.26	1417.47	2994.8		7	388	68.2	6	K.EGLELPEDEEEK.K
	HsFLAG-MOCK_300mM_T	2.8099	0.2341	1167.72	1168.35	4413.6		1	487.2	75	2	K.KTKFENLCK.I
	HsFLAG-MOCK_300mM_T	2.911	0.2179	1168.94	1168.35	5882.8		1	1050.9	87.5	2	K.KTKFENLCK.I
	HsFLAG-Control_HeLa_S1(	4.3051	0.3302	1787.57	1788.01	9266.6		1	2131.5	51.8	1	K.HLEINPDHSIIETLR.Q
	HsFLAG-Control_HeLa_NE	4.5439	0.4176	1789.92	1788.01	6445.5		1	1222.4	71.4	4	K.HLEINPDHSIIETLR.Q
	HsFLAG-Control_HeLa_S1(	4.5087	0.3244	3003.82	3004.37	8897.8		1	1496.7	30.8	3	K.DLVILLYETALLSSGFSLEDPQTHANR.I
	HsFLAG-Control_HeLa_S1(	4.0636	0.3203	3004.79	3004.37	7082.1		1	715.8	38.5	1	K.DLVILLYETALLSSGFSLEDPQTHANR.I
gi|5803225|ref|NI	10	33	0.349	255	29174	4.7	U		tyrosine 3/tryptophan 5 -monooxygenase activation protein, epsilon polypeptide [Homo sa			
*	HsFLAG-MOCK_300mM_T	2.5416	0.2887	1237.59	1238.39	4153.5		2	394.9	54.5	1	K.HLIPAANTGESK.V
*	HsHeLa3_Ti_106.1935.193	3.206	0.3518	1237.6	1238.39	4525.7		1	806.4	77.3	2	K.HLIPAANTGESK.V
*	HsFLAG-Control_293_Ti_2(	3.1003	0.2777	1238.19	1238.39	3501.1		1	875.5	81.8	6	K.HLIPAANTGESK.V
*	HsFLAG-Control_HeLa_NE	2.9473	0.196	1238.35	1238.39	3739.8		1	960.2	81.8	3	K.HLIPAANTGESK.V
*	HsHeLa3_Ti_102.1598.159	2.6098	0.2372	1194.68	1195.32	3865.9		1	301.8	65	2	K.EAAENSLVAYK.A
*	HsHeLa3_Ti_105.1866.186	3.4293	0.3151	1822.34	1821.1	4207.1		1	658.5	62.5	2	K.AASDIAMTELPPTHPIR.L
*	HsFLAG-Control_HeLa_S1(	5.0871	0.4949	2088.4	2089.22	6566.8		1	2164.1	75	13	K.AAFDDAIAELDTLSEESYK.D
	HsHeLa3_Ti_102.2409.240	5.4964	0.4395	2181.77	2182.28	6994.4		1	1369.3	63.9	2	R.DNLTLWTSDMQGDGEEQNK.E
*	HsFLAG-Control_293_Ti_2(	2.3856	0.1179	1289.26	1290.28	10240.8		9	771.2	60	1	K.EALQDVEDENQ.-
*	Hs293FLP_TREX_Ti_101.0	2.8756	0.2038	1289.99	1290.28	5483.3		2	701	70	1	K.EALQDVEDENQ.-
gi|89061489|ref|X	68	315	0.345	869	100139	9.9	U		PREDICTED: similar to Bcl-2-associated transcription factor 1 (Btf) isoform 1 [Homo sapie			
	Hs293FLP-MG_Ti_103.116	4.2686	0.2971	1442.85	1442.57	4496.5		2	911.5	75	9	K.KAEGEPQEESPLK.S
	HsF-IP-293-MG_Ti_105.15	4.2602	0.2754	2608.4	2609.68	4613.8		1	427	42.9	3	K.SQEEPKDTFEHDPSESIDEFNK.S

Hs293FLP-MG_Ti_306.237	3.692	0.4131	2608.41	2609.68	4254.9	1	519.8	47.6	1	K.SQEEPKDTFEHDPSESIDEFNK.S
Hs293FLP-MG_Ti_203.190	4.7394	0.2621	2608.75	2609.68	7028.8	1	1057.3	36.9	1	K.SQEEPKDTFEHDPSESIDEFNK.S
Hs293FLP-MG_Ti_203.190	4.0194	0.4754	2608.86	2609.68	4719.7	1	683.3	52.4	2	K.SQEEPKDTFEHDPSESIDEFNK.S
Hs283FLP_Ti_105.1581.15	4.0195	0.3453	2608.88	2609.68	4522.5	1	351.3	40.5	5	K.SQEEPKDTFEHDPSESIDEFNK.S
HsFLAG-Control_HeLa_NE	3.8143	0.3422	2608.92	2609.68	5472.9	1	396.8	40.5	1	K.SQEEPKDTFEHDPSESIDEFNK.S
HsF-IP-293-MG_Ti_105.18	4.8778	0.3121	2609.15	2609.68	5020.4	1	769.3	35.7	5	K.SQEEPKDTFEHDPSESIDEFNK.S
HsHeLa_Control_Ti_103.20	3.6894	0.2965	2609.65	2609.68	4258.9	1	715.4	39.3	1	K.SQEEPKDTFEHDPSESIDEFNK.S
HsFLAG-Control_HeLa_NE	4.4793	0.2928	2609.78	2609.68	5503.5	1	994.4	39.3	2	K.SQEEPKDTFEHDPSESIDEFNK.S
Hs283FLP_Ti_104.2388.23	4.4679	0.2976	2609.93	2609.68	4879.3	1	929.9	39.3	4	K.SQEEPKDTFEHDPSESIDEFNK.S
Hs293FLP-MG_Ti_105.200	3.5827	0.2809	2610.54	2609.68	4295.5	1	410.6	42.9	4	K.SQEEPKDTFEHDPSESIDEFNK.S
Hs293FLP-MG_Ti_105.200	3.8551	0.2815	2611.6	2609.68	4440.2	1	544.1	34.5	1	K.SQEEPKDTFEHDPSESIDEFNK.S
HsHeLa_Control_Ti_103.21	3.6537	0.3622	2612.16	2609.68	4472.1	1	539.3	47.6	4	K.SQEEPKDTFEHDPSESIDEFNK.S
HsFLAG-Control_HeLa_NE	5.0441	0.3677	1910.23	1910.95	5038.6	1	1211.9	73.3	5	K.DTFEHDPSESIDEFNK.S
Hs293FLP-MG_Ti_202.289	4.8623	0.4437	2081.58	2082.19	4344.8	1	1036	63.2	16	K.SSATSGDIWPGLSAYDNSPR.S
HsHeLa_Control-MG_Ti_20	3.6063	0.4059	1843.57	1842.93	6122.5	1	906.8	63.3	2	K.NTPSQHSHSIQHSPER.S
Hs293FLP_Ti_306.2264.22	3.4083	0.2608	1721.99	1720.89	6373.3	1	727.9	57.1	4	R.YSPSQNSPIHHIPSR.R
Hs283FLP_Ti_102.1419.14	2.3846	0.4217	1501.45	1502.53	6003.2	1	511.6	53.8	1	R.SSFYPDGGDQETAK.T
HsHeLa_Control_Ti_102.14	2.3205	0.185	1501.61	1502.53	5733	3	363.9	46.2	2	R.SSFYPDGGDQETAK.T
Hs293FLP-MG_Ti_102.160	2.0577	0.285	1501.68	1502.53	5072.4	3	309.8	42.3	2	R.SSFYPDGGDQETAK.T
HsF-IP-293_Ti_102.1268.1	3.085	0.2893	1502.22	1502.53	2840.5	1	554.7	76.9	1	R.SSFYPDGGDQETAK.T
HsF-IP-293-MG_Ti_102.14	2.4381	0.266	1502.35	1502.53	5606.8	1	399.1	50	2	R.SSFYPDGGDQETAK.T
HsF-IP-293-MG_Ti_102.14	3.0554	0.2523	1502.37	1502.53	2747.5	1	404.6	65.4	2	R.SSFYPDGGDQETAK.T
HsHeLa_Control-MG_Ti_10	2.3845	0.2616	1502.55	1502.53	5796.6	1	489.2	53.8	1	R.SSFYPDGGDQETAK.T
Hs293FLP-MG_Ti_102.161	2.7868	0.2594	1502.6	1502.53	2467.8	1	354.4	65.4	1	R.SSFYPDGGDQETAK.T
Hs283FLP_Ti_102.1417.14	2.6933	0.235	1502.68	1502.53	2778.5	1	458.9	69.2	2	R.SSFYPDGGDQETAK.T
HsFLAG-Control_HeLa_NE	3.0327	0.3137	1503	1502.53	3285.7	1	495.9	69.2	4	R.SSFYPDGGDQETAK.T
Hs293FLP-MG_Ti_202.172	3.7527	0.499	1788.52	1788.87	5741.7	1	1215.2	71.9	1	R.SSFYPDGGDQETAKTGK.F
HsF-IP-293-MG_Ti_106.22	5.3436	0.3611	2245.89	2246.31	5886.4	1	1606.5	69.4	10	K.GRAEGEWEDQEALDYFSDK.E
Hs293FLP-MG_Ti_105.253	4.6412	0.468	2033.75	2033.07	7949.2	1	2032.6	75	10	R.AEGEWEDQEALDYFSDK.E
Hs283FLP_Ti_102.1357.13	5.838	0.4935	1922.53	1922.82	6981.6	1	2089.5	80	22	K.FNDSEGDDTEETEDYR.Q
HsHeLa_Control-MG_Ti_20	4.1149	0.4	1776.87	1777.89	7495.1	1	1082.7	66.7	6	K.SFATASHRNTEEEGLK.Y
Hs293FLP_Ti_303.1251.12	2.0747	0.0942	1466.85	1467.62	2740	1	222.5	54.2	1	K.ETGYVVERPSTTK.D
HsFLAG-Control_HeLa_NE	4.0119	0.3318	1467.43	1467.62	7006.1	1	904.1	70.8	20	K.ETGYVVERPSTTK.D
Hs293FLP-MG_Ti_203.146	2.5808	0.1428	1467.49	1467.62	3517	1	306.8	58.3	2	K.ETGYVVERPSTTK.D
Hs293FLP-MG_Ti_303.121	3.8984	0.3154	1467.56	1467.62	5823	1	926.4	75	4	K.ETGYVVERPSTTK.D
HsFLAG-Control_293_Ti_2	3.0228	0.2083	1467.57	1467.62	8359.9	1	553.9	58.3	2	K.ETGYVVERPSTTK.D
HsHeLa_Control-MG_Ti_20	3.6018	0.2921	1710.03	1710.88	6504.2	1	707.8	60.7	1	K.ETGYVVERPSTTKDK.H
HsHeLa_Control-MG_Ti_20	3.4975	0.2166	1573.57	1573.83	7924.3	1	1333	75	2	K.LKDLFDYSPPLHK.N
HsFLAG-Control_HeLa_NE	2.2798	0.1683	1332.18	1332.5	5588.9	8	369	55	1	K.DLFDYSPPLHK.N
Hs283FLP_Ti_105.1871.18	3.4646	0.2425	1332.32	1332.5	6364.4	2	1002	75	11	K.DLFDYSPPLHK.N
HsHeLa_Control_Ti_103.23	2.8874	0.2104	1332.55	1332.5	5500.6	1	944.3	75	2	K.DLFDYSPPLHK.N
HsHeLa_Control-MG_Ti_10	3.3112	0.0852	1222.98	1222.34	6714.1	4	787.4	72.2	11	K.STFREESPLR.I
HsFlag1P_Ti_106.2169.21	4.0871	0.3181	1369.95	1370.57	7811	1	1066	72.7	10	K.MIASDSHRPEVK.L
HsFlag1P_Ti_106.2364.23	3.6088	0.3892	1812.35	1813.08	5930.8	1	790.6	65.6	14	K.MAPVPLDDSNRPASLTK.D
Hs283FLP_Ti_106.2095.20	3.1316	0.2854	1439.69	1439.7	5682.1	1	896.3	75	11	K.DRLLASTLVHSVK.K
HsF-IP-293-MG_Ti_105.16	2.4818	0.2632	1167.54	1168.42	4506.2	1	365.5	60	3	R.LLASTLVHSVK.K
HsFLAG-Control_HeLa_NE	2.5169	0.3168	1167.62	1168.42	5843.7	1	497.1	65	1	R.LLASTLVHSVK.K
HsFLAG-Control_MG_293_	2.1901	0.222	1167.65	1168.42	5958.2	9	371.3	55	1	R.LLASTLVHSVK.K
HsFLAG-Control_HeLa_NE	2.68	0.2024	1167.67	1168.42	5487.1	4	425.6	60	2	R.LLASTLVHSVK.K

	Hs283FLP_Ti_106.2063.20	2.3436	0.2039	1167.67	1168.42	4435.6		3	465	70	2	R.LLASTLVHSVK.K
	HsHeLa_Control-MG_Ti_10	2.281	0.1774	1167.72	1168.42	4403.9		7	321	55	1	R.LLASTLVHSVK.K
	HsF-IP-293-MG_Ti_105.17	3.7119	0.3023	1167.77	1168.42	5656.8		1	1443.5	90	9	R.LLASTLVHSVK.K
	HsFLAG-Control_HeLa_NE	3.5225	0.2403	1168.4	1168.42	5524		1	1141.3	85	2	R.LLASTLVHSVK.K
	HsFLAG-Control_HeLa_NE	3.4651	0.2726	1168.41	1168.42	5303.9		1	1092.6	85	2	R.LLASTLVHSVK.K
	HsHeLa_Control_Ti_106.28	3.1839	0.2792	1168.53	1168.42	5034.1		1	1106.1	85	2	R.LLASTLVHSVK.K
	Hs283FLP_Ti_106.2060.20	3.5571	0.2799	1168.53	1168.42	5104.5		1	852	75	7	R.LLASTLVHSVK.K
	HsHeLa_Control-MG_Ti_10	3.4683	0.2555	1168.55	1168.42	4937.9		1	1048.5	85	8	R.LLASTLVHSVK.K
	HsHeLa_Control_Ti_106.28	3.8897	0.3442	1297.34	1296.6	7805.9		1	1502.1	77.3	1	R.LLASTLVHSVKK.E
	Hs293FLP_Ti_306.3180.31	4.2947	0.3775	2049.47	2049.34	9191.7		1	977.1	50	3	K.STSESFIQHIVSLVHHVK.E
	Hs293FLP-MG_Ti_206.326	4.6544	0.4146	2049.64	2049.34	10764.5		1	1393.5	55.9	2	K.STSESFIQHIVSLVHHVK.E
	Hs293FLP-MG_Ti_206.326	3.8436	0.3622	2049.97	2049.34	5190.3		1	983.8	44.1	1	K.STSESFIQHIVSLVHHVK.E
	Hs293FLP_Ti_306.3178.31	3.9343	0.3553	2050.54	2049.34	4792.1		1	768.2	39.7	2	K.STSESFIQHIVSLVHHVK.E
	Hs293FLP-MG_Ti_205.173	3.7302	0.2231	1158.39	1158.34	5834		1	1464.2	94.4	5	R.RIDISPSTLR.K
	HsHeLa_Control-MG_Ti_20	4.2638	0.3814	1897.7	1897.96	7641.9		1	1155.2	63.3	11	R.GTFHDDRDDGVDYWAK.R
	HsHeLa_Control-MG_Ti_10	5.7904	0.3491	2358.89	2359.39	6813.3		1	1730.2	63.2	13	K.YQGDGIVEDEEETMENNEEK.K
	HsF-IP-293-MG_Ti_103.17	4.0181	0.3086	2486.6	2487.57	9684.8		1	872.7	45	8	K.YQGDGIVEDEEETMENNEEKK.D
gi|4503529|ref|N	9	72	0.345	406	46154	5.5	U	eukaryotic translation initiation factor 4A, isoform 1 [Homo sapiens]				
	HsFLAG-Control_HeLa_NE	4.3475	0.477	1828.66	1829.07	5470.9		1	956.4	66.7	13	R.GIYAYGFEKPSAIQQR.A
	HsFLAG-Control_HeLa_NE	4.8509	0.4125	1396.71	1395.51	5929.6		1	1620.3	84.6	3	K.GYDVIAQAQSGTGK.T
*	HsFLAG-Control_HeLa_S1	5.1355	0.3741	1905.93	1905.24	8122.7		1	1580.9	65.6	7	K.TATFAISILQQIELDLK.A
	HsFLAG-Control_HeLa_NE	3.5644	0.2417	1142.43	1141.36	5618.9		1	1590.1	85	7	K.ATQALVLAPTR.E
	HsFLAG-Control_HeLa_NE	2.9952	0.1609	1170.29	1170.31	4761		2	738.5	81.2	3	K.DQIYDIFQK.L
*	HsHeLa3_Ti_103.3368.336	2.6614	0.214	2460.08	2460.85	7317.9		6	368.6	31.8	1	K.LNSNTQVVLLSATMPSDVLEVTK.K
	HsFLAG-Control_HeLa_NE	3.3775	0.2405	1115.66	1115.36	4998.5		2	1015	88.9	15	R.VLITTDLLAR.G
	HsFLAG-Control_HeLa_S1	5.2214	0.4321	2146.44	2145.42	9669.9		1	1812.5	61.1	22	R.GIDVQQVSLVINYDLPTNR.E
*	HsFLAG-Control_HeLa_S1	3.6339	0.3506	2427.95	2428.71	6410.6		3	425.2	40	1	R.DIETFYNTSIEEMPLNVADLI.-
gi|13514813|ref|	26	104	0.344	662	73272	7.2	U	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 3 [Homo sapiens]				
gi|13514817|ref|	26	104	0.344	662	73272	7.2	U	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 3 [Homo sapiens]				
	HsGST-MOCK_Ti_102.272	4.8053	0.4074	3624.15	3623.87	6156.7		1	783.2	27.4	2	K.SDEDDWSKPLPPSERLEQELFSGGNTGINFEK.Y
	HsFLAG-Control_HeLa_S1	5.3353	0.4903	1883.37	1884.05	7684.1		1	1935.1	75	3	R.LEQELFSGGNTGINFEK.Y
	HsGST-MOCK_Ti_405.487	6.0723	0.4615	2332.19	2333.69	9106.9		1	2019.5	41.7	1	K.TAAFLLPILSQIYSDGPGEALR.A
	HsHeLa_Control-MG_Ti_20	5.4106	0.447	2332.6	2333.69	8756.4		1	2295.4	44	2	K.TAAFLLPILSQIYSDGPGEALR.A
	HsGST-MOCK_Ti_304.481	6.1656	0.4572	2332.76	2333.69	6759.1		1	1721.7	64.3	11	K.TAAFLLPILSQIYSDGPGEALR.A
	HsFLAG-Control_HeLa_NE	5.8579	0.4604	2333.32	2333.69	8356.7		1	2154.7	44	2	K.TAAFLLPILSQIYSDGPGEALR.A
	HsHeLa_Control-MG_Ti_20	5.3027	0.4394	2333.53	2333.69	8010.1		1	1560.5	57.1	4	K.TAAFLLPILSQIYSDGPGEALR.A
	HsHeLa3_Ti_104.4623.462	4.6618	0.3988	2333.76	2333.69	7437.9		1	1356.7	39.3	1	K.TAAFLLPILSQIYSDGPGEALR.A
	HsFLAG-Control_HeLa_NE	5.3776	0.3583	2333.94	2333.69	5423.6		1	1068.7	57.1	6	K.TAAFLLPILSQIYSDGPGEALR.A
	HsHeLa3_Ti_105.4551.455	4.8978	0.4303	2334.59	2333.69	6231.3		1	1310.8	57.1	3	K.TAAFLLPILSQIYSDGPGEALR.A
	HsGST-MOCK_Ti_305.288	3.3787	0.181	1358.41	1358.62	6011.2		5	809.5	72.7	5	K.QYPISLVLAPTR.E
	HsGST-MOCK_Ti_102.159	4.31	0.3866	1889.78	1889.13	3983.7		1	931.3	65.6	5	R.VRPCVVYGGADIGQQIR.D
	HsGST-MOCK_Ti_102.143	3.4108	0.2907	1181.52	1181.35	6575.9		2	1213	85	2	R.GCHLLVATPGR.L
	HsGST-MOCK_Ti_303.267	3.1278	0.2572	1337.33	1337.6	5377.8		1	865.1	80	2	R.MLDMGFEPQIR.R
	HsHeLa_Control_Ti_103.42	4.0259	0.2653	1560.87	1558.77	7756.3		1	1819.1	83.3	2	R.DFLDEYIFLAVGR.V
	HsFLAG-Control_HeLa_S1	2.5499	0.1769	1163.05	1164.26	9379.1		1	1254.5	75	1	R.VGSTSENITQK.V
	HsHeLa_Control_Ti_106.37	4.5524	0.2611	1448.71	1448.71	5559.7		1	1429.6	83.3	3	K.RSFLLDLLNATGK.D
	HsGST-MOCK_Ti_102.271	4.4398	0.1874	1449.05	1448.71	5808.4		4	1760	58.3	2	K.RSFLLDLLNATGK.D
	HsHeLa_Control_Ti_103.37	4.62	0.3021	1293.29	1292.52	7028		1	1921.9	86.4	4	R.SFLLDLLNATGK.D
	HsGST-MOCK_Ti_102.226	3.6	0.2792	2614.27	2614.71	7170.3		1	1056.5	35.2	1	K.GADSLEDFLYHEGYACTSIHGDR.S

	HsGST-MOCK_Ti_103.134	3.4856	0.286	1301.78	1301.4	4049.4		1	491.1	77.8	3	R.DREEALHQFR.S
	HsGST-MOCK_Ti_405.217	4.4769	0.4241	1169.52	1169.41	7969.3		1	2001	86.4	16	K.SPILVATAVAAR.G
	HsGST-MOCK_Ti_103.249	2.9633	0.3145	2083.82	2084.3	6082		4	410.8	46.9	1	K.HVINFDLPSDIEEYVHR.I
	HsGST-MOCK_Ti_103.247	4.8039	0.3748	2085.22	2084.3	6002.3		1	1189.1	45.3	2	K.HVINFDLPSDIEEYVHR.I
	HsGST-MOCK_Ti_404.319	3.989	0.393	1525.26	1525.7	8108.9		1	1203.9	69.2	19	R.VGNLGLATSFFNER.N
	HsGST-MOCK_Ti_302.390	2.6522	0.2065	1128.46	1129.34	7594.7		2	867.9	72.2	1	K.DLLDLLVEAK.Q
gi|4826760|ref|N	16	160	0.34	415	45672	5.6	U	heterogeneous nuclear ribonucleoprotein F [Homo sapiens]				
*	HsHeLa3_Ti_106.3082.308	4.0915	0.3212	3755.52	3754.04	6864.5		1	630.6	25	2	R.GLPWSCSVEDVQNFLSDCTIHDGAAGVHFIYTR.E
*	HsFLAG-Control_HeLa_NE	3.0634	0.3552	1710.28	1710.79	6719.6		1	870.3	60	2	R.QSGEAFVELGSEDDVK.M
*	HsFLAG-MOCK_300mM_T	3.9191	0.4346	1633.51	1631.66	6511.9		1	1450.7	73.3	4	K.HSGPNSADSANDGFVR.L
*	HsFLAG-Control_HeLa_NE	5.6087	0.3785	1868.59	1869.08	6985.5		1	2352	78.1	24	K.ITGEAFVQFASQELAEK.A
*	HsGST-MOCK_Ti_102.279	4.2549	0.3983	3475	3476.71	9180.6		1	1122.4	26.6	2	R.MRPGAYSTGYGGYEEYSGLSDGYGFTTDLFGR.D
	HsFLAG-Control_HeLa_S1	3.9094	0.2338	1996.83	1998.2	9892.6		2	1192.3	40.6	1	K.ATENDIYNFFSPLNPVR.V
	HsFLAG-Control_HeLa_NE	4.6608	0.3601	1997.35	1998.2	7568.7		1	1568.7	68.8	16	K.ATENDIYNFFSPLNPVR.V
	HsFLAG-Control_293_Ti_2	4.7208	0.3986	1997.49	1998.2	7549.3		1	1676.5	71.9	55	K.ATENDIYNFFSPLNPVR.V
	HsGST-MOCK_Ti_403.397	4.7263	0.4323	1997.5	1998.2	7501		1	1361.2	65.6	2	K.ATENDIYNFFSPLNPVR.V
	HsFLAG-Control_HeLa_S1	4.3947	0.4897	1997.59	1998.2	7565.5		1	1326.5	65.6	6	K.ATENDIYNFFSPLNPVR.V
	HsFLAG-Control_HeLa_NE	4.2241	0.188	1998.1	1998.2	8148.8		8	882.3	35.9	1	K.ATENDIYNFFSPLNPVR.V
	HsFLAG-Control_HeLa_NE	5.2012	0.4834	1998.25	1998.2	8235.9		1	1839.9	68.8	23	K.ATENDIYNFFSPLNPVR.V
	Hs293FLP-MG_Ti_202.411	4.5072	0.2946	1998.27	1998.2	7716.3		1	1486.3	46.9	2	K.ATENDIYNFFSPLNPVR.V
	HsFLAG-Control_HeLa_NE	4.903	0.1706	1998.31	1998.2	8396.7		1	1484.8	43.8	2	K.ATENDIYNFFSPLNPVR.V
	HsFLAG-Control_HeLa_NE	2.6268	0.1908	1092.55	1093.23	6937.7		1	767.6	72.2	2	R.VHIEIGPDGR.V
	HsFLAG-Control_HeLa_NE	3.4554	0.2844	1093.46	1093.23	5275.7		1	1166.4	83.3	16	R.VHIEIGPDGR.V
gi|54291727|ref|N	13	47	0.337	258	29135	7	U	spindlin family, member 2 [Homo sapiens]				
gi|56682949|ref|N	13	47	0.337	258	29158	7.2	U	spindlin-like protein 2 [Homo sapiens]				
gi|56682947|ref|N	13	47	0.337	258	29158	7.2	U	spindlin-like protein 2 [Homo sapiens]				
gi|56682945|ref|N	13	47	0.337	258	29158	7.2	U	spindlin-like protein 2 [Homo sapiens]				
	HsFLAG-Control_HeLa_NE	3.0838	0.1501	1430.22	1430.47	8322.8		2	872.4	62.5	1	K.TPNAQEAEGQQTR.A
	HsHeLa_Control-MG_Ti_10	4.7712	0.4162	1912.73	1912.11	8148.4		1	1643	70	2	R.ISHGWKEGDEPITQWK.G
	HsHeLa_Control-MG_Ti_10	5.1045	0.4244	1813	1812.03	4668.3		1	1150.5	67.6	8	R.VASSHISDANLANTIIGK.A
	HsHeLa_Control-MG_Ti_10	4.0915	0.3401	1777.54	1777.04	6757.4		1	1720	76.9	1	K.DPVLYMYQLLDDYK.E
	HsFlag1P_Ti_106.3196.319	5.5281	0.375	2346.24	2347.65	10130.9		1	2660	66.7	4	K.DPVLYMYQLLDDYKEGDLR.I
	HsFLAG-Control_HeLa_S1	4.5343	0.3515	2347.02	2347.65	4881.8		1	856.9	38.9	1	K.DPVLYMYQLLDDYKEGDLR.I
	HsF-IP-293-MG_Ti_106.272	5.0438	0.2755	2347.34	2347.65	9931.9		1	2671.7	66.7	2	K.DPVLYMYQLLDDYKEGDLR.I
	HsFLAG-Control_HeLa_NE	2.7657	0.1821	854.29	854.037	3938.9		1	651.2	91.7	2	K.PSVYFIK.F
	HsFLAG-Control_HeLa_NE	4.0442	0.3492	1789.83	1789.98	4977.2		1	817.4	46.2	1	K.FDDDFHIYVYDLVK.K
	HsFLAG-Control_HeLa_S1	3.9146	0.3163	1790.12	1789.98	4844.5		1	1279.7	55.8	3	K.FDDDFHIYVYDLVK.K
	HsFLAG-Control_HeLa_NE	4.7853	0.4088	1790.36	1789.98	8202.8		1	2020.3	80.8	5	K.FDDDFHIYVYDLVK.K
	HsFLAG-Control_HeLa_S1	5.8606	0.4583	1790.46	1789.98	8612.6		1	2552	84.6	10	K.FDDDFHIYVYDLVK.K
	HsFLAG-Control_HeLa_S1	4.7497	0.4247	1791.38	1789.98	8548.6		1	1784.2	76.9	7	K.FDDDFHIYVYDLVK.K
gi|21040371|ref|N	12	50	0.335	427	49130	5.7	U	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39 isoform 1 [Homo sapiens]				
	HsFLAG-Control_HeLa_NE	2.9102	0.2152	1296.6	1297.41	4190.9		1	218.6	54.5	2	K.GSYVSIHSSGFR.D
	HsFLAG-Control_HeLa_NE	3.3999	0.3467	1297.35	1297.41	6239.4		1	1014.2	72.7	2	K.GSYVSIHSSGFR.D
	HsFLAG-Control_HeLa_NE	3.1536	0.356	1297.62	1297.41	5696.1		1	730.8	68.2	3	K.GSYVSIHSSGFR.D
	HsFLAG-MOCK_300mM_T	5.1172	0.3001	3653.38	3654.03	4854.3		1	730.6	28.2	2	R.AIVDCGFEHPSEVQHECIPQAILGMDVLCQAK.S
	HsFLAG-Control_HeLa_NE	3.0844	0.2693	1294.89	1293.43	7691.3		1	1289.5	77.3	1	K.NCPHVVVGTPGR.I
	HsFLAG-Control_HeLa_NE	3.4418	0.3925	1463.16	1463.72	5746.5		1	821.1	72.7	4	K.LTLHGLQQYYVK.L
	HsFLAG-Control_HeLa_NE	3.6145	0.3768	1464	1463.72	6104.4		1	861.3	72.7	2	K.LTLHGLQQYYVK.L
*	HsFLAG-Control_HeLa_S1	3.5729	0.2601	2295.02	2296.7	8983		1	1021.6	50	2	R.CMALAQLLVEQNFPAIAIHR.G

	HsFLAG-Control_HeLa_NE	3.7388	0.3438	1260.68	1260.53	7837.1		1	1712.5	90	1	R.RILVATNLFGR.G
	HsFLAG-Control_HeLa_S1	3.8361	0.2249	1104.14	1104.34	5719.5		1	1117.8	83.3	14	R.ILVATNLFGR.G
	HsFLAG-Control_HeLa_NE	4.782	0.4338	1480.11	1480.62	6927.2		1	1731.5	80.8	16	K.GLAITFVSDENDAK.I
*	HsFLAG-Control_HeLa_NE	3.8132	0.1533	3536.69	3536.87	10613.9		1	935.3	24.1	1	K.ILNDVQDRFEVNVAELPEEIDISTYIEQSR.-
gi|4507143|ref|N	3	8	0.333	162	18762	8.7	U		sorting nexin 3 isoform a [Homo sapiens]			
	HsFLAG-Control_HeLa_NE	5.1714	0.2769	3555.36	3555.97	9112.3		1	1335.2	27.3	2	R.LITKPQNLNDAYGPPSNFLEIDVSNPQTVGVGR.G
	HsFLAG-Control_HeLa_NE	2.2128	0.1182	832.59	833.018	4619.6		3	399.9	75	1	K.TNLPIFK.L
	HsFLAG-Control_HeLa_NE	4.6542	0.392	1643.94	1642.68	3987.3		1	836.7	76.9	5	R.GDDGIFDDNFIEER.K
gi|25453472|ref|	9	22	0.331	281	31122	5	U		eukaryotic translation elongation factor 1 delta isoform 2 [Homo sapiens]			
gi|25453474|ref|	9	22	0.144	647	71408	6.4	U		eukaryotic translation elongation factor 1 delta isoform 1 [Homo sapiens]			
	HsHeLa3_Ti_104.1528.152	4.8195	0.4698	2185.3	2186.3	7501.5		1	1101	47.8	3	K.SLAGSSGPGASSGTSGDHGELVVR.I
	HsFLAG-Control_HeLa_S1	3.7254	0.2887	1359.28	1359.52	7795.7		1	1366.3	77.3	1	R.IASLEVENQSLR.G
	HsFLAG-Control_HeLa_S1	3.713	0.2044	1300.52	1300.5	7733.2		1	1557.5	81.8	3	R.GVVQELQQAISK.L
	HsHeLa3_Ti_106.1858.185	3.0676	0.2947	1424.74	1424.62	6575.4		1	882.4	62.5	1	R.ATAPQTQHVSPMR.Q
	HsFLAG-Control_MG_293_	2.0266	0.1299	726.64	726.938	3702.4		1	463.1	83.3	3	K.KPALVAK.S
	HsHeLa3_Ti_103.2748.274	3.7792	0.2643	1374.83	1374.58	7375.9		1	1566.3	79.2	1	R.SIQLDGLVWGASK.L
	HsGST-MOCK_Ti_304.189	2.9994	0.3378	1474.47	1475.65	4272.6		2	535	63.6	3	R.KLQIQCVVEDDK.V
	HsGST-MOCK_Ti_404.199	4.8653	0.3375	1474.84	1475.65	7647.6		1	2151.3	90.9	5	R.KLQIQCVVEDDK.V
	HsGST-MOCK_Ti_101.077	4.8945	0.3341	1475.3	1475.65	7192.3		1	1660.3	86.4	2	R.KLQIQCVVEDDK.V
gi|4758504|ref|N	4	15	0.33	261	26923	7.8	U		hydroxyacyl-Coenzyme A dehydrogenase, type II isoform 1 [Homo sapiens]			
*	Hs293FLP-MG_Ti_203.353	4.5517	0.5278	1813.74	1814.09	8178.5		1	1715.4	65.8	1	K.GLVAVITGGASGLGLATAER.L
*	HsFLAG-Control_293_Ti_2	4.9921	0.4171	2197.02	2196.47	6445.5		1	784	45.5	10	R.LVGQGASAVLLDLPNSGGEAQAK.K
*	Hs293FLP-MG_Ti_204.181	3.7194	0.498	1849.56	1851.03	7100.3		1	681.7	59.4	1	K.KLGNNCVFAPADVTSEK.D
*	HsHeLa_Control-MG_Ti_20	6.0284	0.3869	2880.1	2880.27	9621.7		1	2386.9	38	3	R.LGDPAEYAHLVQAIIENPFLNGEVIR.L
gi|7019485|ref|N	7	35	0.33	191	21868	5.4	U		programmed cell death 6 [Homo sapiens]			
	Hs293FLP-MG_Ti_203.393	4.6801	0.4089	3191.57	3190.5	8001.6		1	828.5	26.8	2	K.DRSGVISDTELQQALSNGTWTPFNPVTVR.S
	HsHeLa_Control-MG_Ti_20	4.1809	0.329	2918.73	2919.22	6930.2		1	1003.4	42.3	4	R.SGVISDTELQQALSNGTWTPFNPVTVR.S
	Hs293FLP-MG_Ti_202.431	4.2992	0.2749	2919.43	2919.22	7920.8		2	651.2	27.9	1	R.SGVISDTELQQALSNGTWTPFNPVTVR.S
*	HsHeLa_Control-MG_Ti_20	3.9883	0.2535	1442.44	1442.61	6433.9		1	1289.9	75	7	K.AGVNFSEFTGVWK.Y
*	HsHeLa_Control-MG_Ti_20	3.7243	0.3234	1342.26	1342.5	5882.2		1	1071.4	83.3	7	K.YITDWQNVFR.T
*	Hs293FLP-MG_Ti_203.235	2.3835	0.3205	1356.56	1357.55	6245.9		1	679.5	70	1	R.LSDQFHDILIR.K
*	HsHeLa_Control-MG_Ti_20	4.2041	0.2757	1357.85	1357.55	8001.4		1	1594.4	85	13	R.LSDQFHDILIR.K
gi|4506645|ref|N	2	8	0.329	70	8218	10.1	U		ribosomal protein L38 [Homo sapiens]			
*	HsGST-MOCK_Ti_103.196	4.4816	0.2776	1578.57	1576.88	6968.5		1	1797.8	87.5	6	R.KIEEIKDFLLTAR.R
*	HsGST-MOCK_Ti_404.272	2.9826	0.2254	1229.56	1229.46	7540.3		2	687.7	66.7	2	R.YLYTLVITDK.E
gi|4758302|ref|N	17	91	0.327	104	12259	5.9	U		enhancer of rudimentary homolog [Homo sapiens]			
*	HsHeLa_Control-MG_Ti_20	5.7567	0.5199	2056.71	2056.14	7458.8		1	1813	75	51	R.TYADYESVNECMEGVCK.M
*	HsFLAG-Control_HeLa_NE	3.5185	0.3103	1328.12	1329.41	4744.2		4	511.6	65	2	R.ADTQTYQPYNK.D
*	HsF-IP-293-MG_Ti_102.11	2.3533	0.2235	1328.18	1329.41	4555.5		1	331.2	55	2	R.ADTQTYQPYNK.D
*	Hs293FLP_TREX_Ti_102.1	2.2731	0.3091	1328.35	1329.41	4429.4		1	413.5	65	1	R.ADTQTYQPYNK.D
*	Hs293FLP-MG_Ti_102.103	1.9606	0.3226	1328.49	1329.41	3743.6		3	288	60	1	R.ADTQTYQPYNK.D
*	HsFLAG-Control_HeLa_NE	2.439	0.2217	1328.55	1329.41	6219		1	587.5	65	1	R.ADTQTYQPYNK.D
*	Hs283FLP_Ti_102.1173.11	2.7337	0.273	1328.57	1329.41	4622		5	347	55	1	R.ADTQTYQPYNK.D
*	HsF-IP-293-MG_Ti_102.11	3.4114	0.3154	1328.62	1329.41	5194		1	841.9	75	2	R.ADTQTYQPYNK.D
*	HsHeLa_Control_Ti_102.10	2.3573	0.3181	1328.68	1329.41	4483.3		1	415.8	65	2	R.ADTQTYQPYNK.D
*	HsFLAG-MOCK_300mM_T	3.5707	0.2422	1329.28	1329.41	6066.4		1	787	70	9	R.ADTQTYQPYNK.D
*	Hs293FLP_TREX_Ti_102.1	3.6393	0.2883	1329.3	1329.41	5099.9		1	1017.3	80	2	R.ADTQTYQPYNK.D
*	Hs283FLP_Ti_102.1165.11	3.3405	0.2277	1329.39	1329.41	4804.6		1	770.1	75	2	R.ADTQTYQPYNK.D
*	HsFLAG-Control_HeLa_NE	2.6617	0.2666	1329.58	1329.41	5126.9		1	477.5	65	2	R.ADTQTYQPYNK.D

*	HsHeLa_Control_Ti_102.10	3.6473	0.3001	1330.11	1329.41	5301.2		1	830.7	75	2	R.ADTQTYQPYNK.D
*	Hs293FLP-MG_Ti_102.107	3.5789	0.2266	1330.49	1329.41	4850.4		4	589	70	2	R.ADTQTYQPYNK.D
*	HsFLAG-Control_HeLa_NE	3.5597	0.3191	1871.5	1872.04	5456.2		1	940.5	67.9	7	R.ADTQTYQPYNKDWIK.E
*	HsFlag1P_Ti_104.2021.202	3.0758	0.1253	2128.3	2129.33	5849.4		1	645.1	56.2	2	R.ADTQTYQPYNKDWIKEK.I
gi|4501881|ref|N	20	161	0.326	377	42051	5.4	U		alpha 1 actin precursor [Homo sapiens]			
gi|4885049|ref|N	20	161	0.326	377	42019	5.4	U		cardiac muscle alpha actin proprotein [Homo sapiens]			
	HsFLAG-Control_HeLa_S1	2.2896	0.2133	976.42	977.021	5697.3		5	418.5	61.1	1	K.AGFAGDDAPR.A
	HsFLAG-Control_Hela_Ti_1	3.0127	0.1884	976.63	977.021	5102.4		1	1237.5	88.9	9	K.AGFAGDDAPR.A
	HsHeLa_Control_Ti_102.11	2.1727	0.108	976.67	977.021	4557.8		2	513.5	66.7	1	K.AGFAGDDAPR.A
	HsFLAG-MOCK_150mM_T	3.2886	0.2636	978.67	977.021	5248.4		1	1406.5	88.9	20	K.AGFAGDDAPR.A
	HsFLAG-Control_HeLa_S1	2.6516	0.2088	946.02	946.137	3258.8		2	623.5	87.5	1	R.AVFPSIVGR.P
	HsFLAG-MOCK_300mM_T	3.5305	0.3215	1199.52	1199.44	7004.5		2	801.6	75	15	R.AVFPSIVGRPR.H
	HsFLAG-MOCK_300mM_T	2.8034	0.3247	1171.52	1172.41	5485.7		1	609.4	65	3	R.HQGVMVGMGQK.D
	HsHeLa3_Ti_106.1966.196	2.937	0.3448	1171.61	1172.41	5543.4		1	647.3	65	2	R.HQGVMVGMGQK.D
	HsHeLa3_Ti_106.1967.196	3.1676	0.3309	1172.92	1172.41	4063.3		1	693.8	80	1	R.HQGVMVGMGQK.D
	HsFLAG-MOCK_300mM_T	3.105	0.361	1173.72	1172.41	4167.5		1	841.2	85	2	R.HQGVMVGMGQK.D
	HsFLAG-MOCK_300mM_T	5.2956	0.4824	2351.94	2352.6	7863.3		1	2199.1	66.7	2	R.HQGVMVGMGQKDSYVGDEAQSK.R
	HsFLAG-Control_HeLa_S1	3.424	0.33	1199.08	1199.22	4776.6		2	971.4	85	4	K.DSYVGDEAQSK.R
	HsFLAG-MOCK_300mM_T	4.3505	0.1577	1962.79	1962.18	6559.2		1	1122.5	66.7	4	K.YPIEHGIITNWDDMEK.I
	HsFLAG-Control_Hela_Ti_1	3.2795	0.3331	1515.45	1516.7	7777.5		1	997.2	75	12	K.IWHHTFYNELR.V
	HsFLAG-MOCK_300mM_T	2.4013	0.1049	1515.69	1516.7	5047.5		1	338.5	60	1	K.IWHHTFYNELR.V
	HsHeLa_Control-MG_Ti_10	3.3547	0.3682	1518.65	1516.7	5691.8		1	740.7	75	4	K.IWHHTFYNELR.V
	HsFLAG-Control_HeLa_S1	4.0056	0.3243	1959.67	1957.23	5828.4		1	593.6	55.9	3	R.VAPEEHPTLLTEAPLNPK.A
	HsFLAG-Control_293_Ti_2	2.3671	0.1397	1000.32	999.167	7387.7		9	624.4	71.4	2	R.DLTDYLMK.I
	HsHeLa_Control-MG_Ti_20	5.1912	0.2593	1792.4	1791.96	5309.1		1	1957.5	86.7	64	K.SYELPDGQVITIGNER.F
	HsHeLa_Control-MG_Ti_10	2.6274	0.294	1161.67	1162.39	4080.9		1	437	65	10	K.EITALAPSTMK.I
gi|5453990|ref|N	7	13	0.325	249	28723	6	U		proteasome activator subunit 1 isoform 1 [Homo sapiens]			
	HsFLAG-Control_HeLa_S1	4.0117	0.2953	1269.45	1269.44	5555.9		2	1124.6	85	1	K.TENLLGSYFPK.K
	HsFLAG-Control_HeLa_S1	3.4619	0.3172	1415.43	1413.57	7475.7		1	701.5	58.3	4	K.EPALNEANLSNLK.A
	HsFLAG-Control_HeLa_S1	3.4651	0.3362	1261.56	1261.5	3498.4		4	495.7	68.2	1	K.APLDIPVPDPVK.E
	HsFLAG-Control_HeLa_S1	3.4385	0.288	1519.36	1518.79	4013		2	466.6	61.5	2	K.APLDIPVPDPVKEK.E
	HsFLAG-Control_HeLa_S1	4.295	0.2818	2280.34	2280.67	8483.2		2	1126.4	52.8	2	K.DVIEQLNLVTTWLQLQIPR.I
	HsFLAG-Control_HeLa_S1	2.5057	0.1405	1504.64	1502.62	6543.7		2	603.5	68.2	1	R.QLVHELDEAEYR.D
*	HsFLAG-Control_HeLa_S1	4.0935	0.3617	1398.07	1396.67	8360		1	1613.2	81.8	2	R.NAYAVLYDIILK.N
gi|4505409|ref|N	4	18	0.322	152	17298	8.4	U		non-metastatic cells 2, protein (NM23B) expressed in [Homo sapiens]			
gi|66392227|ref|N	4	18	0.322	152	17298	8.4	U		non-metastatic cells 2, protein (NM23B) expressed in [Homo sapiens]			
gi|66392205|ref|N	4	18	0.322	152	17298	8.4	U		non-metastatic cells 2, protein (NM23B) expressed in [Homo sapiens]			
gi|66392203|ref|N	4	28	0.184	267	30137	8.9	U		NME1-NME2 protein [Homo sapiens]			
gi|66392192|ref|N	4	18	0.322	152	17298	8.4	U		non-metastatic cells 2, protein (NM23B) expressed in [Homo sapiens]			
	HsHeLa_Control-MG_Ti_20	3.8743	0.2064	1345.49	1345.59	6946.5		6	915.1	68.2	8	R.TFIAIKPDGVQR.G
	Hs293FLP_Ti_305.2093.20	2.9077	0.2113	1178.01	1176.4	6241		1	826.7	72.2	5	K.DRPFFPGLVK.Y
	HsF-IP-293_Ti_205.1656.1	3.1597	0.1115	1786.66	1787.04	7174.9		3	745.9	56.2	2	R.VMLGETNPADSKPGTIR.G
	Hs293FLP_TREX_Ti_104.1	2.1945	0.1136	1069.37	1070.19	3659.5		1	365.4	66.7	3	R.NIIHGSDSVK.S
gi|4507793|ref|N	8	22	0.322	152	17138	6.6	U		ubiquitin-conjugating enzyme E2N [Homo sapiens]			
	HsFLAG-Control_HeLa_NE	1.9653	0.0863	1036.55	1037.29	6171.5		8	489.4	61.1	2	R.LLAEPVPGIK.A
*	HsFLAG-Control_HeLa_S1	4.8589	0.3684	2196.64	2197.46	6063.6		1	1132.3	57.9	7	R.YFHVVIAGPQDSPFEGGTFK.L
*	HsFLAG-Control_HeLa_NE	4.7876	0.2597	2196.98	2197.46	6019.2		1	696.5	47.4	2	R.YFHVVIAGPQDSPFEGGTFK.L
*	HsFLAG-Control_HeLa_S1	4.6427	0.2606	2197.14	2197.46	5489.4		1	1197.6	42.1	2	R.YFHVVIAGPQDSPFEGGTFK.L
*	HsFLAG-Control_HeLa_S1	3.9031	0.282	2197.48	2197.46	6811.2		1	858.1	50	1	R.YFHVVIAGPQDSPFEGGTFK.L

*	HsFLAG-Control_HeLa_NE	5.0106	0.3735	2198.93	2197.46	7056.2		1	1566.3	44.7	2	R.YFHVVIAGPQDSPFEGGTFK.L
	HsFLAG-Control_HeLa_NE	2.2374	0.1709	985.41	986.115	5569.4		3	594.8	78.6	3	K.IYHPNVDK.L
	HsFLAG-Control_HeLa_S1	4.1792	0.3064	1204.19	1204.28	9508.9		1	2276.3	90	3	K.TNEAQAIETAR.A
gi|49574541|ref|N	2	4	0.321	109	11601	7.8	U		hypothetical protein LOC113386 [Homo sapiens]			
*	Hs293FLP-MG_Ti_202.378	3.4158	0.2625	1600.86	1600.86	4340.9		2	798.1	69.2	1	R.DPWYSTVGLLPPVR.A
*	Hs293FLP-MG_Ti_202.302	4.0851	0.4894	2247.75	2247.53	6811.3		1	715.7	47.5	3	K.TEQGPTGVTMTSNPITWGQIK.K
gi|5803137|ref|N	2	4	0.318	157	17170	8.9	U		RNA binding motif protein 3 isoform a [Homo sapiens]			
gi|63054840|ref|N	2	4	0.556	90	9668	4.8	U		RNA binding motif protein 3 isoform b [Homo sapiens]			
	HsHeLa3_Ti_104.4219.422	4.0525	0.2935	3498.05	3496.9	6957.5		1	642.8	24.2	2	K.LFVGGLNFNTDEQALEDHFSSFGPISEVVVVK.D
	HsHeLa3_Ti_106.2590.259	4.1592	0.4415	1983.03	1983.25	6339.6		1	1326.5	61.8	2	R.GFGFITFTNPEHASVAMR.A
gi|14110414|ref|N	11	23	0.317	306	32835	8.2	U		heterogeneous nuclear ribonucleoprotein D isoform c [Homo sapiens]			
gi|14110420|ref|N	11	23	0.273	355	38434	7.8	U		heterogeneous nuclear ribonucleoprotein D isoform a [Homo sapiens]			
	HsHeLa3_Ti_103.0707.070	3.205	0.2524	1971.73	1972.98	7003.9		2	626.7	47.1	1	K.IDASKNEEDEGHSNSSPR.H
	HsHeLa3_Ti_103.2727.272	3.6095	0.2337	1357.22	1356.58	5439.5		1	1313.4	86.4	2	K.MFIGGLSWDTTK.K
	HsHeLa3_Ti_105.2386.238	3.3375	0.2791	1484.65	1484.75	5195		1	1139.9	79.2	2	K.MFIGGLSWDTTKK.D
	HsHeLa3_Ti_105.3002.300	2.8793	0.2666	915.6	915.123	2537.7		6	545.2	85.7	2	R.GFGFVLFK.E
	HsHeLa3_Ti_104.1771.177	4.6677	0.2891	1619.75	1617.84	7068		1	2274.4	78.6	4	K.KIFVGGLSPDTPEEK.I
	HsHeLa3_Ti_103.1874.187	2.5831	0.3016	1488.81	1489.67	6337.8		1	530.1	53.8	1	K.IFVGGLSPDTPEEK.I
	HsHeLa3_Ti_103.1866.186	4.8348	0.2472	1489.94	1489.67	6412.6		1	1324.3	76.9	2	K.IFVGGLSPDTPEEK.I
	HsHeLa3_Ti_105.3136.313	3.4757	0.1879	2432.29	2431.72	5246		3	440.3	42.5	3	K.IREYFGGFGEVESIELPMDNK.T
	HsHeLa3_Ti_102.3414.341	3.7385	0.3291	2162.32	2162.38	7472.3		1	618.6	44.4	1	R.EYFGGFGEVESIELPMDNK.T
	HsHeLa3_Ti_105.2478.247	4.3636	0.4322	1733.05	1731.95	5512.6		1	1039.4	73.1	3	R.GFCFITFKEEEPVK.K
	HsHeLa3_Ti_106.1846.184	2.6852	0.2626	917.56	918.04	5033.3		1	602.6	71.4	2	K.YHNVGLSK.C
gi|4506901|ref|N	5	25	0.317	164	19330	11.6	U		splicing factor, arginine/serine-rich 3 [Homo sapiens]			
*	Hs293FLP_TREX_Ti_102.1	3.3868	0.2654	1249.63	1249.37	6142.3		1	1337.2	81.8	4	K.VYVGNLGNNGNK.T
*	HsGST-MOCK_Ti_305.220	2.8124	0.3226	1043.37	1044.2	4716.5		3	727.7	75	6	R.AFGYYGPLR.S
	HsHeLa_Control-MG_Ti_20	4.0134	0.3097	1622.36	1622.78	7266		1	1224.3	73.1	12	R.NPPGFAFVEFEDPR.D
*	HsGST-MOCK_Ti_304.313	2.891	0.1581	2321.5	2321.51	4845.3		1	310.2	42.5	2	R.NPPGFAFVEFEDPRDAADAVR.E
*	HsGST-MOCK_Ti_104.127	2.8901	0.1946	1125.49	1124.25	5275.6		6	680.7	77.8	1	R.NRGPPPSWGR.R
gi|34577110|ref|N	9	18	0.316	364	39420	8.1	U		aldolase A [Homo sapiens]			
gi|4557305|ref|N	9	18	0.316	364	39420	8.1	U		aldolase A [Homo sapiens]			
gi|34577112|ref|N	9	18	0.316	364	39420	8.1	U		aldolase A [Homo sapiens]			
	HsHeLa3_Ti_102.1703.170	3.7499	0.4137	1333.4	1333.48	6129.3		1	1382.1	76.9	1	K.GILAADESTGSIAK.R
	HsHeLa3_Ti_102.1690.169	2.4184	0.3637	1333.65	1333.48	4457.7		1	470.4	61.5	1	K.GILAADESTGSIAK.R
	HsHeLa3_Ti_102.1367.136	3.7466	0.317	1491.4	1491.56	6130.3		1	847.2	66.7	3	R.LQSIGTENTEENR.R
	HsHeLa3_Ti_106.2806.280	3.8688	0.3347	3115.36	3115.57	10693.9		1	621.4	23.1	1	R.QLLLTADDRVNPCIGGVILFHETLYQK.A
	HsHeLa3_Ti_105.2874.287	4.8429	0.2048	2107.74	2108.42	7145.9		1	1163.7	38.2	3	K.IGEHTPSALAIMENANVLAR.Y
	HsHeLa3_Ti_105.2862.286	4.5914	0.4418	2108.93	2108.42	4633.3		1	811.5	57.9	3	K.IGEHTPSALAIMENANVLAR.Y
	HsHeLa3_Ti_103.1446.144	2.1033	0.1778	763.77	763.955	6992.1		2	713.3	75	2	K.VLAAVYK.A
	Hs293FLP_TREX_Ti_106.2	3.8714	0.2796	1289.6	1289.44	7119.9		1	1376.3	81.8	2	K.RALANSLACQGK.Y
	HsHeLa3_Ti_103.2179.217	3.8984	0.3719	2230.55	2229.37	5228		1	783.9	52.4	2	K.YTPSGQAGAAASESLFVSNHAY.-
gi|89047143|ref|X	48	155	0.313	1848	213671	7.2	U		PREDICTED: myosin VB isoform 1 [Homo sapiens]			
gi|89047438|ref|X	48	155	0.313	1848	213641	7.2	U		PREDICTED: similar to Myosin-5B (Myosin Vb) isoform 5 [Homo sapiens]			
	Hs283FLP_Ti_102.2467.24	4.5141	0.4208	1835.5	1834.03	5736.2		1	1155.5	71.4	6	R.LEDETILEYPIDVQR.N
	HsFLAG-Control_293_Ti_1	3.1998	0.3473	2985.89	2987.38	9516		1	491.7	30.8	2	R.NPDILVGENDLTALSYLHEPAVLHNLK.V
	HsFLAG-Control_293_Ti_1	4.0441	0.3285	2986.64	2987.38	4144		1	487.8	28.8	2	R.NPDILVGENDLTALSYLHEPAVLHNLK.V
	HsFLAG-Control_293_Ti_1	2.9882	0.3546	1346.45	1347.47	4838.8		1	465.2	61.5	1	K.NQSIIVSGESGAGK.T
	HsFLAG-Control_293_Ti_2	3.863	0.277	1346.79	1347.47	6221.8		1	1506	80.8	5	K.NQSIIVSGESGAGK.T
	HsFLAG-Control_293_Ti_1	5.0198	0.5791	1803.17	1803.92	5108.4		1	1357.1	78.1	2	R.YFATVGGSASETNIEEK.V

	HsFLAG-Control_293_Ti_1	2.3489	0.3134	1500.45	1501.78	7347.3		1	444.8	46.4	2	K.VLASSPIMEAIGNAK.T
	HsFLAG-Control_MG_293_	3.9652	0.3977	1501.59	1501.78	5445.7		1	598	57.1	4	K.VLASSPIMEAIGNAK.T
	HsFLAG-Control_293_Ti_1	5.9249	0.491	2143.98	2143.42	8806.5		1	2185.4	70.6	2	R.NYHIFYQLCAAAGLPEFK.E
	HsFLAG-Control_293_Ti_1	5.977	0.4083	3487.85	3488.61	9815.9		1	1226.2	28.2	3	K.ELALTSAEDFFYTSQGGDTSIEGVDDAEDFEK.T
	HsFLAG-Control_293_Ti_1	4.8326	0.4568	1792.62	1792.13	6881.2		1	1488.5	68.8	2	K.IIASILHLGSVAIQAER.D
	HsFLAG-Control_293_Ti_1	4.3336	0.4445	2219.31	2221.27	5806.5		1	850.7	55.6	4	R.DGDSCSISPQDVYLSNFCR.L
	HsFLAG-Control_MG_293_	4.012	0.3475	1261.8	1261.48	9899.8		1	1586.9	80	2	K.TMSLQQVINAR.N
	HsFLAG-Control_293_Ti_1	3.8786	0.3307	2822.16	2823.14	7546.9		1	649.5	30.7	1	K.EQIPWTLIDFYDNQPCIDLIEAK.L
	HsFLAG-Control_293_Ti_1	3.3527	0.3285	2822.89	2823.14	7496.8		1	456.3	36.4	10	K.EQIPWTLIDFYDNQPCIDLIEAK.L
	HsFLAG-Control_293_Ti_1	4.5501	0.2511	1418.32	1418.59	7813.6		1	1868.9	86.4	13	K.LGILDLLDEECK.V
	HsFLAG-Control_293_Ti_1	2.8274	0.2463	1299.6	1300.45	9166.2		1	828.1	65	1	K.VEYLSDGFLEK.N
	HsFLAG-Control_293_Ti_1	3.8103	0.2728	1300.3	1300.45	6466.2		1	1491.6	85	1	K.VEYLSDGFLEK.N
	HsFLAG-Control_293_Ti_1	3.3274	0.2744	1736.94	1735.94	9591.8		1	1121.5	65.4	1	K.NRDTVYEEQINILK.A
	HsFLAG-Control_293_Ti_1	4.0714	0.3136	1465.37	1465.64	7588.7		1	1207.7	72.7	2	R.DTVYEEQINILK.A
	Hs283FLP_Ti_106.2540.25	4.5589	0.2383	1418.59	1417.6	6406.8		1	1741.8	90.9	7	K.FPLVADLFHDDK.D
	HsFLAG-Control_293_Ti_1	3.5956	0.234	1075.78	1076.28	9662.3		1	1513.8	83.3	1	R.AAVVIQAFTR.A
	HsFLAG-Control_293_Ti_1	3.7918	0.3434	1859.06	1859.99	9143.1		1	1060.6	60	6	K.ELVHYQQSPGEDTSLR.L
	HsFLAG-Control_293_Ti_1	2.7516	0.0979	2493.33	2494.69	10736.3		7	409.7	35	1	K.EQLNNQILCQSKDEFAQNSVK.E
	HsFLAG-Control_293_Ti_1	5.2259	0.4353	4369.94	4369.56	8724.3		1	828.3	22.4	4	R.RNPSNQSSLESDSNYPSISTSEIGDTEDALQQVEEIGLEK.A
	HsFLAG-Control_293_Ti_1	4.235	0.3935	2756.69	2757.03	4865.8		1	694.2	41.7	7	K.KVQAEPPQTDIDLDPNADLAYNSLK.R
	HsFLAG-Control_293_Ti_1	4.445	0.2412	2756.96	2757.03	8496.7		1	1750.2	38.5	3	K.KVQAEPPQTDIDLDPNADLAYNSLK.R
	HsFLAG-Control_293_Ti_1	4.0791	0.4035	2626.77	2628.85	4062.8		1	486.5	45.7	4	K.VQAEPPQTDIDLDPNADLAYNSLK.R
	HsFLAG-Control_293_Ti_1	3.7355	0.4474	2858.78	2860.07	10941.7		1	817.1	36.5	4	K.AVADQATQNNSSHGSPDSYSLLLNQLK.L
	HsFLAG-Control_293_Ti_2	4.1818	0.3748	2859.77	2860.07	9747.7		1	866.3	38.5	1	K.AVADQATQNNSSHGSPDSYSLLLNQLK.L
	HsFLAG-Control_293_Ti_1	5.6805	0.3483	2860.16	2860.07	7885.3		1	1534.9	35.6	5	K.AVADQATQNNSSHGSPDSYSLLLNQLK.L
	HsFLAG-Control_293_Ti_1	3.7798	0.2695	2473.85	2474.73	10175.1		1	686.2	42.5	2	R.LLEAQLQAQSLEHEEEVEHLK.A
	HsFLAG-Control_293_Ti_1	4.2861	0.3268	2473.85	2474.73	7908.3		1	1243.5	40	2	R.LLEAQLQAQSLEHEEEVEHLK.A
	HsFLAG-Control_293_Ti_1	4.0001	0.292	1731.55	1729.89	11190.5		1	2118.3	70	3	K.KAQDLEAAQALAQSER.K
	HsFLAG-Control_293_Ti_1	5.0703	0.3861	1601.36	1601.71	10092.6		1	2750.1	82.1	2	K.AQDLEAAQALAQSER.K
	HsFLAG-Control_293_Ti_1	3.7982	0.3359	1191.81	1192.23	5896.7		2	1230.7	88.9	1	R.HADYTNDDLK.V
	HsFLAG-Control_293_Ti_1	3.4528	0.1451	1383.46	1383.63	6455.4		1	933.5	70.8	2	K.VHSLLTSTINGIK.K
	HsFLAG-Control_293_Ti_1	3.1579	0.2472	1383.62	1383.63	5748		1	617.9	66.7	3	K.VHSLLTSTINGIK.K
	HsFLAG-Control_293_Ti_1	1.9092	0.2085	1057.35	1058.14	3541.7		2	249.9	78.6	1	K.NFDLTEYR.Q
	HsFLAG-Control_293_Ti_1	5.1365	0.4351	1889.45	1890.23	7874.5		1	1992.7	76.7	6	R.QVLSDLSIQIYQQLIK.I
	HsFLAG-Control_293_Ti_1	3.1379	0.1949	2035.97	2037.47	6352.4		1	750.6	53.1	1	K.QLFYMINAVTLNNLLLR.K
	HsFLAG-Control_293_Ti_1	4.0757	0.2687	1451.5	1451.62	7259.7		1	1630.5	85	3	R.YNISQLEEWLR.G
	HsFLAG-Control_293_Ti_1	2.675	0.1762	1451.53	1451.62	4350.3		1	251.3	60	1	R.YNISQLEEWLR.G
	HsFLAG-Control_293_Ti_1	3.9755	0.3459	2631.89	2633.08	8560.7		1	863.9	43.5	1	R.NLHQSGAVQTMEPLIQAAQLLQLK.K
	HsFLAG-Control_293_Ti_1	4.8994	0.2878	2633.04	2633.08	7126.9		1	817.3	30.4	1	R.NLHQSGAVQTMEPLIQAAQLLQLK.K
	HsFLAG-Control_293_Ti_1	4.4345	0.4107	2482.92	2483.66	6920.6		1	1273.2	52.4	9	K.TQEDAEAICSLCTSLSTQQIVK.I
	HsFLAG-Control_293_Ti_1	3.9336	0.2947	1751.65	1751.98	5697.5		1	770.7	69.2	6	K.ILNLYTPLNEFEER.V
	HsFLAG-Control_293_Ti_1	3.6649	0.1336	1255.08	1255.41	5723.7		1	794.6	75	2	R.NDPQQLLLDAK.H
gi|4758356|ref|N		7	11	0.311	380	42593	8.6	U	flap structure-specific endonuclease 1 [Homo sapiens]			
*	HsFLAG-Control_HeLa_NE	3.0778	0.144	1126.37	1126.34	6180.6		1	1413.3	90	1	K.LIADVAPSAIR.E
*	HsHeLa3_Ti_106.2240.224	3.8289	0.3417	1488.84	1488.77	6765.9		1	1219.3	75	1	K.PVYVFDGKPPQLK.S
*	HsFLAG-Control_HeLa_NE	4.4733	0.4182	1728.47	1728.86	7184.4		1	1758	80	3	K.QLQQAQAAGAEQEVEK.F
*	HsHeLa3_Ti_105.3584.358	3.1503	0.3773	2758.21	2758.17	3764.7		1	369.9	38	1	K.HLLSLMGIPYLDAPSEAEASCAALVK.A
*	HsHeLa3_Ti_103.3152.315	3.0694	0.2929	2349.25	2348.66	9806.5		1	509.2	35	1	K.VYAAATEDMDCLTFGSPVLMR.H

*	HsFLAG-Control_HeLa_NE	3.0002	0.2754	2323.49	2323.61	7149.3		1	380.7	36.8	3	K.EAHQLFLEPEVLDPESVELK.W
*	HsHeLa3_Ti_102.1953.195	2.9396	0.1289	1374.76	1374.49	3557.4		5	454.4	75	1	K.WSEPNEEELIK.F
gi|9507215|ref|N	20	418	0.31	449	50094	5.1	U	tubulin, alpha 8 [Homo sapiens]				
	HsFLAG-Control_HeLa_S1	4.2449	0.3005	2415.72	2416.66	8163.2		1	1212.2	36.2	4	R.QLFHPEQLITGKEDAANNYAR.G
	HsHeLa_Control-MG_Ti_10	3.4137	0.2652	2416.42	2416.66	7726.4		1	627.9	45	8	R.QLFHPEQLITGKEDAANNYAR.G
	HsGST-MOCK_Ti_103.173	4.1081	0.2897	2416.8	2416.66	6806.6		1	1048.6	36.2	1	R.QLFHPEQLITGKEDAANNYAR.G
	HsFLAG-Control_HeLa_NE	3.5321	0.3633	2417.37	2416.66	8286.1		1	502	42.5	3	R.QLFHPEQLITGKEDAANNYAR.G
	HsFLAG-Control_MG_293_	3.4903	0.1725	1719.53	1719.9	7713.5		1	803	61.5	17	R.NLDIERPTYTNLNR.L
	HsFLAG-Control_HeLa_S1	4.6066	0.4074	1488.47	1488.77	7506.5		1	1467.1	76.9	9	R.LISQIVSSITASLR.F
	HsFLAG-Control_HeLa_S1	4.684	0.43	1488.49	1488.77	7157.4		1	1312.2	73.1	22	R.LISQIVSSITASLR.F
	HsHeLa_Control-MG_Ti_20	5.0495	0.4454	1488.53	1488.77	8030.6		1	1907.4	80.8	39	R.LISQIVSSITASLR.F
	HsFLAG-Control_HeLa_S1	4.722	0.3946	1488.57	1488.77	8151.1		1	1172.8	69.2	9	R.LISQIVSSITASLR.F
	HsFLAG-Control_HeLa_S1	4.3035	0.346	1488.75	1488.77	5615.6		1	1324.7	55.8	2	R.LISQIVSSITASLR.F
	HsFLAG-Control_HeLa_S1	4.1471	0.2471	1489.29	1488.77	5256.5		3	867.3	50	2	R.LISQIVSSITASLR.F
	HsFLAG-Control_HeLa_NE	4.6049	0.3537	1489.3	1488.77	6361.1		1	1211.5	73.1	15	R.LISQIVSSITASLR.F
	HsFLAG-Control_HeLa_NE	4.3453	0.2295	1489.54	1488.77	5799.3		1	1231.8	53.8	2	R.LISQIVSSITASLR.F
	HsFLAG-Control_HeLa_S1	3.7596	0.3173	1490.02	1488.77	5380.1		1	894.9	50	1	R.LISQIVSSITASLR.F
	HsFLAG-Control_HeLa_NE	5.8208	0.383	2410.89	2410.69	6224.2		1	1491.8	62.5	149	R.FDGALNVDLTEFQTNLVPYPR.I
	HsHeLa_Control-MG_Ti_20	3.7919	0.422	1755.69	1755.98	6153.4		1	806.5	65.4	7	K.RTIQFVDWCPTGFK.V
	HsFLAG-Control_HeLa_S1	4.5938	0.4395	1599.28	1599.79	7004.1		1	1203.6	75	4	R.TIQFVDWCPTGFK.V
	HsHeLa-FLAG-IP_S100_Ti_	4.1491	0.409	1825.53	1826.1	3764.8		1	755.9	64.7	121	K.VGINYQPPTVVPGGDLAK.V
	HsF-IP-293-MG_Ti_104.26	2.8488	0.3461	1865.28	1866.11	9656.2		1	1217.8	59.4	2	R.AVCMLSNTTAIAEAWAR.L
	HsGST-MOCK_Ti_404.302	2.6983	0.1597	2332.29	2331.52	9294.4		1	579.2	42.1	1	R.AFVHWYVGEGMEEGEFSEAR.E
gi|13489099|ref|N	4	14	0.31	290	32494	4.8	U	potassium channel tetramerisation domain containing 17 [Homo sapiens]				
*	HsFLAG-Control_293_Ti_2	5.1167	0.4883	2397.14	2396.67	7510.9		1	1236.9	52.5	3	K.DMAEEGVLEEAEFYNIGPLIR.I
*	HsFLAG-Control_293_Ti_2	5.2202	0.5072	2527.35	2528.78	6812.4		1	1301	57.5	2	R.VLQCQEEELTQMVSTMSDGWR.F
*	HsFLAG-Control_293_Ti_2	2.937	0.2826	1601.46	1601.67	5481.3		4	352.1	46.4	2	K.ELHSTPNGLSSESSR.K
*	HsFLAG-Control_293_Ti_2	7.6093	0.4459	3902.56	3905	9341.3		1	1797.7	30.5	7	K.STEEQLEEQQQQEEEVEEVEVEQVQVEADAQEK.G
gi|4506005|ref|N	7	11	0.309	327	37187	6.2	U	protein phosphatase 1, catalytic subunit, beta isoform 1 [Homo sapiens]				
gi|46249376|ref|N	7	11	0.309	327	37187	6.2	U	protein phosphatase 1, catalytic subunit, beta isoform 1 [Homo sapiens]				
	HsHeLa3_Ti_106.2992.299	4.6683	0.3871	2198.1	2197.62	7004.8		1	1387.3	63.9	1	K.SREIFLSQPILLELEAPLK.I
	HsFLAG-Control_HeLa_NE	4.2579	0.3786	1954.03	1954.36	4463.2		1	777.4	65.6	3	R.EIFLSQPILLELEAPLK.I
	HsHeLa3_Ti_103.4158.415	3.0674	0.2613	2583.37	2583.86	4462.4		2	247.8	38.1	1	R.LFEYGGFPPEANYLFLGDYVDR.G
	HsHeLa3_Ti_104.2893.289	3.2713	0.3242	1199.72	1199.4	5387.2		1	846.3	87.5	2	K.YPENFFLLR.G
	HsGST-MOCK_Ti_302.394	4.6892	0.3549	2116.37	2115.32	6732.6		1	1086.5	61.8	2	K.TFTDCFNCLPIAAIVDEK.I
	HsHeLa3_Ti_106.2355.235	3.9058	0.2397	2249.87	2249.48	6344.4		1	712	52.8	1	K.IFCCHGGLSPDLQSMEQIR.R
	HsHeLa3_Ti_104.2112.211	3.636	0.3626	1640.78	1640.79	5993.4		1	991.5	65.4	1	R.AHQVVEDGYEFFAK.R
gi|63029937|ref|N	40	229	0.307	854	98113	5.2	U	heat shock protein 90kDa alpha (cytosolic), class A member 1 isoform 1 [Homo sapiens]				
	HsFLAG-Control_HeLa_S1	2.4492	0.1648	1291.51	1292.39	4628.6		1	302.8	59.1	1	R.ELISNSSDALDK.I
	HsFLAG-Control_HeLa_S1	3.2785	0.2502	1292.15	1292.39	6546.2		1	726.9	68.2	10	R.ELISNSSDALDK.I
	HsFLAG-Control_HeLa_S1	3.3867	0.2554	1292.42	1292.39	5189		5	656.4	68.2	3	R.ELISNSSDALDK.I
	HsFLAG-Control_HeLa_S1	2.678	0.2106	1039.44	1040.12	6287.3		3	663.1	75	4	R.YESLTDPSK.L
	HsFLAG-Control_HeLa_NE	2.7149	0.2011	1039.45	1040.12	6815.8		1	815.2	81.2	4	R.YESLTDPSK.L
	HsFLAG-Control_HeLa_NE	3.4808	0.2474	1040.52	1040.12	3725.7		4	589.2	87.5	2	R.YESLTDPSK.L
	HsFLAG-Control_HeLa_S1	3.2975	0.1427	1192.37	1191.42	7693.8		3	1304.4	88.9	6	R.ELHINLIPNK.Q
	HsFLAG-Control_HeLa_NE	4.4034	0.1007	1243.05	1243.45	5205.6		1	1215	86.4	20	K.ADLINNLGTIAK.S
	HsFLAG-Control_HeLa_S1	5.634	0.452	2257.72	2257.29	8942.2		1	2330.1	65.8	16	K.HNDDEQYAWESSAGGSFTVR.T
	HsFLAG-Control_HeLa_S1	3.3042	0.2832	1312.18	1312.33	6777.7		1	777.6	77.8	15	K.EDQTEYLEER.R
	HsFLAG-Control_HeLa_S1	3.9401	0.3021	1779.66	1780.08	5732.9		1	1407.9	51.8	1	K.HSQFIGYPITLFVEK.E

	HsFLAG-Control_HeLa_S1	4.6022	0.3566	1780.14	1780.08	7627		1	1659.1	75	6	K.HSQFIGYPITLFVEK.E
	HsFLAG-Control_HeLa_S1	5.013	0.4458	1780.42	1780.08	6666.5		1	1717.5	82.1	8	K.HSQFIGYPITLFVEK.E
	HsFLAG-Control_HeLa_S1	3.5901	0.1509	1151.58	1152.25	8718.8		6	968.9	75	4	K.YIDQEELNK.T
	HsFLAG-Control_HeLa_S1	5.4991	0.3687	1834.65	1834.89	6758.2		1	2036.9	85.7	32	R.NPDDITNEEYGEFYK.S
	HsFLAG-Control_HeLa_NE	4.7198	0.3685	1528.53	1528.66	7778.9		1	1591.3	79.2	15	K.SLTNDWEDHLAVK.H
	HsFLAG-Control_HeLa_S1	3.1275	0.2534	1349.94	1349.49	5003.1		1	677	75	4	K.HFSVEGQLEFR.A
	HsFLAG-Control_HeLa_NE	3.7466	0.2381	1264.71	1265.41	6070.2		1	1041.7	83.3	10	R.RAPFDLFENR.K
	HsFLAG-Control_HeLa_NE	2.4384	0.1143	948.48	949.051	8413.3		8	681.8	75	1	K.FYEQFSK.N
	HsFLAG-Control_HeLa_S1	2.5696	0.1448	1168.59	1169.24	5147.3		2	436.5	66.7	3	K.LGIHEDSQNR.K
	HsFLAG-Control_HeLa_NE	2.8368	0.2315	1169.2	1169.24	6356.4		7	602.8	66.7	3	K.LGIHEDSQNR.K
	HsFLAG-Control_HeLa_S1	2.8613	0.2441	1169.35	1169.24	6648.7		1	820.8	72.2	5	K.LGIHEDSQNR.K
	HsFLAG-Control_HeLa_NE	2.6665	0.1841	1297.57	1297.41	8151.2		1	940.5	70	1	K.LGIHEDSQNRK.K
	HsFLAG-Control_HeLa_S1	3.73	0.4072	1551.39	1551.71	7872.1		1	1334.4	73.1	1	R.YYTSASGDEMVSLK.D
	HsFLAG-Control_HeLa_NE	3.403	0.3361	1224.51	1225.39	6426		2	721.8	66.7	5	K.HIYYITGETK.D
	HsFLAG-Control_HeLa_S1	3.2831	0.3573	1224.53	1225.39	6930.1		1	843.9	72.2	6	K.HIYYITGETK.D
	Hs283FLP_Ti_105.1393.13	3.1232	0.3785	1224.58	1225.39	5786.9		1	754.6	72.2	2	K.HIYYITGETK.D
	HsFLAG-Control_HeLa_S1	3.2689	0.4124	1224.59	1225.39	6192.5		1	931.4	77.8	1	K.HIYYITGETK.D
	HsFLAG-Control_HeLa_S1	3.3338	0.3832	1224.82	1225.39	3650.2		1	668.6	77.8	1	K.HIYYITGETK.D
	HsFLAG-Control_HeLa_NE	3.3596	0.3489	1225.24	1225.39	3715.7		1	927.2	88.9	4	K.HIYYITGETK.D
	HsFLAG-Control_HeLa_S1	3.247	0.3207	1225.56	1225.39	3672.2		1	869.1	88.9	1	K.HIYYITGETK.D
	HsFLAG-Control_HeLa_S1	3.7466	0.3254	1236.22	1236.33	7080.7		2	1140	80	13	K.DQVANSAFVER.L
	HsFLAG-Control_HeLa_S1	2.5834	0.3358	1416.47	1417.47	3338.4		1	318	63.6	2	K.EGLELPEDEEEK.K
	HsFLAG-Control_HeLa_NE	2.8612	0.171	1417.26	1417.47	2994.8		7	388	68.2	6	K.EGLELPEDEEEK.K
	HsFLAG-MOCK_300mM_T	2.8099	0.2341	1167.72	1168.35	4413.6		1	487.2	75	2	K.KTKFENLCK.I
	HsFLAG-MOCK_300mM_T	2.911	0.2179	1168.94	1168.35	5882.8		1	1050.9	87.5	2	K.KTKFENLCK.I
	HsFLAG-Control_HeLa_S1	4.3051	0.3302	1787.57	1788.01	9266.6		1	2131.5	51.8	1	K.HLEINPDHSIIETLR.Q
	HsFLAG-Control_HeLa_NE	4.5439	0.4176	1789.92	1788.01	6445.5		1	1222.4	71.4	4	K.HLEINPDHSIIETLR.Q
	HsFLAG-Control_HeLa_S1	4.5087	0.3244	3003.82	3004.37	8897.8		1	1496.7	30.8	3	K.DLVILLYETALLSSGFSLEDPQTHANR.I
	HsFLAG-Control_HeLa_S1	4.0636	0.3203	3004.79	3004.37	7082.1		1	715.8	38.5	1	K.DLVILLYETALLSSGFSLEDPQTHANR.I
gi|4827071|ref|N	4	11	0.305	177	19463	7.7	U		zinc finger protein 9 [Homo sapiens]			
*	HsFLAG-MOCK_150mM_T	4.0835	0.3929	1776.53	1776.95	4965.5		1	1137.7	75	3	R.GFQFVSSSLPDICYR.C
*	HsFLAG-MOCK_150mM_T	4.4738	0.4289	1777.29	1776.71	7424.1		1	2314.1	80.8	1	K.DCDLQEDACYNCGR.G
*	HsFLAG-MOCK_150mM_T	4.0251	0.3622	1486.51	1486.56	8543.7		1	1407.1	77.3	2	K.CYSCGEFGHIQK.D
*	HsFLAG-MOCK_150mM_T	4.5357	0.4368	1433.96	1433.49	7047.3		1	1296.2	75	5	R.CGETGHVAINCSK.T
gi|4826860|ref|N	2	4	0.305	128	14174	8.5	U		NHP2 non-histone chromosome protein 2-like 1 [Homo sapiens]			
gi|51317376|ref|	2	4	0.305	128	14174	8.5	U		NHP2 non-histone chromosome protein 2-like 1 [Homo sapiens]			
	HsFLAG-Control_HeLa_NE	2.638	0.2628	1200.4	1200.38	4105.2		1	567.7	80	1	K.AYPLADAHLTK.K
	HsFLAG-MOCK_300mM_T	4.4606	0.202	3141.39	3138.65	6294		1	918.3	29.6	3	R.GISEFIVMAADAEPLEIILHLPLLCEDK.N
gi|31542947|ref|	10	38	0.304	573	61055	5.9	U		chaperonin [Homo sapiens]			
gi|41399285|ref|	10	38	0.304	573	61055	5.9	U		chaperonin [Homo sapiens]			
	HsFLAG-MOCK_300mM_T	5.7423	0.3515	2115.75	2114.57	8543.1		1	2266.7	45	1	R.ALMLQGVDLLADAVAVTMGPK.G
	HsFLAG-Control_HeLa_NE	5.3575	0.4769	2560.34	2561.72	7694		1	1034.5	47.9	5	K.LVQDVANNTNEEAGDGTTTATVLAR.S
	HsFLAG-Control_HeLa_NE	2.915	0.2935	2041.92	2042.25	8372.4		1	685.1	50	1	K.PVTTPEEIAQVATISANGDK.E
	Hs293FLP_TREX_Ti_102.2	3.3907	0.3559	1390.23	1390.58	4072.4		1	1090.3	81.8	2	R.GYISPYFINTSK.G
	HsFLAG-Control_293_Ti_2	2.7786	0.1954	1605.27	1602.75	6264.6		1	338.6	54.2	1	K.CEFQDAYVLLSEK.K
	HsHeLa_Control-MG_Ti_20	4.209	0.31	2049.14	2048.39	6268.8		1	796.3	52.8	1	K.KISSIQSIVPALEIANAHR.K
	HsFLAG-Control_HeLa_NE	2.2193	0.1673	844.51	845.027	7946.7		7	620.6	71.4	3	K.VGEVIVTK.D
	HsFLAG-Control_HeLa_NE	3.4295	0.3174	1234.26	1234.31	8156.8		1	1020.2	72.7	3	K.VGGTSDVEVNEK.K
	HsFLAG-Control_HeLa_NE	2.6929	0.245	1772.26	1772.92	7382.7		1	675.9	56.7	2	R.CIPALDSLTPANEDQK.I

	HsFLAG-Control_HeLa_NE	6.0057	0.3814	2870.06	2870.31	7241.4		1	1924	38.9	19	R.TALLDAAGVASLLTTAEVVVTEIPKEEK.D
gi|4504897|ref|N	11	33	0.302	529	57862	5.4	U	karyopherin alpha 2 [Homo sapiens]				
gi|89042174|ref|	11	33	0.302	529	57862	5.4	U	PREDICTED: similar to Importin alpha-2 subunit (Karyopherin alpha-2 subunit) (SRP1-alp				
gi|89042170|ref|	11	33	0.302	529	57862	5.4	U	PREDICTED: similar to Importin alpha-2 subunit (Karyopherin alpha-2 subunit) (SRP1-alp				
	Hs293FLP-MG_Ti_302.159	4.0965	0.4024	1878.34	1877.96	4415.8		1	763.4	65.6	2	R.NVSSFPDDATSPLQENR.N
	Hs293FLP-MG_Ti_303.187	4.108	0.3001	1690.97	1689.82	5974.2		1	1090.4	71.4	3	R.NNQGTVNWSVDDIVK.G
	Hs293FLP-MG_Ti_302.151	4.6149	0.4105	1900.8	1902.03	7951.6		1	1828.8	67.6	3	K.GINSSNVENQLQATQAAR.K
	Hs293FLP-MG_Ti_305.280	3.421	0.3744	2842.61	2844.03	7110		1	899.8	40	5	R.TDCSPIQFESAWALTNIASGTSEQTK.A
	Hs293FLP-MG_Ti_306.291	5.4679	0.1826	1943.55	1944.28	6190.6		1	1683.2	50	2	K.NPAPPIDAVEQILPTLVR.L
	HsFLAG-Control_HeLa_S1	3.2688	0.3874	1944.32	1944.28	5818.7		1	531.1	50	2	K.NPAPPIDAVEQILPTLVR.L
	Hs293FLP-MG_Ti_306.266	2.7796	0.2547	1549.58	1550.88	4762.3		1	342.7	57.1	2	K.LLGASELPIVTPALR.A
	HsFLAG-Control_HeLa_NE	3.8492	0.2303	1550.75	1550.88	4988.1		3	617.5	60.7	4	K.LLGASELPIVTPALR.A
	Hs293FLP-MG_Ti_306.266	3.9873	0.3009	1551.72	1550.88	4100.6		1	675.5	67.9	4	K.LLGASELPIVTPALR.A
	HsFLAG-Control_HeLa_S1	4.7065	0.2881	3355.83	3354.83	7409.4		1	894.6	27.3	2	R.AIGNIVTGTDEQTQVVIDAGALAVFPSLLTNPK.T
	HsFLAG-Control_HeLa_S1	5.1557	0.4961	1971.72	1972.38	9575.3		1	2769.4	73.5	4	K.IILVILDAISNIFQAAEK.L
gi|34147540|ref|N	4	7	0.3	140	14564	8.5	U	hypothetical protein LOC114984 [Homo sapiens]				
*	HsHeLa3_Ti_105.1530.153	3.5574	0.293	1932.91	1933.17	4046.7		1	705.7	55.6	2	K.ASQEPSPKPGTEVIPAAPR.K
*	HsHeLa3_Ti_106.1936.193	2.8558	0.2311	1263.67	1264.43	5897.9		4	368.5	60	1	K.ALLQTHPEAQR.A
*	HsHeLa3_Ti_106.1934.193	3.0039	0.2284	1264.66	1264.43	4956.1		1	693.2	75	2	K.ALLQTHPEAQR.A
*	HsHeLa3_Ti_102.1289.128	3.309	0.2616	1311.61	1311.43	3631.2		1	668.5	77.3	2	R.AIEAAPQEPEQK.R
gi|41151097|ref|	4	10	0.299	214	24627	10.1	U	PREDICTED: similar to ribosomal protein L10 isoform 1 [Homo sapiens]				
gi|89057215|ref|	4	10	0.299	214	24627	10.1	U	PREDICTED: similar to ribosomal protein L10 isoform 4 [Homo sapiens]				
gi|89057211|ref|	4	10	0.299	214	24627	10.1	U	PREDICTED: similar to ribosomal protein L10 isoform 1 [Homo sapiens]				
gi|89052350|ref|	4	10	0.299	214	24627	10.1	U	PREDICTED: similar to ribosomal protein L10 isoform 4 [Homo sapiens]				
gi|5174431|ref|N	4	10	0.299	214	24577	10.1	U	ribosomal protein L10 [Homo sapiens]				
	HsGST-MOCK_Ti_102.273	6.5622	0.5053	3282.16	3283.56	8243.1		1	2573.8	39.3	1	K.AKVDEFPLCGHMVSDEYEQLSSEALEAAR.I
	HsF-IP-293-MG_Ti_106.18	2.155	0.1527	1188.66	1189.36	3924.9		6	197	59.1	1	R.GAFGKPQGTVAR.V
	HsF-IP-293-MG_Ti_102.23	3.6793	0.1568	1546.36	1545.66	6663.1		2	1880.3	83.3	2	K.FNADEFEDMVAEK.R
	HsGST-MOCK_Ti_102.139	3.4877	0.2356	1115.55	1115.28	4787.3		1	958.4	83.3	6	K.RLIPDGCGVK.Y
gi|24307939|ref|N	9	44	0.298	541	59671	5.6	U	chaperonin containing TCP1, subunit 5 (epsilon) [Homo sapiens]				
*	HsFLAG-Control_293_Ti_1	3.6907	0.248	3115.1	3115.38	7439.5		1	540.6	31	2	K.SQDDEIGDGTTGVVVLAGALLEEAEQLLDR.G
*	HsHeLa_Control-MG_Ti_20	5.3369	0.4713	3116.94	3115.38	5386.4		1	909.2	32.8	8	K.SQDDEIGDGTTGVVVLAGALLEEAEQLLDR.G
*	HsFLAG-Control_HeLa_NE	4.1096	0.3957	2186.04	2186.51	7983		1	702.7	44.7	4	K.ISDSVLVDIKDTEPLIQTAK.T
*	HsFLAG-Control_HeLa_S1	3.8651	0.3445	1611.35	1611.93	7708.9		1	945	61.5	5	K.IAILTCPFEPPKPK.T
*	HsHeLa_Control-MG_Ti_20	4.0692	0.4256	1434.4	1434.59	6931.6		1	1408.8	81.8	2	K.HKLDVTSVEDYK.A
*	HsFLAG-Control_HeLa_S1	3.961	0.2203	3382.49	3381.7	7874.5		2	529.5	23.3	1	K.ETGANLAICQWGFDDEANHLLLQNNLPAVR.W
*	HsHeLa_Control-MG_Ti_20	2.6364	0.2309	1739.59	1740.01	9012.4		1	727.4	53.1	1	R.WVGGPEIELIAIATGGR.I
*	HsFLAG-Control_HeLa_S1	5.3166	0.3031	1668.45	1668.93	8272		1	1989.9	73.3	20	K.LGFAGLVQEISFGTTK.D
*	HsFLAG-Control_HeLa_S1	4.6295	0.5095	2195.19	2196.39	9521.4		1	1939.7	57.1	1	R.VVYGGGAAEISCALAVSQEADK.C
gi|21735625|ref|N	6	18	0.298	245	27745	4.8	U	tyrosine 3/tryptophan 5 -monooxygenase activation protein, zeta polypeptide [Homo sapie				
gi|4507953|ref|N	6	18	0.298	245	27745	4.8	U	tyrosine 3/tryptophan 5 -monooxygenase activation protein, zeta polypeptide [Homo sapie				
	HsHeLa3_Ti_102.1435.143	2.7583	0.2969	1548.62	1549.59	3559.8		1	213.6	50	1	K.SVTEQGAELSNEER.N
	HsHeLa3_Ti_102.1431.143	4.2821	0.3336	1549.69	1549.59	7395.9		1	1521.3	73.1	5	K.SVTEQGAELSNEER.N
	HsFLAG-MOCK_300mM_T	3.2778	0.422	2439.22	2438.65	8500		1	723.2	42.9	1	K.SVTEQGAELSNEERNLLSVAYK.N
	HsFLAG-MOCK_300mM_T	3.4045	0.2878	1505.62	1505.67	6944.9		1	1332.9	69.2	2	R.VVSSIEQKTEGAEK.K
	HsFLAG-Control_HeLa_S1	3.9585	0.294	2041.03	2042.21	10559.1		1	1559.9	58.8	1	K.GIVDQSQQAYQEAFEISK.K
	HsFLAG-Control_HeLa_NE	4.8185	0.429	2133.81	2133.27	6873.5		1	1374.3	63.9	8	K.TAFDEAIAELDTLSEESYK.D
gi|34147630|ref|N	13	51	0.297	455	49875	7.6	U	Tu translation elongation factor, mitochondrial [Homo sapiens]				
*	HsHeLa_Control-MG_Ti_20	3.5039	0.4202	1810.39	1811.01	6607.1		1	1224.2	68.8	1	R.DKPHVNVGTIGHVDHGK.T

*	Hs293FLP_Ti_302.1308.13	3.8038	0.2962	1495.01	1493.57	7842.9		1	1569.9	81.8	4	K.KYEEIDNAPEER.A
*	HsHeLa_Control-MG_Ti_20	4.8924	0.4745	1674.36	1674.85	7870.2		1	1702.9	73.3	3	R.GITINAAHVEYSTAAR.H
*	HsGST-MOCK_Ti_406.228	2.6155	0.0936	1770.24	1771.85	10711.7		5	692.9	50	1	R.HYAHTDCPGHADYVK.N
*	HsHeLa_Control-MG_Ti_20	4.0632	0.421	1771.34	1771.85	8511.3		1	1376	75	3	R.HYAHTDCPGHADYVK.N
*	HsGST-MOCK_Ti_104.129	4.2042	0.3084	1771.6	1771.85	8142.1		1	2990.9	58.9	2	R.HYAHTDCPGHADYVK.N
*	Hs293FLP-MG_Ti_203.436	3.9538	0.2669	2939.74	2940.29	5591.8		1	611.4	28.8	3	R.ELLTEFGYKGEETPVIVGSALCALEGR.D
*	Hs293FLP-MG_Ti_203.474	4.9575	0.3622	3692.69	3693.15	6799.1		1	572.4	24.2	6	R.ELLTEFGYKGEETPVIVGSALCALEGRDPELGLK.S
*	Hs293FLP-MG_Ti_202.312	2.1516	0.22	1542.63	1543.8	3896.1		1	467.3	57.7	1	K.LLDAVDTYIPVPAR.D
*	Hs293FLP-MG_Ti_202.313	4.161	0.3099	1542.71	1543.8	6319.7		1	1658.6	80.8	4	K.LLDAVDTYIPVPAR.D
*	HsHeLa_Control-MG_Ti_20	4.2046	0.3442	1543.66	1543.8	5543.3		1	1360.5	76.9	8	K.LLDAVDTYIPVPAR.D
*	HsFLAG-Control_293_Ti_2	4.8842	0.3629	1644.64	1644.95	3916.1		1	1098.5	78.6	12	K.PFLLPVEAVYSVPGR.G
*	Hs293FLP-MG_Ti_204.141	3.5572	0.2081	1373.3	1373.47	8693.2		1	1454.9	77.3	3	K.KGDECELLGHSK.N
gi|50592996|ref|N	38	352	0.296	450	50433	4.9	U		tubulin, beta, 4 [Homo sapiens]			
	HsF-IP-293-MG_Ti_102.233	4.2116	0.3257	1617.72	1616.87	4090.1		1	901.5	75	15	R.AILVDLEPGTMDSVR.S
	HsGST-MOCK_Ti_102.286	3.2049	0.3313	1958.45	1960.15	8017.5		1	762.8	52.9	1	K.GHYTEGAELVDSVLDVVR.K
	HsFLAG-Control_HeLa_S1	4.1642	0.2955	1959.3	1960.15	8544.6		2	1215.8	38.2	2	K.GHYTEGAELVDSVLDVVR.K
	HsGST-MOCK_Ti_403.395	4.7164	0.3422	1959.33	1960.15	10548.9		1	1301.9	55.9	1	K.GHYTEGAELVDSVLDVVR.K
	HsFLAG-Control_HeLa_NE	5.3562	0.4242	1959.63	1960.15	11243.1		1	2825.8	70.6	3	K.GHYTEGAELVDSVLDVVR.K
	Hs293FLP_Ti_303.3357.33	4.1617	0.1819	1959.92	1960.15	7405		2	1468.9	42.6	6	K.GHYTEGAELVDSVLDVVR.K
	HsHeLa_Control-MG_Ti_10	6.1452	0.4266	1959.96	1960.15	8101.6		1	2856.7	79.4	5	K.GHYTEGAELVDSVLDVVR.K
	Hs293FLP-MG_Ti_205.353	4.315	0.1813	1959.98	1960.15	9417.8		1	1643	41.2	5	K.GHYTEGAELVDSVLDVVR.K
	Hs293FLP-MG_Ti_204.367	6.6846	0.431	1959.98	1960.15	10282.1		1	3961.5	82.4	8	K.GHYTEGAELVDSVLDVVR.K
	Hs293FLP_Ti_306.3198.31	6.98	0.3863	1960.01	1960.15	9148.7		1	3744.2	85.3	7	K.GHYTEGAELVDSVLDVVR.K
	HsFLAG-Control_HeLa_S1	4.5919	0.2553	1960.03	1960.15	7594.6		1	1242.3	41.2	2	K.GHYTEGAELVDSVLDVVR.K
	HsHeLa_Control-MG_Ti_10	3.5165	0.1922	1960.13	1960.15	6171.6		3	834.7	35.3	1	K.GHYTEGAELVDSVLDVVR.K
	HsHeLa_Control-MG_Ti_20	4.3353	0.2198	1960.22	1960.15	8005.9		1	1897.4	47.1	2	K.GHYTEGAELVDSVLDVVR.K
	HsFLAG-Control_HeLa_S1	5.8707	0.417	1960.53	1960.15	9914.1		1	3928.7	82.4	2	K.GHYTEGAELVDSVLDVVR.K
	HsHeLa_Control-MG_Ti_20	6.9239	0.4578	1960.6	1960.15	10283.3		1	4222.7	85.3	8	K.GHYTEGAELVDSVLDVVR.K
	HsHeLa_Control_Ti_105.38	6.5934	0.4301	1960.92	1960.15	9241.8		1	3541.4	82.4	7	K.GHYTEGAELVDSVLDVVR.K
	HsFLAG-Control_HeLa_NE	4.632	0.1653	1961.1	1960.15	7796.1		7	1433.4	44.1	1	K.GHYTEGAELVDSVLDVVR.K
	HsHeLa_Control_Ti_105.38	3.9939	0.1774	1961.13	1960.15	6245.6		2	1192.6	45.6	2	K.GHYTEGAELVDSVLDVVR.K
	HsFLAG-Control_HeLa_S1	4.764	0.2325	1961.21	1960.15	8029.8		1	1535	42.6	2	K.GHYTEGAELVDSVLDVVR.K
	HsFLAG-Control_HeLa_S1	6.9041	0.4463	1961.25	1960.15	11475.7		1	4165.7	82.4	14	K.GHYTEGAELVDSVLDVVR.K
	HsFLAG-Control_HeLa_S1	5.9828	0.4073	1961.57	1960.15	10193.9		1	3020.1	76.5	5	K.GHYTEGAELVDSVLDVVR.K
	HsGST-MOCK_Ti_102.285	4.2626	0.1599	1962	1960.15	7062.2		4	1185.6	41.2	1	K.GHYTEGAELVDSVLDVVR.K
	Hs293FLP_Ti_306.3098.30	6.1016	0.4085	2088.19	2088.33	9030.4		1	2434	72.2	2	K.GHYTEGAELVDSVLDVVRK.E
	HsHeLa_Control_Ti_106.36	2.6425	0.3564	2089.18	2088.33	10954.4		1	669	41.7	1	K.GHYTEGAELVDSVLDVVRK.E
	HsFLAG-MOCK_300mM_T	4.8098	0.3951	2089.85	2088.33	6163.4		1	1098.1	41.7	3	K.GHYTEGAELVDSVLDVVRK.E
	Hs293FLP_Ti_305.3017.30	5.121	0.3371	2090.41	2088.33	6587.3		1	1579.1	48.6	9	K.GHYTEGAELVDSVLDVVRK.E
	HsFLAG-Control_MG_293_	4.3284	0.3282	1320.01	1320.59	8983.2		1	1855	86.4	18	R.IMNTFSVVPSPK.V
	HsFLAG-Control_293_Ti_2	2.3562	0.2676	1130.49	1131.28	3790.3		1	334.2	72.2	1	R.FPGQLNADLR.K
	HsFLAG-Control_HeLa_S1	3.3308	0.1729	1130.86	1131.28	4313.3		1	873.6	88.9	23	R.FPGQLNADLR.K
	HsFLAG-Control_MG_293_	3.206	0.113	1130.88	1131.28	3899.4		1	816.9	88.9	6	R.FPGQLNADLR.K
	HsFLAG-Control_HeLa_S1	2.9598	0.1628	1259.33	1259.45	6893.9		1	1452.3	90	5	R.FPGQLNADLRK.L
	HsHeLa_Control-MG_Ti_10	3.4275	0.2361	1272.73	1272.59	5940.6		2	973.4	75	2	R.KLAVNMVPFPR.L
	HsF-IP-293-MG_Ti_104.212	3.5921	0.3097	1145.56	1144.42	4625.3		1	875.9	88.9	19	K.LAVNMVPFPR.L
	HsHeLa-FLAG-IP_S100_Ti_	3.5217	0.3098	1692.35	1692.97	3844.5		1	610.2	67.9	9	R.ALTVPELTQQMFDAK.N
	HsHeLa-FLAG-IP_S100_Ti_	2.9555	0.2199	1068.25	1066.2	7345.1		2	1221.1	81.2	2	K.NMMAACDPR.H
	HsFLAG-Control_HeLa_S1	4.2481	0.345	1697.72	1697.89	5597.6		1	913.8	69.2	79	K.NSSYFVEWIPNNVK.V

*	Hs283FLP_Ti_103.2794.27	5.1829	0.4392	1875.9	1875.15	4237		1	1173	71.9	70	K.MSSTFIGNSTAIQELFK.R
	HsHeLa_Control-MG_Ti_10	3.5998	0.3059	1388.48	1386.61	7275		1	1173.3	80	3	K.RISEQFTAMFR.R
gi|14670350|ref|N	29	71	0.291	998	112416	6.4	U	general transcription factor II, i isoform 1 [Homo sapiens]				
gi|14670354|ref|N	29	71	0.297	977	110106	7.4	U	general transcription factor II, i isoform 3 [Homo sapiens]				
gi|14670352|ref|N	29	71	0.297	978	110280	6.7	U	general transcription factor II, i isoform 2 [Homo sapiens]				
	HsFLAG-Control_HeLa_NE	2.8495	0.0973	1302.39	1301.44	5418.3		1	844.3	80	2	K.HPENYDLATLK.W
	HsHeLa3_Ti_105.1675.167	2.5927	0.2664	1272.62	1273.44	4605.7		3	439.2	58.3	2	R.SILSPGGSCGPIK.V
	HsFLAG-Control_HeLa_NE	3.7084	0.2931	1729.02	1729.93	4652.6		1	729.5	62.5	2	K.ANELPQPPVPEPANAGK.R
	HsFLAG-Control_HeLa_NE	5.1862	0.4159	3471.36	3470.99	8294.7		1	1390.3	30.8	1	K.AKGPVTIPYPLFQSHVEDLYVEGLPEGIPFR.R
	HsFLAG-Control_HeLa_NE	3.8949	0.2478	3271.61	3271.74	3424.7		1	330.2	27.7	3	K.GPVTIPYPLFQSHVEDLYVEGLPEGIPFR.R
	HsFLAG-Control_HeLa_NE	3.1689	0.1623	1400.62	1400.57	7310.3		2	846.1	70.8	1	R.EDLQLDKPASGVK.E
	HsFLAG-Control_HeLa_NE	3.18	0.3169	1252.37	1252.41	8166		1	1160.8	72.7	1	K.KFAEALGSTEAK.A
	HsFLAG-Control_HeLa_NE	2.3131	0.2165	1123.52	1124.24	9161.8		1	957.5	65	1	K.FAEALGSTEAK.A
	HsFLAG-Control_HeLa_NE	3.2349	0.2143	1124.08	1124.24	4860.3		1	1620.3	90	1	K.FAEALGSTEAK.A
	HsFLAG-Control_HeLa_NE	4.3228	0.3444	2357.75	2358.62	5991.2		1	881.2	55.3	2	K.FEAHPNDLYVEGLPENIPFR.S
	HsFLAG-Control_HeLa_NE	2.9452	0.1359	1063.22	1063.2	5447.9		1	1227.3	93.8	4	R.SPSWYGIPR.L
	HsFLAG-MOCK_300mM_T	4.3991	0.3836	1865.78	1866.08	7391.7		1	1526.3	76.7	1	K.RPELLTHSTTEVTQPR.T
	HsFLAG-Control_HeLa_NE	3.8786	0.3368	1865.93	1866.08	6700.4		1	424.1	53.3	2	K.RPELLTHSTTEVTQPR.T
	HsFLAG-Control_HeLa_NE	5.2462	0.3918	1867.62	1866.08	8768		1	2200.3	51.7	2	K.RPELLTHSTTEVTQPR.T
	HsFLAG-MOCK_300mM_T	3.984	0.4102	1868.84	1866.08	7763.3		1	1205.5	43.3	1	K.RPELLTHSTTEVTQPR.T
	HsFLAG-Control_HeLa_NE	2.7354	0.1485	1458.94	1459.6	8972.5		6	583.9	54.5	1	R.TNTPVKEDWNVR.I
	HsFLAG-Control_HeLa_NE	4.7837	0.2459	1250.49	1248.47	4835.1		1	1335	90.9	5	K.FAQALGLTEAVK.V
	HsFLAG-Control_HeLa_NE	5.1574	0.4427	2896.06	2897.3	7001.6		1	1269.7	52.1	7	K.VPYPVFESNPEFLYVEGLPEGIPFR.S
	HsFLAG-Control_HeLa_NE	4.745	0.4849	2897.08	2897.3	5312.2		1	744	45.8	5	K.VPYPVFESNPEFLYVEGLPEGIPFR.S
	HsFLAG-Control_HeLa_NE	3.5712	0.3321	2897.37	2897.3	7093.6		1	787.9	29.2	1	K.VPYPVFESNPEFLYVEGLPEGIPFR.S
	HsFLAG-Control_HeLa_NE	4.5094	0.3707	2898.64	2897.3	4877.7		1	1072.3	35.4	3	K.VPYPVFESNPEFLYVEGLPEGIPFR.S
	HsFLAG-Control_HeLa_NE	3.6155	0.283	1061.03	1061.23	5953.9		1	923.5	87.5	5	R.SPTWFGIPR.L
	HsFLAG-Control_HeLa_NE	5.5258	0.4681	2364.7	2365.56	5882.3		1	1250.9	59.5	4	K.VPEIEVTVEGPNNNNPQTSAVR.T
	HsFLAG-Control_HeLa_NE	5.4502	0.4674	2364.8	2365.56	9003		1	1604.6	40.5	3	K.VPEIEVTVEGPNNNNPQTSAVR.T
	HsFLAG-Control_HeLa_NE	4.1029	0.2623	1644.8	1644.83	6134.9		1	935.7	64.3	3	R.TPTQTNGSNVPFKPR.G
	HsFLAG-Control_HeLa_NE	3.3378	0.2806	1229.23	1229.33	6218		6	787.7	77.8	2	R.EFSFEAWNAK.I
	HsFLAG-Control_HeLa_NE	3.0837	0.203	2889.48	2890.26	6407		2	219.4	27.1	2	K.VPFALFESFPEDFYVEGLPEGVPFR.R
	HsFLAG-Control_HeLa_NE	3.2716	0.1198	1031.26	1031.2	6255.7		1	1018.5	93.8	3	R.RPSTFGIPR.L
	HsFLAG-Control_HeLa_NE	2.9824	0.1933	1037.23	1036.21	2673.1		9	542.4	87.5	1	R.ILDSAEFIK.F
gi|20127486|ref|N	7	29	0.288	434	47047	5.4	U	mannose 6 phosphate receptor binding protein 1 [Homo sapiens]				
*	HsFLAG-Control_HeLa_S1	4.8848	0.3976	1528.42	1528.79	7918.1		1	1802.3	73.3	13	R.TLTAAAVSGAQPILSK.L
*	HsFLAG-Control_HeLa_NE	3.774	0.3045	1572.11	1572.72	4075.4		1	619.5	73.1	2	K.LEPQIASASEYAHR.G
*	HsFLAG-Control_HeLa_S1	3.1791	0.1696	2068.5	2066.36	7421		1	546.4	47.1	1	R.GLDKLEENLPILQQPTEK.V
*	HsFLAG-Control_HeLa_S1	5.3196	0.4361	1578.05	1577.69	8974.2		1	1998.6	75	6	K.DTVATQLSEAVDATR.G
*	HsFLAG-Control_HeLa_S1	3.5065	0.3754	2068.59	2068.21	6103		1	383.1	44.1	1	K.SEEWADNHLPLTDAELAR.I
*	HsFLAG-Control_HeLa_S1	5.2393	0.4258	1837.69	1836.01	9850.5		1	2567.9	75	5	R.IATSLDGFDVASVQQQR.Q
*	HsFLAG-Control_HeLa_S1	3.6527	0.2777	2996	2996.26	11011.3		2	826.4	25	1	R.QVEDLQATFSSIHSFQDLSSSILAQSR.E
gi|4506457|ref|N	9	34	0.287	317	36876	4.4	U	reticulocalbin 2, EF-hand calcium binding domain [Homo sapiens]				
*	HsFLAG-Control_293_Ti_1	3.4441	0.295	1707.43	1707.88	7605.6		1	874.6	60.7	1	R.EALLGVQEDVDEYVK.L
*	HsFLAG-Control_293_Ti_1	4.6665	0.4739	2215.84	2216.28	8681.2		1	1330.5	58.3	7	R.VIDFDENTALDDAEEESFR.K
*	HsFLAG-Control_293_Ti_1	2.5998	0.1656	2343.62	2344.45	9162.9		1	440.4	39.5	1	R.VIDFDENTALDDAEEESFRK.L
*	HsFLAG-Control_293_Ti_1	3.9812	0.3755	1818.19	1818.94	8744.5		1	1068.4	60	5	K.NGDGFVSLEEFLGDYR.W
*	HsFLAG-Control_293_Ti_1	3.666	0.3423	1943	1943.12	6042.8		1	938.5	66.7	3	R.WDPTANEDPEWILVEK.D
*	Hs293FLP-MG_Ti_203.360	4.3001	0.2629	2770.24	2771.01	7426.5		2	751.5	41.3	1	K.KLSEEEILENPDLFLTSEATDYGR.Q

*	HsFLAG-Control_293_Ti_1(	4.2361	0.2446	2770.81	2771.01	10643.2		1	1255.2	31.5	3	K.KLSEEEILENPDLFLTSEATDYGR.Q
*	HsFLAG-Control_293_Ti_1(	4.6084	0.3643	2771.43	2771.01	7671.9		1	1149.3	50	8	K.KLSEEEILENPDLFLTSEATDYGR.Q
*	HsFLAG-Control_293_Ti_1(	4.256	0.4118	2642.35	2642.83	6286.4		1	757.9	47.7	5	K.LSEEEILENPDLFLTSEATDYGR.Q
gi|4503745|ref|NI	46	119	0.286	2647	280759	6.1	U	filamin 1 (actin-binding protein-280) [Homo sapiens]				
*	HsFlag1P_Ti_102.2428.242	2.7245	0.2146	1417.7	1416.57	4734.7		1	419.1	62.5	1	R.IANLQTDLSDGLR.L
	HsHeLa_Control-MG_Ti_20	4.0112	0.3224	1227.4	1227.53	5098.2		1	1284	90	3	R.LIALLEVLSQK.K
*	HsHeLa_Control-MG_Ti_20	2.5246	0.09	1286.59	1286.52	3698.3		2	626.1	80	1	K.LPQLPITNFSR.D
*	HsHeLa_Control-MG_Ti_20	4.0442	0.3287	2314.92	2314.47	7580.4		1	843.1	47.6	1	R.SAGQGEVLVYVEDPAGHQEEAK.V
*	HsHeLa_Control-MG_Ti_20	2.6495	0.127	1752.15	1751.98	4992.9		4	349.8	46.4	3	R.TFSVWYVPEVTGTHK.V
*	HsHeLa_Control-MG_Ti_20	3.9072	0.2597	1284.42	1284.54	6461.3		1	1489	86.4	4	K.VTVLFAGQHIAK.S
*	HsFLAG-Control_293_Ti_2(	2.5071	0.196	1653.87	1653.83	4758.3		8	286.8	46.9	1	K.VTAQGPGLEPSGNIANK.T
*	HsFLAG-Control_MG_293_	3.688	0.4601	1869.31	1868.97	6005.5		3	416.3	50	2	R.SPYTVTVGGQACNPSACR.A
*	HsHeLa_Control-MG_Ti_20	3.2148	0.1966	2538.01	2537.71	6870.2		1	499	42.5	1	R.YWPQEAGEYAVHVLCNSEDIR.L
*	HsFlag1P_Ti_105.1934.193	4.1068	0.3702	1647.48	1647.87	5318.5		1	1133.2	70	2	K.TGVAVNKPAEFTVDAK.H
*	HsHeLa_Control-MG_Ti_20	4.6372	0.3796	1785.37	1785.96	8293.4		1	959.9	60	1	R.VQVQDNEGCPVEALVK.D
*	HsHeLa_Control-MG_Ti_20	4.1858	0.2726	1699.52	1699.95	6133		1	942.3	66.7	3	R.TGVELGKPTHFTVNAK.A
*	HsFLAG-Control_HeLa_S1(	3.9335	0.4293	2287	2287.58	7732.2		1	1049.1	52.4	5	K.YTPVQQGPVGVNVTYGGDPIPK.S
*	HsHeLa_Control-MG_Ti_20	4.399	0.311	1534.37	1534.75	5830.7		1	1119.4	71.4	3	K.SPFSVAVSPSLDLSK.I
*	HsHeLa_Control-MG_Ti_20	3.692	0.1746	4000.77	4001.53	7427.4		1	567.3	20.8	1	R.FLPREEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK.V
*	HsHeLa_Control-MG_Ti_10	5.1486	0.4181	3487.54	3487.89	5414.7		1	592.5	26.6	3	R.EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK.V
*	HsFLAG-MOCK_300mM_T	3.8786	0.3316	1430.32	1430.56	6111.2		1	1114.8	70	6	K.AFGPGLQGGSAGSPAR.F
*	HsHeLa_Control-MG_Ti_20	4.489	0.5355	2763.71	2765.02	7205.3		1	1109.3	50	3	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E
*	HsHeLa_Control-MG_Ti_20	2.869	0.281	1109.19	1109.27	7579.7		1	994	75	2	R.ALTQTGGPHVK.A
*	HsHeLa_Control-MG_Ti_20	5.7175	0.4588	4298.74	4299.57	6049.3		1	1193.6	28.9	2	K.VEYTPYEEGLHSVDVTYDGSPVPSSPFQVPVTEGCDPSR.V
*	HsHeLa_Control-MG_Ti_20	4.1971	0.4224	1635.17	1635.82	6552.2		1	1044.8	66.7	3	R.VHGPGIQSGTTNKPNK.F
*	HsHeLa_Control-MG_Ti_20	2.84	0.2378	1167.36	1168.29	4668.7		2	406.1	55	2	K.VPVHDVTDASK.V
*	HsHeLa_Control-MG_Ti_20	3.0872	0.2517	1168.14	1168.29	5490.8		1	1141.7	90	1	K.VPVHDVTDASK.V
*	HsHeLa_Control-MG_Ti_20	6.0972	0.4649	2544.44	2545.77	10345		1	2361.3	58.7	7	K.GLVEPVDVVDNADGTQTVNYVPSR.E
*	HsFLAG-MOCK_300mM_T	3.696	0.3104	4438.07	4437.82	5986.4		1	604.2	20.6	1	K.GLVEPVDVVDNADGTQTVNYVPSREGPYSISVLYGDEEVPR.S
*	HsHeLa_Control-MG_Ti_20	4.1704	0.355	2343.48	2343.64	3896.3		1	560	50	11	K.ASGPGLNTTGVPASLPVEFTIDAK.D
*	HsFLAG-Control_293_Ti_2(	3.749	0.2162	1938.98	1939.17	9057.5		1	1227.5	52.8	2	K.DAGEGLLAVQITDPEGKPK.K
*	HsHeLa_Control-MG_Ti_20	3.6138	0.3683	2588.14	2588.8	5689.7		1	980.6	34.1	1	K.KTHIQDNHDGTYTVAYVPDVTGR.Y
*	HsHeLa_Control-MG_Ti_20	4.7974	0.4223	2946.22	2947.28	5067.8		1	991.6	35.2	1	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S
*	HsHeLa_Control-MG_Ti_20	4.697	0.4131	2946.79	2947.28	7849.7		1	1320.1	46.3	2	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S
*	HsFLAG-Control_293_Ti_2(	2.8521	0.3032	1589.66	1589.76	6989.7		1	623.4	57.7	1	R.YAPSEAGLHEMDIR.Y
*	HsHeLa_Control-MG_Ti_20	3.6905	0.2797	1603.3	1603.73	3664.3		1	571.1	69.2	3	K.YNEQHVPGSPFTAR.V
*	Hs293FLP-MG_Ti_203.455	3.8073	0.2511	3765.65	3765.26	3365.5		1	391.6	25	2	K.VGSAADIPINISETDLSLLTATVVPPSGREEPCLLK.R
*	HsHeLa_Control-MG_Ti_20	1.9087	0.3179	1154.44	1155.34	2519.9		3	306.1	65	1	R.NGHVGISFVPK.E
*	HsHeLa_Control-MG_Ti_20	2.5015	0.2198	1148.52	1149.29	2274.7		1	193.4	61.1	2	K.ETGEHLVHVK.K
*	HsHeLa_Control-MG_Ti_20	3.4009	0.2782	1515.98	1516.7	3949.9		1	699.8	73.1	2	K.FADQHVPGSPFSVK.V
*	HsHeLa_Control-MG_Ti_20	5.6398	0.4004	2003.54	2003.28	9509		1	2671.5	72.2	2	K.IPEISIQDMTAQVTSPSGK.T
*	HsHeLa_Control-MG_Ti_20	3.6428	0.3123	1503.49	1503.76	3394.5		1	561.5	76.9	2	R.FVPAEMGTHTVSVK.Y
*	HsHeLa_Control-MG_Ti_20	3.6536	0.3047	1533.61	1534.71	3409.3		2	449.4	65.4	2	R.AEAGVPAEFSIWTR.E
*	HsHeLa_Control-MG_Ti_10	3.9532	0.2955	1419.47	1418.63	6554.7		1	1599.7	83.3	2	R.RLTVSSLQESGLK.V
*	HsHeLa_Control-MG_Ti_20	5.6126	0.5338	2277.47	2278.4	6995.2		1	1939	68.4	3	K.VHSPSGALEECYVTEIDQDK.Y
*	HsHeLa_Control-MG_Ti_20	3.0412	0.2326	1302.39	1302.48	4319.6		1	589.2	72.7	1	K.FNGTHIPGSPFK.I

*	HsHeLa_Control-MG_Ti_20	3.5104	0.2496	1381.14	1380.55	8189.8		2	874.1	58.3	3	K.YGGPYHIGGSPFK.A
*	HsHeLa_Control-MG_Ti_20	5.1175	0.4994	2200.28	2201.44	9175.5		1	1522	57.9	4	R.LVSNHSLHETSSVFVDSLTK.A
*	HsHeLa_Control-MG_Ti_20	4.3178	0.4725	2200.79	2201.44	6809.3		1	1325.1	40.8	2	R.LVSNHSLHETSSVFVDSLTK.A
*	HsHeLa_Control-MG_Ti_20	4.4883	0.4179	1790.35	1790.9	5469.1		1	1051.1	66.7	8	K.ATCAPQHGAPGPGPADASK.V
gi|27436946|ref|N	17	61	0.286	664	74140	7	U	lamin A/C isoform 1 precursor [Homo sapiens]				
gi|27436948|ref|N	17	61	0.3	634	70661	8.4	U	lamin A/C isoform 3 [Homo sapiens]				
	HsHeLa3_Ti_103.1318.131	3.9035	0.1963	1360.52	1360.47	5716.5		1	1048.8	73.1	7	R.SGAQASSTPLSPTR.I
	HsFLAG-Control_HeLa_NE	4.4185	0.2423	1630.17	1630.75	8881.8		1	1914.1	79.2	1	R.LQEKEDLQELNDR.L
	HsFLAG-Control_HeLa_NE	3.1989	0.1656	1132.18	1132.17	6862.3		5	836.4	81.2	2	K.EDLQELNDR.L
	HsFLAG-Control_HeLa_NE	3.8609	0.1834	1149.7	1149.24	6803.3		1	1443.9	88.9	6	R.ITESEEVVSR.E
	HsFLAG-Control_HeLa_NE	3.4433	0.3215	1294.18	1294.41	8383		1	1807.9	81.8	2	K.AAYEAELGDARK.T
	HsFLAG-Control_HeLa_NE	3.468	0.0852	1044.28	1044.15	5337		1	968.1	88.9	2	K.EGDLIAAQAR.L
	HsFLAG-Control_HeLa_NE	3.8782	0.1201	1029.28	1029.18	6594.1		1	1470.5	93.8	4	R.LADALQELR.A
	HsFLAG-Control_HeLa_NE	4.9781	0.4396	1753.59	1753.87	5991.6		1	1074.7	63.3	12	R.NSNLVGAAHEELQQSR.I
	HsHeLa3_Ti_106.2420.242	5.0383	0.3621	1702.14	1700.98	8380.1		1	1848	71.4	4	R.IRIDSLSAQLSQLQK.Q
	HsFLAG-Control_HeLa_NE	4.0637	0.2301	1432.59	1431.63	7785.1		1	1368.3	75	3	R.IDSLSAQLSQLQK.Q
	HsHeLa3_Ti_102.3010.301	4.518	0.2628	1895.78	1895.14	6433.2		1	1493.9	75	2	R.MQQQLDEYQELLDIK.L
	HsHeLa3_Ti_102.1373.137	2.8162	0.3322	1203.55	1204.28	9820		1	1020.9	65	2	R.VAVEEVDEEGK.F
	HsFLAG-Control_HeLa_NE	3.3034	0.2881	1204.23	1204.28	6098.4		1	1425.8	90	5	R.VAVEEVDEEGK.F
	HsFLAG-MOCK_300mM_T	4.2612	0.3747	2535.94	2534.88	8062.9		1	933.6	41.7	1	K.AGQVVTIWAAGAGATHSPPTDLVWK.A
	HsFLAG-Control_HeLa_NE	3.2262	0.3381	1407.4	1407.5	9142.4		1	1132.2	70.8	1	R.TVLCGTCGQPADK.A
	HsHeLa3_Ti_103.1306.130	2.4498	0.2504	1407.47	1407.5	7354.6		3	461	54.2	2	R.TVLCGTCGQPADK.A
	HsHeLa3_Ti_103.1566.156	5.1248	0.4928	2366.08	2366.5	5678.3		1	1179.7	51.9	5	K.ASASGSGAQVGGPISSGSSASSVTVTR.S
gi|4758900|ref|N	11	25	0.283	520	59609	8.2	U	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3 [Homo sapiens]				
	HsFLAG-Control_MG_293_	3.6934	0.2869	1191.41	1191.42	7606		1	1478.6	88.9	4	R.YLNWIGVPTK.V
*	Hs293FLP-MG_Ti_202.218	3.2364	0.2937	1580.31	1580.7	6776.6		1	971.3	64.3	2	K.EGGQIAVFDATNTTR.E
*	Hs293FLP-MG_Ti_203.397	4.3754	0.405	2473.66	2472.78	8948.4		1	1153.5	50	3	K.AFFIESVCDDPTVVASNIMEVK.I
*	Hs293FLP_Ti_303.1609.16	3.9258	0.3603	1945	1943.09	3790.6		1	836.8	63.3	3	K.RISCYEASYQPLDPDK.C
*	Hs293FLP-MG_Ti_202.212	3.814	0.4416	1786.37	1786.9	8635.8		1	1441.6	64.3	1	R.ISCYEASYQPLDPDK.C
*	HsFLAG-Control_MG_293_	4.0917	0.3744	1290.57	1291.33	9216.2		1	1881.3	90	6	R.HGENEHNLQGR.I
	HsFLAG-Control_293_Ti_2	1.9329	0.1065	861.42	862.017	6154.2		1	483.1	83.3	1	R.VWTSQLK.S
*	HsFLAG-Control_MG_293_	3.3734	0.2617	1090.33	1090.22	7382.7		4	1099.9	83.3	1	K.STIQTAEALR.L
*	Hs293FLP-MG_Ti_203.356	3.8119	0.2663	3463.51	3463.7	5932.7		1	833.8	27.7	1	K.ALNEIDAGVCEELTYEEIRDTYPEEYALR.E
*	Hs293FLP-MG_Ti_202.213	4.2093	0.3536	1556.53	1556.67	7703.1		1	1084.4	66.7	2	R.YPTGESYQDLVQR.L
*	Hs293FLP_Ti_305.1367.13	4.0879	0.2434	1497.94	1497.69	5219.1		1	961	73.1	1	R.RNSVTPLASPEPTK.K
gi|4506661|ref|N	11	37	0.282	266	29996	10.6	U	ribosomal protein L7a [Homo sapiens]				
gi|89047383|ref|	11	37	0.282	266	30042	10.6	U	PREDICTED: similar to 60S ribosomal protein L7a isoform 3 [Homo sapiens]				
gi|89047128|ref|	11	37	0.282	266	30042	10.6	U	PREDICTED: similar to 60S ribosomal protein L7a isoform 1 [Homo sapiens]				
	Hs293FLP_TREX_Ti_106.2	2.2821	0.3116	979.56	980.239	5746.7		1	635.5	61.1	2	K.KVAPAPAVVK.K
	Hs293FLP_TREX_Ti_106.2	2.7953	0.2259	980.38	980.239	3474.9		5	599.6	77.8	1	K.KVAPAPAVVK.K
	HsFLAG-MOCK_300mM_T	2.9488	0.3265	980.45	980.239	3792.8		6	622.6	77.8	1	K.KVAPAPAVVK.K
	HsFLAG-Control_293_Ti_2	2.4671	0.2528	852.4	852.065	4300.6		1	524	68.8	14	K.VAPAPAVVK.K
	Hs293FLP_TREX_Ti_102.1	3.3759	0.1809	1217.4	1217.37	5004		1	1151.8	85	2	K.NFGIGQDIQPK.R
	HsFLAG-MOCK_300mM_T	4.1479	0.3958	1570.7	1570.79	4684.5		1	983.1	76.9	8	K.VPPAINQFTQALDR.Q
	Hs293FLP_TREX_Ti_102.1	3.9664	0.3554	1345.7	1346.52	6059.4		1	1044.5	75	3	R.AGVNTVTTLVENK.K
	Hs293FLP_TREX_Ti_103.1	3.5472	0.3606	1474.48	1474.7	5544.8		1	655	61.5	2	R.AGVNTVTTLVENKK.A
	Hs293FLP_TREX_Ti_104.1	4.0049	0.3456	1828.88	1829.97	6597.2		1	1933.9	80	1	R.KTCTTVAFTQVNSEDK.G
	Hs293FLP_TREX_Ti_102.1	3.9068	0.272	1701.47	1701.79	5225		1	1130	75	1	K.TCTTVAFTQVNSEDK.G
	Hs293FLP_TREX_Ti_106.2	3.052	0.2801	1064.33	1065.22	4856.3		1	548.1	72.2	2	R.HWGGNVLGPK.S

gi|5901926|ref|NI	6	10	0.282	227	26227	8.8	U	cleavage and polyadenylation specific factor 5 [Homo sapiens]				
*	HsHeLa3_Ti_103.1947.194	4.0608	0.2043	1755.1	1753.9	4254.1		1	793.4	65.6	2	K.LPGGELNPGEDEVEGLK.R
*	HsHeLa3_Ti_106.2215.221	3.4467	0.1993	1090.45	1089.34	8198.8		1	1442.9	93.8	2	K.RLMTEILGR.Q
*	HsHeLa3_Ti_104.2353.235	2.9922	0.0934	1117.66	1118.36	8579.8		3	855.8	75	1	K.LFLVQLQEK.A
*	HsHeLa3_Ti_104.2345.234	3.4705	0.1549	1119.33	1118.36	4561.5		9	969.2	87.5	1	K.LFLVQLQEK.A
*	Hs293FLP-MG_Ti_204.495	4.6078	0.3517	3115.58	3116.63	10718.1		1	1347	27.7	1	K.LVAAPLFELYDNAPGYGPIISSLPQLLSR.F
*	HsHeLa3_Ti_106.3480.348	3.6632	0.4239	3116.29	3116.63	4015.2		1	510.5	39.3	3	K.LVAAPLFELYDNAPGYGPIISSLPQLLSR.F
gi|56788366|ref|N	12	28	0.275	652	70755	7.9	U	phosphatidylinositol-binding clathrin assembly protein isoform 1 [Homo sapiens]				
gi|56788368|ref|N	12	28	0.293	610	66393	8.8	U	phosphatidylinositol-binding clathrin assembly protein isoform 2 [Homo sapiens]				
	HsFLAG-Control_HeLa_NE	2.6836	0.2628	1456.43	1457.63	8205.5		1	507.4	50	1	R.ITAAQHSVTGSAVSK.T
	HsHeLa3_Ti_106.1827.182	3.3388	0.3985	1456.66	1457.63	5315.1		1	425.6	53.6	2	R.ITAAQHSVTGSAVSK.T
	HsFLAG-Control_HeLa_NE	4.623	0.4486	1457.6	1457.63	6593.8		1	1739.4	82.1	1	R.ITAAQHSVTGSAVSK.T
	HsHeLa3_Ti_105.1236.123	4.169	0.3575	1458.57	1457.63	6435.3		1	1243.9	71.4	2	R.ITAAQHSVTGSAVSK.T
	HsHeLa3_Ti_105.1262.126	2.5447	0.1789	1084.46	1085.26	5745.5		1	548.9	61.1	1	K.ATTHEIMGPK.K
	HsHeLa3_Ti_103.3474.347	4.279	0.3544	1428.27	1426.61	5766		1	1512.7	90.9	3	R.NTLFNLSNFLDK.S
	HsHeLa3_Ti_103.2522.252	4.0966	0.3566	1475.49	1475.66	5000.7		1	960.5	75	2	K.SGLQGYDMSTFIR.R
	HsHeLa3_Ti_103.3559.355	2.6762	0.4074	1708.9	1709	6802.2		1	621	53.6	1	R.LFAAYNEGIINLLEK.Y
	HsHeLa3_Ti_104.5048.504	5.0099	0.4158	3773.92	3774.18	10639.9		1	975.4	23.6	2	K.VAEQVGIDRGDIPDLSQAPSSLLDALEQHLASLEGK.K
	HsFLAG-Control_HeLa_NE	5.0189	0.4322	1922.69	1923.17	7309.9		1	1195.2	57.9	7	R.ATTLSNAVSSLASTGLSLTK.V
	HsHeLa3_Ti_104.3239.323	6.4198	0.4391	3370.93	3370.78	6363.6		1	1162	30.5	1	K.STNVIVDSGGFDELGGLLKPTVASQNQNLPVAK.L
	HsHeLa3_Ti_102.4165.416	5.2235	0.3465	2474.24	2474.73	6047.2		1	1024.3	50	5	K.LVSDDLDSSLANLVGNLGIGNGTTK.N
gi|4506411|ref|NI	10	16	0.273	587	63542	4.7	U	Ran GTPase activating protein 1 [Homo sapiens]				
*	HsFLAG-Control_HeLa_NE	2.8422	0.2774	1136.28	1136.29	4810.9		1	1019.9	85	1	K.TQVAGGQLSFK.G
*	HsFLAG-Control_HeLa_NE	3.1377	0.2427	1136.63	1136.29	8330.3		1	712.3	65	1	K.TQVAGGQLSFK.G
*	HsFLAG-Control_HeLa_NE	2.8936	0.1628	1216.44	1216.34	6430.8		1	864.2	77.3	1	R.LEGNTVGVEAAR.V
*	HsFLAG-MOCK_300mM_T	5.0885	0.4962	4751.55	4751.43	6601.5		1	1080.9	23.9	2	R.LRTEIPPALISLGEGLITAGAQLVELDLSDNAFGPDGV QGFEALLK.S
*	HsFLAG-MOCK_300mM_T	2.9664	0.2059	1100.6	1100.3	5404.3		5	687.3	70	1	K.SSAQGKPLALK.V
*	HsFLAG-Control_HeLa_NE	3.6418	0.1133	1408.61	1408.55	6468.9		2	1049	77.3	2	R.VINLNDNTFTEK.G
*	HsFLAG-Control_HeLa_NE	3.724	0.2836	1551.31	1549.73	7982.3		1	1075.4	70.8	1	R.QVEVINFGDCLVR.S
*	HsFLAG-Control_HeLa_NE	4.9497	0.4261	1719.47	1719.84	7777.4		1	1794	73.3	2	K.SSVLIAQQTDTSDPEK.V
*	HsFLAG-Control_HeLa_NE	4.5405	0.4032	1694.6	1693.81	6999.3		1	1275.1	71.4	4	K.AFNSSSFNSNTFLTR.L
*	HsFLAG-MOCK_300mM_T	2.7156	0.1751	2578.8	2577.99	3933.9		1	250.1	32.6	1	K.ALAPLLLAFVTKPNSALESCSFAR.H
gi|45827706|ref|N	7	15	0.273	341	37671	8.5	U	quaking homolog, KH domain RNA binding isoform HQK-5 [Homo sapiens]				
gi|45827712|ref|N	7	15	0.292	319	35248	7.4	U	quaking homolog, KH domain RNA binding isoform HQK-7B [Homo sapiens]				
gi|45827710|ref|N	7	15	0.286	325	35978	6.2	U	quaking homolog, KH domain RNA binding isoform HQK-7 [Homo sapiens]				
gi|45827708|ref|N	7	15	0.292	319	35131	7.4	U	quaking homolog, KH domain RNA binding isoform HQK-6 [Homo sapiens]				
	HsHeLa3_Ti_106.2839.283	3.7658	0.3327	2037.06	2036.32	4017.3		1	536.1	59.4	2	K.LMSSLPNFCGIFNHLER.L
	HsHeLa3_Ti_102.1590.159	2.7387	0.3095	1488.43	1488.57	4556.2		3	425.1	58.3	1	K.DMYNDTLNGSTEK.R
	HsHeLa3_Ti_102.1586.158	3.331	0.2613	1490	1488.57	8892.5		1	1426	75	3	K.DMYNDTLNGSTEK.R
	HsHeLa3_Ti_104.2264.226	5.0846	0.3568	1953.08	1951.23	6848.3		1	1535.1	67.6	4	K.RSAELPDAVGPIVQLQEK.L
	HsHeLa3_Ti_104.3367.336	2.9227	0.2436	1653.98	1654	7167.2		1	643.6	53.8	2	K.MQLMELAILNGTYR.D
	HsHeLa3_Ti_105.2480.248	3.8611	0.3185	1644.87	1643.88	6480.3		1	1332.6	65.6	1	K.SPALAFSLAATAQAAPR.I
	HsHeLa3_Ti_106.2430.243	3.375	0.4031	1465.89	1465.79	5878.2		1	674.8	61.5	2	R.TPTPAGPTIMPLIR.Q
gi|5453543|ref|NI	7	17	0.272	323	36788	7.9	U	aldo-keto reductase family 1, member C1 [Homo sapiens]				
	HsHeLa_Control-MG_Ti_20	4.9003	0.4852	2179.71	2180.39	7914.1		1	1927.1	69.4	1	R.HIDSAHLYNNEEQVGLAIR.S
	HsHeLa_Control-MG_Ti_20	2.9992	0.1893	1158.57	1159.28	8800.5		1	1327.5	87.5	2	K.REDIFYTSK.L
	HsHeLa_Control-MG_Ti_20	3.5613	0.3033	3126.24	3127.65	8920.1		1	466.9	32.7	4	K.NLQLDYVDLYLIHFPVSVKPGEEVIPK.D

	HsHeLa_Control-MG_Ti_20	5.8065	0.4856	3126.75	3127.65	6812.3		1	1504.3	35.6	6	K.NLQLDYVDLYLIHFPVSVKPGEEVIPK.D
	HsHeLa_Control-MG_Ti_20	5.0274	0.436	3670.03	3671.19	7067.5		1	803.5	25.8	2	K.NLQLDYVDLYLIHFPVSVKPGEEVIPKDENGK.I
	HsHeLa_Control-MG_Ti_20	2.6218	0.1304	1011.47	1011.26	4836.1		8	501.6	75	1	K.RTPALIALR.Y
	HsHeLa_Control-MG_Ti_20	3.2941	0.2454	2224.39	2223.44	8018.3		1	778.3	47.2	1	R.YLTLDIFAGPPNYPFSDEY.-
gi|34740329|ref|	9	17	0.267	378	39595	9	U	heterogeneous nuclear ribonucleoprotein A3 [Homo sapiens]				
	HsGST-MOCK_Ti_102.247	3.6654	0.2381	2441.67	2442.69	4085.2		1	916.2	45	1	K.LFIGGLSFETTDDSLREHFEK.W
	HsGST-MOCK_Ti_103.126	2.8392	0.2115	1381.44	1381.57	3984.4		5	468.1	70.8	1	R.EDSVKPGAHLTVK.K
	HsGST-MOCK_Ti_303.228	4.4364	0.3509	1883.8	1884.1	7735.5		1	1594	73.3	2	K.IFVGGIKEDTEEYNLR.D
	HsGST-MOCK_Ti_305.252	3.3382	0.3493	1870.41	1871.02	7264.3		2	564.3	50	1	K.RGFAFVTFDDHDTVDK.I
	HsGST-MOCK_Ti_103.179	4.4864	0.2692	1872.37	1871.02	8163.6		1	2203.2	51.7	1	K.RGFAFVTFDDHDTVDK.I
	HsGST-MOCK_Ti_303.270	3.998	0.4061	1715.11	1714.83	6098.4		1	1319.7	75	2	R.GFAFVTFDDHDTVDK.I
	HsGST-MOCK_Ti_104.111	3.7099	0.3367	1472.35	1472.57	6891.1		3	788.8	68.2	2	K.YHTINGHNCEVK.K
	HsGST-MOCK_Ti_105.108	3.2225	0.3178	1599.91	1600.74	9934.8		1	1133.1	66.7	2	K.YHTINGHNCEVKK.A
*	HsFLAG-MOCK_300mM_T	4.717	0.4394	1913.38	1911.9	6653.5		1	1242.4	59.5	5	R.SSGSPYGGGYGSGGGSGGYGSR.R
gi|22129784|ref|	3	14	0.266	184	20036	4.2	U	hypothetical protein LOC55352 [Homo sapiens]				
*	HsHeLa_Control-MG_Ti_20	4.7594	0.5052	1982.24	1983.06	3079.2		1	516.8	65.8	7	R.GAPPSPEAGFATADHSGQER.E
*	HsFLAG-Control_293_Ti_1	2.9311	0.3381	1922.58	1923	5161.4		3	214.2	40	5	K.EQPGDLFNEDWDSELK.A
*	HsFLAG-Control_293_Ti_2	2.6632	0.314	1503.28	1504.57	8142.6		1	760.5	58.3	2	K.MVFETGQFDDAED.-
gi|4507389|ref|N	26	137	0.264	772	87230	9.6	U	elongin A [Homo sapiens]				
*	Hs293FLP-MG_Ti_303.407	4.303	0.4089	1828.37	1828.16	3118.8		1	627.9	67.6	84	K.LSTLPITVDILAETGVGK.T
*	Hs293FLP-MG_Ti_306.211	2.8331	0.3941	1167.62	1168.3	4339.5		1	462.8	72.2	2	R.KHEHVGSFAR.D
*	Hs293FLP-MG_Ti_306.212	2.0705	0.1821	1039.79	1040.13	4957.4		1	436.8	75	2	K.HEHVGSFAR.D
*	Hs293FLP-MG_Ti_306.213	2.5152	0.2025	1040.01	1040.13	5215.6		2	573.6	75	1	K.HEHVGSFAR.D
*	Hs293FLP-MG_Ti_302.235	2.116	0.0884	859.63	860.001	6106		6	514.1	75	1	R.DLVAQWK.K
*	Hs293FLP-MG_Ti_304.149	3.2445	0.3182	2016.67	2016.17	6540.6		1	895.2	59.4	2	K.LVPVERNAEPDEQDFEK.S
*	Hs293FLP-MG_Ti_302.108	2.1255	0.0868	1321.31	1322.33	4654.7		7	329.2	60	2	R.NAEPDEQDFEK.S
*	Hs293FLP-MG_Ti_306.242	5.4759	0.4749	2230.25	2230.36	8971.3		1	1569.8	61.8	4	R.DALQKEEEMEGDYQETWK.A
*	Hs293FLP-MG_Ti_306.243	5.5374	0.3628	2231.05	2230.36	7768.2		1	2420.7	51.5	2	R.DALQKEEEMEGDYQETWK.A
*	Hs293FLP-MG_Ti_303.148	4.4584	0.3243	1674.59	1674.73	4752.9		1	1261.8	87.5	5	K.EEEMEGDYQETWK.A
*	Hs293FLP-MG_Ti_306.216	3.3979	0.1475	1236.99	1237.45	7070.1		1	1059.2	83.3	1	R.KLSELERPHK.V
*	Hs293FLP-MG_Ti_305.108	2.546	0.1354	1109.62	1109.27	6690.8		1	848.6	81.2	1	K.LSELERPHK.V
*	Hs293FLP-MG_Ti_302.125	4.5922	0.3561	1639.3	1639.76	6027.2		1	1358.9	80.8	2	R.SLEEDQEPIVSHQK.P
*	Hs293FLP-MG_Ti_304.126	4.1739	0.4296	1921.6	1922.1	5478.4		1	644.1	56.2	9	R.SLEEDQEPIVSHQKPGK.G
*	Hs293FLP-MG_Ti_304.067	3.2536	0.2212	971.39	970.033	4708.8		1	904.2	87.5	2	R.RPPSGDNAR.E
*	Hs293FLP-MG_Ti_305.118	3.1967	0.3832	1667.5	1667.83	5706.5		1	512.7	53.6	1	K.KCLPPSEAASDNHLK.K
*	Hs293FLP-MG_Ti_304.123	2.8668	0.2771	1539.28	1539.65	2941.6		1	214	57.7	5	K.CLPPSEAASDNHLK.K
*	Hs293FLP-MG_Ti_302.134	2.5715	0.3341	1068.22	1068.13	4731		5	423.6	72.2	1	K.QGLDSFDTGK.G
*	Hs293FLP-MG_Ti_302.141	2.1464	0.2446	1070.22	1068.13	2190.8		8	118.1	55.6	1	K.QGLDSFDTGK.G
*	Hs293FLP-MG_Ti_306.294	2.9361	0.2529	2300.27	2301.73	5152.4		1	966.1	57.5	1	K.VPDVLPVLPDLPLPAIQANYR.P
*	Hs293FLP-MG_Ti_302.149	4.4536	0.5056	1743.77	1742.8	6691.6		1	1118.1	66.7	2	K.AFSSPQEEEEAGFTGR.R
*	Hs293FLP-MG_Ti_306.235	2.7839	0.1216	1901.12	1901	4710.6		1	484.2	61.5	1	R.DFKEERPEEYESWR.E
*	Hs293FLP-MG_Ti_306.220	2.2804	0.162	1267.4	1268.46	3958.3		8	378.7	65	1	K.NIQFAHANKPK.G
*	Hs293FLP-MG_Ti_306.221	4.1602	0.2803	1269.42	1268.46	8000.2		2	1413	80	2	K.NIQFAHANKPK.G
*	Hs293FLP-MG_Ti_302.120	1.9601	0.1551	1033.32	1034.16	3293.5		3	258.6	60	1	K.FGTGGAAVPEK.I
*	Hs293FLP-MG_Ti_302.120	2.6989	0.1806	1034.58	1034.16	5189.5		1	753.8	80	1	K.FGTGGAAVPEK.I
gi|30089997|ref|	6	15	0.264	387	43236	6.1	U	actin-like 6A isoform 2 [Homo sapiens]				
gi|4757718|ref|N	6	15	0.238	429	47461	5.6	U	actin-like 6A isoform 1 [Homo sapiens]				
gi|30089999|ref|	6	15	0.264	387	43236	6.1	U	actin-like 6A isoform 2 [Homo sapiens]				
	HsHeLa3_Ti_105.2366.236	4.4142	0.4789	2026.01	2026.27	3588.2		1	502.6	52.9	3	K.SEASLHPVLMSEAPWNTR.A

	HsHeLa3_Ti_106.3010.301	5.3342	0.3715	2274.03	2274.65	5645.8		1	1080.6	61.8	2	K.LTELMFEHYNIPAFFLCK.T
	HsFLAG-Control_HeLa_NE	3.5028	0.2438	1121.46	1121.28	7511.6		2	1395.7	85	1	K.TAVLTAFANGR.S
	HsFLAG-Control_HeLa_NE	6.3223	0.3311	3093.16	3093.51	8853.3		1	1768.3	32.8	6	R.STGLILDSGATHTTAIPVHDGYVLQQGIVK.S
	HsHeLa3_Ti_103.2258.225	3.943	0.3834	1497.56	1496.69	6358.3		1	1507.8	79.2	2	K.SPLAGDFITMQCR.E
	HsHeLa3_Ti_103.2158.215	2.8927	0.1078	1317.57	1316.5	3989.3		5	538.6	68.2	1	K.IPEGLFDPSNVK.G
gi|29568109|ref|N	37	113	0.263	1966	225146	7.7	U	dedicator of cytokinesis 4 [Homo sapiens]				
*	HsFLAG-Control_293_Ti_2	3.4473	0.2339	1011.71	1012.2	5061.1		1	1291.5	87.5	5	K.YGVVIASFR.G
*	HsFLAG-Control_293_Ti_1	4.3967	0.1738	2134.65	2133.45	7553.2		1	1276.7	60.5	3	R.GTVPYGLSLEIGDTVQILEK.C
*	HsFLAG-Control_293_Ti_2	3.8412	0.2774	2484.37	2485.83	3891		1	348.3	42.9	2	K.GQFEMVIPTEDSVITEMTSTLR.D
*	HsFLAG-Control_293_Ti_2	4.7001	0.268	1725.01	1725.94	8194.4		1	1762.1	75	3	R.LDWGNEQLGLDLVPR.K
*	HsFLAG-Control_293_Ti_1	4.0316	0.3367	1569.02	1569.71	8555.2		1	962.1	65.4	2	R.EYSSVFSHGVSITR.K
*	HsFLAG-Control_293_Ti_2	3.1731	0.156	1137.07	1137.28	7829.6		2	1305.3	87.5	2	R.NDLYITIER.G
*	HsFLAG-Control_293_Ti_2	3.4709	0.3552	1744.53	1744.02	4139.6		1	423.9	57.1	1	K.LFGFSFVPLMQEDGR.T
*	HsFLAG-Control_293_Ti_2	2.4744	0.1138	1459.64	1460.67	5783.5		5	392.4	50	1	R.TLPDGTHELIVHK.C
*	HsFLAG-Control_293_Ti_2	3.0856	0.1969	1460.65	1460.67	4235.5		2	464	70.8	1	R.TLPDGTHELIVHK.C
*	HsFLAG-Control_293_Ti_2	2.3837	0.2734	1306.34	1307.51	5280		2	316.5	59.1	1	K.GIFLGNNNQAMK.A
*	HsFLAG-Control_293_Ti_2	3.3908	0.2277	1306.98	1307.51	5680.8		1	796.9	72.7	1	K.GIFLGNNNQAMK.A
*	HsFLAG-Control_MG_293_	3.5255	0.2882	1361.05	1361.6	8206		1	1221.3	77.3	1	K.LTQNGDMLDLLK.W
*	HsFLAG-Control_293_Ti_2	4.4192	0.2327	2197.59	2198.43	7679		2	1427.8	41.7	1	K.FLQDTLDTLFGILDENSQK.Y
*	HsFLAG-Control_293_Ti_1	4.7432	0.3459	2197.76	2198.43	8229.9		1	2477.6	66.7	9	K.FLQDTLDTLFGILDENSQK.Y
*	HsFLAG-Control_293_Ti_2	3.0065	0.2585	1698.32	1698.83	4722.2		3	320	50	2	R.LFSLATGGQNEEEFR.C
*	HsFLAG-Control_293_Ti_1	2.2516	0.0915	985.52	986.112	7157.5		4	587	78.6	3	R.FFLSQESK.G
*	HsFLAG-Control_293_Ti_1	5.1626	0.4592	2587.94	2587.93	7955.9		1	1108.2	45.8	10	K.GSGALSQSQAVFLSSFPAVYSELLK.L
*	HsFLAG-Control_293_Ti_1	4.1238	0.3532	2890.6	2891.29	7039.6		1	662.7	26	6	R.EVANLVQDTLGSLPTILHVDDSLQAIK.L
*	HsFLAG-Control_293_Ti_1	3.013	0.2291	1207.51	1207.47	5306.7		1	819.8	83.3	1	R.ILSNVFCLIK.K
*	HsFLAG-Control_293_Ti_2	3.4453	0.3059	1873.89	1875.15	6742.8		2	319.2	43.8	1	R.TILEITSRPQPSSSAMR.F
*	HsFLAG-Control_293_Ti_1	4.6914	0.5072	2245.37	2244.56	6954.4		1	1247.6	61.1	2	R.FQFQDVTGEFVACLLSLLR.Q
*	HsFLAG-Control_293_Ti_1	4.9876	0.3533	2088.64	2089.48	7988.4		1	1737.4	61.1	4	R.LVANNVIITTVLYLSDALR.K
*	HsFLAG-Control_MG_293_	3.8185	0.2649	1233.41	1233.41	7377.6		1	1425.7	81.8	6	R.ESGVSLIATVTR.L
*	HsFLAG-Control_293_Ti_2	3.4468	0.2907	1415.83	1415.64	5111.8		1	855.2	77.3	2	K.IGCTVSLLNFYK.T
*	HsFLAG-Control_293_Ti_2	3.3739	0.3606	1730.38	1728.86	5297.6		1	883.9	70.8	2	R.KIAEQYESYYDYR.N
*	HsFLAG-Control_293_Ti_2	4.2067	0.2077	1534.1	1534.8	6408.1		1	1040	69.2	5	R.TSLYLVQSLPGISR.W
*	HsFLAG-Control_293_Ti_2	4.7316	0.2884	2044.38	2044.33	6770.6		1	955.3	58.8	12	R.EVVEMSPLENAIEVLENK.N
*	HsFLAG-Control_293_Ti_2	2.7662	0.1347	1107.24	1107.22	4662.9		1	852.4	87.5	3	K.TLISQCQTR.Q
*	HsFLAG-Control_MG_293_	2.7745	0.2957	1259.15	1259.32	5606.8		1	580.4	62.5	1	R.NSAPASVSPDGTR.V
*	HsFLAG-Control_293_Ti_2	3.5493	0.329	1259.98	1260.44	7213.2		1	1089.4	80	4	R.RSPLSYPAVNR.Y
*	HsFLAG-Control_MG_293_	2.8675	0.1382	1104.58	1104.25	6745.7		2	775.8	72.2	1	R.SPLSYPAVNR.Y
*	HsFLAG-Control_293_Ti_2	4.9764	0.3675	1988.5	1988.17	8121.6		1	1060.8	62.5	6	R.ERPCSAIYPTPVEPSQR.M
*	HsFLAG-Control_MG_293_	2.8078	0.21	1196.37	1197.29	5152.1		2	317.1	63.6	1	R.HTTSVSPSPAGR.S
*	HsFLAG-Control_293_Ti_2	2.5641	0.2936	1196.68	1197.29	6530.9		2	844.7	68.2	1	R.HTTSVSPSPAGR.S
*	Hs293FLP_Ti_305.2753.27	5.6418	0.4178	3872.94	3870.22	4448.8		1	593.2	25	3	K.GSVQSFTPSPVEYHSPGLISNSPVLSGSYSSGISSLSR.C
*	HsFLAG-Control_293_Ti_1	5.4011	0.4492	4172.9	4171.53	9382.6		1	916.7	23.7	3	R.CSTSETSGFENQVNEQSAPLPVPVPVPVPSYGGEEPVRK.E
*	HsFLAG-Control_293_Ti_2	1.9018	0.1465	1208.35	1209.34	3194.9		3	152.8	61.1	1	K.TPPPYSVYER.T
gi|4504183|ref|N	6	14	0.262	210	23356	5.6	U	glutathione transferase [Homo sapiens]				
*	HsHeLa_Control-MG_Ti_20	5.1778	0.4105	1887.01	1885.08	7365.5		1	1485.6	73.3	2	K.FQDGDLTLYQSNTILR.H
*	HsHeLa_Control-MG_Ti_20	4.2329	0.4337	2126.73	2127.45	4940.4		1	868.6	63.2	4	K.ALPGQLKPFETLLSQNQGGK.T
*	HsHeLa_Control-MG_Ti_20	4.3167	0.2326	2127.47	2127.45	7401.6		1	1226.4	39.5	1	K.ALPGQLKPFETLLSQNQGGK.T

*	Hs293FLP_Ti_306.2891.28	3.6957	0.4217	2130.13	2127.45	3499.8		1	547.6	57.9	2	K.ALPGQLKPFETLLSQNQGGK.T
*	HsHeLa_Control-MG_Ti_20	3.9949	0.354	1905.51	1905.16	6451.6		1	1201.7	61.8	1	K.AFLASPEYVNLPINGNGK.Q
*	HsHeLa_Control-MG_Ti_20	4.0492	0.388	2033.79	2033.29	6251.6		1	1095.1	63.9	4	K.AFLASPEYVNLPINGNGKQ.-
gi|4503475|ref|N	36	156	0.261	463	50470	9	U	eukaryotic translation elongation factor 1 alpha 2 [Homo sapiens]				
	HsGST-MOCK_Ti_105.161	5.0627	0.3697	1589.75	1589.84	7575.5		1	2410.8	82.1	28	K.THINIVVIGHVDSGK.S
	HsHeLa_Control-MG_Ti_20	2.1168	0.0805	1120.6	1121.28	4071.8		2	445.4	66.7	1	K.STTTGHLIYK.C
	HsFLAG-Control_HeLa_NE	3.2571	0.3469	1121.08	1121.28	8100.5		1	1088.6	72.2	19	K.STTTGHLIYK.C
	HsFLAG-Control_293_Ti_2	3.0545	0.334	1121.22	1121.28	8815.4		1	1167	77.8	9	K.STTTGHLIYK.C
	HsGST-MOCK_Ti_102.404	3.739	0.3542	2910.16	2911.26	7190.7		1	546.8	32.1	2	K.NMITGTSQADCAVLIVAAGVGEFEAGISK.N
	HsGST-MOCK_Ti_303.534	4.7274	0.3861	2912.77	2911.26	8229.7		1	1623.9	33	4	K.NMITGTSQADCAVLIVAAGVGEFEAGISK.N
	HsGST-MOCK_Ti_405.245	2.884	0.275	1314.28	1315.56	3797.5		1	422.1	63.6	2	R.EHALLAYTLGVK.Q
	Hs293FLP-MG_Ti_204.231	3.1474	0.3715	1314.52	1315.56	6113		1	627.9	63.6	1	R.EHALLAYTLGVK.Q
	HsFLAG-Control_HeLa_NE	3.8894	0.3764	1314.54	1315.56	7099.1		1	843.2	68.2	1	R.EHALLAYTLGVK.Q
	HsFLAG-Control_HeLa_S1	3.3633	0.3249	1314.54	1315.56	6442.6		1	682.8	63.6	1	R.EHALLAYTLGVK.Q
	HsHeLa3_Ti_105.2226.222	3.7276	0.3842	1314.65	1315.56	5432.8		1	771	68.2	6	R.EHALLAYTLGVK.Q
	HsGST-MOCK_Ti_405.244	3.0462	0.2235	1314.83	1315.56	6532.9		2	861.4	72.7	2	R.EHALLAYTLGVK.Q
	HsHeLa_Control-MG_Ti_10	3.4703	0.3478	1314.83	1315.56	5679.7		1	655	63.6	2	R.EHALLAYTLGVK.Q
	HsFLAG-Control_HeLa_S1	4.0957	0.3505	1315.1	1315.56	6796.4		1	1542.9	86.4	7	R.EHALLAYTLGVK.Q
	HsFLAG-Control_HeLa_S1	3.3605	0.3219	1315.28	1315.56	7637		1	1057.6	72.7	3	R.EHALLAYTLGVK.Q
	HsGST-MOCK_Ti_305.236	3.3426	0.261	1315.47	1315.56	3468.6		1	431.4	68.2	3	R.EHALLAYTLGVK.Q
	HsGST-MOCK_Ti_305.236	3.4506	0.2703	1315.48	1315.56	5538.1		1	959.1	81.8	7	R.EHALLAYTLGVK.Q
	HsFLAG-Control_HeLa_NE	3.1986	0.3053	1315.53	1315.56	6457.5		2	1086.8	77.3	2	R.EHALLAYTLGVK.Q
	HsFLAG-Control_HeLa_S1	3.6587	0.3109	1315.58	1315.56	6360.4		2	555.9	59.1	3	R.EHALLAYTLGVK.Q
	HsHeLa3_Ti_105.2218.221	3.3286	0.2525	1316.68	1315.56	6114.4		2	1130.5	81.8	2	R.EHALLAYTLGVK.Q
	HsHeLa_Control-MG_Ti_10	3.3203	0.2631	1316.86	1315.56	6340.9		1	1163.7	81.8	6	R.EHALLAYTLGVK.Q
	HsGST-MOCK_Ti_102.183	2.8304	0.2663	1317.2	1315.56	6447.2		1	1041.9	77.3	1	R.EHALLAYTLGVK.Q
	Hs293FLP_Ti_306.2670.26	3.2917	0.2924	1342.8	1342.62	4781.3		1	708	75	11	K.PLRLPLQDVYK.I
	HsHeLa_Control_Ti_106.31	3.1476	0.2914	1342.85	1342.62	5204.3		1	841.7	75	4	K.PLRLPLQDVYK.I
	HsHeLa3_Ti_106.2360.236	4.1661	0.2161	1343.33	1342.62	6881.1		1	1536.8	60	2	K.PLRLPLQDVYK.I
	HsGST-MOCK_Ti_102.184	4.1506	0.2292	1343.6	1342.62	6531.1		1	1475	57.5	2	K.PLRLPLQDVYK.I
	Hs293FLP-MG_Ti_204.174	1.8645	0.2129	1025.5	1026.22	4916.9		7	205.7	55	1	K.IGGIGTVPVGR.V
	Hs293FLP-MG_Ti_304.147	1.8582	0.2752	1025.51	1026.22	4087.8		7	177.1	55	1	K.IGGIGTVPVGR.V
	HsFLAG-Control_Hela_Ti_1	1.9211	0.1678	1025.52	1026.22	5051.1		4	266.3	60	1	K.IGGIGTVPVGR.V
	HsFLAG-Control_293_Ti_2	2.1086	0.236	1025.57	1026.22	5224.8		4	263.8	60	2	K.IGGIGTVPVGR.V
	HsFLAG-Control_293_Ti_2	3.6738	0.3122	1026.38	1026.22	5169		4	914.7	85	3	K.IGGIGTVPVGR.V
	HsFLAG-Control_MG_293_	3.7743	0.2639	1026.42	1026.22	5236.3		5	894.4	80	1	K.IGGIGTVPVGR.V
	HsFLAG-Control_HeLa_S1	3.4654	0.1423	1026.43	1026.22	4798.2		8	804.6	80	13	K.IGGIGTVPVGR.V
	HsHeLa3_Ti_105.1615.161	3.0073	0.2554	1027.39	1026.22	4582.7		6	778.6	80	1	K.IGGIGTVPVGR.V
*	HsHeLa3_Ti_106.2719.272	3.7293	0.1894	2575.54	2573.07	5594.7		1	496.6	41.3	1	R.VETGILRPGMVVTFAPVNITTEVK.S
	HsFLAG-Control_293_Ti_1	2.1166	0.1645	914.48	915.121	2775.6		1	178.6	75	1	R.QTVAVGVIK.N
gi|4505763|ref|N	8	16	0.261	417	44615	8.1	U	phosphoglycerate kinase 1 [Homo sapiens]				
*	HsHeLa3_Ti_103.2194.219	2.6676	0.2936	1247.73	1248.46	6158		1	560.5	65	2	K.YSLEPVAVELK.S
*	HsHeLa3_Ti_103.2195.219	3.1194	0.2164	1248.59	1248.46	3694.1		1	890.4	85	6	K.YSLEPVAVELK.S
*	HsHeLa3_Ti_103.2951.295	3.4224	0.3007	1770.24	1770.01	6174.7		1	955.6	59.4	1	K.ACANPAAGSVILLENLR.F
	HsHeLa3_Ti_106.2670.267	3.9033	0.1576	1772.39	1770.08	7084.2		1	1132	62.5	2	K.ALESPERPFLAILGGAK.V
	HsHeLa3_Ti_103.2208.221	2.6385	0.0975	1201.74	1202.46	6867		4	596.2	72.2	1	K.IQLINNMLDK.V
*	HsHeLa3_Ti_103.2667.266	4.0074	0.4699	2477.88	2478.7	2724.7		1	514.7	52.1	2	K.TGQATVASGIPAGWMGLDCGPESSK.K
*	HsHeLa3_Ti_106.3127.313	4.3862	0.4102	2108.57	2106.39	7434.4		1	894.8	55.9	1	K.QIVWNGPVGVFEWEAFAR.G
*	HsHeLa3_Ti_102.2969.296	3.1607	0.1704	1098.39	1098.29	6031.7		2	1083.9	75	1	K.VLPGVDALSNI.-

gi|33239451|ref|N		4	14	0.261	261	28769	4.7	U	proliferating cell nuclear antigen [Homo sapiens]				
gi|4505641|ref|NI		4	14	0.261	261	28769	4.7	U	proliferating cell nuclear antigen [Homo sapiens]				
	HsFLAG-Control_293_Ti_2	2.8521	0.1951	1366.81	1366.63	8779.4			1	789.7	58.3	1	R.NLAMGVNLTSMSK.I
	HsHeLa_Control-MG_Ti_20	5.1097	0.3937	2076.54	2076.22	7084.7			1	1415.9	61.1	8	R.AEDNADTLALVFEAPNQEK.V
	HsHeLa3_Ti_102.3375.337	4.1306	0.3896	2468.65	2466.77	4724.2			1	392.8	42.5	1	K.LMDLDVEQLGIPEQEYSCVVK.M
	Hs293FLP_TREX_Ti_104.1	4.0942	0.4064	1584.81	1585.76	4665			1	995	71.4	4	R.DLSHIGDAVVISCAK.D
gi|4502565|ref|NI		5	14	0.261	268	28316	5.2	U	calpain, small subunit 1 [Homo sapiens]				
gi|51599151|ref|N		5	14	0.261	268	28316	5.2	U	calpain, small subunit 1 [Homo sapiens]				
	HsFLAG-Control_HeLa_S1	3.2429	0.2686	2449.11	2448.78	10209.7			3	568.2	32.6	2	R.ILGGVISAISEAAAQYNPEPPPPR.T
	HsFLAG-Control_HeLa_S1	5.1388	0.5263	2449.75	2448.78	8852.2			1	1304.6	34.8	1	R.ILGGVISAISEAAAQYNPEPPPPR.T
	HsHeLa3_Ti_103.4710.471	6.3246	0.4897	2524.98	2524.91	7186.4			1	1716	59.1	7	R.LFAQLAGDDMEVSATELMNILNK.V
	HsHeLa3_Ti_102.1675.167	2.9482	0.2233	1143.09	1142.18	4526.2			2	870.5	83.3	2	K.TDGFGIDTCR.S
	HsHeLa3_Ti_102.1681.168	3.3344	0.4459	1342.58	1342.52	5842			1	601.2	62.5	2	R.SMVAVMDSDTTGK.L
gi|4507791|ref|NI		2	4	0.257	183	20900	7.7	U	ubiquitin-conjugating enzyme E2M [Homo sapiens]				
*	HsFLAG-Control_HeLa_NE	3.8067	0.2958	1888.46	1888	5270			1	655.2	63.3	3	K.TCDISFSDPDDLLNFK.L
*	HsFLAG-Control_HeLa_S1	3.9234	0.1784	3660.75	3661.19	7672.9			1	575	23.3	1	R.EDWKPVLTINSIIYGLQYLFLEPNPEDPLNK.E
gi|5032057|ref|NI		2	5	0.257	105	11740	7.2	U	S100 calcium binding protein A11 (calgizzarin) [Homo sapiens]				
*	HsHeLa3_Ti_104.3125.312	3.4736	0.2526	1308.73	1308.53	6685.1			1	1705.1	85	1	R.CIESLIAVFQK.Y
*	HsHeLa3_Ti_105.4138.413	4.6065	0.4041	1851.71	1851.12	6563.4			1	1619.6	76.7	4	K.TEFLSFMNTELAAFTK.N
gi|21328448|ref|N		4	21	0.256	246	28082	4.8	U	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypep				
gi|4507949|ref|NI		4	21	0.256	246	28082	4.8	U	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypep				
	HsFLAG-Control_HeLa_NE	4.9052	0.3502	1599.02	1599.65	7326.2			1	1394.3	73.1	8	K.AVTEQGHELSNEER.N
	HsHeLa3_Ti_102.1369.136	2.5882	0.2541	1182.57	1183.26	5609.1			1	592.1	65	2	R.YLSEVASGDNK.Q
	HsFLAG-Control_HeLa_S1	4.877	0.4949	2160.24	2160.3	9388.3			1	842.3	47.2	8	K.QTTVSNSQQAYQEAFEISK.K
	HsFLAG-Control_HeLa_S1	4.6071	0.4862	2159.93	2160.3	8158.7			1	1604	61.1	3	K.TAFDEAIAELDTLNEESYK.D
gi|24234688|ref|N		12	47	0.255	679	73681	6.2	U	heat shock 70kDa protein 9B precursor [Homo sapiens]				
*	HsGST-MOCK_Ti_302.274	2.9292	0.1851	2081.13	2079.34	6853.9			2	473.7	45	1	K.GAVVGIDLGTTNSCVAVMEGK.Q
*	HsGST-MOCK_Ti_302.198	3.6786	0.448	1450.74	1451.58	4260			1	732.1	73.1	4	R.TTPSVVAFTADGER.L
*	HsFLAG-Control_MG_293_	5.0887	0.4515	1725.99	1725.9	11174.7			1	1144.2	60.7	10	K.RQAVTNPNNTFYATK.R
*	HsGST-MOCK_Ti_305.339	3.5852	0.203	1554.56	1554.89	6958.4			1	1500.7	76.9	3	K.LYSPSQIGAFVLMK.M
*	Hs293FLP_TREX_Ti_102.1	3.7357	0.3234	1244.77	1243.41	4761.9			1	957.2	77.3	5	K.DAGQISGLNVLR.V
*	HsGST-MOCK_Ti_302.317	5.3077	0.5153	2056.68	2057.18	6344.2			1	968.3	58.3	14	K.STNGDTFLGGEDFDQALLR.H
*	HsHeLa_Control-MG_Ti_10	3.342	0.2842	1363.65	1362.57	5169.1			1	967.1	77.3	2	R.AQFEGIVTDLIR.R
*	HsGST-MOCK_Ti_302.276	3.5814	0.1915	1447.35	1447.69	5582.2			1	1275	73.1	1	K.SDIGEVILVGGMTR.M
*	HsGST-MOCK_Ti_303.224	3.852	0.2342	1291.29	1291.45	7825.9			1	1574.7	85	1	K.VQQTVQDLFGR.A
*	Hs293FLP_TREX_Ti_105.1	2.7979	0.1864	1674.29	1674.9	6864			1	663.3	57.1	2	K.VQQTVQDLFGRAPSK.A
*	HsHeLa_Control-MG_Ti_10	3.6207	0.2843	1595.25	1593.95	3729.1			1	623.2	64.3	3	K.LLGQFTLIGIPPAPR.G
*	HsGST-MOCK_Ti_302.243	5.3014	0.453	2418.95	2419.71	9181.3			1	1298.1	52.4	1	R.EQQIVIQSSGGLSKDDIENMVK.N
gi|23111030|ref|N		3	7	0.253	162	18885	8.4	U	sorting nexin 12 [Homo sapiens]				
*	HsFLAG-MOCK_300mM_T	4.5804	0.2979	3761.81	3761.19	10014.3			1	836.1	23.5	2	R.RLNSKPQDLTDAYGPPSNFLEIDIFNPQTVGVGR.A
*	HsFLAG-Control_HeLa_NE	5.4798	0.4714	3602.9	3605	10241.6			1	1025.5	24.2	4	R.LNSKPQDLTDAYGPPSNFLEIDIFNPQTVGVGR.A
	HsFLAG-Control_HeLa_NE	2.2128	0.1182	832.59	833.018	4619.6			3	399.9	75	1	R.TNLPIFK.L
gi|27363484|ref|N		9	17	0.25	619	67498	5.2	U	E74-like factor 1 (ets domain transcription factor) [Homo sapiens]				
*	HsHeLa3_Ti_102.1185.118	4.5983	0.4378	1435.53	1434.5	4693.2			1	1296.2	84.6	2	K.YADSPGASSPEQPK.R
*	HsHeLa3_Ti_102.2505.250	3.5775	0.371	3088.02	3088.18	5650.5			1	618.5	37.5	1	K.DLIYINDEDPSSSIESSDPSLSSSATSNR.N
*	HsHeLa3_Ti_106.1844.184	2.4805	0.1712	1229.72	1230.41	5078.6			4	448.9	62.5	1	K.GGATTVLKPGNSK.A
*	HsHeLa3_Ti_105.1570.157	4.2587	0.4203	1887.86	1888.13	5200.3			1	856	58.8	2	R.TVHVVQPVQAVPEGEAAR.T
*	HsHeLa3_Ti_102.1782.178	2.8069	0.2301	1898.68	1898.05	10014.9			1	589.4	40.6	1	R.TSTMQDETLNSSVQSIR.T
*	HsHeLa3_Ti_105.1886.188	2.2122	0.0979	1591.84	1592.88	2901.5			3	131.8	46.4	2	R.TIQAPTQVPVVVSPR.N

*	HsHeLa3_Ti_105.1894.189	3.7932	0.3377	1592.61	1592.88	5335.6		1	896	67.9	4	R.TIQAPTQVPVVVSPR.N
*	HsHeLa3_Ti_106.2530.253	3.6015	0.4191	3194.4	3195.55	5779.2		8	227.5	25	2	R.NQQLHTVTLQTVPLTTVIASTDPSAGTGSQK.F
*	HsHeLa3_Ti_106.2250.225	4.0554	0.3405	1836.32	1835.15	3653.7		1	390.2	50	2	R.SSQLVAHPPGTVITSVIK.T
gi|8922789|ref|N	8	41	0.249	357	41739	6.2	U	paraspeckle protein 1 [Homo sapiens]				
*	HsHeLa_Control_Ti_102.30	3.5697	0.3497	1839.78	1839.05	3353.7		1	710.6	73.3	6	R.LFVGNLPTDITEEDFK.R
*	Hs283FLP_Ti_102.1735.17	3.9393	0.29	1312.48	1311.44	3967.6		1	831.9	85	3	R.YGEPSEVFINR.D
*	HsFlag1P_Ti_104.3420.342	5.3161	0.3377	1686.48	1686.99	6896.3		1	1713.1	73.3	4	R.TLAEIAKAELDGTILK.S
*	HsHeLa_Control-MG_Ti_20	2.4594	0.1527	1116.34	1116.31	4102.7		1	538.8	70	5	R.FATHGAALTVK.N
*	HsHeLa_Control_Ti_103.39	5.4072	0.448	2532.82	2533.84	8462.5		1	1437	52.3	10	K.NLSPVVSNELLEQAFSQFGPVEK.A
*	Hs293FLP_Ti_302.3986.39	5.1889	0.3989	2533.3	2533.84	7914		1	1280.2	50	4	K.NLSPVVSNELLEQAFSQFGPVEK.A
*	Hs283FLP_Ti_104.3241.32	3.9085	0.3429	2534.73	2533.84	7130.7		1	1014.3	33	2	K.NLSPVVSNELLEQAFSQFGPVEK.A
*	HsHeLa_Control-MG_Ti_10	3.7086	0.3118	1290.76	1290.51	5000.4		1	1073.4	81.8	7	K.GFVEFAAKPPAR.K
gi|12056465|ref|N	5	15	0.249	321	33784	10.2	U	fibrillarin [Homo sapiens]				
*	Hs293FLP-MG_Ti_204.157	3.3432	0.2344	1667.6	1667.82	6549.7		1	731.9	61.5	1	K.RVSISEGDDKIEYR.A
	Hs283FLP_Ti_106.2291.22	2.811	0.2422	1520.94	1519.83	6650.3		4	530.9	53.6	2	K.LAAAILGGVDQIHIK.P
*	Hs293FLP_Ti_306.2635.26	5.1735	0.4145	1874.91	1873.25	6428.9		1	1569.7	66.7	4	K.LAAAILGGVDQIHIKPGAK.V
*	HsHeLa_Control-MG_Ti_20	7.1087	0.465	3416.23	3418.83	8797.3		1	2261.4	34.4	7	K.VLYLGAASGTTVSHVSDIVGPDGLVYAVEFSHR.S
*	HsHeLa_Control-MG_Ti_20	4.4997	0.3817	1536.67	1534.8	8037.3		1	2088.2	80.8	1	R.DHAVVVGVYRPPPK.V
gi|62420888|ref|N	8	22	0.248	492	54341	6.3	U	dipeptidyl peptidase 7 preproprotein [Homo sapiens]				
*	HsHeLa_Control-MG_Ti_20	3.4213	0.2527	1113.33	1113.31	7019.8		3	1221.1	83.3	3	R.GALLVFAEHR.Y
	HsHeLa_Control-MG_Ti_20	4.6734	0.3665	2226.72	2227.52	7173.3		1	1041.6	36.8	5	R.GHTELLTVEQALADFAELLR.A
	HsHeLa_Control-MG_Ti_20	6.1305	0.5256	2226.76	2227.52	8400.5		1	2554.8	71.1	6	R.GHTELLTVEQALADFAELLR.A
	HsHeLa_Control-MG_Ti_20	4.6441	0.5085	2914.63	2914.34	6039.9		1	963	48.2	3	K.YPHLVAGALAASAPVLAVAGLGDSNQFFR.D
	HsHeLa_Control-MG_Ti_20	2.5488	0.2689	1294.35	1294.36	7508		3	655.1	63.6	1	R.DVTADFEGQSPK.C
	HsHeLa_Control-MG_Ti_20	3.6251	0.2452	1400.41	1398.56	7707.1		1	1838.8	81.8	2	K.DLFLQGAYDTVR.W
	HsHeLa_Control-MG_Ti_20	4.9421	0.4123	1935.25	1935.98	5590.1		1	1116.6	67.6	1	R.LYHSCADPTGCGTGPDAR.A
	HsHeLa_Control-MG_Ti_20	3.4405	0.1877	2133.56	2131.36	7904		1	1104.6	52.5	1	R.AASNIIFSNGNLDPWAGGGIR.R
gi|5453603|ref|N	15	53	0.245	535	57488	6.4	U	chaperonin containing TCP1, subunit 2 [Homo sapiens]				
*	HsFLAG-Control_HeLa_S1	5.3655	0.2547	1518.27	1518.84	6651.2		1	1518.8	75	11	R.LTSFIGAIAIGDLVK.S
*	HsFLAG-Control_HeLa_S1	4.6328	0.481	2287.51	2289.5	9878		1	1501.7	54.8	1	R.VQDDEVGDGTTSVTVLAAELLR.E
*	HsFLAG-Control_HeLa_S1	5.1171	0.46	2288.32	2289.5	8497		1	1344.1	54.8	1	R.VQDDEVGDGTTSVTVLAAELLR.E
*	HsFLAG-Control_HeLa_S1	5.5341	0.3774	2288.48	2289.5	10683.6		1	2192.4	41.7	3	R.VQDDEVGDGTTSVTVLAAELLR.E
*	HsFLAG-Control_HeLa_S1	4.088	0.3266	2288.72	2289.5	9855.9		1	1101.8	34.5	1	R.VQDDEVGDGTTSVTVLAAELLR.E
*	HsFLAG-Control_HeLa_NE	5.2395	0.4922	2288.82	2289.5	7097.2		1	1538.8	59.5	11	R.VQDDEVGDGTTSVTVLAAELLR.E
*	HsFLAG-Control_HeLa_NE	4.8632	0.307	2289.6	2289.5	8789.5		3	1360.5	36.9	2	R.VQDDEVGDGTTSVTVLAAELLR.E
*	HsFLAG-Control_HeLa_S1	5.4686	0.4188	2289.81	2289.5	7393		1	1221.8	54.8	5	R.VQDDEVGDGTTSVTVLAAELLR.E
*	HsFLAG-Control_HeLa_NE	4.0232	0.3127	1657.4	1657.78	7946.4		1	1564.1	66.7	2	R.EALLSSAVDHGSDEVK.F
*	HsFLAG-Control_HeLa_S1	3.1597	0.2403	1252.61	1252.46	6761.6		1	815.8	68.2	3	K.GSGNLEAIHIIK.K
*	HsFLAG-Control_HeLa_S1	2.72	0.3598	2043.98	2042.29	11257.5		1	917.9	47.2	1	K.KLGGSLADSYLDEGFLLDK.K
*	HsFLAG-Control_HeLa_NE	4.9889	0.4497	1913.5	1914.12	7094.3		1	1593	67.6	5	K.LGGSLADSYLDEGFLLDK.K
*	HsFLAG-Control_HeLa_S1	5.4863	0.5067	2098.36	2098.4	7438.9		1	1072.8	55.3	2	R.LALVTGGEIASTFDHPELVK.L
*	HsFLAG-Control_HeLa_S1	4.0485	0.1672	1332.18	1331.43	6934.2		1	1221.8	77.3	2	R.GATQQILDEAER.S
*	HsFLAG-Control_HeLa_S1	4.3039	0.2907	1584.83	1583.87	9663.3		1	1903.1	75	3	R.QVLLSAAEAAEVILR.V
gi|89061568|ref|X	6	14	0.245	367	39994	8.4	U	PREDICTED: similar to Ig gamma-2 chain C region [Homo sapiens]				
	HsHeLa3_Ti_106.2298.229	2.9503	0.2269	1288.79	1288.46	3622.9		8	436.8	63.6	1	K.GPSVFPLAPCSR.S
	HsHeLa3_Ti_103.1803.180	4.0268	0.3434	1426.13	1424.56	8008.5		1	1242.1	69.2	1	R.STSESTAALGCLVK.D
*	HsHeLa3_Ti_106.2646.264	4.9068	0.3289	1795.25	1795.09	7269.1		2	1221.4	63.3	4	R.VVSVLTVVHQDWLNGK.E
	HsHeLa3_Ti_104.1648.164	2.7077	0.2801	1907.07	1906.16	3939.2		3	306.7	50	2	R.EPQVYTLPPSREEMTK.N

	HsHeLa3_Ti_103.1878.187	2.5117	0.1298	1161.73	1162.34	4608.6	9	333.8	66.7	1	K.NQVSLTCLVK.G
	HsHeLa3_Ti_102.3109.310	3.9392	0.2322	2545.91	2545.68	7147	1	1278.7	54.8	5	K.GFYPSDIAVEWESNGQPENNYK.T
gi|24497583|ref|N	5	6	0.245	323	36853	7.9	U	aldo-keto reductase family 1, member C3 [Homo sapiens]			
	HsHeLa_Control-MG_Ti_20	4.9003	0.4852	2179.71	2180.39	7914.1	1	1927.1	69.4	1	R.HIDSAHLYNNEEQVGLAIR.S
	HsHeLa_Control-MG_Ti_20	2.9992	0.1893	1158.57	1159.28	8800.5	1	1327.5	87.5	2	K.REDIFYTSK.L
	HsHeLa_Control-MG_Ti_20	3.6036	0.4104	2236.46	2237.57	7731.6	1	713.5	50	1	R.WVDPNSPVLLEDPVLCALAK.K
	HsHeLa_Control-MG_Ti_20	2.6218	0.1304	1011.47	1011.26	4836.1	8	501.6	75	1	K.RTPALIALR.Y
*	HsHeLa_Control-MG_Ti_20	4.215	0.3578	2667.46	2668.75	8686.6	1	1639.2	59.5	1	R.NLHYFNSDSFASHPNYPYSDEY.-
gi|4503285|ref|N	7	17	0.245	323	36735	7.5	U	aldo-keto reductase family 1, member C2 [Homo sapiens]			
gi|45446745|ref|N	7	17	0.245	323	36735	7.5	U	aldo-keto reductase family 1, member C2 [Homo sapiens]			
	HsHeLa_Control-MG_Ti_20	2.9992	0.1893	1158.57	1159.28	8800.5	1	1327.5	87.5	2	K.REDIFYTSK.L
	HsHeLa_Control-MG_Ti_20	3.5613	0.3033	3126.24	3127.65	8920.1	1	466.9	32.7	4	K.NLQLDYVDLYLIHFPVSVKPGEEVIPK.D
	HsHeLa_Control-MG_Ti_20	5.8065	0.4856	3126.75	3127.65	6812.3	1	1504.3	35.6	6	K.NLQLDYVDLYLIHFPVSVKPGEEVIPK.D
	HsHeLa_Control-MG_Ti_20	5.0274	0.436	3670.03	3671.19	7067.5	1	803.5	25.8	2	K.NLQLDYVDLYLIHFPVSVKPGEEVIPKDENGK.I
	HsHeLa_Control-MG_Ti_20	2.7478	0.1927	1131.26	1131.24	5414.4	2	790.2	77.8	1	K.SIGVSNFNHR.L
	HsHeLa_Control-MG_Ti_20	2.6218	0.1304	1011.47	1011.26	4836.1	8	501.6	75	1	K.RTPALIALR.Y
	HsHeLa_Control-MG_Ti_20	3.2941	0.2454	2224.39	2223.44	8018.3	1	778.3	47.2	1	R.YLTLDIFAGPPNYPFSDEY.-
gi|5032051|ref|N	5	10	0.245	151	16273	10.1	U	ribosomal protein S14 [Homo sapiens]			
gi|68160922|ref|N	5	10	0.245	151	16273	10.1	U	ribosomal protein S14 [Homo sapiens]			
gi|68160915|ref|N	5	10	0.245	151	16273	10.1	U	ribosomal protein S14 [Homo sapiens]			
	Hs293FLP_TREX_Ti_105.2	2.6271	0.2763	1095.18	1095.33	4083.8	3	589.4	77.8	1	K.ELGITALHIK.L
	Hs293FLP_TREX_Ti_104.1	3.448	0.2489	1055.06	1055.18	6598.1	1	1286.1	85	3	K.TPGPGAQSALR.A
	HsFLAG-Control_293_Ti_2	2.0317	0.1701	1055.36	1055.18	2871.1	4	127.9	55	1	K.TPGPGAQSALR.A
	Hs293FLP-MG_Ti_105.119	3.1705	0.331	1055.6	1055.18	6369.1	6	654.2	65	4	K.TPGPGAQSALR.A
	Hs293FLP_TREX_Ti_104.1	3.0484	0.2968	1756.71	1756.95	6353.1	1	709.8	56.7	1	K.IGRIEDVTPIPSDSTR.R
gi|33457332|ref|N	9	13	0.243	606	63877	8.5	U	RAVER1 [Homo sapiens]			
*	HsHeLa3_Ti_103.3360.336	3.9154	0.2604	2345.54	2343.55	6853.6	1	742	47.5	2	R.GLPGDVTNQEVHDLLSDYELK.Y
*	HsHeLa3_Ti_105.3322.332	3.6561	0.1788	2546.37	2546.8	5149.3	2	786.5	34.8	1	K.GTAFVTLLNGEQAEAAINAFHQSR.L
*	HsHeLa3_Ti_105.3332.333	5.1732	0.4343	2547.86	2546.8	8546.9	1	1543.8	50	2	K.GTAFVTLLNGEQAEAAINAFHQSR.L
*	HsFLAG-MOCK_300mM_T	3.1702	0.1786	1353.03	1352.62	4752.6	4	793.8	66.7	2	R.AKSDLLGKPLGPR.T
*	HsFLAG-MOCK_300mM_T	3.4673	0.4168	2280.87	2280.59	9642.2	1	616.9	39.5	1	R.TLYVHWTDAGQLTPALLHSR.C
*	HsFLAG-MOCK_300mM_T	5.6805	0.3339	2281.8	2280.59	4437.6	1	1307.7	47.4	1	R.TLYVHWTDAGQLTPALLHSR.C
*	HsHeLa3_Ti_106.2228.223	5.4886	0.4529	2389.98	2389.6	5027.5	1	1016.2	57.1	1	R.ALSAVHSPTFCQLACGQDGQLK.G
*	HsHeLa3_Ti_106.3022.302	3.6752	0.172	3311.37	3309.59	6008.4	1	567.4	23.3	1	K.GFAVLEYETAEMAEEAQQQADGLSLGGSHLR.V
*	HsHeLa3_Ti_106.2947.294	4.2814	0.275	1616.58	1615.93	7198.5	1	2109.5	73.3	2	R.SMLAALIAAQATALNR.G
gi|57863257|ref|N	11	51	0.243	556	60344	6.1	U	T-complex protein 1 isoform a [Homo sapiens]			
*	HsFLAG-Control_MG_293_	4.293	0.3965	1517.41	1517.78	10541.9	1	2136.4	78.6	1	R.SQNVMAAASIANIVK.S
*	HsFLAG-Control_HeLa_S1	4.382	0.4322	1815.87	1816.1	7640.8	1	1483.5	67.6	4	K.EVGDGTTSVVIIAAELLK.N
*	HsFLAG-Control_HeLa_S1	4.3072	0.391	1764.35	1763.95	7623.7	1	1150.4	67.9	3	R.YINENLIVNTDELGR.D
	HsHeLa_Control-MG_Ti_20	2.7377	0.1445	1923.75	1924.25	7914.3	8	465.8	43.8	1	K.LGVQVVITDPEKLDQIR.Q
	Hs293FLP_TREX_Ti_102.2	3.7157	0.1836	1234.28	1232.43	4032.3	2	856.4	88.9	2	R.ICDDELILIK.N
	HsFLAG-Control_HeLa_S1	2.8846	0.2645	1142.43	1142.31	6093.3	1	845.9	77.8	1	R.SLHDALCVVK.R
	HsFLAG-Control_HeLa_NE	4.546	0.4054	2354.59	2354.71	4705.5	1	847.8	54.5	18	R.SLLVIPNTLAVNAAQDSTDLVAK.L
	HsFLAG-Control_293_Ti_2	4.8314	0.4184	2355.2	2354.71	5823.2	1	672.7	45.5	16	R.SLLVIPNTLAVNAAQDSTDLVAK.L
	HsFLAG-Control_HeLa_S1	5.5299	0.4921	2355.4	2354.71	8122	1	1722.5	40.9	2	R.SLLVIPNTLAVNAAQDSTDLVAK.L
	HsFLAG-Control_HeLa_S1	3.7923	0.2473	1412.11	1412.51	6624.7	1	1026	72.7	2	R.AFHNEAQVNPER.K
	Hs293FLP_Ti_303.1401.14	3.2441	0.313	1572.49	1572.59	7796.7	1	1348.4	67.9	1	K.HGSYEDAVHSGALND.-
gi|38455427|ref|N	9	35	0.243	539	57924	7.8	U	chaperonin containing TCP1, subunit 4 (delta) [Homo sapiens]			
	HsFLAG-Control_HeLa_S1	1.9582	0.0864	837.53	837.951	6829.7	1	621.7	71.4	1	R.FSNISAAK.A

*	HsFLAG-Control_HeLa_S1	2.7041	0.1351	1150.37	1151.37	5981.6		1	1227.1	88.9	1	K.QMQVLHPAAR.M
*	HsFLAG-Control_HeLa_S1	3.1262	0.305	2621.8	2622.85	10125.8		2	464.1	32	1	K.AQDIEAGDGTTSVVIIAGSLLDSCTK.L
*	Hs293FLP_TREX_Ti_106.2	3.1994	0.3397	1457.43	1457.67	3792.4		1	500.1	70.8	2	K.GIHPTIISESFQK.A
*	HsFLAG-Control_HeLa_NE	4.0723	0.4088	1479.34	1479.63	8476.3		1	1445.7	73.1	5	R.ETLLNSATTSLNSK.V
*	HsFLAG-Control_HeLa_NE	4.1746	0.4618	1358.55	1358.54	8187		1	1778.3	83.3	10	K.VIDPATATSVDLR.D
*	HsFLAG-Control_HeLa_S1	4.0617	0.3375	2062.97	2061.3	7353.8		1	782.2	50	2	K.LGGTIDDCELVEGLVLTQK.V
*	HsFLAG-Control_HeLa_NE	3.2128	0.1609	1349.34	1347.61	6048.2		9	660.4	63.6	2	K.IGLIQFCLSAPK.T
*	HsFLAG-Control_HeLa_S1	4.3777	0.3891	1552.91	1551.83	4850.5		1	983.3	73.3	11	R.ALIAGGGAPEIELALR.L
gi|38045913|ref|N	3	14	0.243	177	19654	5.6	U	non-metastatic cells 1, protein (NM23A) expressed in isoform a [Homo sapiens]				
gi|4557797|ref|N	3	14	0.283	152	17149	6.2	U	non-metastatic cells 1, protein (NM23A) expressed in isoform b [Homo sapiens]				
	HsHeLa_Control-MG_Ti_20	3.8743	0.2064	1345.49	1345.59	6946.5		6	915.1	68.2	8	R.TFIAIKPDGVQR.G
	HsF-IP-293_Ti_205.1656.1	3.1597	0.1115	1786.66	1787.04	7174.9		3	745.9	56.2	2	R.VMLGETNPADSKPGTIR.G
	Hs293FLP_TREX_Ti_103.1	3.8718	0.3198	1486.31	1486.58	5491.1		1	1082.2	76.9	4	R.NIIHGSDSVESAEK.E
gi|73622130|ref|N	6	25	0.243	152	16932	8.2	U	BolA-like protein 2 isoform a [Homo sapiens]				
	HsHeLa_Control-MG_Ti_20	5.0862	0.4298	1870.7	1870.97	8452.4		1	1790	73.3	11	R.DLEAEHVEVEDTTLNR.C
	HsFLAG-MOCK_300mM_T	3.9682	0.3119	2512.48	2513.83	7248.1		1	792.9	47.5	3	R.HRLVNACLAEELPHIHAFEQK.T
	HsFLAG-MOCK_300mM_T	5.4896	0.2457	2515.02	2513.83	5986.6		1	1714.4	46.2	2	R.HRLVNACLAEELPHIHAFEQK.T
	HsHeLa_Control-MG_Ti_20	4.9583	0.3283	2219.68	2220.5	11142.3		1	2076.5	61.1	4	R.LVNACLAEELPHIHAFEQK.T
	Hs293FLP_Ti_305.2389.23	4.8302	0.4118	2221.65	2220.5	9190.9		1	1768.2	61.1	4	R.LVNACLAEELPHIHAFEQK.T
	HsHeLa_Control-MG_Ti_20	3.9445	0.2823	2221.97	2220.5	4266.4		1	653.4	40.3	1	R.LVNACLAEELPHIHAFEQK.T
gi|4506631|ref|N	3	6	0.243	115	12784	9.6	U	ribosomal protein L30 [Homo sapiens]				
*	Hs293FLP_TREX_Ti_104.1	2.432	0.2359	1353.45	1354.6	2863.5		7	114.3	54.5	1	K.LVILANNCPALR.K
*	HsGST-MOCK_Ti_305.222	4.2408	0.3329	1354.47	1354.6	8375		1	1791.4	86.4	4	K.LVILANNCPALR.K
*	HsFLAG-MOCK_300mM_T	3.8343	0.2431	1760.2	1758.98	6021.9		1	1246.1	73.3	1	R.VCTLAIIDPGDSDIIR.S
gi|4506597|ref|N	3	8	0.242	165	17819	9.4	U	ribosomal protein L12 [Homo sapiens]				
gi|89032011|ref|	3	8	0.211	190	20667	10.1	U	PREDICTED: similar to 60S ribosomal protein L12 [Homo sapiens]				
gi|89031330|ref|	3	8	0.211	190	20667	10.1	U	PREDICTED: similar to 60S ribosomal protein L12 [Homo sapiens]				
	Hs293FLP_TREX_Ti_102.1	4.1007	0.325	1419.49	1419.54	4967.7		1	1171.6	75	1	R.CTGGEVGATSALAPK.I
	Hs293FLP_TREX_Ti_105.1	2.9049	0.2	882.38	882.091	3455.5		4	528.4	87.5	6	K.IGPLGLSPK.K
	Hs293FLP_TREX_Ti_102.1	4.3368	0.4754	1676.56	1676.79	6765.5		1	1073.1	63.3	1	K.EILGTAQSVGCNVDGR.H
gi|17505234|ref|N	8	15	0.241	440	49324	9.9	U	nucleolar and spindle associated protein 1 isoform 2 [Homo sapiens]				
*	HsGST-MOCK_Ti_102.115	3.1361	0.2559	1853.65	1853.99	5438.2		2	595.2	56.7	2	K.TVRVDPDSQQNHSEIK.I
*	HsGST-MOCK_Ti_404.171	4.8475	0.4363	2120.73	2121.19	5516.1		1	693.5	55.3	1	K.VPSPPDEHQEAENAVSSGNR.D
*	HsGST-MOCK_Ti_103.131	4.0084	0.2913	1515.49	1515.64	7673.6		1	1082	77.3	3	K.HFEEHNSMNELK.Q
	HsGST-MOCK_Ti_404.184	2.8785	0.2341	1159.22	1159.33	7847.6		1	822.5	70	1	R.LSVASTPISQR.R
	HsGST-MOCK_Ti_406.207	2.6612	0.3517	1140.64	1141.27	3263.2		1	330.3	63.6	3	K.SAHVTVSGGTPK.G
	HsFLAG-MOCK_300mM_T	4.7189	0.4608	2033.82	2034.28	6140.9		1	1082.8	60	2	K.SAHVTVSGGTPKGEAVLGTHK.L
	HsGST-MOCK_Ti_403.157	3.7156	0.3913	1389.52	1390.53	9306.4		1	1529.7	75	2	K.LTTEATQTPVSNK.K
	HsGST-MOCK_Ti_104.138	2.6541	0.2335	1512.53	1512.71	3788.1		7	294.8	54.2	1	K.ASLSRPLNYEPHK.G
gi|89030021|ref|	5	7	0.241	261	28492	7.9	U	PREDICTED: far upstream element (FUSE) binding protein 3 isoform 2 [Homo sapiens]				
gi|89030637|ref|	5	7	0.241	261	28492	7.9	U	PREDICTED: similar to Far upstream element binding protein 3 (FUSE binding protein 3)				
	HsFLAG-Control_HeLa_NE	3.0604	0.1305	1407	1406.62	9386		8	897.6	68.2	1	R.TVITEEFKVPDK.M
	HsHeLa3_Ti_106.2111.211	2.8021	0.1606	1070.66	1070.28	4007.8		6	512.7	81.2	1	K.RLLGQIVDR.C
	HsHeLa3_Ti_104.2708.270	4.7219	0.2862	2568.13	2568.8	7995		1	1007.3	47.8	2	R.NGPGFHNDIDSNSTIQEILIPASK.V
	HsHeLa3_Ti_103.1956.195	4.8006	0.3346	1574.04	1573.86	6484		1	1743.8	78.6	2	K.MVMIQDGPLPTGADK.P
	HsHeLa3_Ti_105.2026.202	3.6505	0.3227	1941.72	1940.33	5333.7		3	404.6	47.1	1	K.MVMIQDGPLPTGADKPLR.I
gi|57863301|ref|N	26	84	0.24	1506	164886	8.2	U	CLIP-associating protein 2 [Homo sapiens]				
*	Hs283FLP_Ti_102.1639.16	3.3637	0.3582	2216.72	2217.27	4590.7		1	646.3	50	6	K.SFDDEESVDGNRPSSAASAFK.V
*	Hs293FLP-MG_Ti_202.280	3.8531	0.3886	1584.63	1584.77	3729		1	531.6	69.2	3	K.AFTDVPSIQIYSSR.E

*	Hs293FLP-MG_Ti_205.338	4.8055	0.4008	2098.68	2097.35	8760.2		1	1326.3	58.8	1	R.SLLVAGAAQYDCFFQHLR.L
*	Hs293FLP-MG_Ti_204.235	3.8465	0.4792	1713.58	1713.94	8190.2		1	1186.6	60	1	R.EACITVAHLSTVLGNK.F
*	Hs293FLP_TREX_Ti_103.1	3.0545	0.1274	1348.56	1347.56	3695.9		1	558.1	77.3	7	R.LIPLITSNCTSK.S
*	Hs293FLP_Ti_306.3795.37	4.0121	0.3192	2392.93	2392.67	6767.5		1	961.8	55.6	1	R.SFEFLDLLLQEWQTHSLER.H
*	Hs283FLP_Ti_105.1410.14	2.1317	0.154	1080.62	1081.3	5020.1		9	634.6	72.2	1	R.HAAVLVETIK.K
*	Hs293FLP_Ti_304.1522.15	2.3557	0.1045	1080.66	1081.3	4378.1		2	646	72.2	2	R.HAAVLVETIK.K
*	HsF-IP-293-MG_Ti_105.15	3.0448	0.2681	1082.06	1081.3	5523.1		1	1045	83.3	2	R.HAAVLVETIK.K
*	Hs283FLP_Ti_104.1412.14	2.736	0.2374	1082.34	1081.3	5455.9		1	680.2	77.8	1	R.HAAVLVETIK.K
*	Hs283FLP_Ti_106.1917.19	4.0726	0.3753	1209.61	1209.48	5619.1		1	1395.8	90	2	R.HAAVLVETIKK.G
*	Hs293FLP-MG_Ti_204.253	4.8873	0.3514	2324.88	2325.5	5794.8		1	924.3	55.3	9	R.NHFPGEAETLYNSLEPSYQK.S
*	HsFLAG-Control_293_Ti_2	4.2322	0.3066	1728.81	1728.81	6848.2		1	1264.1	66.7	4	R.SSSSSQESLNRPFSSK.W
*	Hs283FLP_Ti_103.1186.11	4.9083	0.3422	1375.46	1375.48	7089.2		1	1767.1	76.9	4	R.SRSDIDVNAAAGAK.A
*	HsFLAG-Control_293_Ti_2	4.6198	0.4402	1621.27	1620.84	8707.9		1	1185.4	63.3	3	R.VLTTTALSTVSSGVQR.V
*	HsF-IP-293-MG_Ti_102.10	2.6974	0.2254	1017.23	1017.17	4152.6		9	529.1	72.2	1	R.VLVNSASAQK.R
*	Hs283FLP_Ti_104.1711.17	3.9444	0.4584	1681.78	1681.85	4878.4		1	1118.5	73.3	9	R.SFQPLGPGYGISQSSR.L
*	Hs293FLP-MG_Ti_202.349	4.695	0.4013	1731.5	1731.9	10100		1	2287.5	71.9	6	R.VLNTGSDVEEAVADALK.K
*	HsF-IP-293-MG_Ti_102.23	3.3721	0.2674	1369.52	1369.52	10524.3		2	975.9	63.6	1	R.GVTEAIQNFSFR.S
*	HsF-IP-293-MG_Ti_102.07	3.9161	0.3648	1551.15	1551.56	8967.9		2	1518.5	66.7	1	R.AGGDATDSSQTALDNK.A
*	Hs283FLP_Ti_102.2202.22	4.4101	0.3869	1924.51	1925.02	6955.4		1	1919	80	7	R.DYNPYNYSDSISPFNK.S
	HsF-IP-293-MG_Ti_106.30	4.975	0.3926	1442.69	1442.78	8171.1		1	2125.8	87.5	1	K.TILLLLLETLGDK.E
*	Hs293FLP-MG_Ti_202.284	3.4277	0.3576	2094.58	2092.27	7757.7		1	601.6	44.7	1	R.SAEEAASVLATSISPEQCIK.V
	Hs293FLP-MG_Ti_203.369	5.367	0.4306	2113.77	2114.5	9568.9		1	1540.8	58.3	6	K.VLCPIIQTADYPINLAAIK.M
*	Hs293FLP-MG_Ti_202.490	3.3796	0.2963	2889.46	2890.28	5647.7		1	362.9	34	1	K.ETLNLLLPEIMPGLIQGYDNSESSVR.K
*	Hs283FLP_Ti_102.1031.10	3.7221	0.4446	1793.28	1792.81	6298.3		1	850.8	55.6	3	K.RAQTGSGGADPTTDVSGQS.-
gi|89030025|ref|	8	16	0.239	461	49351	8.4	U	PREDICTED: far upstream element (FUSE) binding protein 3 isoform 4 [Homo sapiens]				
gi|89030643|ref|	8	16	0.227	485	52239	8.6	U	PREDICTED: similar to Far upstream element binding protein 3 (FUSE binding protein 3)				
gi|89030641|ref|	8	16	0.239	461	49351	8.4	U	PREDICTED: similar to Far upstream element binding protein 3 (FUSE binding protein 3)				
gi|89030027|ref|	8	16	0.227	485	52239	8.6	U	PREDICTED: far upstream element (FUSE) binding protein 3 isoform 1 [Homo sapiens]				
	HsHeLa3_Ti_106.2111.211	2.8021	0.1606	1070.66	1070.28	4007.8		6	512.7	81.2	1	K.RLLGQIVDR.C
	HsHeLa3_Ti_104.2708.270	4.7219	0.2862	2568.13	2568.8	7995		1	1007.3	47.8	2	R.NGPGFHNDIDSNSTIQEILIPASK.V
	HsHeLa3_Ti_103.1956.195	4.8006	0.3346	1574.04	1573.86	6484		1	1743.8	78.6	2	K.MVMIQDGPLPTGADK.P
	HsHeLa3_Ti_105.2026.202	3.6505	0.3227	1941.72	1940.33	5333.7		3	404.6	47.1	1	K.MVMIQDGPLPTGADKPLR.I
	HsFLAG-Control_HeLa_NE	3.4986	0.1241	1502.4	1502.67	3938.4		1	600.6	70.8	3	R.IQFKPDDGISPER.A
	HsHeLa3_Ti_103.1320.132	1.813	0.1061	1041.59	1042.2	5358.7		4	324.4	66.7	1	R.AAQVMGPPDR.C
	HsFLAG-Control_HeLa_NE	4.2249	0.3994	2248.39	2248.45	4431.8		1	434.6	45.2	3	R.GDWSVGAPGGVQEITYTVPADK.C
	HsHeLa3_Ti_105.1402.140	3.9641	0.3608	1567.83	1567.7	7297.9		1	1372.2	73.1	3	K.SINQQSGAHVELQR.N
gi|4758138|ref|N	13	61	0.238	614	69148	8.9	U	DEAD (Asp-Glu-Ala-Asp) box polypeptide 5 [Homo sapiens]				
*	HsGST-MOCK_Ti_404.187	3.7038	0.281	1390.88	1390.5	8154.9		1	1293	80	2	K.NFYQEHPDLAR.R
*	HsGST-MOCK_Ti_103.109	2.8076	0.2294	1409.14	1409.55	5413		1	387.2	65	1	R.RTAQEVETYRR.S
	HsGST-MOCK_Ti_303.265	3.6573	0.1954	1369.44	1369.57	7837.3		7	895.4	58.3	6	R.GDGPICLVLAPTR.E
*	HsGST-MOCK_Ti_402.256	3.2433	0.2552	1794.64	1793.94	11468		1	1151.8	60.7	1	R.ELAQQVQQVAAEYCR.A
	HsFLAG-Control_HeLa_NE	1.8359	0.1012	1053.37	1054.15	7559.8		5	566	66.7	1	K.STCIYGGAPK.G
*	HsFLAG-Control_HeLa_NE	3.8767	0.2427	1298.37	1296.42	6212.9		1	1375.4	85	4	R.TTYLVLDEADR.M
	HsGST-MOCK_Ti_303.267	3.1278	0.2572	1337.33	1337.6	5377.8		1	865.1	80	2	R.MLDMGFEPQIR.K
*	HsFlag1P_Ti_103.2635.263	3.5657	0.2915	1679.68	1679.83	6958.8		1	827.3	62.5	2	K.SQQERDWVLNEFK.H
	HsFlag1P_Ti_104.2210.221	4.2007	0.3247	1227.42	1227.45	6635		1	1668.4	86.4	19	K.APILIATDVASR.G
	HsFlag1P_Ti_104.2894.289	4.5794	0.3974	2082.79	2083.39	6206.5		1	939.4	55.3	4	K.APILIATDVASRGLDVEDVK.F
	HsFLAG-Control_HeLa_NE	2.6493	0.2241	874.56	874.966	7540.7		5	774.8	78.6	1	R.GLDVEDVK.F
*	HsFLAG-Control_HeLa_NE	3.7113	0.3515	2133.3	2133.28	5119.2		1	623.2	59.4	5	K.FVINYDYPNSSEDYIHR.I

*	HsFLAG-Control_MG_293_	3.7611	0.3594	1576.34	1575.76	9078.9		1	1016.6	61.5	13	K.TGTAYTFFTPNNIK.Q
gi|67782356|ref|N	4	6	0.238	529	51580	8.4	U	corneodesmosin precursor [Homo sapiens]				
*	HsFLAG-Control_Hela_Ti_1	3.1467	0.2878	2506.6	2504.73	5728.2		1	394.6	37	1	K.SYGGYEVVGGSSDSYLVPGMTYSK.G
*	HsFLAG-Control_Hela_Ti_1	3.6619	0.2625	1657.45	1655.85	4686.8		1	596.9	55.9	3	K.GSPGVPSFAAGPPISEGK.Y
*	HsFLAG-Control_293_Ti_1(	4.1364	0.2664	3790.93	3788.13	5131.7		1	643.4	23.7	1	K.YFSSNPIIPSQSAASSAIAFQPVGTGGVQLCGGGSTGSK.G
*	HsFLAG-Control_Hela_Ti_1	3.9333	0.1468	4365.72	4365.47	7908.1		1	566.5	17	1	R.VPSSSSISSSSGLPYHPCGSASQSPCSPPGTGSFSSSSSSQSSGK.I
gi|74099697|ref|N	11	166	0.238	449	49264	6.3	U	heterogeneous nuclear ribonucleoprotein H2 [Homo sapiens]				
gi|9624998|ref|NI	11	166	0.238	449	49264	6.3	U	heterogeneous nuclear ribonucleoprotein H2 [Homo sapiens]				
	Hs293FLP-MG_Ti_204.147	3.8795	0.4268	1685.48	1685.75	7488.8		1	1436.6	70	10	K.HTGPNSPDTANDGFVR.L
	HsFLAG-Control_293_Ti_2(	4.52	0.5046	1685.48	1685.75	8106.6		1	2099.2	80	8	K.HTGPNSPDTANDGFVR.L
	HsFLAG-Control_HeLa_NE	4.3166	0.4328	1686.3	1685.75	6792.2		1	914.4	63.3	5	K.HTGPNSPDTANDGFVR.L
	HsFLAG-Control_293_Ti_2(	4.3669	0.2323	1686.72	1685.75	7063.6		3	1191.3	45	1	K.HTGPNSPDTANDGFVR.L
	HsFLAG-MOCK_300mM_T	4.0472	0.1915	1686.88	1685.75	5906.1		2	1316.5	48.3	1	K.HTGPNSPDTANDGFVR.L
	HsHeLa3_Ti_106.3375.337	4.2045	0.2237	3773.82	3771.29	4292.3		1	378.9	23.5	1	R.GLPFGCSKEEIVQFFSGLEIVPNGMTLPVDFQGR.S
	HsFlag1P_Ti_102.3107.31(	5.4581	0.4545	1841.95	1843	8129.4		1	2087.4	71.9	105	R.STGEAFVQFASQEIAEK.A
	HsFLAG-Control_293_Ti_2(	3.8505	0.4656	1604.09	1602.68	9274.9		1	1651.1	79.2	9	R.DLNYCFSGMSDHR.Y
	HsFLAG-Control_293_Ti_2(	4.4199	0.4232	2029.52	2030.26	9407.7		1	1311.1	59.4	8	R.ATENDIYNFFSPLNPMR.V
	HsFLAG-Control_HeLa_NE	2.6268	0.1908	1092.55	1093.23	6937.7		1	767.6	72.2	2	R.VHIEIGPDGR.V
	HsFLAG-Control_HeLa_NE	3.4554	0.2844	1093.46	1093.23	5275.7		1	1166.4	83.3	16	R.VHIEIGPDGR.V
gi|17737321|ref|N	12	36	0.235	720	82615	5.9	U	engulfment and cell motility 2 [Homo sapiens]				
gi|33469947|ref|N	12	36	0.235	720	82615	5.9	U	engulfment and cell motility 2 [Homo sapiens]				
gi|19718769|ref|N	12	36	0.235	720	82615	5.9	U	engulfment and cell motility 2 [Homo sapiens]				
	HsFLAG-Control_293_Ti_2(	4.6564	0.4107	1996.11	1996.27	4248.8		1	844.2	64.7	3	K.VAIEWPGANAQLLEIDQK.R
	HsFLAG-Control_293_Ti_2(	3.3463	0.2404	2099.78	2100.26	5248.5		1	537.6	53.1	2	K.EVCDGWSLPNPEYYTLR.Y
	HsFLAG-Control_293_Ti_2(	3.9732	0.3434	1655.22	1655.81	7064.8		1	1484.4	73.1	2	R.YADGPQLYITEQTR.S
	HsFLAG-Control_293_Ti_2(	4.0673	0.3892	1370.36	1370.59	7454.5		1	1540.9	79.2	6	K.NGTILQLAISPSR.A
	HsFLAG-Control_293_Ti_2(	5.2671	0.3974	2024.54	2025.37	9121.2		1	1792.4	64.7	1	R.SLAILESMVLNSQSLYQK.I
	Hs293FLP_Ti_303.1442.14	4.6124	0.3908	2049.94	2050.15	3970.8		1	796.1	60.5	1	R.RIAFDAESDPSNAPGSGTEK.R
	HsFLAG-Control_293_Ti_2(	4.7143	0.3186	1893.36	1893.96	6090.4		1	1065.2	61.1	2	R.IAFDAESDPSNAPGSGTEK.R
	HsFLAG-Control_293_Ti_2(	3.0894	0.129	1860.68	1859.11	8246.6		1	944	53.3	1	K.MLCEILQVGELPNEGR.N
	HsFLAG-Control_293_Ti_2(	6.0226	0.5077	2633.92	2634.82	7703.8		1	1722.7	56.8	2	K.VLHYGDLDDNPQGEVTFESLQEK.I
	HsFLAG-Control_293_Ti_2(	4.8548	0.332	1997.71	1998.37	5474.9		1	799.2	58.8	10	R.LLDLENIQIPEAPPPIPK.E
	HsFLAG-Control_293_Ti_2(	4.5241	0.27	1997.83	1998.37	6101.9		1	1791.6	52.9	4	R.LLDLENIQIPEAPPPIPK.E
	HsFLAG-Control_MG_293_	2.8241	0.3272	1463.99	1464.53	8045.4		1	696.1	63.6	2	K.EPSSYDFVYHYG.-
gi|55956919|ref|N	7	15	0.235	332	35968	6.9	U	heterogeneous nuclear ribonucleoprotein AB isoform a [Homo sapiens]				
gi|55956921|ref|N	7	15	0.274	285	30588	7.9	U	heterogeneous nuclear ribonucleoprotein AB isoform b [Homo sapiens]				
	HsHeLa3_Ti_103.2460.246	2.0828	0.1111	1328.69	1328.53	6373.3		5	374.6	50	1	K.MFVGGLSWDTSK.K
	HsHeLa3_Ti_105.2160.216	3.1668	0.2693	1456.79	1456.7	6051.3		2	669.9	62.5	2	K.MFVGGLSWDTSKK.D
	HsHeLa3_Ti_105.3190.319	3.2596	0.1074	929.39	929.15	2854.9		7	591.2	85.7	2	R.GFGFILFK.D
	Hs293FLP_TREX_Ti_104.1	5.1443	0.3386	1632.4	1632.85	5726.1		1	1636.8	82.1	6	K.KIFVGGLNPEATEEK.I
	HsHeLa3_Ti_105.3664.366	3.0226	0.3039	2215.85	2215.48	8491.9		1	1030.4	52.8	1	R.EYFGEFGEIEAIELPMDPK.L
	HsHeLa3_Ti_105.2607.260	3.4495	0.3999	1671.65	1670.95	5015.5		1	820.5	65.4	2	R.GFVFITFKEEEPVK.K
	HsHeLa_Control-MG_Ti_20	2.108	0.2595	990.24	991.135	3482.2		7	185.8	56.2	1	K.KFHTVSGSK.C
gi|32483377|ref|N	3	15	0.235	238	25839	7.5	U	peroxiredoxin 3 isoform b [Homo sapiens]				
gi|5802974|ref|NI	3	15	0.219	256	27693	7.8	U	peroxiredoxin 3 isoform a precursor [Homo sapiens]				
	HsHeLa_Control-MG_Ti_20	5.1113	0.4153	1463	1463.67	9684.9		1	2754.7	84.6	5	R.DYGVLLEGSGLALR.G
	Hs293FLP_TREX_Ti_105.1	2.7992	0.3249	1207.62	1207.38	5786.7		1	771.8	75	1	K.HLSVNDLPVGR.S

	HsHeLa_Control-MG_Ti_20	6.2645	0.4601	3387.88	3387.7	7427.2		1	1234.9	31.7	9	K.AFQYVETHGEVCPANWTPDSPTIKPSPAASK.E
gi|15431301|ref|N	6	11	0.234	248	29226	10.7	U	ribosomal protein L7 [Homo sapiens]				
	Hs293FLP_TREX_Ti_106.2	3.081	0.1865	1339.57	1339.62	4981.4		1	867.6	77.3	1	K.KKEVPAVPETLK.K
	Hs293FLP_TREX_Ti_106.2	3.3372	0.2014	1467.6	1467.79	5733.4		1	975.6	75	1	K.KKEVPAVPETLKK.K
	HsFLAG-MOCK_300mM_T	2.9547	0.3319	1664.07	1663.96	7391.5		1	974.3	61.5	2	R.IVEPYIAWGYPNLK.S
	Hs293FLP_TREX_Ti_105.1	4.7849	0.2846	1327.36	1327.57	4721.8		1	1179.2	86.4	3	K.RIALTDNALIAR.S
	Hs293FLP_TREX_Ti_102.1	3.7636	0.3057	1171.39	1171.38	7116.9		1	1710.7	95	2	R.IALTDNALIAR.S
	Hs293FLP_TREX_Ti_103.1	4.5061	0.3759	2116.68	2117.2	6455		1	721.4	52.8	2	K.TTHFVEGGDAGNREDQINR.L
gi|15809016|ref|N	3	4	0.233	172	19779	4.8	U	myosin regulatory light chain MRCL2 [Homo sapiens]				
gi|5453740|ref|N	3	4	0.234	171	19794	4.8	U	myosin regulatory light chain MRCL3 [Homo sapiens]				
	HsFLAG-MOCK_150mM_T	5.6344	0.4814	2091.58	2092.33	7032		1	1812.2	70.6	2	R.ATSNVFAMFDQSQIQEFK.E
	HsFLAG-Control_HeLa_S1	3.6942	0.3291	1416.01	1416.48	7286.6		1	1258.2	80	1	R.FTDEEVDELYR.E
	HsFLAG-MOCK_300mM_T	2.9454	0.1169	1390.92	1389.55	4933.8		1	656.1	70	1	K.KGNFNYIEFTR.I
gi|5453607|ref|N	14	55	0.232	543	59367	7.6	U	chaperonin containing TCP1, subunit 7 isoform a [Homo sapiens]				
*	Hs293FLP_TREX_Ti_104.1	2.1627	0.3025	1062.42	1063.29	4643.3		4	401.7	61.1	2	K.LLDVVHPAAK.T
*	HsFLAG-Control_HeLa_S1	3.2897	0.3411	1062.99	1063.29	5731		1	1197	88.9	2	K.LLDVVHPAAK.T
*	HsFLAG-Control_HeLa_S1	2.4445	0.2399	1063.66	1063.29	5152.3		1	565.7	72.2	3	K.LLDVVHPAAK.T
*	HsFLAG-Control_HeLa_NE	5.8877	0.5	2253.79	2253.47	6849.8		1	1661.4	64.3	21	K.SQDAEVGDGTTSVTLLAAEFLK.Q
*	HsFLAG-Control_HeLa_NE	6.2374	0.5478	2253.9	2253.47	7964.8		1	2018.5	64.3	12	K.SQDAEVGDGTTSVTLLAAEFLK.Q
*	HsFLAG-Control_HeLa_NE	3.5257	0.2201	2253.96	2253.47	10151.9		1	907.4	29.8	1	K.SQDAEVGDGTTSVTLLAAEFLK.Q
*	HsFLAG-Control_HeLa_S1	3.0882	0.1979	945.87	946.092	6292.2		2	824.9	87.5	2	R.TATQLAVNK.I
*	HsFLAG-Control_HeLa_S1	3.1658	0.421	1918.35	1918.2	12963.3		1	782.1	41.7	2	K.KVQGGALEDSQLVAGVAFK.K
*	HsFLAG-Control_HeLa_S1	2.9903	0.3313	1789.41	1790.03	9923.9		1	720.5	47.1	1	K.VQGGALEDSQLVAGVAFK.K
	HsFLAG-Control_HeLa_S1	3.8345	0.3942	2523.12	2522.77	12160.7		1	1084.7	45	1	R.VHTVEDYQAIVDAEWNILYDK.L
	HsFLAG-Control_HeLa_NE	4.2323	0.3818	1566.47	1566.75	9210.4		1	1263.4	69.2	5	K.LPIGDVATQYFADR.D
	HsFLAG-Control_HeLa_S1	2.4063	0.2126	1133.48	1134.24	8349.9		4	447.5	62.5	1	R.YNFFTGCPK.A
	HsFLAG-Control_HeLa_S1	4.2122	0.4261	2290.76	2290.58	8474.7		1	1046.3	47.6	1	R.INALTAASEAACLIVSVDETIK.N
	HsFLAG-Control_HeLa_NE	5.2274	0.4093	2290.91	2290.58	6375.7		1	1024.6	35.7	1	R.INALTAASEAACLIVSVDETIK.N
gi|54792069|ref|N	2	3	0.232	95	10871	5.5	U	small ubiquitin-like modifier 2 isoform a precursor [Homo sapiens]				
gi|89060987|ref|X	2	3	0.138	160	17755	6.3	U	PREDICTED: similar to SMT3 suppressor of mif two 3 homolog 2 [Homo sapiens]				
gi|89060008|ref|X	2	3	0.138	160	17755	6.3	U	PREDICTED: similar to SMT3 suppressor of mif two 3 homolog 2 [Homo sapiens]				
gi|54792071|ref|N	2	3	0.31	71	8111	5.4	U	small ubiquitin-like modifier 2 isoform b precursor [Homo sapiens]				
	Hs293FLP_TREX_Ti_103.1	3.0964	0.0832	1198.18	1198.28	9247		2	1227.8	77.8	1	K.TENNDHINLK.V
	HsHeLa3_Ti_103.1579.157	3.0052	0.2906	1234.7	1235.38	5822.7		2	416.3	54.5	2	K.VAGQDGSVVQFK.I
gi|31881687|ref|N	6	10	0.231	363	39682	8	U	replication factor C 4 [Homo sapiens]				
gi|4506491|ref|N	6	10	0.231	363	39682	8	U	replication factor C 4 [Homo sapiens]				
	HsFLAG-Control_HeLa_NE	2.5761	0.1017	1230.5	1230.45	5888.1		3	577.3	59.1	1	K.GTSISTKPPLTK.D
	HsGST-MOCK_Ti_404.374	4.3194	0.4574	2046.79	2047.32	6487.7		1	1049.8	55.3	4	K.SLEGADLPNLLFYGPPGTGK.T
	HsFLAG-Control_HeLa_NE	2.7369	0.1891	1208.54	1208.4	6232.2		3	770.1	75	1	K.ISDEGIAYLVK.V
	HsFLAG-Control_HeLa_NE	3.0865	0.2534	1325.49	1326.58	7195.5		3	701.4	62.5	1	K.VITDIAGVIPAEK.I
	HsFLAG-Control_HeLa_NE	3.2128	0.2142	1326.41	1326.58	8702		1	1507.6	75	1	K.VITDIAGVIPAEK.I
	HsFLAG-Control_HeLa_NE	6.3491	0.5007	3087.6	3088.36	11791.9		1	2022.6	33.3	2	K.DLIDEGHAATQLVNQLHDVVVENNLSDK.Q
gi|46276893|ref|N	4	6	0.23	161	17911	6.1	U	elongin B isoform b [Homo sapiens]				
gi|6005890|ref|N	4	6	0.314	118	13133	4.9	U	elongin B isoform a [Homo sapiens]				
	Hs293FLP-MG_Ti_303.146	2.3441	0.2731	1422.34	1423.56	5400.4		1	542.7	63.6	1	R.LYKDDQLLDDGK.T
	Hs293FLP-MG_Ti_303.131	3.5759	0.2897	1424.4	1423.56	5993.4		1	1045.1	77.3	3	R.LYKDDQLLDDGK.T
	HsHeLa_Control-MG_Ti_20	4.6238	0.4249	2638.23	2637.92	9104.2		1	1193.7	33.3	1	K.TLGECGFTSQTARPQAPATVGLAFR.A
	Hs293FLP-MG_Ti_306.241	2.6104	0.3461	1227.49	1228.44	3961.6		1	309.9	68.2	1	R.PQAPATVGLAFR.A
gi|5453549|ref|N	5	9	0.229	271	30540	6.3	U	thioredoxin peroxidase [Homo sapiens]				

*	Hs293FLP_TREX_Ti_105.1	4.0519	0.2751	1293.41	1293.47	8555.5		1	1760	81.8	2	R.VSVADHSLHLSK.A
*	HsHeLa_Control-MG_Ti_10	3.3573	0.3636	1465.64	1465.73	5755.1		1	969.6	75	2	R.IPLLSDLTHQISK.D
*	Hs293FLP-MG_Ti_306.240	3.9691	0.3927	1625.26	1625.74	5697.7		1	1330.6	80.8	1	K.DYGVYLEDSGHTLR.G
	HsHeLa_Control-MG_Ti_20	2.8933	0.2991	1140.68	1141.24	7169.4		1	913.8	77.8	3	K.HGEVCPAGWK.P
*	HsHeLa_Control-MG_Ti_10	4.3364	0.3338	2405.82	2404.65	5461.5		1	970.4	35.2	1	K.HGEVCPAGWKPGSETIIPDPAGK.L
gi|4502549|ref|N	2	24	0.228	149	16838	4.2	U	calmodulin 2 [Homo sapiens]				
gi|5901912|ref|N	2	24	0.228	149	16838	4.2	U	calmodulin 1 (phosphorylase kinase, delta) [Homo sapiens]				
gi|58218968|ref|	2	24	0.228	149	16838	4.2	U	calmodulin 3 [Homo sapiens]				
	HsHeLa3_Ti_102.1822.182	3.7027	0.3618	1266.66	1266.35	5762.1		1	1244.6	81.8	3	K.DGNGYISAAELR.H
	HsHeLa3_Ti_102.3777.377	4.9963	0.381	2490.93	2491.7	5450.3		1	1011.9	54.8	21	R.EADIDGDGQVNYEEFVQMMTAK.-
gi|16751921|ref|	5	16	0.227	110	11284	6.5	U	dermcidin precursor [Homo sapiens]				
*	HsFLAG-Control_Hela_Ti_1	2.704	0.1698	1129.22	1129.17	4873.2		7	527.7	65	2	K.ENAGEDPGLAR.Q
*	HsFLAG-Control_293_Ti_2	4.7558	0.3776	1460.17	1460.62	8454		1	2051.3	76.9	6	K.LGKDAVEDLESVGK.G
*	HsFLAG-Control_Hela_Ti_1	4.2213	0.2867	1162.17	1162.24	5317.6		1	1153.4	85	4	K.DAVEDLESVGK.G
*	HsFLAG-Control_293_Ti_1	4.2005	0.3018	1162.29	1162.24	5093		1	1120.1	85	2	K.DAVEDLESVGK.G
*	HsFLAG-Control_293_Ti_1	2.424	0.2668	1163.46	1162.24	7467.7		9	556.5	65	2	K.DAVEDLESVGK.G
gi|25777711|ref|	2	10	0.225	160	18063	4.5	U	S-phase kinase-associated protein 1A isoform a [Homo sapiens]				
gi|25777713|ref|	2	10	0.221	163	18658	4.5	U	S-phase kinase-associated protein 1A isoform b [Homo sapiens]				
	HsFLAG-Control_HeLa_NE	3.8507	0.3433	1881.56	1880.06	7751.6		1	1135.3	59.4	2	K.LQSSDGEIFEVDVEIAK.Q
	HsFLAG-Control_HeLa_NE	5.4233	0.4006	2136.9	2137.48	9430.1		1	1577.3	58.3	8	K.VDQGTLFELILAANYLDIK.G
gi|4503483|ref|N	15	54	0.224	858	95338	6.8	U	eukaryotic translation elongation factor 2 [Homo sapiens]				
*	HsGST-MOCK_Ti_405.467	4.2605	0.3695	2205.35	2205.47	9483		1	914.2	50	8	K.STAISLFYELSENDLNFIK.Q
*	HsHeLa3_Ti_103.3882.388	5.0109	0.2786	2220.93	2221.52	3976.5		1	819.1	64.7	13	R.ALLELQLEPEELYQTFQR.I
*	Hs293FLP_TREX_Ti_102.1	2.8102	0.2061	1015.41	1014.08	4107.1		1	524.2	72.2	1	K.GEGQLGPAER.A
*	HsHeLa3_Ti_103.3627.362	4.0571	0.2568	1496.62	1495.77	7673		1	1415	77.3	6	R.TFCQLILDPIFK.V
*	Hs293FLP_TREX_Ti_103.1	2.198	0.1674	1107.44	1108.32	6209.8		7	458.4	55	1	R.VFSGLVSTGLK.V
*	HsFLAG-Control_MG_293_	2.027	0.1218	1107.52	1108.32	9045.3		2	671.7	60	1	R.VFSGLVSTGLK.V
*	Hs293FLP_TREX_Ti_103.1	3.242	0.1665	1109.5	1108.32	4334		1	890	80	2	R.VFSGLVSTGLK.V
*	Hs293FLP-MG_Ti_202.452	3.4937	0.383	2761.39	2761.15	4847.9		1	472.4	39.6	1	R.YVEPIEDVPCGNIVGLVGVDQFLVK.T
*	Hs293FLP_TREX_Ti_102.1	3.985	0.4356	1595.33	1595.71	8920.2		1	1231.7	65.4	1	R.ETVSEESNVLCLSK.S
*	HsGST-MOCK_Ti_102.180	3.8897	0.239	2143.98	2144.35	8645.9		2	1014.6	39.5	1	K.ARPFPDGLAEDIDKGEVSAR.Q
*	HsHeLa3_Ti_106.2740.274	3.325	0.3199	2234.09	2234.52	6149.4		1	847.8	52.6	2	R.KIWCFGPDGTGPNILTDITK.G
*	HsHeLa3_Ti_103.3610.361	4.6385	0.5003	2107.51	2106.35	6983.4		1	1352.1	63.9	7	K.IWCFGPDGTGPNILTDITK.G
*	Hs293FLP_TREX_Ti_103.1	4.2034	0.4089	1379.36	1379.57	8563.3		1	1910.4	81.8	2	R.CLYASVLTAQPR.L
*	HsHeLa_Control-MG_Ti_10	5.0364	0.4594	1964.9	1963.26	8337.2		1	1975.6	67.6	1	R.GHVFEESQVAGTPMFVVK.A
*	HsHeLa_Control-MG_Ti_20	3.5653	0.2566	1446.57	1445.66	6122.7		1	852.6	70.8	7	K.EGIPALDNFLDKL.-
gi|16933546|ref|	6	19	0.224	317	34274	6	U	ribosomal protein P0 [Homo sapiens]				
gi|4506667|ref|N	6	19	0.224	317	34274	6	U	ribosomal protein P0 [Homo sapiens]				
	Hs293FLP_TREX_Ti_102.2	3.7192	0.2608	1217.02	1218.44	7235.8		1	1472.1	88.9	5	K.IIQLLDDYPK.C
	Hs293FLP_TREX_Ti_102.2	2.6918	0.1248	1217.42	1218.44	8044.9		6	881.5	77.8	1	K.IIQLLDDYPK.C
	HsFLAG-Control_293_Ti_2	1.9261	0.1093	717.4	717.945	9229.4		7	653.9	66.7	1	K.AVVLMGK.N
	Hs293FLP_TREX_Ti_104.1	3.5837	0.2958	1224.39	1222.34	4949.4		1	708	75	5	R.GHLENNPALEK.L
	HsGST-MOCK_Ti_303.337	3.46	0.3459	1314.16	1314.52	8487.9		1	1474.2	77.3	2	K.TSFFQALGITTK.I
	HsFLAG-Control_Hela_Ti_1	4.4724	0.5001	2753.01	2754.16	4979.7		1	1139.4	48.3	5	K.AFLADPSAFVAAAPVAAATTAAPAAAAAPAK.V
gi|4506407|ref|N	2	4	0.224	201	23310	5.3	U	RAN binding protein 1 [Homo sapiens]				
*	Hs293FLP-MG_Ti_203.255	5.0324	0.4019	3935.58	3936.02	8850.2		1	766.4	24.2	2	K.DTHEDHDTSTENTDESNHDPQFEPIVSLPEQEIK.T
	HsFLAG-Control_MG_293_	3.4639	0.2523	1382.24	1382.46	4899.7		1	839.8	80	2	K.TLEEDEEELFK.M
gi|4506617|ref|N	4	15	0.223	184	21397	10.2	U	ribosomal protein L17 [Homo sapiens]				
gi|89039066|ref|	4	15	0.223	184	21313	10.1	U	PREDICTED: similar to 60S ribosomal protein L17 (L23) isoform 5 [Homo sapiens]				

gi|89039064|ref|	4	15	0.223	184	21313	10.1	U	PREDICTED: similar to 60S ribosomal protein L17 (L23) isoform 4 [Homo sapiens]			
gi|89039062|ref|	4	15	0.223	184	21313	10.1	U	PREDICTED: similar to 60S ribosomal protein L17 (L23) isoform 3 [Homo sapiens]			
gi|89039060|ref|	4	15	0.223	184	21313	10.1	U	PREDICTED: similar to 60S ribosomal protein L17 (L23) isoform 2 [Homo sapiens]			
gi|89039058|ref|	4	15	0.223	184	21313	10.1	U	PREDICTED: similar to 60S ribosomal protein L17 (L23) isoform 1 [Homo sapiens]			
gi|89038352|ref|	4	15	0.223	184	21313	10.1	U	PREDICTED: similar to 60S ribosomal protein L17 (L23) isoform 2 [Homo sapiens]			
gi|89038350|ref|	4	15	0.223	184	21313	10.1	U	PREDICTED: similar to 60S ribosomal protein L17 (L23) isoform 1 [Homo sapiens]			
gi|88947794|ref|	4	15	0.223	184	21399	10.1	U	PREDICTED: similar to 60S ribosomal protein L17 (L23) isoform 2 [Homo sapiens]			
gi|88947792|ref|	4	15	0.223	184	21399	10.1	U	PREDICTED: similar to 60S ribosomal protein L17 (L23) isoform 1 [Homo sapiens]			
gi|88943958|ref|	4	15	0.223	184	21455	10.2	U	PREDICTED: similar to 60S ribosomal protein L17 (L23) isoform 6 [Homo sapiens]			
gi|88943956|ref|	4	15	0.223	184	21455	10.2	U	PREDICTED: similar to 60S ribosomal protein L17 (L23) isoform 5 [Homo sapiens]			
gi|88943954|ref|	4	15	0.223	184	21455	10.2	U	PREDICTED: similar to 60S ribosomal protein L17 (L23) isoform 4 [Homo sapiens]			
gi|88943952|ref|	4	15	0.223	184	21455	10.2	U	PREDICTED: similar to 60S ribosomal protein L17 (L23) isoform 3 [Homo sapiens]			
gi|88943950|ref|	4	15	0.223	184	21455	10.2	U	PREDICTED: similar to 60S ribosomal protein L17 (L23) isoform 2 [Homo sapiens]			
gi|88943948|ref|	4	15	0.223	184	21455	10.2	U	PREDICTED: similar to 60S ribosomal protein L17 (L23) isoform 1 [Homo sapiens]			
gi|88942753|ref|	4	15	0.223	184	21399	10.1	U	PREDICTED: similar to 60S ribosomal protein L17 (L23) isoform 2 [Homo sapiens]			
gi|88942751|ref|	4	15	0.223	184	21399	10.1	U	PREDICTED: similar to 60S ribosomal protein L17 (L23) isoform 1 [Homo sapiens]			
	HsHeLa_Control-MG_Ti_20	3.5242	0.2436	1189.1	1189.46	7818.5	1	1089.5	72.2	3	K.SAEFLLHMLK.N
	Hs293FLP-MG_Ti_203.301	4.6944	0.4338	1780.61	1780.03	6847	1	1370.6	70	9	K.GLDVDSLVIEHIQVNK.A
	HsHeLa_Control-MG_Ti_20	3.4181	0.2536	1624.6	1624.83	4546.7	1	596.3	69.2	1	K.EQIVPKPEEEVAQK.K
	HsGST-MOCK_Ti_102.137	2.934	0.3134	1752.67	1753.01	4612.7	1	561.4	60.7	2	K.EQIVPKPEEEVAQKK.K
gi|48762932|ref|	10	20	0.221	548	59621	5.6	U	chaperonin containing TCP1, subunit 8 (theta) [Homo sapiens]			
	HsFLAG-Control_HeLa_S1	3.7321	0.2232	1334.48	1334.56	7369.3	1	1511.3	81.8	1	K.LFVTNDAATILR.E
	HsFLAG-Control_HeLa_NE	3.0197	0.2395	1122.43	1122.27	9013.1	3	868.6	72.2	3	R.ELEVQHPAAK.M
*	HsFLAG-Control_HeLa_S1	3.3415	0.264	1613.06	1612.8	3695.6	1	819.6	73.1	1	K.AHEILPNLVCCSAK.N
*	HsFLAG-Control_HeLa_S1	3.648	0.1603	1147.25	1147.27	9565.4	3	1505.8	83.3	2	R.DIDEVSSLLR.T
*	Hs293FLP_Ti_305.1678.16	3.568	0.2546	1511.98	1511.76	6158.8	1	950.1	64.3	4	K.RLVPGGGATEIELAK.Q
*	HsFLAG-Control_HeLa_S1	3.6874	0.4294	2058.03	2059.25	7214.5	1	708.2	50	1	K.QITSYGETCPGLEQYAIK.K
*	HsFLAG-Control_HeLa_S1	3.6668	0.1848	1150.97	1151.31	6885.3	1	1644.9	94.4	2	K.FAEAFEAIPR.A
*	HsFLAG-Control_HeLa_S1	2.4607	0.1517	1158.31	1159.29	6148.9	1	680.3	72.2	2	K.LYAVHQEGNK.N
*	HsFLAG-Control_HeLa_S1	3.6867	0.2562	1129.52	1129.35	8610.2	1	1595.7	85	3	K.LATNAAVTVLR.V
*	HsFLAG-Control_HeLa_S1	2.0003	0.1521	992.72	993.151	6404.7	2	568.4	60	1	K.PAGGPKPPSGK.K
gi|42544172|ref|	7	9	0.219	581	62711	6.7	U	E74-like factor 2 (ets domain transcription factor) isoform 1 [Homo sapiens]			
gi|6857816|ref|N	7	9	0.238	533	57389	9	U	E74-like factor 2 (ets domain transcription factor) isoform 2 [Homo sapiens]			
	HsHeLa3_Ti_106.3831.383	4.7175	0.3653	2071.68	2070.35	6867.6	1	1108.1	59.4	1	K.GNTTYLWEFLLDLLQDK.N
	HsHeLa3_Ti_102.1274.127	4.6977	0.3908	1671.51	1670.65	7096.8	1	1369.5	71.4	2	K.SETCNEDLAGTTDEK.S
	HsHeLa3_Ti_105.1350.135	2.6597	0.1471	1440.42	1440.56	4837.2	1	714.8	69.2	1	R.VVNITSPGHDASSR.S
	HsHeLa3_Ti_103.2115.211	2.5012	0.3241	2700.3	2701.05	5355.4	1	322.2	31.5	1	K.ISTVAVQSVNAGAPLITSTSPTTATSPK.V
	HsHeLa3_Ti_104.2341.234	3.0336	0.3964	1928.94	1928.25	3761.8	1	335.7	53.1	1	K.IITIPATQLAQCQLQTK.S
	HsHeLa3_Ti_106.2179.217	3.3781	0.4534	1551.18	1550.86	8002.8	1	1051.2	60.7	1	R.ALTPVSIAHGTPVMR.L
	HsHeLa3_Ti_106.2467.246	4.7768	0.4136	2122.04	2121.59	5994.1	1	1065.5	55	2	K.TVTHVVVVSAPSAIALPVTMK.T
gi|4757766|ref|N	8	15	0.219	439	50436	6.3	U	Rho GTPase activating protein 1 [Homo sapiens]			
*	HsFLAG-Control_HeLa_S1	2.6552	0.1294	1213.58	1211.32	7626.8	1	767.7	75	1	R.HQIVEVAGDDK.Y
*	HsFLAG-Control_HeLa_S1	3.3069	0.1444	1407.03	1405.64	5059.2	1	739.7	68.2	3	K.NPEQEPIPIVLR.E
*	HsFLAG-Control_HeLa_S1	2.813	0.3974	2021.76	2021.28	8685.4	1	543	44.1	1	R.ETVAYLQAHALTTEGIFR.R
*	HsFLAG-Control_HeLa_S1	2.6085	0.1178	2312.19	2312.67	6408.5	5	269.4	34.2	1	R.VPATLQVLQTLPEENYQVLR.F
*	HsFLAG-Control_HeLa_NE	4.6438	0.3156	2312.49	2312.67	5192.5	1	678	50	5	R.VPATLQVLQTLPEENYQVLR.F
*	HsFLAG-Control_HeLa_S1	3.9562	0.1532	2312.61	2312.67	5182.2	6	641.3	35.5	1	R.VPATLQVLQTLPEENYQVLR.F
*	HsFLAG-Control_HeLa_S1	4.8296	0.2729	1921.56	1920.18	9253.7	1	1994.5	71.9	2	R.FLTAFLVQISAHSDQNK.M
*	HsFLAG-Control_HeLa_S1	3.0025	0.1061	1969.51	1970.19	4989.5	1	623.6	52.9	1	K.FLLDHQGELFPSPDPSGL.-

gi|23308577|ref|N	14	45	0.216	533	56651	6.7	U	phosphoglycerate dehydrogenase [Homo sapiens]				
*	HsFLAG-Control_HeLa_S1	2.797	0.1609	1298.59	1299.51	8662.6		5	613	59.1	1	K.ILQDGGLQVVEK.Q
*	HsFLAG-Control_HeLa_S1	4.2596	0.2463	1299.28	1299.51	8185.4		1	2222.7	90.9	5	K.ILQDGGLQVVEK.Q
*	HsFLAG-Control_HeLa_S1	3.7534	0.2736	1131.33	1131.27	6365.6		1	1249	85	5	K.VTADVINAAEK.L
*	HsFLAG-Control_HeLa_S1	4.2436	0.3918	1489.41	1489.58	7220.3		1	1217.6	71.4	9	R.AGTGVDNVDLEAATR.K
*	HsFLAG-Control_HeLa_S1	3.3568	0.2833	1618.31	1617.76	8905.7		1	696.1	50	1	R.AGTGVDNVDLEAATRK.G
*	HsHeLa_Control-MG_Ti_20	5.7766	0.4422	2048.68	2049.26	9901.3		1	1494.8	58.3	1	R.ALVDHENVISCPHLGASTK.E
*	HsFLAG-Control_HeLa_S1	5.5782	0.4495	2048.78	2049.26	8441.1		1	1373.5	58.3	2	R.ALVDHENVISCPHLGASTK.E
*	HsFLAG-Control_HeLa_S1	4.6624	0.3136	2050.23	2049.26	9262.2		1	1536.6	40.3	2	R.ALVDHENVISCPHLGASTK.E
*	HsFLAG-Control_HeLa_S1	5.0585	0.5534	2029.69	2030.29	9995.9		1	1173.1	50	2	K.SLTGVVNAQALTSAFSPHTK.P
*	HsFLAG-Control_HeLa_S1	2.6854	0.1328	1345.52	1346.57	7210.8		5	398.8	50	2	K.GTIQVITQGTSLK.N
*	HsFLAG-Control_HeLa_S1	4.2001	0.366	1345.97	1346.57	6432.5		1	1292.8	79.2	5	K.GTIQVITQGTSLK.N
*	HsFLAG-Control_HeLa_S1	3.8303	0.3535	1347.22	1346.57	7450.7		1	1633	79.2	2	K.GTIQVITQGTSLK.N
*	HsFLAG-Control_HeLa_S1	4.6069	0.3931	1625.98	1626.9	5234.8		1	903.9	66.7	7	K.NAGNCLSPAVIVGLLK.E
*	HsFLAG-Control_HeLa_S1	2.6577	0.1196	986.3	987.23	4176.9		3	733.2	85.7	1	R.DLPLLLFR.T
gi|32307148|ref|N	15	56	0.215	1046	116924	6.7	U	O-linked GlcNAc transferase isoform 1 [Homo sapiens]				
*	HsHeLa_Control-MG_Ti_10	2.6237	0.1842	1474.25	1473.73	5440.7		8	457.7	54.2	1	R.MLSFQGLAELAHR.E
	Hs283FLP_Ti_106.1999.19	2.3033	0.1844	1074.57	1075.25	4283		1	513.3	66.7	2	R.SAHFSTLAIK.Q
	HsHeLa_Control_Ti_102.43	5.1897	0.3309	2190.87	2191.53	5183.7		1	1321.2	65.8	21	K.AVTLDPNFLDAYINLGNVLK.E
	HsHeLa_Control_Ti_104.35	2.9291	0.3211	2286.5	2286.56	4625.1		1	312.4	39.5	2	R.AIELQPHFPDAYCNLANALK.E
	HsF-IP-293-MG_Ti_102.16	2.658	0.3262	1657.42	1656.71	7401.1		1	650.6	53.6	1	K.GSVAEAEDCYNTALR.L
	Hs293FLP_Ti_304.1758.17	4.0217	0.4033	1783.28	1781.97	6625.3		1	1154.3	66.7	6	R.LCPTHADSLNNLANIK.R
	HsHeLa_Control_Ti_105.36	5.1462	0.3624	2556.9	2556.88	7516.5		1	1007.3	45.7	7	K.ALEVFPEFAAAHSNLASVLQQQGK.L
	HsHeLa_Control_Ti_106.29	4.7165	0.4207	2122.26	2119.39	5439.1		1	874.4	55.3	1	R.AIQINPAFADAHSNLASIHK.D
	HsHeLa_Control_Ti_102.21	2.8144	0.1837	1394.44	1393.5	3050.6		3	442.4	62.5	2	K.DSGNIPEAIASYR.T
	HsHeLa_Control-MG_Ti_10	3.0676	0.249	1344.1	1343.61	6020.6		1	1056.8	72.7	1	K.KLVSIVADQLEK.N
	Hs283FLP_Ti_102.1902.19	2.7057	0.2068	1216	1215.43	5744		6	560.5	65	1	K.LVSIVADQLEK.N
	HsHeLa_Control-MG_Ti_10	4.2227	0.3564	2423.01	2423.65	4955.4		1	997.7	57.9	4	R.SQYGLPEDAIVYCNFNQLYK.I
	HsHeLa_Control_Ti_106.28	2.6137	0.3614	1623.29	1622.91	4231.2		1	678.3	69.2	1	R.IIFSPVAPKEEHVR.R
	HsFlag1P_Ti_104.3185.318	4.7488	0.4245	1847.4	1848.12	7622.3		1	1773.1	68.8	5	R.VAASQLTCLGCLELIAK.N
	Hs283FLP_Ti_103.1375.13	4.0412	0.2068	1366.1	1365.49	5496.2		2	1195.6	85	1	K.NRQEYEDIAVK.L
gi|4503531|ref|N	6	56	0.214	407	46394	5.5	U	eukaryotic translation initiation factor 4A, isoform 2 [Homo sapiens]				
	HsFLAG-Control_HeLa_NE	4.3475	0.477	1828.66	1829.07	5470.9		1	956.4	66.7	13	R.GIYAYGFEKPSAIQQR.A
	HsFLAG-Control_HeLa_NE	4.8509	0.4125	1396.71	1395.51	5929.6		1	1620.3	84.6	3	K.GYDVIAQAQSGTGK.T
*	HsFLAG-Control_HeLa_S1	4.0881	0.4445	1545.49	1545.78	7019.7		1	1315.4	71.4	1	K.LQAEAPHIVVGTPGR.V
	HsFLAG-Control_HeLa_NE	3.3775	0.2405	1115.66	1115.36	4998.5		2	1015	88.9	15	R.VLITTDLLAR.G
	HsFLAG-Control_HeLa_S1	5.2214	0.4321	2146.44	2145.42	9669.9		1	1812.5	61.1	22	R.GIDVQQVSLVINYDLPTNR.E
*	HsFLAG-Control_HeLa_NE	3.2034	0.2903	1479.37	1478.65	7162.5		2	674.3	62.5	2	K.GVAINFVTEEDKR.I
gi|24234747|ref|N	7	17	0.213	390	43062	5.3	U	interleukin enhancer binding factor 2 [Homo sapiens]				
*	HsFLAG-Control_HeLa_NE	3.5749	0.3317	1732.62	1732.97	4773.1		1	737.8	66.7	5	R.VKPAPDETSFSEALLK.R
*	HsFLAG-Control_HeLa_NE	4.7438	0.4595	2101.68	2100.33	4048.2		1	744.4	60.5	3	R.NQDLAPNSAEQASILSLVTK.I
*	HsHeLa3_Ti_104.4007.400	3.4109	0.1166	2584.49	2583.94	4874.1		3	354.6	38.6	1	K.INNVIDNLIVAPGTFEVQIEEVR.Q
*	HsFLAG-Control_HeLa_NE	4.8918	0.3055	2585.37	2583.94	9198.3		1	1711	37.5	1	K.INNVIDNLIVAPGTFEVQIEEVR.Q
*	HsHeLa3_Ti_104.2901.290	4.3742	0.3415	1410.52	1410.7	4854.7		1	1315.9	84.6	4	K.ILPTLEAVAALGNK.V
*	HsHeLa3_Ti_104.2908.291	3.0799	0.4022	1410.75	1410.7	7534.9		1	646.3	57.7	1	K.ILPTLEAVAALGNK.V
*	HsHeLa3_Ti_104.1865.186	3.6178	0.1791	1043.48	1042.27	7171.2		1	2055.5	94.4	2	K.VLQSALAAIR.H
gi|15431295|ref|N	9	25	0.213	211	24261	11.7	U	ribosomal protein L13 [Homo sapiens]				
gi|15431297|ref|N	9	25	0.213	211	24261	11.7	U	ribosomal protein L13 [Homo sapiens]				
	Hs293FLP_TREX_Ti_106.2	3.5193	0.321	1346.98	1346.53	8825.1		1	1102.5	75	2	R.RVATWFNQPAR.K

	Hs293FLP_TREX_Ti_103.1	2.9829	0.2068	1191.36	1190.35	5747.5		1	983.4	88.9	2	R.VATWFNQPAR.K
	Hs293FLP_TREX_Ti_102.2	2.5001	0.1878	951.36	951.067	5651.7		2	939.3	85.7	1	R.GFSLEELR.V
	Hs293FLP_TREX_Ti_102.1	2.2863	0.2085	1232.42	1233.32	4297.7		2	238.2	60	1	K.STESLQANVQR.L
	HsF-IP-293-MG_Ti_102.124	3.7563	0.3187	1233.15	1233.32	6321.4		1	1432.1	85	4	K.STESLQANVQR.L
	HsFLAG-MOCK_300mM_T	4.2406	0.2782	1233.38	1233.32	6665.6		1	1638.9	90	2	K.STESLQANVQR.L
	Hs293FLP_TREX_Ti_104.1	3.6726	0.2513	1474.58	1474.66	7070.8		1	1100.7	66.7	2	K.STESLQANVQRLK.E
	Hs293FLP-MG_Ti_105.198	3.9903	0.3168	1383.35	1383.69	6048.4		2	1075.6	75	10	K.LATQLTGPVMPVR.N
	HsHeLa_Control-MG_Ti_10	2.1957	0.2205	1383.92	1383.69	2842.6		9	102.2	50	1	K.LATQLTGPVMPVR.N
gi|27436929|ref|N	21	251	0.212	641	70405	6	U	heat shock 70kDa protein 1-like [Homo sapiens]				
	HsF-IP-293-MG_Ti_102.174	2.6315	0.2566	1487.66	1488.59	3419.2		1	176.5	58.3	2	R.TTPSYVAFTDTER.L
	Hs293FLP-MG_Ti_202.217	3.2886	0.3043	1487.89	1488.59	4372.6		1	860.7	83.3	12	R.TTPSYVAFTDTER.L
	HsFLAG-Control_HeLa_NE	3.2444	0.2808	1487.89	1488.59	4634.5		1	570.4	66.7	57	R.TTPSYVAFTDTER.L
	HsHeLa_Control-MG_Ti_20	2.4813	0.2055	1488.47	1488.59	3249.8		1	121.1	50	1	R.TTPSYVAFTDTER.L
	HsHeLa_Control-MG_Ti_20	3.6044	0.4296	1489.1	1488.59	3675.9		1	589.8	75	9	R.TTPSYVAFTDTER.L
	HsFLAG-MOCK_300mM_T	3.2112	0.1491	2159.14	2157.39	6487.7		1	523.9	44.7	2	R.TTPSYVAFTDTERLIGDAAK.N
	HsGST-MOCK_Ti_302.323	3.467	0.4254	1615.76	1615.88	4904.2		1	879.9	76.9	1	K.AFYPEEISSMVLTK.L
	Hs293FLP-MG_Ti_202.302	2.4988	0.215	1197.55	1198.41	3227.7		3	256.7	59.1	2	K.DAGVIAGLNVLR.I
	HsFLAG-Control_HeLa_S1	4.4911	0.242	1198.36	1198.41	6241.2		1	1789.9	90.9	34	K.DAGVIAGLNVLR.I
	Hs293FLP-MG_Ti_202.302	4.3885	0.222	1198.53	1198.41	6626.9		1	1848	90.9	8	K.DAGVIAGLNVLR.I
	HsHeLa_Control-MG_Ti_20	5.5061	0.3911	1661.88	1660.91	4282.5		1	1591.7	86.7	75	R.IINEPTAAAIAYGLDK.G
	HsFLAG-Control_293_Ti_2	4.5503	0.4103	1677.37	1676.7	7130.1		1	1456.7	70	19	K.ATAGDTHLGGEDFDNR.L
	HsGST-MOCK_Ti_403.434	4.8873	0.4836	2303.72	2305.61	7751.9		1	1475.4	54.5	11	K.SINPDEAVAYGAAVQAAILMGDK.S
	HsGST-MOCK_Ti_403.436	5.5284	0.3617	2305.81	2305.61	9393.7		1	2713.4	44.3	1	K.SINPDEAVAYGAAVQAAILMGDK.S
	HsGST-MOCK_Ti_303.335	2.5776	0.2963	2786.6	2788.04	7450.8		1	473.9	37	1	K.QTQIFTTYSDNQPGVLIQVYEGER.A
	Hs293FLP-MG_Ti_204.321	4.2945	0.5036	2787.69	2788.04	6064.2		1	769.6	45.7	4	K.QTQIFTTYSDNQPGVLIQVYEGER.A
	Hs293FLP-MG_Ti_205.311	5.4004	0.3198	2788.58	2788.04	11083.1		1	1393.9	33.7	2	K.QTQIFTTYSDNQPGVLIQVYEGER.A
	HsFLAG-Control_HeLa_S1	3.5026	0.3748	2788.84	2788.04	6443.9		1	586	41.3	2	K.QTQIFTTYSDNQPGVLIQVYEGER.A
	HsFLAG-Control_HeLa_NE	3.9327	0.3083	2788.9	2788.04	14432.1		5	820.7	26.1	2	K.QTQIFTTYSDNQPGVLIQVYEGER.A
	Hs293FLP_Ti_302.3136.31	4.1608	0.366	2789.84	2788.04	7098.1		1	800.1	31.5	1	K.QTQIFTTYSDNQPGVLIQVYEGER.A
	HsFLAG-Control_MG_293_	3.8888	0.3065	1289.5	1288.46	6627.1		1	1451.2	85	5	K.NALESYAFNMK.S
gi|14141152|ref|N	11	28	0.208	730	77516	8.7	U	heterogeneous nuclear ribonucleoprotein M isoform a [Homo sapiens]				
gi|14141154|ref|N	11	28	0.22	691	73561	8.7	U	heterogeneous nuclear ribonucleoprotein M isoform b [Homo sapiens]				
	HsFLAG-Control_HeLa_NE	2.216	0.0821	1066.37	1067.19	3681.6		6	361.8	75	1	R.FEPYANPTK.R
	HsFLAG-Control_HeLa_NE	3.868	0.2018	1265.72	1265.5	4996.7		1	1034.7	85	8	R.AFITNIPFDVK.W
	HsFLAG-Control_HeLa_NE	3.7321	0.3596	1427.65	1427.64	4358.7		1	607.8	66.7	5	R.LGSTVFVANLDYK.V
	HsFLAG-Control_HeLa_NE	2.9836	0.1007	1104.05	1104.2	6868		6	1034.5	83.3	1	R.ADILEDKDGK.S
	Hs293FLP_TREX_Ti_102.1	3.2779	0.0827	1116.31	1115.32	5455.2		2	1117.1	88.9	1	R.INEILSNALK.R
	HsFLAG-Control_HeLa_NE	3.2831	0.3074	1285.68	1285.36	5859.7		2	478.6	60.7	1	K.QGGGGGGGSVPGIER.M
	HsFLAG-MOCK_300mM_T	3.2819	0.1854	1873.97	1873.11	6297.9		1	439.7	47.1	2	R.MGAGLGHGMDRVGSEIER.M
	HsFLAG-MOCK_300mM_T	2.8053	0.3653	1615.63	1614.88	7348.6		1	653.6	53.6	1	R.MGPLGLDHMASSIER.M
	HsFLAG-MOCK_300mM_T	3.8495	0.4435	2036.26	2036.17	5789.9		1	776.9	45.5	4	R.GNFGGSFAGSFGGAGGHAPGVAR.K
	Hs293FLP_TREX_Ti_104.1	4.6316	0.3392	1566.56	1566.72	4920.3		1	1704.6	87.5	3	K.FNECGHVLYADIK.M
	HsFLAG-MOCK_300mM_T	2.6979	0.164	1665.42	1664.82	4947.3		1	932	60.7	1	K.GCGVVKFESPEVAER.A
gi|4506633|ref|NI	4	4	0.208	125	14463	10.5	U	ribosomal protein L31 [Homo sapiens]				
	Hs293FLP_TREX_Ti_102.1	3.2685	0.1907	989.51	989.117	6740.7		1	1268.9	87.5	1	R.SAINEVVTR.E
	Hs293FLP_TREX_Ti_106.2	1.9224	0.154	757.65	757.911	3434.5		4	254.8	75	1	R.IHGVGFK.K
*	Hs293FLP_TREX_Ti_101.0	2.901	0.1704	1145.31	1146.2	7342.2		1	753	77.8	1	K.NLQTVNVDEN.-
*	Hs293FLP_TREX_Ti_101.0	2.9897	0.2234	1147.22	1146.2	3924		1	761.6	83.3	1	K.NLQTVNVDEN.-
gi|4506605|ref|NI	3	21	0.207	140	14865	10.5	U	ribosomal protein L23 [Homo sapiens]				

*	HsFLAG-Control_293_Ti_2	4.6787	0.3493	1970.77	1971.23	5128.4		1	965.6	63.2	18	R.ISLGLPVGAVINCADNTGAK.N
*	HsGST-MOCK_Ti_106.201	2.2358	0.1769	1018.44	1019.28	5355.3		2	574	81.2	1	K.KVHPAVVIR.Q
*	HsGST-MOCK_Ti_106.200	2.6347	0.365	1020.6	1019.28	3875.3		1	603	87.5	2	K.KVHPAVVIR.Q
gi|46195723|ref|	7	15	0.206	490	54774	10.1	U	ribosomal L1 domain containing 1 [Homo sapiens]				
*	Hs293FLP_TREX_Ti_104.1	3.3333	0.2626	1128.19	1128.28	7113.1		1	1247.8	83.3	1	K.AVDALLTHCK.S
*	Hs293FLP_TREX_Ti_103.2	3.6781	0.1854	1332.61	1331.6	5725.5		1	1094.4	81.8	2	K.TVSQIISLQTLK.K
*	HsFLAG-Control_HeLa_NE	3.6559	0.4081	1532.56	1532.74	8390.3		1	1290	70.8	1	R.LLSSFDFFLTDAR.I
*	Hs293FLP_TREX_Ti_104.1	2.7401	0.1813	1116.15	1116.3	4862.8		1	812.7	87.5	1	K.LPEKWESVK.L
*	HsFLAG-Control_HeLa_NE	4.5597	0.4946	2070.16	2071.29	8419.2		1	1157.5	55.6	7	K.SAALPIFSSFVSNWDEATK.R
*	Hs293FLP_TREX_Ti_102.1	5.1239	0.3092	2020.37	2021.19	6076.7		1	1129.8	57.9	2	K.TASVLSKDDVAPESGDTTVK.K
*	Hs293FLP_TREX_Ti_104.2	3.0193	0.356	1968.31	1969.2	6543.7		1	505.2	47.1	1	K.ATNESEDEIPQLVPIGKK.T
gi|60218913|ref|	4	12	0.205	185	21228	7.9	U	calcyclin binding protein isoform 2 [Homo sapiens]				
gi|7656952|ref|N	4	12	0.167	228	26210	8.2	U	calcyclin binding protein isoform 1 [Homo sapiens]				
	HsFLAG-Control_HeLa_S1	2.3756	0.2702	1488.6	1488.77	7067		1	535.6	53.6	1	K.PAAVVAPITTGYTVK.I
	HsFLAG-Control_HeLa_S1	3.5256	0.4431	1489.17	1488.77	5662.8		1	1084.9	67.9	6	K.PAAVVAPITTGYTVK.I
	HsFLAG-Control_HeLa_S1	3.9528	0.4105	1491.28	1488.77	4601.4		1	1042.8	71.4	4	K.PAAVVAPITTGYTVK.I
	HsFLAG-Control_HeLa_S1	4.9689	0.3279	2683.02	2683.04	9671.2		2	873.7	30.7	1	K.IYITLTGVHQVPTENVQVHFTER.S
gi|40254861|ref|	13	42	0.204	1087	114543	7.1	U	ubiquitin associated protein 2-like [Homo sapiens]				
*	HsFLAG-MOCK_300mM_T	2.795	0.1631	2065.24	2065.17	6711.1		1	472.3	46.9	1	R.ARGNWEQPQNQNQTQHK.Q
*	HsFLAG-MOCK_300mM_T	2.9909	0.372	2129.71	2130.17	5980.1		1	512.2	44.1	1	K.NQDECVIALHDCNGDVNR.A
*	HsFLAG-MOCK_300mM_T	4.411	0.4103	2210.9	2211.5	5372.2		1	998.4	57.9	3	R.AINVLLEGNPDTHSWEMVGK.K
*	HsFLAG-Control_HeLa_NE	4.5976	0.4675	2241.35	2242.27	7169.3		1	1034	58.3	10	R.TATEEWGTEDWNEDLSETK.I
*	HsFLAG-MOCK_300mM_T	5.2636	0.464	2349.92	2348.53	4737		1	1034.9	59.1	2	K.GFGDVGEAKGGSTTGSQFLEQFK.T
*	HsFLAG-Control_HeLa_NE	3.2623	0.2024	1487.53	1487.61	9764.6		1	1125.5	61.5	1	K.GGSTTGSQFLEQFK.T
*	HsFLAG-Control_HeLa_NE	4.2917	0.3574	1387.65	1387.49	11560.5		1	2081.4	79.2	9	K.NPSDSAVHSPFTK.R
*	HsFLAG-MOCK_300mM_T	3.4805	0.2352	2130.94	2131.47	7537		1	901.5	52.9	1	K.RQAFTPSSTMMEVFLQEK.S
*	HsFLAG-Control_HeLa_NE	3.6458	0.3911	1960.63	1961.22	3449.8		1	410.4	50	3	K.SPAVATSTAAPPPPSSPLPSK.S
*	HsFLAG-Control_HeLa_NE	3.7205	0.2392	1337.57	1337.48	6766.8		2	746.5	68.2	1	R.RYPSSISSSPQK.D
*	HsFLAG-Control_HeLa_NE	2.9255	0.1046	2597.63	2597.8	8184.9		1	457.3	32	2	K.NGFSSVQATQLQTTQSVEGATGSAVK.S
*	HsFLAG-Control_HeLa_NE	3.8245	0.1943	2283.97	2284.62	3691.5		1	395.1	50	6	R.FPLDYYSIPFPTPTTPLTGR.D
*	HsFLAG-Control_HeLa_S1	3.7144	0.2938	1525.47	1525.61	7405.4		1	1115.6	67.9	2	R.DGSLASNPYSGDLTK.F
gi|4504865|ref|N	14	28	0.203	711	73161	7.3	U	KH-type splicing regulatory protein (FUSE binding protein 2) [Homo sapiens]				
*	HsHeLa3_Ti_102.1597.159	2.6114	0.2573	992.58	993.064	2874.7		5	365	75	1	K.DAFADAVQR.A
*	HsHeLa3_Ti_102.1601.160	3.3329	0.14	993.46	993.064	5263.6		1	1547.6	93.8	2	K.DAFADAVQR.A
*	HsHeLa3_Ti_102.2075.207	5.01	0.4512	2154.87	2155.29	6132.2		1	892.6	50	5	K.IGGDAATTVNNSTPDFGFGGQK.R
*	HsHeLa3_Ti_104.3205.320	4.1088	0.4202	2226.18	2225.58	7346.2		1	1370.2	40.8	2	R.TSMTEEYRVPDGMVGLIIGR.G
*	HsHeLa3_Ti_104.2811.281	3.5663	0.3863	1227.56	1227.51	6687.7		1	1691.1	90.9	2	R.VPDGMVGLIIGR.G
*	HsHeLa3_Ti_103.1595.159	2.184	0.2667	1354.79	1355.49	3638.4		1	308.2	58.3	2	K.VQISPDSGGLPER.S
*	HsHeLa3_Ti_103.1596.159	4.0649	0.2719	1355.77	1355.49	4802.3		1	971.9	75	1	K.VQISPDSGGLPER.S
*	HsHeLa3_Ti_103.1515.151	2.2186	0.2626	1302.65	1303.46	5379.7		6	362.4	50	1	R.SVSLTGAPESVQK.A
*	HsHeLa3_Ti_103.3078.307	4.4457	0.401	1594.53	1593.86	8173.5		1	1741.6	79.2	3	K.VQQACEMVMDILR.E
*	HsHeLa3_Ti_104.1824.182	3.9042	0.1915	1080.69	1080.27	6166.7		1	1561.7	95	2	R.IGGGIDVPVPR.H
*	HsHeLa3_Ti_103.2611.261	3.9623	0.1056	1185.64	1185.41	5272.6		2	1289.9	94.4	2	R.IINDLLQSLR.S
*	HsHeLa3_Ti_103.1807.180	2.6494	0.2016	1535.06	1534.71	8843.2		2	1031.6	61.5	1	K.AINQQTGAFVEISR.Q
*	HsHeLa3_Ti_106.1894.189	4.4018	0.2837	2110.02	2110.33	5768.5		1	1194.3	63.9	3	K.KIGQQPQQPGAPPQQDYTK.A
*	HsHeLa3_Ti_104.1367.136	3.6195	0.2457	1981.93	1982.16	4350.9		1	994.9	64.7	1	K.IGQQPQQPGAPPQQDYTK.A
gi|66346679|ref|	5	6	0.203	408	44965	8.6	U	SERPINE1 mRNA binding protein 1 isoform 1 [Homo sapiens]				
gi|66346681|ref|	5	6	0.206	402	44257	8.7	U	SERPINE1 mRNA binding protein 1 isoform 2 [Homo sapiens]				
	HsGST-MOCK_Ti_402.371	6.338	0.4332	1944.6	1945.09	8660.2		1	2538.7	80	1	R.FDQLFDDESDPFEVLK.A

	Hs293FLP_TREX_Ti_102.0	3.6106	0.3335	1460.72	1461.53	10064.2		1	1057.2	56.7	1	K.SAAQAAAQTNSNAAGK.Q
	HsGST-MOCK_Ti_103.118	3.1142	0.1515	1368.11	1368.62	5680.5		4	635.9	68.2	2	K.KEETQPPVALKK.E
	HsGST-MOCK_Ti_105.151	4.9824	0.3926	2243.03	2243.4	9109.7		1	1648	40	1	K.RGGSGSHNWGTVKDELTESPK.Y
	HsGST-MOCK_Ti_103.139	4.7432	0.4888	2112.62	2113.23	7324.6		1	1419.5	61.8	1	K.SKSEEAHAEDSVMDHHFR.K
gi|21361331|ref|	17	36	0.202	1500	164939	6.7	U	carbamoyl-phosphate synthetase 1, mitochondrial [Homo sapiens]				
*	HsHeLa_Control-MG_Ti_20	4.273	0.4568	1383.56	1383.54	8473.1		1	2237.4	83.3	2	K.AQTAHIVLEDGTK.M
*	HsHeLa_Control-MG_Ti_20	5.9432	0.4194	3387.66	3389.7	6765.5		1	1000.9	29.7	2	K.GYSFGHPSSVAGEVVFNTGLGGYPEAITDPAYK.G
*	HsHeLa_Control-MG_Ti_20	3.9202	0.3576	1734.36	1734.9	5872		1	1176.6	75	1	K.IEFEGQPVDFVDPNK.Q
*	HsHeLa_Control-MG_Ti_20	3.119	0.2252	1750.54	1750.95	5685.2		1	792	60.7	1	R.GAEVHLVPWNHDFTK.M
*	HsHeLa_Control-MG_Ti_20	4.31	0.3405	1933.21	1931.24	6368.4		1	1296.7	63.2	4	K.EPLFGISTGNLITGLAAGAK.T
*	HsHeLa_Control-MG_Ti_20	2.9887	0.2276	1726.41	1726.07	4606.4		1	448.8	53.1	1	K.ATTITSVLPKPALVASR.V
*	HsHeLa_Control-MG_Ti_20	3.7666	0.3144	2309.03	2310.7	3607.2		1	407.6	50	3	K.QADTVYFLPITPQFVTEVIK.A
*	HsHeLa_Control-MG_Ti_20	5.1565	0.4141	1591.66	1590.81	4881.3		1	1180.6	78.6	5	K.IAPSFAVESIEDALK.A
*	HsHeLa_Control-MG_Ti_20	3.261	0.3118	1595.4	1593.75	9902.9		1	854.3	50	1	R.SAYALGGLGSGICPNR.E
*	HsHeLa_Control-MG_Ti_20	4.5182	0.2411	3414.84	3414.86	4516		1	417.9	25.8	1	R.ILDIYHQEACGGCIISVGGQIPNNLAVPLYK.N
*	HsHeLa_Control-MG_Ti_20	3.8557	0.2549	1223.23	1222.42	5572.6		1	1337.1	85	2	R.SIFSAVLDELK.V
*	HsHeLa_Control-MG_Ti_20	4.5636	0.3582	1639.3	1638.95	5930		1	1413.1	78.6	4	K.AFAISGPFNVQFLVK.G
*	HsHeLa_Control-MG_Ti_20	3.4739	0.3081	1279.38	1279.48	5475.2		1	1281.1	86.4	2	K.TLGVDFIDVATK.V
*	HsHeLa_Control-MG_Ti_20	4.1146	0.4872	2013.69	2014.38	6285.6		1	817.5	58.8	2	K.HLPTLDHPIIPADYVAIK.A
*	HsHeLa_Control-MG_Ti_20	3.8312	0.3361	2414.33	2416.64	7322.1		1	1136.9	52.4	2	R.CEMASTGEVACFGEGIHTAFLK.A
*	HsHeLa_Control-MG_Ti_10	4.1549	0.3069	1590.23	1589.79	6777.5		1	1380.7	76.9	2	R.FLGVAEQLHNEGFK.L
*	HsHeLa_Control-MG_Ti_20	4.1361	0.1782	1728.17	1727.91	5844.7		1	763.7	60	1	R.DGSIDLVINLPNNNTK.F
gi|34419635|ref|	33	234	0.202	643	71028	6.1	U	heat shock 70kDa protein 6 (HSP70B') [Homo sapiens]				
	HsF-IP-293-MG_Ti_102.17	2.6315	0.2566	1487.66	1488.59	3419.2		1	176.5	58.3	2	R.TTPSYVAFTDTER.L
	HsFLAG-Control_HeLa_NE	3.2444	0.2808	1487.89	1488.59	4634.5		1	570.4	66.7	57	R.TTPSYVAFTDTER.L
	Hs293FLP-MG_Ti_202.217	3.2886	0.3043	1487.89	1488.59	4372.6		1	860.7	83.3	12	R.TTPSYVAFTDTER.L
	HsHeLa_Control-MG_Ti_20	2.4813	0.2055	1488.47	1488.59	3249.8		1	121.1	50	1	R.TTPSYVAFTDTER.L
	HsHeLa_Control-MG_Ti_20	3.6044	0.4296	1489.1	1488.59	3675.9		1	589.8	75	9	R.TTPSYVAFTDTER.L
	HsFLAG-Control_MG_293_	4.0254	0.3882	1613.23	1613.77	5127		1	1241.4	78.6	2	K.SQAALNPHNTVFDAK.R
*	HsFLAG-Control_MG_293_	4.0742	0.2754	1169.65	1170.35	6353.2		1	2020.7	90.9	4	K.DAGAIAGLNVLR.I
	Hs293FLP-MG_Ti_202.294	4.8775	0.4462	1687.76	1688.92	5341.9		1	1731.2	83.3	3	R.IINEPTAAAIAYGLDR.R
	HsGST-MOCK_Ti_303.271	5.3019	0.4188	1687.89	1688.92	6005.7		1	1770	80	5	R.IINEPTAAAIAYGLDR.R
	HsFLAG-Control_293_Ti_2	4.1753	0.1988	1687.96	1688.92	6399		1	1885.4	51.7	1	R.IINEPTAAAIAYGLDR.R
	HsFLAG-Control_HeLa_S1	4.903	0.4088	1688.25	1688.92	7186.8		1	1733	73.3	10	R.IINEPTAAAIAYGLDR.R
	HsFLAG-Control_HeLa_S1	3.9936	0.1641	1688.33	1688.92	7417.7		1	1534	45	1	R.IINEPTAAAIAYGLDR.R
	HsFLAG-Control_HeLa_S1	5.0183	0.3954	1688.36	1688.92	5572.8		1	1466.9	76.7	6	R.IINEPTAAAIAYGLDR.R
	Hs283FLP_Ti_102.2353.23	3.8797	0.1309	1688.68	1688.92	7756.8		2	1564.1	46.7	1	R.IINEPTAAAIAYGLDR.R
	HsFLAG-Control_HeLa_NE	4.519	0.1849	1688.87	1688.92	8251.2		1	1695	48.3	2	R.IINEPTAAAIAYGLDR.R
	Hs293FLP_Ti_302.2512.25	5.4892	0.4056	1689.01	1688.92	4983.8		1	1547.6	80	6	R.IINEPTAAAIAYGLDR.R
	HsF-IP-293-MG_Ti_102.22	4.8927	0.3179	1689.03	1688.92	5477.4		1	1448.1	76.7	2	R.IINEPTAAAIAYGLDR.R
	HsF-IP-293-MG_Ti_102.23	4.2375	0.1806	1689.14	1688.92	8011.1		1	1686.5	46.7	1	R.IINEPTAAAIAYGLDR.R
	Hs293FLP-MG_Ti_202.294	5.0798	0.1684	1689.4	1688.92	8497.4		1	2183.9	51.7	2	R.IINEPTAAAIAYGLDR.R
	HsFLAG-Control_HeLa_S1	3.5964	0.1281	1689.42	1688.92	8134.2		1	1438.2	45	1	R.IINEPTAAAIAYGLDR.R
	HsFLAG-Control_HeLa_NE	5.5152	0.4246	1689.75	1688.92	5197.5		1	1487.3	76.7	18	R.IINEPTAAAIAYGLDR.R
	HsHeLa_Control-MG_Ti_10	5.0746	0.318	1689.79	1688.92	5333.8		1	1131.8	70	9	R.IINEPTAAAIAYGLDR.R
	HsFLAG-Control_293_Ti_2	4.5503	0.4103	1677.37	1676.7	7130.1		1	1456.7	70	19	K.ATAGDTHLGGEDFDNR.L
	HsGST-MOCK_Ti_404.277	3.9207	0.2533	1543.5	1543.69	5188.1		1	843.1	72.7	4	R.ARFEELCSDLFR.S
	HsGST-MOCK_Ti_102.200	3.7463	0.1191	1543.86	1543.69	7015		1	1515	52.3	1	R.ARFEELCSDLFR.S
	Hs293FLP_Ti_303.2415.24	4.2742	0.302	1545.2	1543.69	4892.3		1	1270.4	86.4	21	R.ARFEELCSDLFR.S

	HsFLAG-Control_HeLa_S1	3.4883	0.2705	1316.29	1316.42	7134.9		5	1058.9	77.8	8	R.FEELCSDLFR.S
	HsFLAG-Control_HeLa_NE	2.0048	0.1567	902.47	903.02	4539.8		5	443.3	71.4	4	R.STLEPVEK.A
	HsFLAG-Control_MG_293_	3.1449	0.1938	1082.22	1082.24	5278.9		5	835.3	87.5	7	K.LLQDFFNGK.E
	HsFLAG-MOCK_300mM_T	3.5405	0.2578	1568.26	1566.8	8502.8		1	1323.3	75	1	K.LLQDFFNGKELNK.S
	HsFLAG-Control_MG_293_	2.37	0.1055	1183.56	1184.38	4415.4		2	447.5	65	2	R.FELSGIPPAPR.G
	HsFLAG-Control_MG_293_	3.253	0.2405	1184.35	1184.38	3642.9		1	911.3	80	11	R.FELSGIPPAPR.G
	HsFLAG-Control_MG_293_	2.8795	0.2759	1457.63	1457.53	8283.2		1	706.6	53.8	1	R.QGDPSTGPIIEEVD.-
gi|13654237|ref|N	52	122	0.201	4128	469093	7.1	U		protein kinase, DNA-activated, catalytic polypeptide [Homo sapiens]			
	HsFLAG-Control_293_Ti_1	4.1025	0.3982	2620.81	2620.97	8093.6		1	734.3	39.6	4	R.GLGQECVLSSSPAVLALQTSLVFSR.D
*	HsFLAG-Control_293_Ti_1	2.1132	0.1403	970.4	971.194	7312.6		1	826.6	75	1	K.LPVLAGCLK.G
*	HsFLAG-Control_293_Ti_1	2.7859	0.1552	971.39	971.194	4972.2		4	1022.5	81.2	1	K.LPVLAGCLK.G
*	HsFLAG-Control_293_Ti_2	2.2131	0.1914	972.08	971.194	6546.6		1	717.5	75	2	K.LPVLAGCLK.G
	HsHeLa3_Ti_104.2845.284	3.4697	0.3397	1240.83	1240.41	4478		1	749.5	80	1	K.GLSSLLCNFTK.S
	HsHeLa3_Ti_103.3232.323	3.4894	0.2767	1151.28	1150.36	6891.4		1	1430.4	80	1	K.AALSALESFLK.Q
	HsHeLa_Control-MG_Ti_20	3.4787	0.2784	1497.87	1497.7	9752		5	755.6	58.3	2	R.NCISTVVHQGLIR.I
	HsFLAG-Control_293_Ti_2	3.6929	0.2242	1576.24	1575.72	9065.4		1	961.7	61.5	2	K.NLSSNEAISLEEIR.I
	HsFLAG-Control_MG_293_	4.7414	0.3429	1443.73	1444.73	7832.2		1	2205.6	84.6	11	R.VVQMLGSLGGQINK.N
	HsHeLa3_Ti_106.3187.318	3.9772	0.4159	1317.47	1316.63	6966.3		1	1509.8	85	1	K.PVIFLDVFLPR.V
	HsFLAG-Control_293_Ti_1	3.502	0.3672	1177.05	1177.27	7630.5		1	1692.2	94.4	1	R.LACDVDQVTR.Q
	Hs293FLP-MG_Ti_206.036	2.5996	0.1291	2274.01	2275.67	9324.3		2	405.1	38.2	1	R.QLYEPLVMQLIHWFTNNK.K
*	HsFLAG-Control_293_Ti_1	4.2052	0.4162	2945.35	2946.33	8376.3		1	1090.8	44.2	1	K.KFESQDTVALLEAILDGIVDPVDSTLR.D
	HsHeLa3_Ti_104.2277.227	2.5135	0.1518	1340.59	1339.54	5790.3		5	559.5	63.6	1	R.LGASLAFNNIYR.E
	HsHeLa_Control-MG_Ti_20	4.1308	0.3038	3881.13	3881.38	10987.6		1	808.6	21.4	1	K.DVLKEEGVSFLINTFEGGGCGQPSGILAQPTLLYLR.G
	HsHeLa3_Ti_103.3043.304	4.9432	0.464	1817.23	1816.11	5348.7		1	945.1	64.7	9	R.TVGALQVLGTEAQSSLLK.A
	HsGST-MOCK_Ti_405.461	3.9577	0.4637	2075.42	2077.45	10891.3		1	546.3	38.9	4	K.AVAFFLESIAMHDIIAAEK.C
	Hs293FLP-MG_Ti_202.339	4.1709	0.2788	2564.82	2563.79	8715.1		1	926.5	43.2	3	K.ITAQSIEELCAVNLYGPDAQVDR.S
	HsGST-MOCK_Ti_106.258	3.6844	0.2005	3145.03	3144.6	9761.7		1	1021.7	26.8	1	R.AGLLHNILPSQSTDLHHSVGTELLSLVYK.G
	HsHeLa3_Ti_106.2587.258	2.7438	0.3035	1769.86	1769.12	6736.9		1	590.1	46.4	1	R.VLEQLIVAHFPMQSR.E
	HsHeLa3_Ti_105.0183.018	3.5405	0.1139	2712.72	2710.18	8143.1		1	1045.5	31.8	1	K.FLDALELSQSPMLLELMTEVLCR.E
	HsFLAG-Control_MG_293_	4.7715	0.4663	2048.58	2048.23	6917.1		1	1012.4	58.8	7	K.INQVFHGSCITEGNELTK.T
	HsGST-MOCK_Ti_405.261	3.767	0.3536	1620.47	1620.85	9165		1	1087.9	66.7	2	K.FYQGFLFSEKPEK.N
	HsHeLa3_Ti_104.4096.409	4.113	0.1818	1445.7	1445.74	5008.4		1	1452.5	86.4	2	K.NLLIFENLIDLK.R
	HsHeLa3_Ti_103.2700.270	3.2755	0.3281	1610.26	1609.84	6289		1	723.9	62.5	1	R.YNFPVEVEVPMER.K
	HsHeLa3_Ti_103.1531.153	3.0746	0.4023	1468.85	1468.56	5223.3		1	859	73.1	3	R.SLGPPQGEEDSVPR.D
	HsFLAG-Control_293_Ti_1	2.7964	0.2496	1206.02	1206.47	5280.4		1	773.8	75	2	K.LGNPIVPLNIR.L
	HsHeLa3_Ti_105.2328.232	2.8598	0.2438	1679.08	1679.96	9457		3	729.8	53.8	1	K.LVINTEEVFRPYAK.H
	HsHeLa3_Ti_103.3480.348	4.1041	0.3019	1519.03	1518.71	6128.5		1	1582.7	83.3	2	K.NILEESLCELVAK.Q
	HsGST-MOCK_Ti_405.313	3.3821	0.2384	2085.88	2086.32	7656.6		2	374.3	38.2	1	R.ELLNPVVEFVSHPSTTCR.E
	HsFLAG-Control_293_Ti_1	4.8425	0.3215	2121.4	2120.5	8927		1	1749.4	63.9	4	K.DVLIQGLIDENPGLQLIIR.N
	HsFLAG-Control_MG_293_	3.5782	0.1871	1218.7	1219.47	6476.9		1	1055.2	80	2	R.LLALNSLYSPK.I
	HsHeLa3_Ti_103.2587.258	4.3484	0.3929	2297.06	2296.6	6795.5		1	864.5	50	1	R.STVLTPMFVETQASQGTLQTR.T
	HsFLAG-Control_293_Ti_2	3.4641	0.2916	1136.05	1136.29	8789.8		1	1248.6	83.3	1	R.HGDLPDIQIK.H
	HsGST-MOCK_Ti_104.204	2.9316	0.2539	2159.73	2159.54	5223.6		7	301.3	36.8	1	K.HSSLITPLQAVAQRDPIIAK.Q
	HsGST-MOCK_Ti_104.203	3.631	0.2803	2159.84	2159.54	6624.6		1	1050.1	36.8	1	K.HSSLITPLQAVAQRDPIIAK.Q
	HsHeLa3_Ti_105.3771.377	3.4924	0.2966	1340.66	1340.61	4079		1	640.4	77.3	3	K.QLFSSLFSGILK.E
	HsFLAG-Control_293_Ti_2	1.9429	0.1407	951.43	952.182	5040		4	582.6	75	1	R.LLPAELPAK.R
	HsFLAG-Control_293_Ti_1	3.0489	0.2561	2299.4	2298.48	5060.4		5	303	44.1	1	K.DFWELASLDCYNHLAEWK.S
	HsHeLa3_Ti_103.3747.374	2.9151	0.0953	2238.73	2237.58	7309.3		2	701	50	1	K.IWSEPFYQETYLPYMIR.S

	HsGST-MOCK_Ti_302.392	5.1482	0.4262	1904.41	1905.2	9603.5		1	2985.4	78.1	6	K.LLLQGEADQSLLTFIDK.A
	HsFLAG-Control_293_Ti_1	5.2701	0.4395	2181.91	2182.52	9211.5		1	2616	69.4	9	K.LQSVQALTEIQEFISFISK.Q
*	HsHeLa3_Ti_102.2659.266	2.6302	0.1714	1770.14	1769.95	3670.9		3	299	50	1	K.TVSLLDENNVSSYLSK.N
	Hs293FLP-MG_Ti_202.308	4.1735	0.4413	2173.55	2174.38	5438.6		1	771.8	55.3	6	R.IIANALSSEPACLAEIEEDK.A
	HsGST-MOCK_Ti_405.359	3.3844	0.2706	2180.3	2178.59	10326.5		1	838.1	50	1	R.LLQIIERYPEETLSLMTK.E
	HsFLAG-Control_293_Ti_1	3.6633	0.2795	3976.29	3977.37	9350.4		1	540.8	19.1	1	K.DQAVAVQHSVEEITDNYPQAIVYPFIISSESYSFK.D
	HsFLAG-Control_293_Ti_1	4.1278	0.2877	3002.5	3004.41	11045.4		1	1174	27.9	3	K.SKLDQGGVIQDFINALDQLSNPELLFK.D
	HsHeLa3_Ti_103.3803.380	3.5816	0.2067	1639.77	1637.93	5589.9		2	733.3	61.5	2	K.LSDFNDITNMLLLK.M
	HsHeLa3_Ti_103.3707.370	2.5412	0.2549	2394.72	2395.66	6747.1		1	359.3	37.5	1	R.VEQLFQVMNGILAQDSACSQR.A
*	HsHeLa3_Ti_104.4719.471	4.3303	0.3091	1629.63	1629.94	7099.7		1	1725.7	80.8	2	R.LGLIEWLENTVTLK.D
*	HsFLAG-Control_293_Ti_2	2.6878	0.2475	1420.85	1421.61	10444.3		6	877.1	63.6	1	K.DLLLNTMSQEEK.A
	HsFLAG-Control_293_Ti_1	3.5291	0.2914	1632.53	1632.72	4662.4		1	773.9	71.4	2	R.AQEPESGLSEETQVK.C
gi|27734703|ref|N		4	4	0.2	330	37221	6.3	U	hypothetical protein LOC283742 [Homo sapiens]			
*	HsHeLa3_Ti_103.1770.177	2.8812	0.2804	1199.55	1199.39	5723.2		1	956.4	80	1	K.GPLLEEQALTK.A
*	HsHeLa3_Ti_103.4160.416	3.0448	0.3136	2480.4	2480.74	6277.4		1	536.5	38.6	1	K.AAEGGLSSPEFSELCIWLGSQIK.S
*	HsHeLa3_Ti_103.4460.446	4.6366	0.3214	2172.71	2170.44	6518.5		1	1017.1	55.6	1	K.NSEVYQEVQAMFDTLGIPK.S
*	HsHeLa3_Ti_102.1723.172	3.0457	0.3044	1565.62	1563.68	8152.7		1	1159.9	70.8	1	K.MDLNSEQAEQLER.I
gi|10800138|ref|N		3	9	0.198	126	13936	10.3	U	H2B histone family, member B [Homo sapiens]			
gi|66912162|ref|N		3	9	0.198	126	13920	10.3	U	histone 2, H2bf [Homo sapiens]			
gi|4504271|ref|N		3	9	0.198	126	13906	10.3	U	H2B histone family, member K [Homo sapiens]			
gi|4504269|ref|N		3	9	0.198	126	13892	10.3	U	H2B histone family, member J [Homo sapiens]			
gi|4504265|ref|N		3	9	0.198	126	13906	10.3	U	H2B histone family, member G [Homo sapiens]			
gi|4504263|ref|N		3	9	0.198	126	13989	10.3	U	H2B histone family, member E [Homo sapiens]			
gi|4504261|ref|N		3	9	0.198	126	13922	10.3	U	H2B histone family, member D [Homo sapiens]			
gi|4504259|ref|N		3	9	0.198	126	13952	10.3	U	H2B histone family, member C [Homo sapiens]			
gi|4504257|ref|N		3	9	0.198	126	13906	10.3	U	H2B histone family, member A [Homo sapiens]			
gi|21396484|ref|N		3	9	0.198	126	13906	10.3	U	H2B histone family, member H [Homo sapiens]			
gi|21166389|ref|N		3	9	0.198	126	13906	10.3	U	H2B histone family, member L [Homo sapiens]			
gi|20336752|ref|N		3	9	0.198	126	13936	10.3	U	H2B histone family, member B [Homo sapiens]			
gi|18105048|ref|N		3	9	0.198	126	13890	10.3	U	H2B histone family, member T [Homo sapiens]			
gi|11036646|ref|N		3	9	0.198	126	13944	10.4	U	H2B histone family, member S [Homo sapiens]			
	Hs293FLP-MG_Ti_105.159	2.3675	0.2884	1265.5	1266.44	5744.3		1	525.4	61.1	1	R.KESYSVYVYK.V
	Hs293FLP-MG_Ti_105.156	3.659	0.2277	1267.24	1266.44	4674.6		1	868.1	83.3	4	R.KESYSVYVYK.V
	HsFlag1P_Ti_105.3933.393	4.8638	0.5024	1743.99	1745.02	10137.7		1	2353.4	75	4	K.AMGIMNSFVNDIFER.I
gi|10835230|ref|N		1	3	0.197	61	6070	8	U	metallothionein 1G [Homo sapiens]			
gi|88974819|ref|X		1	3	0.067	178	18903	8.4	U	PREDICTED: hypothetical protein XP_498969 [Homo sapiens]			
gi|5174764|ref|N		1	3	0.197	61	6042	7.8	U	metallothionein 2A [Homo sapiens]			
gi|28866966|ref|N		1	3	0.197	61	6137	7.8	U	metallothionein 1M [Homo sapiens]			
gi|10835232|ref|N		1	3	0.197	61	6068	8	U	metallothionein 1X [Homo sapiens]			
	HsFLAG-MOCK_150mM_T	3.9348	0.4427	1446.47	1446.43	9073		1	1586	81.8	3	K.SCCSCCPVGCAK.C
gi|35493811|ref|N		11	55	0.196	530	59380	10.1	U	RNA-binding region containing protein 2 isoform a [Homo sapiens]			
gi|4757926|ref|N		11	55	0.198	524	58657	10.1	U	RNA-binding region containing protein 2 isoform b [Homo sapiens]			
gi|35493829|ref|N		11	55	0.279	373	40541	6.3	U	RNA-binding region containing protein 2 isoform c [Homo sapiens]			
gi|35493822|ref|N		11	55	0.283	367	39818	6.6	U	RNA-binding region containing protein 2 isoform d [Homo sapiens]			
gi|35493817|ref|N		11	55	0.279	373	40541	6.3	U	RNA-binding region containing protein 2 isoform c [Homo sapiens]			
	HsHeLa_Control_Ti_102.31	3.0608	0.0842	1272.35	1272.4	5737.4		1	1062	80	2	R.DLEEFFSTVGK.V
	HsFLAG-Control_HeLa_NE	3.6188	0.3643	2391.66	2392.76	6035.3		1	556.6	43.2	3	K.GIAYVEFVDVSSVPLAIGLTGQR.V
	HsFLAG-Control_HeLa_NE	4.5568	0.4319	2392.66	2392.76	9161.6		1	1251.9	33	2	K.GIAYVEFVDVSSVPLAIGLTGQR.V
	HsHeLa3_Ti_104.2473.247	2.3954	0.4214	1551.68	1552.86	7863.6		1	777.1	57.1	1	R.VLGVPIIVQASQAEK.N

	HsFLAG-Control_HeLa_NE	3.2534	0.2862	1552.81	1552.86	7033		1	737.5	57.1	2	R.VLGVPIIVQASQAEK.N
	Hs293FLP-MG_Ti_203.276	4.365	0.3913	1553.59	1552.86	3284.7		1	668.7	75	22	R.VLGVPIIVQASQAEK.N
	HsHeLa3_Ti_104.2463.246	4.144	0.3784	1553.79	1552.86	3060.7		1	760.5	82.1	2	R.VLGVPIIVQASQAEK.N
	HsFLAG-Control_HeLa_NE	4.9435	0.4651	1829.7	1830.86	7134.8		1	1364.2	65.6	17	R.TDASSASSFLDSDELER.T
	HsFLAG-Control_HeLa_NE	3.3244	0.1326	991.23	991.089	6104.5		1	1177.4	88.9	2	R.TGIDLGTTGR.L
	HsGST-MOCK_Ti_105.147	3.3066	0.439	1238.54	1238.43	9798.2		1	1485.6	80	1	K.HGGVIHIYVDK.N
	HsHeLa_Control_Ti_106.34	2.6017	0.3543	1693.27	1692.93	5444.2		1	563.2	50	1	K.CPSIAAAIAAVNALHGR.W
gi|4826734|ref|N	8	24	0.196	526	53426	9.4	U	fusion (involved in t(12;16) in malignant liposarcoma) isoform a [Homo sapiens]				
*	HsFLAG-Control_HeLa_NE	6.9768	0.4157	3587.24	3587.75	10060		1	2365	33.1	9	R.HDSEQDNSDNNTIFVQGLGENVTIESVADYFK.Q
*	HsFLAG-Control_HeLa_NE	3.7472	0.3555	1664	1662.84	4078.6		1	929.7	66.7	2	K.LKGEATVSFDDPPSAK.A
	HsFLAG-Control_HeLa_S1	3.1093	0.3568	1420.76	1421.5	8011.9		1	1098.8	65.4	3	K.GEATVSFDDPPSAK.A
	HsFLAG-Control_HeLa_NE	2.937	0.2157	1023.19	1023.13	5824.6		1	1015.2	87.5	4	K.AAIDWFDGK.E
*	HsFLAG-MOCK_300mM_T	2.8818	0.288	1896.47	1896.11	5992.6		1	817.2	59.4	1	K.AAIDWFDGKEFSGNPIK.V
*	HsGST-MOCK_Ti_404.234	3.388	0.4386	1814.01	1813.91	7582.7		1	727.6	61.5	2	K.CPNPTCENMNFSWR.N
*	HsGST-MOCK_Ti_104.128	4.6709	0.513	2253.41	2254.36	5051.1		1	1442.2	67.4	2	K.APKPDGPGGGPGGSHMGGNYGDDR.R
*	HsGST-MOCK_Ti_104.128	3.6633	0.3522	2255.6	2254.36	5519.2		1	1011.7	38	1	K.APKPDGPGGGPGGSHMGGNYGDDR.R
gi|4506761|ref|N	2	2	0.196	97	11203	7.4	U	S100 calcium-binding protein A10 [Homo sapiens]				
*	HsFLAG-MOCK_300mM_T	2.6719	0.2594	1095.61	1095.24	3415		4	619.3	81.2	1	K.GYLTKEDLR.V
*	HsGST-MOCK_Ti_403.248	2.6325	0.2289	1209.42	1209.34	4994.7		1	729.2	83.3	1	K.EFPGFLENQK.D
gi|88948848|ref|	2	6	0.196	107	11186	9.1	U	PREDICTED: hypothetical protein XP_950274 [Homo sapiens]				
	HsHeLa-FLAG-IP_S100_Ti_	2.8382	0.1203	932.36	933.006	3007.7		7	641.4	92.9	1	K.LLEGEESR.L
	HsHeLa-FLAG-IP_S100_Ti_	4.3215	0.1842	1477.47	1476.71	8315.4		1	1887.4	87.5	5	R.LESGMQNMSIHTK.T
gi|5031931|ref|N	3	10	0.195	215	23384	4.6	U	nascent-polypeptide-associated complex alpha polypeptide [Homo sapiens]				
*	HsFLAG-MOCK_300mM_T	3.991	0.2185	1551.84	1550.88	5870.5		1	1385.7	83.3	5	K.NILFVITKPDVYK.S
*	Hs293FLP_TREX_Ti_102.2	4.6715	0.4282	1484.95	1485.63	9384.2		1	1707.8	73.1	4	K.SPASDTYIVFGEAK.I
*	HsFLAG-Control_HeLa_S1	2.5519	0.1492	1615.3	1615.78	9381.8		2	688.3	57.1	1	K.IEDLSQQAQLAAAEK.F
gi|4503423|ref|N	2	6	0.195	164	17748	6.6	U	dUTP pyrophosphatase isoform 2 [Homo sapiens]				
gi|70906444|ref|N	2	6	0.227	141	15395	6.5	U	dUTP pyrophosphatase isoform 3 [Homo sapiens]				
gi|70906441|ref|N	2	6	0.127	252	26563	9.4	U	dUTP pyrophosphatase isoform 1 precursor [Homo sapiens]				
	HsGST-MOCK_Ti_403.270	2.9871	0.1544	1707.62	1706.85	8757.9		1	1109.7	67.9	1	K.HFIDVGAGVIDEDYR.G
	HsGST-MOCK_Ti_402.307	4.5182	0.4462	2067.77	2068.25	7254.6		1	1790.8	75	5	R.IFYPEIEEVQALDDTER.G
gi|4507651|ref|N	3	5	0.194	248	28522	4.7	U	tropomyosin 4 [Homo sapiens]				
gi|89028749|ref|	3	5	0.224	214	24866	5.1	U	PREDICTED: similar to tropomyosin 4 [Homo sapiens]				
gi|51467148|ref|	3	5	0.224	214	24926	5	U	PREDICTED: similar to tropomyosin 4 [Homo sapiens]				
	HsFLAG-MOCK_300mM_T	3.7804	0.2326	1885.9	1885.09	7915.4		1	1326.7	44.6	1	R.RIQLVEEELDRAQER.L
	Hs293FLP_TREX_Ti_104.1	4.3686	0.233	1444.9	1444.67	9084.8		1	1752.4	79.2	3	R.LATALQKLEEAEK.A
	HsHeLa_Control-MG_Ti_10	2.9692	0.2388	2341.94	2341.5	10550.9		2	761.3	42.1	1	K.EENVGLHQTLDQTLNELNCI.-
gi|34594669|ref|N	5	8	0.194	237	26927	6.8	U	HCCA2 protein [Homo sapiens]				
*	HsHeLa_Control-MG_Ti_20	3.1815	0.1511	1216.34	1216.38	6626.6		1	999.5	88.9	2	R.KAYLEPEHTK.A
*	HsFlag1P_Ti_106.2812.281	4.1073	0.3687	1705.57	1706.04	8219.2		1	1209.2	69.2	2	R.ITDFQFKELVVLPR.E
	HsFLAG-Control_293_Ti_2	2.426	0.1213	825.39	826.027	3728.7		6	344.9	83.3	1	K.ELVVLPR.E
*	HsFLAG-Control_293_Ti_2	3.0839	0.2053	1264.12	1264.42	5205.1		1	761.4	75	2	K.LVTDEDVFPTK.Y
*	HsHeLa_Control-MG_Ti_20	2.7482	0.0849	1298.61	1298.44	5399.3		2	576.5	70	1	R.EFPSSFESLVR.K
gi|67782328|ref|N	13	28	0.192	1722	182686	7	U	trinucleotide repeat containing 6B isoform 1 [Homo sapiens]				
	HsHeLa_Control-MG_Ti_20	5.8275	0.3555	3187.08	3187.53	9148.7		1	1087.7	28.1	4	K.VPEVTKPSLSQPTAASPIGSSPSPPVNGGNNAK.R
*	Hs293FLP-MG_Ti_204.325	3.5672	0.274	2989.86	2990.22	8288.9		1	548.3	24.1	1	R.IGPGSGFSNFNPNSNPSAWPALVQEGTSR.K
*	HsHeLa_Control_Ti_102.13	4.4246	0.4734	2209.82	2210.28	6919.4		1	1086.6	52.4	1	K.GALETDNSNSSAQVSTVGQTSR.E
*	HsHeLa_Control-MG_Ti_20	3.7253	0.3534	1989.22	1990.11	6952		1	1303.7	64.7	2	K.GHPLPENQGNAQAPCWGR.S
*	HsHeLa_Control-MG_Ti_20	4.1572	0.2028	1990.78	1990.11	6895		1	1914.7	51.5	1	K.GHPLPENQGNAQAPCWGR.S

*	HsHeLa_Control-MG_Ti_20	5.0235	0.4008	2242.85	2243.49	7146.3		1	1488.8	44.4	2	R.SYRPTHPDCQAVLQTLLSR.T
*	HsHeLa_Control-MG_Ti_10	5.9871	0.3165	3722.64	3722.88	6529.4		1	1615.1	31.2	3	K.NSNWESSASKPVSGWGEGGQNEIGTWGNGGNASLASK.G
	HsHeLa_Control-MG_Ti_20	3.75	0.3507	1476.9	1476.55	7400.4		1	1278.9	67.9	1	K.GGSHGLFGNSTAQSR.G
	HsHeLa_Control-MG_Ti_10	3.5359	0.2017	3129.73	3127.4	4963		4	449.2	25	1	R.GGSPYNQFDIIPGDTLGGHTGPAGDSWLPAK.S
	HsFLAG-Control_293_Ti_2(	6.3886	0.4317	3766.82	3765.13	5331.3		1	1184.2	30	7	K.GIQNIDPESDPYVTPGSVLGGTATSPIVDTDHQLLR.D
	HsHeLa_Control-MG_Ti_20	4.3594	0.4181	3900.73	3902.05	5159.1		1	492.4	23	2	R.DNTTGSNSSLNTSLPSPGAWPYSASDNSFTNVHSTSAK.F
	HsFLAG-MOCK_300mM_T	2.5037	0.25	1988.67	1989.16	5129		3	268.7	38.2	1	K.STWSPDPIGHNPTHLSNK.M
	HsHeLa_Control-MG_Ti_10	5.062	0.4198	3689.8	3687.11	7620.6		1	694.8	23.5	2	R.LASASTWSDGGSVRPSYWLVLHNLTPQIDGSTLR.T
gi|4506583|ref|NI	9	17	0.192	616	68138	7.2	U	replication protein A1, 70kDa [Homo sapiens]				
*	HsFLAG-Control_HeLa_S1(	3.394	0.3446	1485.41	1486.58	9434.7		1	1637	66.7	1	K.AAGPSLSHTSGGTQSK.V
*	HsHeLa_Control-MG_Ti_10	2.3544	0.3878	1485.61	1486.58	5058.9		2	269.3	43.3	1	K.AAGPSLSHTSGGTQSK.V
*	HsHeLa_Control-MG_Ti_10	3.311	0.4488	1486.55	1486.58	5405.3		1	951.4	66.7	4	K.AAGPSLSHTSGGTQSK.V
*	HsFLAG-Control_HeLa_S1(	3.3501	0.3639	1403.56	1403.66	4849.5		1	751	75	2	K.VVPIASLTPYQSK.W
*	HsHeLa_Control-MG_Ti_10	4.534	0.415	1448.76	1448.67	7227.7		1	2032	83.3	2	K.SKDSLVDIIGICK.S
*	HsFLAG-Control_HeLa_S1(	2.788	0.2959	1407.31	1405.55	7304.2		1	533.4	58.3	1	K.VVTATLWGEDADK.F
*	HsFLAG-Control_HeLa_NE	3.0877	0.1726	2205.98	2206.5	9621.5		6	662.8	40	1	R.SLSVLSSSTIIANPDIPEAYK.L
*	HsHeLa_Control-MG_Ti_10	4.8541	0.1793	2009.86	2009.18	7583.1		1	2230.2	69.4	4	R.GWFDAEGQALDGVSISDLK.S
*	HsHeLa_Control-MG_Ti_10	2.646	0.2114	2546.46	2546.8	6814.9		1	493.7	40.9	1	K.SENLGQGDKPDYFSSVATVVYLR.K
gi|34932414|ref|N	11	64	0.191	471	54232	8.9	U	non-POU domain containing, octamer-binding [Homo sapiens]				
*	HsFLAG-MOCK_300mM_T	2.8917	0.1414	1145.86	1144.32	6197.4		1	798	72.2	1	K.AGEVFIHKDK.G
*	HsFLAG-Control_HeLa_NE	5.4696	0.4091	2668.64	2669.95	7010.2		1	1077.8	50	12	R.NLPQYVSNELLEEAFSVFGQVER.A
*	HsFLAG-Control_293_Ti_1(	5.5133	0.424	2668.76	2669.95	10060.2		1	1959.7	54.5	19	R.NLPQYVSNELLEEAFSVFGQVER.A
*	HsFLAG-Control_HeLa_NE	4.6452	0.4418	2669.33	2669.95	8265.6		1	1259.7	36.4	3	R.NLPQYVSNELLEEAFSVFGQVER.A
*	HsGST-MOCK_Ti_406.364	3.7252	0.1932	2669.4	2669.95	8162.5		1	1171.3	36.4	1	R.NLPQYVSNELLEEAFSVFGQVER.A
*	Hs283FLP_Ti_106.3244.32	3.5353	0.2008	2669.79	2669.95	7195.9		1	812.5	30.7	1	R.NLPQYVSNELLEEAFSVFGQVER.A
*	Hs283FLP_Ti_105.4217.42	5.1611	0.3675	2670.03	2669.95	10888.2		1	2045.6	52.3	12	R.NLPQYVSNELLEEAFSVFGQVER.A
*	Hs283FLP_Ti_105.1387.13	2.5891	0.2802	1233.9	1232.43	6290		1	985.7	68.2	1	K.GIVEFSGKPAAR.K
	HsGST-MOCK_Ti_103.109	4.3871	0.3215	1541.56	1541.72	8485.2		1	1508.1	81.8	5	R.RMEELHNQEVQK.R
*	HsHeLa_Control-MG_Ti_10	4.1919	0.4811	2165.03	2164.44	6260.8		1	1062.1	57.1	1	R.FGQAATMEGIGAIGGTPPAFNR.A
	HsFLAG-Control_HeLa_NE	2.8838	0.299	1072.5	1073.19	4173.1		2	502.1	70	8	R.AAPGAEFAPNK.R
gi|89037397|ref|X	30	92	0.19	2028	228228	6.2	U	PREDICTED: hypothetical protein LOC440193 isoform 1 [Homo sapiens]				
gi|89037763|ref|X	30	92	0.19	2028	228212	6.2	U	PREDICTED: similar to DVL-binding protein DAPLE isoform 9 [Homo sapiens]				
	HsHeLa_Control-MG_Ti_10	2.4386	0.1368	1081.02	1081.18	3952.6		8	272	68.8	2	K.HVNNDVNLR.I
	HsHeLa_Control-MG_Ti_20	3.0553	0.2499	1081.49	1081.18	3888.2		1	706.6	93.8	4	K.HVNNDVNLR.I
	HsHeLa_Control-MG_Ti_10	3.5154	0.345	1631.02	1630.9	6937.3		1	1453.1	73.1	1	K.VLLLVLGCAVQCER.K
	HsHeLa_Control-MG_Ti_10	4.0074	0.2952	1495.76	1494.69	5711.6		1	981.4	75	6	R.DYLQAQHPPSPIK.S
	Hs283FLP_Ti_102.1330.13	3.8859	0.383	1871.72	1870.88	3550.4		1	402.4	52.8	8	K.SSSADSTPSPTSSLSSEDK.Q
	Hs293FLP-MG_Ti_104.142	4.3789	0.2271	1457.96	1456.64	5393.2		1	1192	79.2	2	K.VKQENIQLAADAR.S
	HsHeLa_Control-MG_Ti_10	3.5203	0.3533	1475.84	1474.61	6876.7		4	805.6	66.7	4	K.ENQSLQSTIQGLR.D
	HsHeLa_Control_Ti_102.21	3.8544	0.2623	1261.4	1261.42	4593.5		1	978.3	77.3	2	R.DASLVLEESGLK.C
	Hs283FLP_Ti_102.2739.27	3.6572	0.2866	1775.92	1775.91	7172.1		1	1311.3	78.6	6	K.QSNQDLETLSEELIR.E
	HsHeLa_Control-MG_Ti_10	3.0918	0.3859	1268.63	1269.4	4967.6		1	556.2	63.6	2	K.ALHQTVTEANGK.L
	HsHeLa_Control-MG_Ti_20	3.2149	0.3804	1269.46	1269.4	4580.6		1	453.1	63.6	2	K.ALHQTVTEANGK.L
	HsHeLa_Control-MG_Ti_20	3.3412	0.3703	1269.48	1269.4	6189.5		1	969.1	72.7	2	K.ALHQTVTEANGK.L
	HsHeLa_Control-MG_Ti_10	3.9838	0.4058	1269.67	1269.4	7604.9		1	1445.8	81.8	2	K.ALHQTVTEANGK.L

	HsHeLa_Control-MG_Ti_20	5.4591	0.3586	3040	3041.34	9540.4		1	2482.7	37.5	2	R.KVTSLETATEKVEALEHESQGLQLENR.T
	HsHeLa_Control-MG_Ti_20	5.6116	0.4009	2914.55	2913.17	9018.5		1	2242.5	39	3	K.VTSLETATEKVEALEHESQGLQLENR.T
	HsHeLa_Control_Ti_102.33	5.4945	0.313	1916.38	1916.14	5290.9		1	1528.2	78.1	9	K.SLDTLQNVSLQLEGLER.D
	HsHeLa_Control_Ti_102.28	4.748	0.3613	1705.96	1705.82	6961.4		1	1651.3	75	4	K.TQTLESELGELEAER.Q
	HsHeLa_Control-MG_Ti_10	5.1275	0.4153	2587.06	2586.91	7493.9		1	1044	50	2	K.EQLQHLETQNVTFSSQILTLQK.Q
	Hs283FLP_Ti_104.1409.14	3.3123	0.2061	2047.15	2047.23	7658.9		1	550.6	44.1	1	K.QSAFLQEHNTTLQTQTAK.L
	HsHeLa_Control-MG_Ti_10	4.3331	0.287	3156.54	3156.48	5781.7		2	465.6	24.1	2	K.LQVENSTLSSQSAALTAQYTLLQNHHTAK.E
	HsHeLa_Control-MG_Ti_20	2.9596	0.1168	1136.71	1136.34	8264.8		2	1102.8	81.2	1	R.VNFLHHQLK.G
	HsHeLa_Control-MG_Ti_10	2.1222	0.2025	1313.84	1314.4	4590.5		5	262.5	45	1	K.GEYEELHAHTK.E
	HsHeLa_Control-MG_Ti_10	3.8767	0.288	1316.35	1314.4	8494.2		1	1395.6	80	4	K.GEYEELHAHTK.E
	HsHeLa_Control-MG_Ti_10	2.9306	0.2367	1257.89	1257.36	4863.1		1	638.6	72.2	1	K.LDNHCELLSR.L
	Hs293FLP-MG_Ti_102.262	4.897	0.3411	2626.22	2624.82	6482.6		1	864.4	45.8	8	K.STVDSPPWQLESSDPASPAASQPLR.S
	HsHeLa_Control_Ti_102.13	4.5345	0.4469	2047.79	2047.07	4678		1	1488.9	77.8	4	R.SQAENPDTPALGSNCAEER.D
	HsHeLa_Control-MG_Ti_10	3.1378	0.37	1924.49	1925.03	3993.7		1	323.3	47.2	4	R.TCSTSATTTAPSNSTPIAR.H
	HsHeLa_Control_Ti_103.24	4.0093	0.2938	2494.4	2493.57	4965.8		1	576.5	47.5	1	K.GYNSDDNLCEPSLEFEVPNHR.Q
	HsHeLa_Control-MG_Ti_20	2.7714	0.1956	1497.34	1496.62	3534.4		1	260.2	58.3	1	R.QYVSRPSSLESSR.N
	HsHeLa_Control-MG_Ti_10	2.8726	0.1501	1164.78	1164.35	4943.3		3	778.2	75	1	R.AFSLASADLLR.A
gi|11863154|ref|N	7	10	0.19	511	57210	6.2	U	archain [Homo sapiens]				
*	HsFLAG-MOCK_300mM_T	4.8082	0.3926	3089.06	3086.44	7213.2		1	948.7	28.2	2	K.APGFGGFGSSAVSGGSTAAMITETIIETDKPK.V
*	HsFLAG-MOCK_300mM_T	3.5666	0.2956	1465.96	1464.67	5311.8		1	797.1	75	2	K.KGVQLQTHPNVDK.K
*	HsFLAG-MOCK_300mM_T	3.654	0.2272	1336.78	1336.49	6492.9		1	1139	77.3	1	K.GVQLQTHPNVDK.K
*	HsFLAG-MOCK_300mM_T	3.6743	0.2943	1467.16	1464.67	5865.7		1	886.2	70.8	2	K.GVQLQTHPNVDKK.L
*	HsFLAG-MOCK_300mM_T	2.3084	0.1405	1319.62	1320.62	4235.4		7	321.9	50	1	K.KLFTAESLIGLK.N
*	HsFLAG-Control_HeLa_NE	2.6395	0.2665	2688.98	2689	7147.5		1	437.5	35.4	1	K.SGSLEFSIAGQPNDFFPVQVSFVSK.K
*	HsFLAG-Control_HeLa_NE	2.7775	0.1977	1807.23	1807.05	7966.8		3	583	50	1	R.FSTETTFLVDKYEIL.-
gi|7706310|ref|NI	9	37	0.189	402	47620	10	U	LUC7-like 2 [Homo sapiens]				
*	HsHeLa_Control-MG_Ti_20	5.2293	0.5201	1866.12	1867	7993.3		1	2338.5	76.7	10	K.SHLLNCCPHDVLSGTR.M
*	HsHeLa_Control-MG_Ti_10	2.135	0.088	823.92	823.971	4061.7		3	537.8	83.3	4	K.VHDLALR.A
	Hs293FLP_Ti_303.1279.12	2.8366	0.2292	1167.66	1168.29	4978		1	557.6	66.7	1	R.VHELNEEIGK.L
	HsHeLa_Control-MG_Ti_20	2.9432	0.147	1168.12	1168.29	5296.9		1	676.8	77.8	1	R.VHELNEEIGK.L
	Hs293FLP_Ti_303.1278.12	3.1115	0.1986	1170.57	1168.29	4706.3		1	711	83.3	1	R.VHELNEEIGK.L
*	Hs293FLP-MG_Ti_201.046	5.1149	0.3732	1617.4	1617.71	7062.6		1	1870.9	78.6	13	K.VEQLGAEGNVEESQK.V
	HsHeLa_Control-MG_Ti_10	1.9477	0.1266	844.78	844.946	3744.8		1	350.9	64.3	3	R.LADHFGGK.L
*	HsHeLa_Control-MG_Ti_20	2.8551	0.0864	1098.47	1098.33	5379.3		3	1040	87.5	3	K.LHLGFIEIR.E
*	HsHeLa_Control-MG_Ti_20	3.4429	0.2076	1384	1383.43	5777.4		2	916.7	80	1	R.FRDQDLASCDR.D
gi|14591909|ref|N	6	12	0.189	297	34363	9.7	U	ribosomal protein L5 [Homo sapiens]				
*	Hs293FLP_TREX_Ti_102.2	3.5941	0.3635	1223.23	1223.38	8240.9		1	1735.3	88.9	2	R.DIICQIAYAR.I
	Hs293FLP_TREX_Ti_104.1	2.9722	0.3363	1338.29	1339.49	4891.1		1	705.9	57.7	2	K.GAVDGGLSIPHSTK.R
	Hs293FLP_TREX_Ti_103.1	4.1716	0.2622	1339.27	1339.49	4845.2		1	1253.4	76.9	2	K.GAVDGGLSIPHSTK.R
*	Hs293FLP_TREX_Ti_104.1	3.5179	0.2293	1187.29	1186.27	4818.2		3	730	77.8	2	K.RFPGYDSESK.E
	Hs293FLP_TREX_Ti_104.1	2.5259	0.2273	1131.38	1130.25	5746.3		5	515	75	1	K.EFNAEVHRK.H
*	Hs293FLP_TREX_Ti_106.2	3.5276	0.3794	1499.47	1498.68	6714.1		1	1128.1	75	3	K.AHAAIRENPVYEK.K
gi|19923485|ref|N	8	48	0.188	432	51466	9.8	U	cisplatin resistance-associated overexpressed protein [Homo sapiens]				
gi|52426743|ref|N	8	48	0.188	432	51466	9.8	U	cisplatin resistance-associated overexpressed protein [Homo sapiens]				
	HsHeLa_Control-MG_Ti_10	4.715	0.3591	2014.79	2013.19	5420.5		1	1054.2	70	14	K.YYLCGFCPAELFTNTR.S
	HsHeLa_Control_Ti_103.28	2.3911	0.2409	1320.72	1321.52	3618.4		1	203	55	1	R.YLQSLLAEVER.R
	HsHeLa_Control_Ti_103.28	3.869	0.1804	1321.88	1321.52	5100.8		1	1376.5	85	5	R.YLQSLLAEVER.R
	HsF-IP-293-MG_Ti_103.13	4.9884	0.4648	1716.6	1715.86	7799.9		1	1872.8	70.6	12	R.LALSQNQQSSGAAGPTGK.N
	Hs293FLP-MG_Ti_104.126	4.6347	0.377	2217.24	2216.37	6776.2		1	1282.6	59.5	3	R.LALSQNQQSSGAAGPTGKNEEK.I

	Hs293FLP-MG_Ti_103.137	3.1	0.1619	1144.76	1144.31	8391.7		2	1711.7	93.8	3	K.LVEQLKEER.E
	Hs293FLP-MG_Ti_102.206	4.3169	0.4334	1502.39	1500.6	6177.5		1	1303.4	76.9	9	R.STTSTIESFAAQEK.Q
	HsHeLa_Control-MG_Ti_20	2.8696	0.1936	1047.38	1047.19	8470		1	1110	81.2	1	K.ATVEELKEK.L
gi|34577083|ref|N	2	3	0.188	224	25545	8.7	U	ras suppressor protein 1 isoform 2 [Homo sapiens]				
gi|6912638|ref|NI	2	3	0.152	277	31540	8.6	U	ras suppressor protein 1 isoform 1 [Homo sapiens]				
	HsFLAG-Control_HeLa_NE	5.5854	0.3289	2822.82	2820.17	5312.7		1	944.3	37	2	K.NLEVLNFFNNQIEELPTQISSLQK.L
	HsFLAG-Control_HeLa_NE	3.0516	0.2123	2021.55	2021.27	4179.2		3	509.1	52.9	1	R.ALYLSDNDFEILPPDIGK.L
gi|23308579|ref|N	2	3	0.188	160	18697	4.5	U	unactive progesterone receptor, 23 kD [Homo sapiens]				
	Hs293FLP_TREX_Ti_102.2	3.4478	0.4062	1446.09	1446.57	7189		1	1242.3	75	2	K.LTFSCLGGSDNFK.H
*	HsHeLa_Control-MG_Ti_10	2.6648	0.25	2070.1	2068.22	6562.9		2	430	46.9	1	K.HLNEIDLFHCIDPNDSK.H
gi|4504425|ref|NI	3	6	0.186	215	24894	5.7	U	high-mobility group box 1 [Homo sapiens]				
	HsHeLa3_Ti_104.2319.231	2.6019	0.1928	1498.04	1497.68	7096.5		1	627.9	59.1	1	K.MSSYAFFVQTCR.E
*	HsHeLa3_Ti_104.1819.181	2.9239	0.1564	1466.53	1465.56	5900.4		1	823.3	70.8	1	K.HPDASVNFSEFSK.K
	HsGST-MOCK_Ti_104.147	3.5722	0.3969	1521.39	1521.76	5608		1	1015.5	71.4	4	K.IKGEHPGLSIGDVAK.K
gi|5453595|ref|NI	6	13	0.185	475	51673	8	U	adenylyl cyclase-associated protein [Homo sapiens]				
*	HsFLAG-Control_HeLa_S1	5.3021	0.1888	2352.2	2352.69	5378.7		1	1176.2	40.9	1	K.AGAAPYVQAFDSLLAGPVAEYLK.I
*	HsFLAG-Control_HeLa_NE	4.3855	0.3475	2352.66	2352.69	8797.6		1	1004.8	45.5	3	K.AGAAPYVQAFDSLLAGPVAEYLK.I
*	HsFLAG-Control_HeLa_S1	3.6551	0.3843	1758.35	1758.94	6587.8		1	1173.8	66.7	1	R.ALLVTASQCQQPAENK.L
*	HsFLAG-Control_HeLa_S1	3.1641	0.1591	1427.79	1427.68	4660		1	721.4	70.8	2	K.LSDLLAPISEQIK.E
*	HsFLAG-Control_HeLa_S1	4.0109	0.366	1929.51	1929.18	6535.1		4	476.4	44.1	2	R.SALFAQINQGESITHALK.H
*	HsFLAG-Control_HeLa_S1	5.0555	0.3987	2073.56	2074.25	6428.9		1	1515.9	67.6	4	R.VENQENVSNLVIEDTELK.Q
gi|4506685|ref|NI	2	4	0.185	151	17222	10.5	U	ribosomal protein S13 [Homo sapiens]				
*	HsGST-MOCK_Ti_103.175	3.5349	0.233	1382.28	1382.69	3789.8		1	980.2	79.2	2	K.KGLTPSQIGVILR.D
*	HsGST-MOCK_Ti_404.377	3.2119	0.278	1694.35	1694.97	4652.7		1	530.7	64.3	2	K.GLAPDLPEDLYHLIK.K
gi|4505821|ref|NI	2	3	0.185	146	16572	8	U	prolactin-induced protein [Homo sapiens]				
*	HsFLAG-Control_Hela_Ti_1	3.5951	0.3473	1815.72	1816.11	3747.1		1	401.5	56.7	1	K.TYLISSIPLQGAFNYK.Y
*	HsFLAG-Control_293_Ti_1	3.0888	0.3718	1357.72	1357.39	7757.4		1	1260.9	80	2	K.YTACLCDDNPK.T
gi|4506643|ref|NI	3	7	0.185	92	10275	10.4	U	ribosomal protein L37a [Homo sapiens]				
*	Hs293FLP_TREX_Ti_106.2	2.3648	0.1791	1053.47	1054.24	4633.2		1	617.4	75	2	K.KIEISQHAK.Y
*	Hs293FLP_TREX_Ti_106.2	2.8755	0.0877	1054.41	1054.24	5422.9		1	1002	87.5	3	K.KIEISQHAK.Y
	Hs293FLP_TREX_Ti_102.1	2.0743	0.1805	1022.3	1023.06	5628.8		5	343.4	64.3	2	K.YTCSFCGK.T
gi|7706322|ref|NI	3	6	0.184	244	28068	6.7	U	chromosome 14 open reading frame 166 [Homo sapiens]				
*	HsHeLa3_Ti_105.1774.177	4.0372	0.4891	1722.11	1721.88	5932.4		1	976.1	67.9	1	K.LTALDYHNPAGFNCK.D
*	HsFLAG-Control_HeLa_NE	3.6267	0.3406	1813.28	1814.01	8799.8		1	1189.4	60	3	K.NAEPLINLDVNNPDFK.A
*	HsHeLa3_Ti_105.3402.340	4.2302	0.1658	1499.7	1498.83	5807.2		1	1597.9	76.9	2	K.AGVMALANLLQIQR.H
gi|5803227|ref|NI	3	14	0.184	245	27764	4.8	U	tyrosine 3/tryptophan 5 -monooxygenase activation protein, theta polypeptide [Homo sapie				
*	HsFLAG-Control_293_Ti_1	3.7945	0.2291	1532.9	1533.59	9193.5		1	1423.3	69.2	1	K.AVTEQGAELSNEER.N
*	HsHeLa3_Ti_103.3724.372	3.1919	0.3463	1392.73	1392.6	6083		1	1108.3	81.8	2	R.SICTTVLELLDK.Y
*	HsHeLa_Control-MG_Ti_20	5.0264	0.4152	2146.55	2146.27	9674.8		1	1985.8	61.1	11	K.TAFDEAIAELDTLNEDSYK.D
gi|74275346|ref|N	3	4	0.18	334	38340	6	U	S-adenosylmethionine decarboxylase 1 isoform 1 precursor [Homo sapiens]				
gi|74275348|ref|N	3	4	0.323	186	21301	5.1	U	S-adenosylmethionine decarboxylase 1 isoform 2 [Homo sapiens]				
	HsHeLa_Control-MG_Ti_20	4.3662	0.4989	4113.17	4114.42	9402.1		1	1151	26.5	1	K.SDGTYWTIHITPEPEFSYVSFETNLSQTSYDDLIR.K
	HsFLAG-Control_MG_293_	3.5086	0.3111	1372.09	1371.58	5250.8		1	1323.9	86.4	2	K.FVTTLFVNQSSK.C
	HsHeLa_Control-MG_Ti_10	2.8036	0.327	1418.83	1418.68	5120		1	757.1	70.8	1	R.TVLASPQKIEGFK.R
gi|5174445|ref|NI	4	9	0.178	399	45283	7.8	U	lanthionine synthetase C-like protein 1 [Homo sapiens]				
*	HsGST-MOCK_Ti_102.261	5.53	0.405	2508.49	2509.79	8557.9		1	1819.2	57.1	1	K.IPQSHIQQICETILTSGENLAR.K
*	HsGST-MOCK_Ti_104.162	4.435	0.3993	1886.62	1887.2	4447.3		1	1095.8	73.3	4	K.LHSLVKPSVDYVCQLK.F
*	HsGST-MOCK_Ti_305.198	3.1584	0.271	1593.83	1594.69	5393.9		1	571.9	65.4	2	K.FPSGNYPPCIGDNR.D
*	HsGST-MOCK_Ti_302.393	5.5645	0.5147	2380.51	2380.63	7282.7		1	2256.2	72.2	2	K.YLCDAYQCADVIWQYGLLK.K

gi|5174449|ref|N	4	6	0.178	213	22487	10.8	U	H1 histone family, member X [Homo sapiens]				
*	Hs293FLP_TREX_Ti_102.1	3.1612	0.2488	1208.36	1208.4	6344.5		1	927.6	77.8	2	K.YSQLVVETIR.R
*	Hs293FLP_TREX_Ti_102.1	3.3239	0.2893	1342.35	1342.58	7134.1		1	988.6	72.7	2	K.ALVQNDTLLQVK.G
*	Hs293FLP_TREX_Ti_106.2	3.0662	0.2484	1490.7	1488.69	6681.5		1	1116.6	66.7	1	R.RGAPAAATAPAPTAHK.A
*	Hs293FLP_TREX_Ti_105.1	3.6308	0.3374	1332.33	1332.5	4033.1		2	788.7	75	1	R.GAPAAATAPAPTAHK.A
gi|5031973|ref|N	4	12	0.177	440	48121	5.1	U	protein disulfide isomerase-associated 6 [Homo sapiens]				
*	HsHeLa_Control-MG_Ti_20	4.2606	0.2011	1387.23	1387.58	7010.7		1	2109.7	80.8	2	R.TGEAIVDAALSALR.Q
*	HsFLAG-Control_HeLa_NE	4.217	0.4432	1528.74	1528.75	9304.8		1	1356.3	67.9	5	K.LAAVDATVNQVLASR.Y
*	HsHeLa_Control-MG_Ti_20	3.4434	0.1694	2638.52	2638.98	3612		1	252.9	37	4	R.ALDLFSDNAPPPELLEIINEDIAK.R
*	Hs293FLP-MG_Ti_202.428	3.6775	0.3521	2759.44	2759.89	9218.6		1	1085.5	43.8	1	R.DGELPVEDDIDLSDVELDDLGKDEL.-
gi|4502491|ref|N	2	12	0.177	282	31362	4.8	U	complement component 1, q subcomponent binding protein precursor [Homo sapiens]				
*	Hs293FLP-MG_Ti_202.352	3.9469	0.2782	2287.58	2288.56	7379.4		1	1006.3	55.3	3	K.VEEQEPELTSTPNFVVEVIK.N
*	Hs293FLP-MG_Ti_205.021	5.4861	0.4241	3442.19	3441.77	6610.3		1	1127.9	31	9	R.GVDNTFADELVELSTALEHQEYITFLEDLK.S
gi|23510356|ref|N	11	22	0.176	568	65583	6.2	U	RIO kinase 1 isoform 1 [Homo sapiens]				
*	HsFLAG-Control_MG_293_	2.5104	0.4057	1838.36	1838.84	2469.6		1	197.5	56.2	1	R.VVPGQFDDADSSDSENR.D
*	Hs293FLP-MG_Ti_203.212	4.1006	0.3812	1560.66	1560.79	8685.7		1	1065.4	65.4	1	K.LNVTDSVINKVTEK.S
*	HsFLAG-Control_293_Ti_2	3.1438	0.1535	1127.35	1128.27	5672.4		4	1571	88.9	1	R.ATVEQVLDPR.T
*	HsHeLa_Control-MG_Ti_20	4.291	0.3427	1607.56	1606.65	6753.1		1	1177.2	71.4	4	K.EANVYHASTANGESR.A
	HsFLAG-Control_MG_293_	1.9197	0.1308	999.6	1000.2	5172.5		6	308.5	68.8	1	R.HSVAVMTVR.E
	Hs293FLP_Ti_302.1488.14	4.1936	0.2937	1421.45	1420.48	8369.5		1	1733.1	77.3	2	R.SSQDHVDEEVFK.R
	HsFLAG-Control_293_Ti_2	2.8559	0.0989	1396.55	1397.57	4128.1		1	335.5	59.1	2	K.VPALLENQVEER.T
	Hs293FLP-MG_Ti_103.191	2.0878	0.152	1396.73	1397.57	3828.2		1	231.9	54.5	1	K.VPALLENQVEER.T
	HsFLAG-Control_293_Ti_2	3.7808	0.3028	1397.35	1397.57	7746.4		1	1863.1	90.9	2	K.VPALLENQVEER.T
	Hs293FLP-MG_Ti_203.200	3.9443	0.3047	1397.66	1397.57	7861.3		1	1317.3	77.3	2	K.VPALLENQVEER.T
	HsFLAG-Control_MG_293_	3.212	0.2687	1298.49	1298.44	7608.7		1	853.5	75	5	K.KHTTDPDIDKK.E
gi|6631095|ref|N	10	16	0.175	808	90981	5.8	U	minichromosome maintenance protein 3 [Homo sapiens]				
*	HsFLAG-Control_293_Ti_2	4.4297	0.3993	2193.65	2194.27	10145.6		1	1255.5	55.9	3	R.DYLDFLDDEEDQGIYQSK.V
*	HsGST-MOCK_Ti_403.402	3.6231	0.2626	4059.93	4059.43	7395.9		1	668.6	22.9	1	R.YSDLTTLVAFPSSSVYPTKDEENNPLETEYGLSVYK.D
*	HsFLAG-Control_293_Ti_2	4.0613	0.3336	1446.58	1446.59	6398.9		1	1387.6	79.2	3	R.SVDVILDDDLVDK.A
*	HsHeLa3_Ti_105.3382.338	2.7856	0.2419	1315.6	1314.58	6240.9		1	1246.7	77.3	1	K.AILCLLLGGVER.D
*	HsFLAG-Control_293_Ti_2	2.9884	0.1648	1528.31	1525.79	7376.9		2	882.3	60.7	1	R.GDINILLIGDPSVAK.S
*	HsFLAG-Control_MG_293_	3.0786	0.2776	1377.72	1378.54	9742.1		4	824.4	58.3	1	R.CSVLAAANPVYGR.Y
*	HsFLAG-Control_293_Ti_2	2.7218	0.2647	1034.48	1035.15	5137.2		1	561.9	75	1	K.HDNLLHGTK.K
*	HsGST-MOCK_Ti_103.103	3.1095	0.3229	1035.03	1035.15	7557.2		1	1540.1	93.8	2	K.HDNLLHGTK.K
*	HsFLAG-Control_MG_293_	3.1139	0.167	932.87	933.139	5518.8		1	1161.7	92.9	2	K.VALLDVFR.E
*	HsFLAG-Control_293_Ti_2	3.651	0.2884	1838.36	1837.98	7797.4		1	1161	62.5	1	R.DSEEPFSSVEIQAALSK.M
gi|17402900|ref|N	7	10	0.175	644	67560	7.6	U	far upstream element-binding protein [Homo sapiens]				
*	HsHeLa3_Ti_102.1659.166	4.0873	0.3895	1976.62	1975.04	6204.6		1	1132.4	52.6	1	K.IGGDAGTSLNSNDYGYGGQK.R
*	HsHeLa3_Ti_103.0878.087	3.4379	0.2489	1341.6	1341.42	5197.8		1	824.7	77.3	1	K.RPLEDGDQPDAK.K
*	HsHeLa3_Ti_104.2883.288	3.549	0.405	1262.74	1261.53	6066.3		1	1471.4	86.4	2	K.VPDGMVGFIIGR.G
*	HsHeLa3_Ti_103.1575.157	3.8824	0.3118	1596.97	1596.76	5374.3		1	1129.6	75	2	R.SCMLTGTPESVQSAK.R
*	HsHeLa3_Ti_103.1991.199	3.1388	0.3687	1338.09	1337.52	6509.6		1	965.5	70.8	2	R.IGGNEGIDVPIPR.F
*	HsFLAG-MOCK_300mM_T	3.1528	0.1549	1505.03	1504.64	3218.5		4	458.7	66.7	1	R.IQFKPDDGTTPER.I
*	HsHeLa3_Ti_104.2572.257	3.0486	0.19	2910.37	2910.19	4357.7		1	347.7	38.9	1	K.MGQAVPAPTGAPPGGQPDYSAAWAEYYR.Q
gi|5730027|ref|N	10	24	0.174	443	48227	8.7	U	KH domain containing, RNA binding, signal transduction associated 1 [Homo sapiens]				
*	HsFLAG-Control_HeLa_NE	4.0567	0.4145	1385.35	1385.49	4987.8		1	980.2	69.2	6	R.SGSMDPSGAHPSVR.Q
*	HsFLAG-Control_HeLa_NE	3.7115	0.4349	2246.27	2247.53	6300.3		1	499.2	47.4	4	K.DSLDPSFTHAMQLLTAEIEK.I
*	HsFLAG-MOCK_300mM_T	3.1378	0.3135	2510.15	2510.72	7782.3		1	730	45	1	K.IQKGDSKKDDEENYLDLFSHK.N

*	HsFLAG-Control_HeLa_NE	3.6113	0.3061	2140.37	2141.26	10316.7		1	1876.4	61.8	1	K.GDSKKDDEENYLDLFSHK.N
*	HsFLAG-Control_HeLa_NE	4.4611	0.3457	1753.96	1753.86	9626		1	1862.8	76.9	4	K.KDDEENYLDLFSHK.N
*	HsFLAG-Control_HeLa_NE	3.831	0.1647	1754	1753.86	6088.7		2	1041.2	50	2	K.KDDEENYLDLFSHK.N
*	HsFLAG-Control_HeLa_NE	3.8816	0.2599	1626.23	1625.69	7626.2		1	1150.4	70.8	2	K.DDEENYLDLFSHK.N
	HsFLAG-MOCK_300mM_T	3.5951	0.2941	1470.49	1470.8	8215.4		1	1104.8	72.7	2	K.ERVLIPVKQYPK.F
*	HsFLAG-Control_HeLa_NE	2.2158	0.1375	1040.59	1041.24	6188.4		3	481.3	66.7	1	K.ILGPQGNTIK.R
*	HsFLAG-Control_HeLa_NE	3.0714	0.2469	1041.43	1041.24	3570.5		1	676.4	88.9	1	K.ILGPQGNTIK.R
gi|4506715|ref|N	1	3	0.174	69	7841	10.7	U	ribosomal protein S28 [Homo sapiens]				
gi|89042507|ref|X	1	3	0.108	111	12494	10.4	U	PREDICTED: similar to 40S ribosomal protein S28 [Homo sapiens]				
gi|89035017|ref|X	1	3	0.174	69	7841	10.7	U	PREDICTED: similar to 40S ribosomal protein S28 [Homo sapiens]				
gi|89034184|ref|X	1	3	0.174	69	7841	10.7	U	PREDICTED: similar to 40S ribosomal protein S28 [Homo sapiens]				
gi|88959151|ref|X	1	3	0.174	69	7841	10.7	U	PREDICTED: similar to 40S ribosomal protein S28 [Homo sapiens]				
gi|88953906|ref|X	1	3	0.174	69	7841	10.7	U	PREDICTED: similar to 40S ribosomal protein S28 [Homo sapiens]				
	HsFLAG-Control_HeLa_NE	3.6798	0.2664	1361.94	1361.49	7595.4		1	1219.8	72.7	3	R.EGDVLTLLESER.E
gi|4507645|ref|N	3	5	0.173	249	26669	6.9	U	triosephosphate isomerase 1 [Homo sapiens]				
*	HsHeLa3_Ti_103.2759.275	4.2162	0.4302	2193.9	2193.43	4020.7		1	836.2	63.2	2	K.VPADTEVVCAPPTAYIDFAR.Q
	HsHeLa3_Ti_103.1360.136	1.9764	0.1532	1137.57	1138.28	4879.9		4	357	61.1	1	K.IAVAAQNCYK.V
	Hs293FLP_TREX_Ti_103.1	4.2668	0.4557	1459.37	1459.6	3351.5		1	831.4	83.3	2	R.HVFGESDELIGQK.V
gi|71361682|ref|N	25	51	0.172	2115	238257	5.8	U	nuclear mitotic apparatus protein 1 [Homo sapiens]				
*	HsFLAG-Control_HeLa_NE	3.542	0.3077	1353.42	1353.52	4894.7		1	1044.2	86.4	1	R.IHGTEEGQQILK.Q
*	HsGST-MOCK_Ti_102.137	3.1822	0.2526	1440.53	1440.56	4891.2		1	594.5	70.8	1	K.HPSSPECLVSAQK.V
*	HsGST-MOCK_Ti_105.274	4.377	0.3664	2838.34	2838.11	8832.1		1	1040.4	32.6	1	K.LREFASHLQQLQDALNELTEEHSK.A
*	HsFLAG-MOCK_300mM_T	4.2785	0.3316	2569.78	2568.76	7311.5		1	1134.6	38.1	1	R.EFASHLQQLQDALNELTEEHSK.A
*	HsFLAG-Control_HeLa_NE	4.0583	0.3222	2262.97	2262.52	9592.8		1	785.3	42.5	2	K.QQLSSLITDLQSSISNLSQAK.E
*	HsFLAG-Control_HeLa_NE	5.3232	0.387	3186.06	3187.57	8302.3		1	1424.1	32.8	4	R.LTAQVASLTSELTTLNATIQQQDQELAGLK.Q
*	HsFLAG-Control_HeLa_NE	2.6755	0.147	1256.02	1256.4	6470.9		2	830.3	80	1	R.HQVEQLSSSLK.Q
*	HsFLAG-Control_HeLa_NE	2.3132	0.0876	1256.55	1256.4	2553.2		3	153.7	65	1	R.HQVEQLSSSLK.Q
*	HsFLAG-Control_HeLa_NE	4.5955	0.369	1753.65	1754	9526.3		1	2060.9	75	2	K.LEILQQQLQVANEAR.D
*	HsFLAG-Control_HeLa_NE	2.8455	0.1283	1824.15	1823.02	10172		2	652.3	50	1	R.LQQLGEAHQAETEVLR.R
*	Hs293FLP-MG_Ti_203.401	3.2307	0.3401	1871.21	1872.13	9664.7		1	1305.1	59.4	1	R.VEFATLQEALAHALTEK.E
*	HsFLAG-Control_HeLa_NE	4.8382	0.2933	1561.82	1561.69	7607.8		1	2113.1	80.8	6	R.DSALETLQGQLEEK.A
*	HsFLAG-Control_HeLa_NE	4.9966	0.4834	1655.65	1654.78	8400.4		1	1885.3	73.3	3	K.AQELGHSQSALASAQR.E
*	HsFLAG-Control_HeLa_NE	5.2004	0.3141	1804.21	1804.01	7833.3		1	2509.6	80	2	K.NSLISSLEEEVSILNR.Q
*	HsHeLa3_Ti_103.1299.129	4.1032	0.3781	1263.69	1261.38	8204.4		1	1744.5	86.4	8	R.LLQAETASNSAR.A
*	HsGST-MOCK_Ti_305.171	5.0743	0.438	1725.11	1725.87	7900.2		1	1819.2	82.1	3	K.HLCQQLQAEQAAAEK.R
*	HsFLAG-Control_HeLa_NE	2.8024	0.2413	1193.58	1194.38	6538.8		1	574.7	60	1	R.LGHELQQAGLK.T
*	HsFLAG-Control_HeLa_NE	2.8231	0.2005	1194.25	1194.38	5589.8		1	809.4	75	2	R.LGHELQQAGLK.T
*	HsGST-MOCK_Ti_304.314	6.3241	0.5124	3516.46	3516.85	9676.2		1	1833.8	31.5	2	K.SREPQAKPQLDLSIDSLDLSCEEGTPLSITSK.L
*	HsFLAG-Control_HeLa_NE	4.2015	0.4378	2159	2158.55	11359.5		1	1274.5	52.8	2	R.LPPKVESLESLYFTPIPAR.S
*	HsFLAG-Control_HeLa_NE	3.7341	0.4232	2193.63	2194.36	9921.9		1	951.8	47.5	1	R.SQAPLESSLDSLGDVFLDSGR.K
*	HsFLAG-MOCK_300mM_T	3.5639	0.2502	2047.12	2046.16	3203.5		1	753	67.6	1	K.KLDVEEPDSANSSFYSTR.S
*	HsHeLa3_Ti_106.1720.172	2.9177	0.292	1328.76	1327.44	5948.5		1	906.4	73.1	1	R.RSQAGVSSGAPPGR.N
*	HsGST-MOCK_Ti_104.128	4.0043	0.3911	1719.52	1719.9	8064.5		3	757	56.7	2	K.RVSLEPHQGPGTPESK.K
*	HsFLAG-Control_HeLa_NE	3.0007	0.2198	1563.6	1563.71	6669.6		1	528.9	53.6	1	R.VSLEPHQGPGTPESK.K
gi|89062143|ref|X	5	9	0.172	430	47445	6.1	U	PREDICTED: similar to Ig gamma-4 chain C region [Homo sapiens]				
	HsHeLa3_Ti_106.2298.229	2.9503	0.2269	1288.79	1288.46	3622.9		8	436.8	63.6	1	K.GPSVFPLAPCSR.S
	HsHeLa3_Ti_103.1803.180	4.0268	0.3434	1426.13	1424.56	8008.5		1	1242.1	69.2	1	R.STSESTAALGCLVK.D
	HsHeLa3_Ti_106.2848.285	3.5599	0.1238	1807.18	1809.12	6064.8		1	918.8	60	1	R.VVSVLTVLHQDWLNGK.E
	HsHeLa3_Ti_103.1878.187	2.5117	0.1298	1161.73	1162.34	4608.6		9	333.8	66.7	1	K.NQVSLTCLVK.G

	HsHeLa3_Ti_102.3109.310	3.9392	0.2322	2545.91	2545.68	7147		1	1278.7	54.8	5	K.GFYPSDIAVEWESNGQPENNYK.T
gi|38201710|ref|N	12	50	0.171	729	80273	8.3	U	DEAD box polypeptide 17 isoform p82 [Homo sapiens]				
*	HsGST-MOCK_Ti_103.193	3.5467	0.2944	1520.57	1520.77	8941.2		1	1254.7	72.7	2	K.KWDLSELPKFEK.N
*	HsGST-MOCK_Ti_103.193	3.9635	0.1962	1521.99	1520.77	5332.3		1	1687.8	65.9	1	K.KWDLSELPKFEK.N
	HsGST-MOCK_Ti_303.265	3.6573	0.1954	1369.44	1369.57	7837.3		7	895.4	58.3	6	R.GDGPICLVLAPTR.E
*	HsFLAG-Control_HeLa_NE	4.7057	0.3663	1692.68	1692.82	7858.2		1	1737.2	71.4	7	R.ELAQQVQQVADDYGK.C
	HsFLAG-Control_HeLa_NE	1.8359	0.1012	1053.37	1054.15	7559.8		5	566	66.7	1	K.STCIYGGAPK.G
	HsGST-MOCK_Ti_303.267	3.1278	0.2572	1337.33	1337.6	5377.8		1	865.1	80	2	R.MLDMGFEPQIR.K
	HsFlag1P_Ti_104.2210.221	4.2007	0.3247	1227.42	1227.45	6635		1	1668.4	86.4	19	K.APILIATDVASR.G
	HsFlag1P_Ti_104.2894.289	4.5794	0.3974	2082.79	2083.39	6206.5		1	939.4	55.3	4	K.APILIATDVASRGLDVEDVK.F
	HsFLAG-Control_HeLa_NE	2.6493	0.2241	874.56	874.966	7540.7		5	774.8	78.6	1	R.GLDVEDVK.F
*	HsGST-MOCK_Ti_303.233	3.3671	0.2812	2118.67	2119.25	5168.5		1	467.1	50	1	K.FVINYDYPNSSEDYVHR.I
*	HsFLAG-Control_MG_293_	3.8601	0.427	1417.71	1417.6	7369.4		1	1180.8	70.8	5	K.GTAYTFFTPGNLK.Q
	HsFLAG-Control_HeLa_NE	3.7084	0.3561	1456.27	1456.51	9318.2		1	1233.7	65.4	1	R.SSQSSSQQFSGIGR.S
gi|4502643|ref|N	7	45	0.171	531	58024	6.7	U	chaperonin containing TCP1, subunit 6A isoform a [Homo sapiens]				
*	HsFLAG-Control_HeLa_S1	5.4594	0.4244	2545.32	2545.85	8401.4		1	1334.7	47.9	14	K.VATAQDDITGDGTTSNVLIIGELLK.Q
	HsFLAG-Control_HeLa_S1	6.8988	0.492	2206.72	2207.57	7755.3		1	2378.2	70	5	K.VHAELADVLTEAVVDSILAIK.K
	HsFLAG-Control_HeLa_S1	4.2557	0.2912	2207.9	2207.57	7718.5		3	905.2	33.8	1	K.VHAELADVLTEAVVDSILAIK.K
	Hs293FLP_Ti_306.4003.40	4.2625	0.3443	2208.26	2207.57	7837.1		1	1103	50	1	K.VHAELADVLTEAVVDSILAIK.K
	HsFLAG-Control_HeLa_S1	2.9141	0.184	1264.25	1263.43	6367.5		1	1051	77.3	2	K.GIDPFSLDALSK.E
	HsFLAG-Control_HeLa_NE	4.8851	0.3477	1770.01	1769.14	6623.7		1	1756.6	71.9	12	R.AQLGVQAFADALLIIPK.V
	HsFLAG-Control_HeLa_NE	4.6981	0.4435	1763.63	1763	7618.5		1	1684	73.3	10	K.VLAQNSGFDLQETLVK.I
gi|20070125|ref|N	5	10	0.171	508	57116	4.9	U	prolyl 4-hydroxylase, beta subunit [Homo sapiens]				
*	HsFLAG-Control_Hela_Ti_1	5.0771	0.3054	2936.99	2937.27	9229.3		1	1711.4	31	2	R.TGPAATTLPDGAAAESLVESSEVAVIGFFK.D
*	Hs293FLP-MG_Ti_202.454	2.8122	0.2801	2714.68	2714.99	5719.5		1	401.6	37.5	1	K.QFLQAAEAIDDIPFGITSNSDVFSK.Y
*	HsHeLa_Control-MG_Ti_20	3.5425	0.325	1965.38	1966.24	6084.4		1	921.2	62.5	2	K.HNQLPLVIEFTEQTAPK.I
*	HsHeLa_Control-MG_Ti_20	5.0161	0.3739	1966.3	1966.24	5651		1	1202	46.9	2	K.HNQLPLVIEFTEQTAPK.I
*	HsHeLa_Control-MG_Ti_20	4.1992	0.372	1833.98	1835.03	8888.2		1	2415.6	78.6	3	K.ILFIFIDSDHTDNQR.I
gi|16579885|ref|N	14	37	0.171	427	47697	11.1	U	ribosomal protein L4 [Homo sapiens]				
*	Hs293FLP_TREX_Ti_103.2	2.3791	0.1648	988.41	989.203	4738.9		1	536.7	75	2	K.NVTLPAVFK.A
*	Hs293FLP_TREX_Ti_106.2	3.9795	0.3025	1762.58	1762.97	6274.2		1	1156.3	67.9	4	R.RGPCIIYNEDNGIIK.A
*	HsGST-MOCK_Ti_303.223	3.1785	0.184	1607.34	1606.78	6018.9		1	793	65.4	1	R.GPCIIYNEDNGIIK.A
*	HsFLAG-Control_293_Ti_2	3.0543	0.2832	1270	1269.53	3215		1	427.1	72.7	5	R.NIPGITLLNVSK.L
	Hs293FLP_TREX_Ti_105.1	3.0873	0.1897	1281.4	1281.45	7000.5		1	1102.4	77.8	2	R.KLDELYGTWR.K
*	HsFLAG-Control_293_Ti_2	2.1849	0.1272	956.33	957.118	7948.8		1	825.3	70	1	K.AAAAAAALQAK.S
*	Hs293FLP_TREX_Ti_102.1	2.617	0.1118	956.43	957.118	8836.6		1	1421.6	75	2	K.AAAAAAALQAK.S
*	Hs293FLP-MG_Ti_102.135	2.0988	0.1262	956.48	957.118	7657.2		1	906.4	65	2	K.AAAAAAALQAK.S
*	HsFLAG-Control_293_Ti_2	4.4872	0.1236	957.09	957.118	8189.6		1	2394.4	95	4	K.AAAAAAALQAK.S
*	Hs293FLP-MG_Ti_102.134	4.4588	0.086	957.52	957.118	6768.5		1	2233.4	95	4	K.AAAAAAALQAK.S
*	Hs293FLP_TREX_Ti_102.1	4.4473	0.1056	958.31	957.118	7312.8		1	2347.7	95	2	K.AAAAAAALQAK.S
*	HsHeLa_Control-MG_Ti_10	4.2754	0.0949	958.55	957.118	7408.5		1	2461.2	95	4	K.AAAAAAALQAK.S
*	Hs293FLP_TREX_Ti_103.1	5.4018	0.3601	1416.48	1416.57	7654.8		1	2204.6	82.1	2	K.AAAAAAALQAKSDEK.A
	Hs293FLP_TREX_Ti_106.2	2.9032	0.2376	1125.71	1125.4	7089.2		5	1071.7	72.7	2	K.AAVAGKKPVVGK.K
gi|31563378|ref|N	3	6	0.171	245	26599	4.7	U	integrin beta 4 binding protein isoform a [Homo sapiens]				
gi|4504771|ref|N	3	6	0.171	245	26599	4.7	U	integrin beta 4 binding protein isoform a [Homo sapiens]				
	HsHeLa_Control-MG_Ti_20	3.3618	0.2903	2085.63	2086.32	5039.7		1	405.4	50	1	R.HGLLVPNNTTDQELQHIR.N
	HsHeLa_Control-MG_Ti_20	3.9255	0.3393	2086.66	2086.32	7096		1	1526.6	48.5	1	R.HGLLVPNNTTDQELQHIR.N
	HsFLAG-MOCK_300mM_T	4.304	0.3784	2585.21	2585.87	6197.5		1	597.3	43.5	4	K.TSIEDQDELSSLLQVPLVAGTVNR.G
gi|15431288|ref|N	3	6	0.171	217	24831	9.9	U	ribosomal protein L10a [Homo sapiens]				

*	Hs293FLP_TREX_Ti_103.1	4.0776	0.3762	1893.23	1893.98	5985		1	1105	70	3	K.FSVCVLGDQQHCDEAK.A
	HsGST-MOCK_Ti_303.268	2.7753	0.1705	1452.89	1452.71	3831.3		1	607.5	75	1	K.AVDIPHMDIEALK.K
*	HsFLAG-Control_293_Ti_2	2.2737	0.1007	811.49	812	4830.2		1	633	85.7	2	R.ILGPGLNK.A
gi|4502201|ref|N	2	4	0.171	181	20697	6.8	U	ADP-ribosylation factor 1 [Homo sapiens]				
gi|66879664|ref|N	2	4	0.171	181	20697	6.8	U	ADP-ribosylation factor 1 [Homo sapiens]				
gi|66879662|ref|N	2	4	0.171	181	20697	6.8	U	ADP-ribosylation factor 1 [Homo sapiens]				
gi|66879660|ref|N	2	4	0.171	181	20697	6.8	U	ADP-ribosylation factor 1 [Homo sapiens]				
gi|4502209|ref|N	2	4	0.172	180	20530	6.8	U	ADP-ribosylation factor 5 [Homo sapiens]				
gi|4502203|ref|N	2	4	0.171	181	20601	7.4	U	ADP-ribosylation factor 3 [Homo sapiens]				
	HsFLAG-Control_HeLa_NE	2.8325	0.2149	2323.54	2324.68	4710.8		2	276.2	37.5	2	K.LGEIVTTIPTIGFNVETVEYK.N
	Hs293FLP_TREX_Ti_105.2	2.9605	0.2248	1091.96	1090.31	6960.4		4	1003.9	77.8	2	R.DAVLLVFANK.Q
gi|13128992|ref|N	3	3	0.17	176	18419	9.4	U	hypothetical protein MGC2803 [Homo sapiens]				
*	HsGST-MOCK_Ti_405.204	1.9613	0.1931	1106.4	1107.25	5770		9	330.4	54.5	1	K.GGPGSTLSFVGK.R
*	HsGST-MOCK_Ti_405.204	2.9747	0.3624	1106.95	1107.25	6468.1		1	882.5	72.7	1	K.GGPGSTLSFVGK.R
*	HsFLAG-MOCK_300mM_T	2.737	0.1821	2036.83	2035.26	8538.5		1	630.6	47.1	1	K.KQKTEDEVLTSKGDAWAK.Y
gi|4507195|ref|N	25	67	0.168	2364	274630	5.6	U	spectrin, beta, non-erythrocytic 1 isoform 1 [Homo sapiens]				
	HsHeLa_Control-MG_Ti_20	3.6659	0.4837	1978.91	1979.16	6118.1		1	623.6	56.2	1	K.TAGYPNVNIHNFTTSWR.D
	HsHeLa_Control-MG_Ti_10	5.7495	0.4072	2485.89	2484.73	9319.6		1	2418.5	41.7	2	K.SNAHYNLQNAFNLAEQHLGLTK.L
	HsFLAG-Control_HeLa_NE	3.7666	0.3027	1722.39	1722.85	9166.6		1	1270.8	67.9	1	K.LLDPEDISVDHPDEK.S
	HsHeLa_Control-MG_Ti_20	5.4697	0.4777	2185.36	2185.45	9125.3		1	1788.4	61.1	14	K.FANSLVGVQQQLQAFNTYR.T
	HsFLAG-Control_HeLa_NE	4.0704	0.2917	2022.17	2023.25	6167.4		2	812.1	55.6	6	R.LVSQDNFGFDLPAVEAATK.K
	HsHeLa_Control-MG_Ti_10	3.7671	0.2724	1265.71	1265.5	3580.7		1	901.9	85	2	K.HLLGVEDLLQK.H
	HsFLAG-Control_HeLa_NE	4.6418	0.42	2052.36	2052.2	7628.2		1	1247.7	61.1	3	K.IVSSSDVGHDEYSTQSLVK.K
	HsFlag1P_Ti_104.3099.309	4.6181	0.357	2319.54	2320.53	8608.8		1	1093	50	3	K.DALLSALSIQNYHLECNETK.S
	HsFlag1P_Ti_105.3421.342	3.2246	0.3661	1893.32	1894.19	5548.6		1	487.8	50	1	R.LAEISDVWEEMKTTLK.N
	Hs293FLP_Ti_304.1261.12	2.8291	0.1554	1097.19	1096.27	5622.2		2	662.6	75	1	K.LLTQHENIK.N
	HsFlag1P_Ti_105.2266.226	4.3426	0.3537	1524.63	1525.7	7652.4		1	1878.3	83.3	1	R.LQALDTGWNELHK.M
	HsHeLa_Control-MG_Ti_20	3.6898	0.2976	1833.69	1834.05	2820.9		1	394.7	64.3	2	R.QNLLSQSHAYQQFLR.D
	HsFlag1P_Ti_104.3259.325	4.3457	0.2628	1923.48	1924.13	10090.5		1	2857.4	82.1	2	K.FLQDCQELSLWINEK.M
	HsFLAG-Control_HeLa_NE	4.6725	0.4922	1888.6	1889.03	7770.9		1	1589.2	68.8	2	K.EIEELQSQAQALSQEGK.S
	HsHeLa_Control-MG_Ti_20	1.8772	0.1552	943.45	944.038	2530.1		2	138	75	1	K.EIHQFNR.D
	HsFlag1P_Ti_105.3208.320	3.0756	0.285	1616.06	1615.87	4785.3		1	489.1	66.7	2	K.QLWGLLIEETEKR.H
	HsHeLa_Control-MG_Ti_10	5.1985	0.4872	2340.67	2339.57	7669.4		1	1832.9	46.1	2	K.HQILEQAVEDYAETVHQLSK.T
	HsHeLa_Control-MG_Ti_20	2.8857	0.3354	1312.78	1311.39	8336.7		7	704.3	63.6	1	R.ALVADSHPESER.I
	HsFlag1P_Ti_105.2024.202	3.8258	0.2344	1375.09	1374.58	6821.1		3	1293.7	77.3	1	R.TQILAASYELHK.F
	HsFlag1P_Ti_104.3489.348	3.4352	0.2274	2092.66	2093.3	9625.2		2	869.7	47.2	4	R.DASVAEAWLLGQEPYLSSR.E
*	HsFLAG-Control_Hela_Ti_1	3.5219	0.383	1368.11	1368.58	7487.6		1	1376.8	73.1	3	K.TALPAQSAATLPAR.T
*	HsFLAG-Control_HeLa_S1	3.4515	0.2897	1756.37	1757	4137.1		1	450.3	53.1	7	K.TAASGIPYHSEVPVSLK.E
*	HsHeLa_Control-MG_Ti_10	2.8587	0.1137	2243.78	2241.39	6661.5		2	558.3	44.7	1	K.DDEEMNTWIQAISSAISSDK.H
*	HsHeLa_Control-MG_Ti_20	4.6103	0.5059	1545.3	1545.61	8109.4		1	1939.8	78.6	1	K.HEVSASTQSTPASSR.A
*	Hs293FLP_Ti_304.1842.18	4.1563	0.4432	2061.45	2060.31	5040.3		1	593.4	50	3	R.AQTLPTSVVTITSESSPGKR.E
gi|24432106|ref|N	9	19	0.168	923	102902	5.2	U	p30 DBC protein [Homo sapiens]				
gi|40548408|ref|N	9	19	0.168	923	102902	5.2	U	p30 DBC protein [Homo sapiens]				
	HsHeLa3_Ti_104.2023.202	3.4473	0.299	1588.6	1586.79	4214.6		1	589.2	60.7	2	K.AAYNPGQAVPWNAVK.V
	HsFLAG-Control_HeLa_S1	3.7552	0.4418	1499.24	1499.8	4270.1		1	634.7	67.9	2	K.SPAPPLLHVAALGQK.Q
	HsFLAG-Control_HeLa_NE	4.3456	0.386	2165.78	2164.24	5158.4		1	986.8	59.5	3	K.EAAPDAGAEPITADSDPAYSSK.V
	HsHeLa3_Ti_103.3115.311	3.9656	0.3035	1591.8	1589.87	4532.7		1	733.7	69.2	3	K.VLLLSSPGLEELYR.C
	HsFLAG-Control_HeLa_S1	4.0825	0.3696	1550.13	1550.76	6000		1	779.4	66.7	4	R.FAEFQYLQPGPPR.R
	HsFLAG-Control_HeLa_S1	3.6761	0.3138	3383.19	3382.49	6716.6		5	370.8	21.9	1	K.AAEAAPPTQEAQGETEPTEQAPDALEQAADTSR.R

	HsFLAG-Control_HeLa_NE		4.0821	0.3522	2605.58	2605.95	6360.3		1	704.4	43.8	1	R.QEGLDGGLPEEVLFGNLDLLPPPGK.S
	HsFLAG-Control_HeLa_NE		3.6456	0.2393	2606.52	2605.95	7541.2		1	784.1	29.2	1	R.QEGLDGGLPEEVLFGNLDLLPPPGK.S
	HsHeLa3_Ti_106.2486.248		5.0062	0.4229	1880.04	1879.17	8411.9		1	1467.6	61.8	2	K.ALVSHNGSLINVGSLLQR.A
gi|72534660|ref|N		3	21	0.168	238	27367	11.8	U	splicing factor, arginine/serine-rich 7, 35kDa [Homo sapiens]				
*	Hs293FLP_TREX_Ti_104.1		4.3143	0.404	1720.47	1720.92	6469.5		1	775.3	56.2	5	K.VYVGNLGTGAGKGELER.A
*	Hs293FLP_TREX_Ti_103.1		2.7702	0.2787	1074.26	1074.22	7943.1		1	895.4	81.2	4	R.AFSYYGPLR.T
	HsHeLa_Control-MG_Ti_20		4.0134	0.3097	1622.36	1622.78	7266		1	1224.3	73.1	12	R.NPPGFAFVEFEDPR.D
gi|16306492|ref|N		2	2	0.167	240	27503	7.1	U	cell division cycle 2 protein isoform 2 [Homo sapiens]				
gi|4502709|ref|N		2	2	0.135	297	34095	8.4	U	cell division cycle 2 protein isoform 1 [Homo sapiens]				
	HsFLAG-Control_HeLa_S1		2.7605	0.1583	2213.56	2213.54	9440.4		2	538.2	36.8	1	R.YSTPVDIWSIGTIFAELATK.K
	HsFLAG-Control_293_Ti_2		3.0792	0.2705	2289.71	2290.49	5554.3		1	410.2	44.7	1	R.ALGTPNNEVWPEVESLQDYK.N
gi|4759160|ref|N		1	2	0.167	126	13916	10.3	U	small nuclear ribonucleoprotein polypeptide D3 [Homo sapiens]				
*	Hs293FLP_Ti_304.1577.15		3.9912	0.4083	2415.45	2415.59	6351.3		1	1010.5	52.5	2	K.VLHEAEGHIVTCETNTGEVYR.G
gi|6912280|ref|N		4	5	0.166	338	38274	5.5	U	AHA1, activator of heat shock 90kDa protein ATPase homolog 1 [Homo sapiens]				
*	HsFLAG-Control_HeLa_S1		2.7806	0.1242	2511.62	2509.78	9734.5		1	472.4	38.1	1	K.TLFLAVQVQNEEGKCEVTEVSK.L
*	HsFLAG-Control_HeLa_S1		2.5725	0.1635	1485.25	1485.63	6691.8		1	655.4	68.2	1	K.ETFLTSPEELYR.V
*	HsFLAG-Control_HeLa_S1		3.7862	0.3773	2445.15	2446.72	8308.4		1	893.3	45.2	2	R.VFTTQELVQAFTHAPATLEADR.G
*	HsFLAG-Control_HeLa_S1		4.8492	0.3378	2446.86	2446.72	6469.2		1	926.2	35.7	1	R.VFTTQELVQAFTHAPATLEADR.G
gi|28882049|ref|N		3	5	0.166	320	35244	5.5	U	replication factor C 2 (40kD) isoform 2 [Homo sapiens]				
gi|31563534|ref|N		3	5	0.15	354	39157	6.4	U	replication factor C 2 (40kD) isoform 1 [Homo sapiens]				
	HsFLAG-Control_HeLa_NE		3.7738	0.2571	1446.46	1446.56	5293.9		1	937.7	75	2	K.LNEIVGNEDTVSR.L
	HsFLAG-Control_HeLa_S1		3.0542	0.2209	1635.55	1634.87	5666		1	590.3	50	1	R.EGNVPNIIIAGPPGTGK.T
	HsFLAG-Control_HeLa_NE		3.4772	0.3151	2564.75	2563.83	9058.3		1	713.5	38.6	2	R.QALNNLQSTFSGFGFINSENVFK.V
gi|4504803|ref|N		15	36	0.165	1142	131956	7.7	U	janus kinase 1 [Homo sapiens]				
*	HsHeLa_Control-MG_Ti_20		3.8395	0.1222	3002.06	3002.39	7000.5		6	480.8	26	1	K.KTEVNLEAPEPGVEVIFYLSDREPLR.L
*	HsHeLa_Control-MG_Ti_20		4.5654	0.4736	2035.57	2036.26	5861.6		1	1210.9	68.8	4	R.ISPLCHNLFALYDENTK.L
*	Hs293FLP-MG_Ti_203.499		4.3255	0.5113	2868.03	2869.24	9297.5		1	1004.2	38	2	K.IPDATPLLDASSLEYLFAQGQYDLVK.C
*	HsHeLa_Control-MG_Ti_20		4.9669	0.3983	2868.73	2869.24	8999		1	1278.7	44	3	K.IPDATPLLDASSLEYLFAQGQYDLVK.C
*	HsHeLa_Control-MG_Ti_20		5.1218	0.3156	2870.36	2869.24	7316.3		1	1386.7	34	2	K.IPDATPLLDASSLEYLFAQGQYDLVK.C
*	HsHeLa_Control-MG_Ti_20		2.9676	0.144	1134.26	1134.32	8139.5		5	1248	87.5	1	K.RYIPETLNK.S
*	HsHeLa_Control-MG_Ti_20		5.4564	0.0855	2156.68	2157.39	7607.4		1	2241.3	66.7	3	K.LSSHEEALSFVSLVDGYFR.L
*	HsHeLa_Control-MG_Ti_20		3.9864	0.252	1379.54	1379.61	5988		1	1157.1	85	2	K.HIVYLYGVCVR.D
*	HsFLAG-Control_MG_293_		2.8517	0.1533	1544.51	1544.71	5730.9		1	736.2	62.5	1	R.IPWIAPECVEDSK.N
*	HsHeLa_Control-MG_Ti_20		3.3426	0.2596	1566.98	1566.75	4464.2		1	705.2	71.4	1	K.SLKPESGGNHIADLK.K
*	HsHeLa_Control-MG_Ti_20		2.9982	0.1456	1694.46	1694.93	6116.6		1	541.4	56.7	1	K.SLKPESGGNHIADLKK.E
*	HsHeLa_Control-MG_Ti_20		2.9168	0.1719	1130.2	1130.29	5376		2	894.7	87.5	2	R.NLYHENIVK.Y
*	HsHeLa_Control-MG_Ti_20		2.8982	0.2333	1282.39	1282.44	8025.7		5	905.9	70	1	R.NVLVESEHQVK.I
*	HsHeLa_Control-MG_Ti_10		3.6007	0.3271	2146.71	2146.4	5479.2		1	620	56.2	1	K.RLPCPPNCPDEVYQLMR.K
*	HsHeLa_Control-MG_Ti_20		4.6744	0.3853	1710.42	1710.97	6861.3		1	1767.1	78.6	11	R.TSFQNLIEGFEALLK.-
gi|24119203|ref|N		3	7	0.165	248	29033	4.8	U	tropomyosin 3 isoform 2 [Homo sapiens]				
	HsFLAG-MOCK_300mM_T		3.7804	0.2326	1885.9	1885.09	7915.4		1	1326.7	44.6	1	R.RIQLVEEELDRAQER.L
	Hs293FLP_TREX_Ti_104.1		4.3686	0.233	1444.9	1444.67	9084.8		1	1752.4	79.2	3	R.LATALQKLEEAEK.A
	HsHeLa_Control-MG_Ti_10		3.8528	0.1147	1689.98	1689.82	8374.2		1	1405.2	75	3	K.YSQKEDKYEEEIK.I
gi|29029559|ref|N		13	45	0.164	971	110417	5.8	U	CSE1 chromosome segregation 1-like protein [Homo sapiens]				
	HsFLAG-Control_HeLa_S1		5.3664	0.3032	2435	2434.84	8186.1		1	2065.4	43.8	1	K.FLESVEGNQNYPLLLLTLLEK.S
	HsHeLa-FLAG-IP_S100_Ti_		3.193	0.3625	2435.22	2434.84	7520		1	502.1	40	4	K.FLESVEGNQNYPLLLLTLLEK.S
	HsFLAG-Control_HeLa_S1		4.0163	0.3033	1589.64	1589.79	10064.2		1	1061.2	61.5	3	R.FQSGDFHVINGVLR.T
	HsFLAG-Control_HeLa_S1		4.0758	0.3687	1675.75	1676.05	5504.8		1	1006.9	71.4	2	K.LVLDAFALPLTNLFK.A
*	HsFLAG-Control_HeLa_S1		5.5135	0.4338	1929.19	1930.16	8316.8		1	1748	65.6	10	K.LLQTDDEEEAGLLELLK.S

*	HsFLAG-Control_HeLa_NE	3.5724	0.3848	1811.87	1812.94	10393.3		1	1717.6	71.4	1	K.NLFEDQNTLTSICEK.V
*	HsFLAG-Control_HeLa_S1	4.6425	0.4397	1888.59	1888.9	7668.2		1	1353.2	66.7	10	R.AADEEAFEDNSEEYIR.R
*	HsFLAG-Control_HeLa_S1	4.7549	0.3262	1354.27	1352.57	6953.9		1	1840.7	83.3	1	K.DAAIYLVTSLASK.A
*	HsFLAG-Control_HeLa_NE	5.4242	0.3708	2806.13	2806.27	9613.6		1	1793.7	35	2	R.GPNNATLFTAAEIAPFVEILLTNLFK.A
*	HsFLAG-Control_HeLa_S1	4.6011	0.3311	2806.16	2806.27	6162.7		1	650.4	40	5	R.GPNNATLFTAAEIAPFVEILLTNLFK.A
*	HsFLAG-Control_HeLa_S1	7.1393	0.3647	2808.07	2806.27	9562		1	2437.9	39	4	R.GPNNATLFTAAEIAPFVEILLTNLFK.A
*	HsFLAG-Control_HeLa_S1	3.2422	0.3046	1105.59	1106.18	3416		1	784.9	72.7	1	R.GSNTIASAAADK.I
*	HsFLAG-Control_HeLa_S1	3.0314	0.096	1072.35	1072.34	4610		6	606.9	77.8	1	K.IPGLLGVFQK.L
gi|67189747|ref|N	6	13	0.163	288	32728	10.6	U	ribosomal protein L6 [Homo sapiens]				
gi|89027564|ref|X	6	13	0.173	272	30905	10.5	U	PREDICTED: similar to 60S ribosomal protein L6 (TAX-responsive enhancer element bin				
gi|89027562|ref|X	6	13	0.173	272	30905	10.5	U	PREDICTED: similar to 60S ribosomal protein L6 (TAX-responsive enhancer element bin				
gi|89027560|ref|X	6	13	0.223	211	24310	10.5	U	PREDICTED: similar to 60S ribosomal protein L6 (TAX-responsive enhancer element bin				
gi|89027558|ref|X	6	13	0.173	272	30905	10.5	U	PREDICTED: similar to 60S ribosomal protein L6 (TAX-responsive enhancer element bin				
gi|89027556|ref|X	6	13	0.222	212	24343	10.5	U	PREDICTED: similar to 60S ribosomal protein L6 (TAX-responsive enhancer element bin				
gi|89027554|ref|X	6	13	0.173	272	30905	10.5	U	PREDICTED: similar to 60S ribosomal protein L6 (TAX-responsive enhancer element bin				
gi|89027552|ref|X	6	13	0.173	272	30905	10.5	U	PREDICTED: similar to 60S ribosomal protein L6 (TAX-responsive enhancer element bin				
gi|89025441|ref|X	6	13	0.173	271	30777	10.5	U	PREDICTED: similar to 60S ribosomal protein L6 (TAX-responsive enhancer element bin				
gi|89025439|ref|X	6	13	0.173	271	30777	10.5	U	PREDICTED: similar to 60S ribosomal protein L6 (TAX-responsive enhancer element bin				
gi|89025437|ref|X	6	13	0.224	210	24182	10.5	U	PREDICTED: similar to 60S ribosomal protein L6 (TAX-responsive enhancer element bin				
gi|89025435|ref|X	6	13	0.223	211	24215	10.5	U	PREDICTED: similar to 60S ribosomal protein L6 (TAX-responsive enhancer element bin				
gi|89025433|ref|X	6	13	0.173	271	30777	10.5	U	PREDICTED: similar to 60S ribosomal protein L6 (TAX-responsive enhancer element bin				
gi|89025431|ref|X	6	13	0.173	271	30777	10.5	U	PREDICTED: similar to 60S ribosomal protein L6 (TAX-responsive enhancer element bin				
	Hs293FLP_TREX_Ti_104.1	3.755	0.3511	1284.53	1285.53	5189		1	642	66.7	2	K.VLATVTKPVGGDK.N
	Hs293FLP_TREX_Ti_104.1	3.4107	0.261	1285.41	1285.53	5347.3		1	819.1	70.8	5	K.VLATVTKPVGGDK.N
	HsFLAG-MOCK_300mM_T	2.9349	0.1974	1286.31	1285.53	6480.2		3	672.8	66.7	2	K.VLATVTKPVGGDK.N
	Hs293FLP_TREX_Ti_102.1	1.9579	0.27	1139.46	1140.24	5012.1		2	276.4	62.5	1	R.YYPTEDVPR.K
	HsFLAG-Control_Hela_Ti_1	3.3518	0.3263	1765.01	1765.15	7676.4		1	721	53.1	1	K.QLASGLLLVTGPLVLNR.V
	Hs293FLP_TREX_Ti_102.1	1.9737	0.1386	866.5	867.033	5435.6		1	659.8	85.7	2	K.FVIATSTK.I
gi|4506585|ref|N	3	4	0.163	270	29247	6.1	U	replication protein A2, 32kDa [Homo sapiens]				
*	HsHeLa_Control-MG_Ti_10	3.1144	0.3189	2511.95	2511.66	3705.8		1	452	50	1	R.QWVDTDDTSSENTVVPPETYVK.V
*	HsHeLa_Control-MG_Ti_10	3.9091	0.2433	1645.83	1645.82	4830		3	700.6	65.4	2	K.ACPRPEGLNFQDLK.N
*	HsHeLa_Control-MG_Ti_10	1.8456	0.2046	888.82	889.058	4987.6		3	387.2	71.4	1	K.HMSVSSIK.Q
gi|15431306|ref|N	6	12	0.163	257	28025	11	U	ribosomal protein L8 [Homo sapiens]				
gi|4506663|ref|N	6	12	0.163	257	28025	11	U	ribosomal protein L8 [Homo sapiens]				
	Hs293FLP_TREX_Ti_105.1	3.1272	0.2393	1460.58	1460.68	3863.4		2	530.6	69.2	1	K.DIIHDPGRGAPLAK.V
	HsFLAG-MOCK_300mM_T	4.3817	0.3992	1689.67	1689.82	7829.6		1	1315.2	63.3	1	R.ASGNYATVISHNPETK.K
	Hs293FLP_TREX_Ti_105.1	4.0528	0.3475	1817.42	1818	7333.2		1	1002.9	56.2	2	R.ASGNYATVISHNPETKK.T
	Hs293FLP_TREX_Ti_103.1	2.9887	0.2442	941.5	942.106	5650.3		1	471.7	65	1	R.AVVGVVAGGGR.I
	HsFLAG-Control_MG_293_	3.6661	0.3252	942.22	942.106	6523.4		1	1669.9	85	6	R.AVVGVVAGGGR.I
	HsFLAG-MOCK_300mM_T	3.4756	0.3353	942.4	942.106	5581.5		1	1573.4	85	1	R.AVVGVVAGGGR.I
gi|4506693|ref|N	1	3	0.163	135	15550	9.8	U	ribosomal protein S17 [Homo sapiens]				
gi|89059266|ref|X	1	3	0.163	135	15602	9.6	U	PREDICTED: similar to 40S ribosomal protein S17 [Homo sapiens]				
gi|51476007|ref|X	1	3	0.163	135	15602	9.6	U	PREDICTED: similar to 40S ribosomal protein S17 [Homo sapiens]				
	HsFLAG-Control_Hela_Ti_1	4.5985	0.4231	2489.37	2490.68	7324.5		1	1330.5	57.1	3	R.DNYVPEVSALDQEIIEVDPDTK.E
gi|4503265|ref|N	4	6	0.162	482	53487	8.5	U	dihydrolipoamide branched chain transacylase [Homo sapiens]				
*	Hs283FLP_Ti_105.1345.13	3.8601	0.2651	2632.95	2632.71	5141.6		8	478.6	29.5	1	K.DSEEDVVETPAVSHDEHTHQEIK.G
*	HsFlag1P_Ti_104.2981.298	3.5469	0.2013	1491.43	1491.77	5746.9		1	1142.9	81.8	2	R.ILKEDILNYLEK.Q
*	HsHeLa_Control-MG_Ti_20	2.556	0.273	2049.78	2050.28	4792.6		1	265.9	46.9	1	K.IPHFGYCDEIDLTELVK.L
*	Hs283FLP_Ti_103.3215.32	3.6269	0.2952	2880.84	2881.22	5757.3		1	495.2	27	2	K.AASLGLLQFPILNASVDENCQNITYK.A

gi|89031528|ref|X	3	4	0.161	261	29663	9.5	U	PREDICTED: similar to ribosomal protein S3a isoform 2 [Homo sapiens]				
gi|89033501|ref|X	3	4	0.161	261	29663	9.5	U	PREDICTED: similar to ribosomal protein S3a isoform 4 [Homo sapiens]				
	HsFLAG-Control_293_Ti_1	2.7091	0.2616	1952.81	1953.16	8138.8		1	428.8	46.9	1	R.VFEVSLADLQNDEVAFR.K
	HsFLAG-Control_293_Ti_2	2.8582	0.3372	1346.13	1346.49	8117.1		1	682.5	65	1	R.KTSYAQHQQVR.Q
	Hs293FLP-MG_Ti_204.252	3.2536	0.3231	1705.53	1705.92	4408.4		1	515.8	61.5	2	K.ACQSIYPLHDVFVR.K
gi|30410794|ref|N	3	10	0.161	254	29506	6	U	proteasome activator subunit 3 isoform 1 [Homo sapiens]				
gi|30410796|ref|N	3	10	0.154	267	30887	6.1	U	proteasome activator subunit 3 isoform 2 [Homo sapiens]				
	HsFLAG-Control_HeLa_NE	4.8523	0.4428	1682.41	1681.88	8368.8		1	1908.7	75	3	R.ITSEAEDLVANFFPK.K
	HsFLAG-Control_HeLa_S1	3.875	0.2263	1287.5	1287.46	8275.6		1	1415.2	80	4	K.SNQQLVDIIEK.V
	HsFLAG-Control_HeLa_NE	4.3787	0.3957	1670.31	1669.79	7554.1		1	2096.5	78.6	3	R.TVESEAASYLDQISR.Y
gi|4507191|ref|N	29	73	0.16	2472	284281	5.3	U	spectrin, alpha, non-erythrocytic 1 (alpha-fodrin) [Homo sapiens]				
*	Hs283FLP_Ti_106.2436.24	5.429	0.4792	2368.5	2367.62	5616		1	1310.7	62.5	1	K.EAIVTSEELGQDLEHVEVLQK.K
*	HsFLAG-Control_HeLa_NE	4.1997	0.2112	1606.71	1606.82	6167.8		1	997.9	70.8	2	K.LIQEQHPEEELIK.T
*	HsFLAG-Control_HeLa_NE	2.6276	0.1568	1086.06	1086.28	10943.8		1	1543.5	83.3	1	R.DLASVQALLR.K
*	HsHeLa_Control-MG_Ti_20	4.2445	0.2867	1678.13	1678.93	5081.3		1	734.5	67.9	1	R.LQQSHPLSATQIQVK.R
*	HsHeLa_Control-MG_Ti_20	6.1914	0.4643	2127.69	2128.34	8858.3		1	2541.1	67.5	7	K.ALINADELASDVAGAEALLDR.H
*	HsFLAG-Control_HeLa_NE	4.1413	0.1508	2128.53	2128.34	11102.5		1	1757.3	36.2	2	K.ALINADELASDVAGAEALLDR.H
*	HsFLAG-Control_HeLa_NE	5.724	0.5185	2128.7	2128.34	8291.8		1	2285.4	65	4	K.ALINADELASDVAGAEALLDR.H
*	HsFLAG-Control_HeLa_NE	4.2329	0.345	2147.33	2148.25	6898.4		1	1445.5	60	1	K.SADESGQALLAAGHYASDEVR.E
*	HsHeLa_Control-MG_Ti_20	4.3664	0.3848	1708.47	1708.92	8934.8		1	1406.8	69.2	2	R.AQLADSFHLQQFFR.D
*	Hs293FLP_Ti_303.1455.14	3.0607	0.4432	1590.58	1588.68	5279.5		1	961.9	69.2	1	K.HQAFEAELSANQSR.I
*	HsHeLa_Control-MG_Ti_10	4.0638	0.3215	1533.52	1532.66	8317		1	1419.2	81.8	1	K.LREANQQQQFNR.N
*	Hs293FLP_Ti_305.1451.14	3.9955	0.4051	1557.84	1557.71	6138.1		1	1490.9	80.8	1	K.HQALQAEIAGHEPR.I
*	Hs293FLP_Ti_304.2547.25	3.1888	0.1791	1487	1484.69	5810		3	528.9	59.1	1	K.ELVLALYDYQEK.S
*	HsHeLa_Control-MG_Ti_10	4.6519	0.2672	1418.73	1417.65	7251.1		1	1865.2	83.3	5	K.KGDILTLLNSTNK.D
*	Hs293FLP-MG_Ti_105.137	3.5146	0.2305	1326.34	1325.47	4861.5		1	1028	81.8	2	R.SQLLGSAHEVQR.F
*	Hs293FLP_Ti_303.1939.19	4.4721	0.4674	2329.18	2329.49	8090.9		1	1482.5	57.5	1	K.NQALNTDNYGHDLASVQALQR.K
*	HsHeLa_Control-MG_Ti_20	3.9486	0.2423	2876.2	2877.19	6586.9		1	1036.6	32	2	R.AGTFQAFEQFGQQLLAHGHYASPEIK.Q
*	HsFLAG-Control_HeLa_NE	4.2952	0.4237	2295.88	2295.51	9873.9		1	734.2	42.5	3	R.EAFLNTEDKGDSLDSVEALIK.K
*	HsHeLa_Control-MG_Ti_20	5.2969	0.4174	1972.73	1973.28	7818.9		1	1994.5	63.9	9	K.IAALQAFADQLIAAGHYAK.G
*	Hs293FLP-MG_Ti_205.377	4.9059	0.3069	1973.07	1973.28	5887.7		1	1171.2	41.7	2	K.IAALQAFADQLIAAGHYAK.G
*	HsFlag1P_Ti_105.3218.321	5.0468	0.4859	1631.03	1631.92	9179.1		1	2724.7	84.6	6	R.LAALADQWQFLVQK.S
*	HsGST-MOCK_Ti_102.138	4.0933	0.1982	1874.71	1875.05	7509.4		1	1573.4	70	1	K.KLSDDNTIGKEEIQQR.L
*	HsFLAG-MOCK_300mM_T	3.4463	0.3402	1437.71	1437.51	8580.3		1	977.4	68.2	1	K.KNNHHEENISSK.M
*	Hs293FLP_TREX_Ti_102.2	3.2027	0.1702	1205.42	1205.39	6573.5		1	1264.4	85	4	R.DLSSVQTLLTK.Q
*	HsFlag1P_Ti_105.3011.301	3.6485	0.2722	1311.26	1311.56	5289.2		1	945.9	80	1	R.KVEDLFLTFAK.K
*	Hs293FLP_Ti_302.3886.38	2.9786	0.1949	2299.6	2299.42	6797.4		1	483.7	39.5	1	K.ASAFNSWFENAEEDLTDPVR.C
*	Hs293FLP-MG_Ti_202.326	5.1751	0.426	1952.5	1953.07	9740		1	2958.3	73.5	6	R.SSLSSAQADFNQLAELDR.Q
*	HsFlag1P_Ti_105.2843.284	4.1616	0.4332	1802.74	1802	5263.6		1	1123.6	75	2	K.GRELPTAFDYVEFTR.S
*	HsFLAG-Control_HeLa_NE	3.2017	0.2687	1588.1	1588.76	6137.6		3	453.4	58.3	2	R.ELPTAFDYVEFTR.S
gi|4504983|ref|N	3	5	0.16	250	26188	8.5	U	galectin 3 [Homo sapiens]				
*	HsHeLa3_Ti_106.2455.245	3.3301	0.145	1644.26	1642.01	5737.5		2	740.2	57.1	3	R.MLITILGTVKPNANR.I
*	HsHeLa3_Ti_104.1863.186	3.229	0.1392	1325.58	1325.55	6804.9		7	849.6	70	1	K.IQVLVEPDHFK.V
*	HsHeLa3_Ti_106.2068.206	2.7391	0.3564	1651.2	1650.84	8583.7		1	873.6	57.7	1	K.VAVNDAHLLQYNHR.V
gi|17298690|ref|N	5	10	0.159	542	58172	5.3	U	fuse-binding protein-interacting repressor isoform b [Homo sapiens]				
gi|17978512|ref|N	5	10	0.154	559	59876	5.3	U	fuse-binding protein-interacting repressor isoform a [Homo sapiens]				
	HsFLAG-Control_HeLa_NE	3.2345	0.3073	1762.69	1763.04	4477.6		1	509.5	60	4	K.LGLPPLTPEQQEALQK.A
	HsFLAG-Control_HeLa_NE	2.7476	0.3483	1878.78	1878.09	8215.3		1	739.1	53.3	1	R.VYVGSIYYELGEDTIR.Q
	HsFLAG-Control_HeLa_NE	4.9305	0.438	1820.53	1818.98	7791.1		1	2382.5	83.3	3	R.IYVASVHQDLSDDDIK.S

	HsHeLa3_Ti_102.3627.362	3.7216	0.3213	2389.5	2388.61	6882.4			1	851.4	47.6	1	K.AQSSQDAVSSMNLFDLGGQYLR.V
	HsFLAG-Control_HeLa_NE	3.0383	0.1482	1827.64	1824.81	9146.4			4	582.8	46.7	1	K.DIDDDLEGEVTEECGK.F
gi|4506621|ref|NI		3	4	0.159	145	17258	10.6	U	ribosomal protein L26 [Homo sapiens]				
gi|89034466|ref|X		3	4	0.159	145	17282	10.5	U	PREDICTED: similar to 60S ribosomal protein L26-like 1 [Homo sapiens]				
gi|89033748|ref|X		3	4	0.159	145	17268	10.4	U	PREDICTED: similar to 60S ribosomal protein L26-like 1 [Homo sapiens]				
gi|7705813|ref|NI		3	4	0.159	145	17256	10.6	U	ribosomal protein L26-like 1 [Homo sapiens]				
	Hs293FLP_TREX_Ti_102.1	3.1355	0.257	1088.36	1088.21	4753.5			1	824.6	87.5	1	R.KDDEVQVVR.G
	Hs293FLP_TREX_Ti_106.2	2.753	0.3933	1418.46	1418.6	4224.7			1	332.3	53.8	1	K.ANGTTVHVGIHPSK.V
	Hs293FLP_TREX_Ti_106.2	4.0291	0.3748	1418.59	1418.6	7306.7			1	1198.8	69.2	2	K.ANGTTVHVGIHPSK.V
gi|28570172|ref|N		3	4	0.158	329	35886	8.3	U	NADP-dependent leukotriene B4 12-hydroxydehydrogenase [Homo sapiens]				
*	HsHeLa_Control-MG_Ti_20	3.2647	0.2319	1655.44	1654.82	5775.7			1	849	65.4	1	K.HFVGYPTNSDFELK.T
*	HsHeLa_Control-MG_Ti_10	3.1157	0.2499	1928.52	1928.15	5097.4			1	564.5	52.8	1	K.GTIVLASPGWTTHSISDGK.D
*	HsHeLa_Control-MG_Ti_20	3.8665	0.3272	2073.35	2074.43	2910			1	279.4	58.3	2	R.TGPLPPGPPPEIVIYQELR.M
gi|8393159|ref|NI		1	13	0.158	146	15921	4.4	U	calmodulin-like skin protein [Homo sapiens]				
*	HsFLAG-Control_Hela_Ti_1	5.767	0.5056	2264.58	2264.45	7702.9			1	1735.6	59.1	13	K.AFSAVDTDGNGTINAQELGAALK.A
gi|4506787|ref|NI		18	37	0.157	1657	189251	6.5	U	IQ motif containing GTPase activating protein 1 [Homo sapiens]				
*	HsFLAG-Control_HeLa_S1	2.9727	0.2635	1533.25	1533.68	4646.8			2	532.2	68.2	1	K.IFYPETTDIYDR.K
*	HsFLAG-Control_HeLa_S1	4.3422	0.3532	2962.33	2960.36	8128.6			1	1034.6	28.6	1	K.IGGILANELSVDEAALHAAVIAINEAIDR.R
*	HsFLAG-Control_HeLa_S1	4.439	0.3331	2562.39	2563.91	11000.6			1	947.8	41.3	3	K.VNTFSALANIDLALEQGDALALFR.A
*	HsFLAG-Control_HeLa_S1	2.6459	0.1328	1027.34	1026.22	8052.9			5	1158.9	83.3	1	R.ALQSPALGLR.G
*	HsFLAG-Control_HeLa_S1	4.83	0.3499	1296.84	1296.6	9274.5			1	2296.2	83.3	1	R.LAAVALINAAIQK.G
*	HsFLAG-Control_HeLa_S1	4.58	0.3228	1884.49	1884.14	7684.3			1	1358.9	42.6	1	R.ILAIGLINEALDEGDAQK.T
*	HsFLAG-Control_HeLa_S1	3.553	0.3201	1885	1884.14	10565.4			2	866.7	47.1	2	R.ILAIGLINEALDEGDAQK.T
*	HsFLAG-Control_HeLa_NE	5.5538	0.4174	1885.14	1884.14	7943.1			1	2567	79.4	5	R.ILAIGLINEALDEGDAQK.T
*	HsFLAG-Control_HeLa_S1	2.8266	0.1727	1153.49	1154.4	8510.1			2	724.2	65	3	K.TLQALQIPAAK.L
*	HsFLAG-Control_HeLa_S1	3.8261	0.3775	2057.33	2056.33	7727.6			1	917.9	52.9	3	K.LEGVLAEVAQHYQDTLIR.A
*	HsFLAG-Control_HeLa_S1	4.7881	0.3927	1938.55	1938.19	7572.6			1	1216.3	58.3	6	K.FALGIFAINEAVESGDVGK.T
*	HsFLAG-Control_HeLa_S1	2.8025	0.1075	1602.27	1601.81	7404.1			1	632.1	62.5	1	K.QIPAITCIQSQWR.G
*	HsFLAG-Control_HeLa_S1	4.0879	0.325	2429.03	2427.81	8562.7			1	1030.9	50	1	K.LEAYQHLFYLLQTNPTYLAK.L
*	HsFLAG-Control_HeLa_NE	4.0537	0.3173	1939.83	1940.16	4783.6			1	764.2	62.5	3	K.LPYDVTPEQALAHEEVK.T
*	HsFLAG-Control_HeLa_S1	3.0103	0.3851	1698.45	1698.84	6099.2			1	601.3	61.5	2	R.FFQTACDVPELQDK.F
*	HsFLAG-Control_HeLa_S1	2.7702	0.175	1644.5	1644.82	8122.6			1	1671.1	76.9	1	K.FNVDEYSDLVTLTK.P
*	HsFLAG-Control_HeLa_NE	2.8833	0.1763	1236.4	1235.38	7189.9			1	1251.8	88.9	1	K.YQELINDIAR.D
*	HsFLAG-Control_HeLa_S1	4.113	0.4557	2052.95	2053.27	7425.8			1	1199.3	61.8	1	K.NVIFEISPTEEVGDFEVK.A
gi|5902076|ref|NI		4	6	0.157	248	27745	10.4	U	splicing factor, arginine/serine-rich 1 (splicing factor 2, alternate splicing factor) [Homo sap				
*	Hs293FLP_TREX_Ti_103.2	2.9346	0.1493	1258.27	1257.48	5428.1			2	623.4	75	1	R.IYVGNLPPDIR.T
*	Hs293FLP_TREX_Ti_102.2	2.8494	0.1537	1028.33	1029.13	7621			6	829.7	78.6	2	K.DIEDVFYK.Y
*	HsFLAG-Control_HeLa_NE	2.8166	0.1761	1079.2	1079.2	5978.2			1	1003.8	88.9	1	R.DGTGVVEFVR.K
*	Hs293FLP_TREX_Ti_103.1	3.2393	0.2315	1163.56	1163.23	4297.7			1	810.5	83.3	2	R.SHEGETAYIR.V
gi|5453555|ref|NI		5	9	0.157	216	24423	7.5	U	ras-related nuclear protein [Homo sapiens]				
*	HsHeLa3_Ti_103.1584.158	1.8576	0.2981	1015.7	1016.18	4929.8			1	572.2	70	1	K.LVLVGDGGTGK.T
*	Hs293FLP_TREX_Ti_102.1	3.9199	0.3217	1516.54	1516.71	4081.6			2	959	83.3	4	R.VCENIPIVLCGNK.V
*	Hs293FLP_TREX_Ti_102.1	2.9307	0.2104	1214.34	1215.35	4801.9			1	393	72.2	2	K.NLQYYDISAK.S
*	HsHeLa3_Ti_103.1734.173	2.7727	0.1521	1214.68	1215.35	5395			3	421.8	72.2	1	K.NLQYYDISAK.S
*	HsFLAG-Control_HeLa_NE	2.5077	0.1152	1215.43	1215.35	6020.5			5	691.6	72.2	1	K.NLQYYDISAK.S
gi|4502389|ref|NI		1	2	0.157	89	10059	6.1	U	barrier to autointegration factor 1 [Homo sapiens]				
gi|88959141|ref|X		1	2	0.163	86	9740	6.1	U	PREDICTED: similar to barrier to autointegration factor 1 [Homo sapiens]				
gi|88953904|ref|X		1	2	0.163	86	9740	6.1	U	PREDICTED: similar to barrier to autointegration factor 1 [Homo sapiens]				
	HsFLAG-Control_293_Ti_2	3.3511	0.3931	1297.29	1297.54	7119.5			1	1029.4	69.2	2	K.PVGSLAGIGEVLGK.K

gi|30315658|ref|N	21	54	0.156	2155	251417	5.6	U		spectrin, beta, non-erythrocytic 1 isoform 2 [Homo sapiens]			
*	HsHeLa_Control-MG_Ti_10	3.1814	0.2362	2801.72	2801.04	4765.8		2	263.2	30	2	R.TSSISGPLSPAYTGQVPYNYNQLEGR.F
	HsHeLa_Control-MG_Ti_20	3.6659	0.4837	1978.91	1979.16	6118.1		1	623.6	56.2	1	K.TAGYPNVNIHNFTTSWR.D
	HsHeLa_Control-MG_Ti_10	5.7495	0.4072	2485.89	2484.73	9319.6		1	2418.5	41.7	2	K.SNAHYNLQNAFNLAEQHLGLTK.L
	HsFLAG-Control_HeLa_NE	3.7666	0.3027	1722.39	1722.85	9166.6		1	1270.8	67.9	1	K.LLDPEDISVDHPDEK.S
	HsHeLa_Control-MG_Ti_20	5.4697	0.4777	2185.36	2185.45	9125.3		1	1788.4	61.1	14	K.FANSLVGVQQQLQAFNTYR.T
	HsFLAG-Control_HeLa_NE	4.0704	0.2917	2022.17	2023.25	6167.4		2	812.1	55.6	6	R.LVSQDNFGFDLPAVEAATK.K
	HsHeLa_Control-MG_Ti_10	3.7671	0.2724	1265.71	1265.5	3580.7		1	901.9	85	2	K.HLLGVEDLLQK.H
	HsFLAG-Control_HeLa_NE	4.6418	0.42	2052.36	2052.2	7628.2		1	1247.7	61.1	3	K.IVSSSDVGHDEYSTQSLVK.K
	HsFlag1P_Ti_104.3099.309	4.6181	0.357	2319.54	2320.53	8608.8		1	1093	50	3	K.DALLSALSIQNYHLECNETK.S
	HsFlag1P_Ti_105.3421.342	3.2246	0.3661	1893.32	1894.19	5548.6		1	487.8	50	1	R.LAEISDVWEEMKTTLK.N
	Hs293FLP_Ti_304.1261.12	2.8291	0.1554	1097.19	1096.27	5622.2		2	662.6	75	1	K.LLTQHENIK.N
	HsFlag1P_Ti_105.2266.226	4.3426	0.3537	1524.63	1525.7	7652.4		1	1878.3	83.3	1	R.LQALDTGWNELHK.M
	HsHeLa_Control-MG_Ti_20	3.6898	0.2976	1833.69	1834.05	2820.9		1	394.7	64.3	2	R.QNLLSQSHAYQQFLR.D
	HsFlag1P_Ti_104.3259.325	4.3457	0.2628	1923.48	1924.13	10090.5		1	2857.4	82.1	2	K.FLQDCQELSLWINEK.M
	HsFLAG-Control_HeLa_NE	4.6725	0.4922	1888.6	1889.03	7770.9		1	1589.2	68.8	2	K.EIEELQSQAQALSQEGK.S
	HsHeLa_Control-MG_Ti_20	1.8772	0.1552	943.45	944.038	2530.1		2	138	75	1	K.EIHQFNR.D
	HsFlag1P_Ti_105.3208.320	3.0756	0.285	1616.06	1615.87	4785.3		1	489.1	66.7	2	K.QLWGLLIEETEKR.H
	HsHeLa_Control-MG_Ti_10	5.1985	0.4872	2340.67	2339.57	7669.4		1	1832.9	46.1	2	K.HQILEQAVEDYAETVHQLSK.T
	HsHeLa_Control-MG_Ti_20	2.8857	0.3354	1312.78	1311.39	8336.7		7	704.3	63.6	1	R.ALVADSHPESER.I
	HsFlag1P_Ti_105.2024.202	3.8258	0.2344	1375.09	1374.58	6821.1		3	1293.7	77.3	1	R.TQILAASYELHK.F
	HsFlag1P_Ti_104.3489.348	3.4352	0.2274	2092.66	2093.3	9625.2		2	869.7	47.2	4	R.DASVAEAWLLGQEPYLSSR.E
gi|55743153|ref|N	6	10	0.156	514	58604	6.2	U		WD repeat domain 26 [Homo sapiens]			
*	HsHeLa_Control-MG_Ti_20	4.1988	0.2713	1996.2	1995.28	7012.4		1	968.5	56.2	2	K.DTTVIIWQVDPDTHLLK.L
*	HsHeLa_Control-MG_Ti_20	4.0938	0.3525	2372.74	2373.51	8866.4		1	1299.6	52.6	1	R.GQFYQCDLDGNLLDSWEGVR.V
*	HsHeLa_Control-MG_Ti_20	2.9989	0.2055	1128.53	1128.23	6333.1		2	927.5	83.3	2	K.TVLASDTHQR.I
*	HsHeLa_Control-MG_Ti_20	4.0873	0.3516	2162.55	2163.48	11083.4		1	1219.9	52.8	2	R.LALLNVATQGVHLWDLQDR.V
*	HsHeLa_Control-MG_Ti_20	3.6647	0.2758	2162.84	2163.48	6482.2		1	1043.3	38.9	1	R.LALLNVATQGVHLWDLQDR.V
*	HsHeLa_Control-MG_Ti_20	4.3623	0.2286	1580.65	1580.78	5639.5		1	818	73.1	2	K.RSELPIAELTGHTR.T
gi|15431303|ref|N	3	7	0.156	192	21863	10	U		ribosomal protein L9 [Homo sapiens]			
gi|67944630|ref|N	3	7	0.156	192	21863	10	U		ribosomal protein L9 [Homo sapiens]			
	HsFLAG-Control_293_Ti_2	3.7277	0.4088	2113.59	2114.4	5346.6		1	498.4	47.2	2	K.TILSNQTVDIPENVDITLK.G
	Hs293FLP_TREX_Ti_104.1	3.0605	0.1702	1300.02	1299.51	6496.3		1	1616.1	90	2	R.KFLDGIYVSEK.G
	Hs293FLP_TREX_Ti_102.2	3.6884	0.289	1171.18	1171.34	3512.6		1	734	83.3	3	K.FLDGIYVSEK.G
gi|46249412|ref|N	13	41	0.155	1396	152978	5.1	U		latent transforming growth factor beta binding protein 1 isoform LTBP-1S [Homo sapiens]			
gi|46249414|ref|N	13	41	0.126	1722	186838	6	U		latent transforming growth factor beta binding protein 1 isoform LTBP-1L [Homo sapiens]			
	HsF-IP-293-MG_Ti_106.199	3.503	0.2411	1406.69	1406.63	3791.5		3	809.1	79.2	1	K.LCQIPVHGASVPK.L
	Hs283FLP_Ti_102.2678.26	3.4824	0.3189	2475.79	2476.71	4636.5		1	459.5	43.2	3	K.IGFGPDPTFSSCVPDPPVISEEK.G
	Hs283FLP_Ti_103.1372.13	2.705	0.426	1815.12	1815.98	7578.8		1	542.9	47.1	1	R.EHGPGVAEPEVATAPPEK.E
	Hs283FLP_Ti_104.1465.14	4.6682	0.3866	2206.88	2206.27	8566		1	1353.3	61.8	2	K.CVDIDECTQVQHLCSQGR.C
	Hs283FLP_Ti_106.1612.16	2.6714	0.3461	1139.39	1139.19	4417		1	626.9	81.2	2	R.HLCAHGQCR.N
	Hs283FLP_Ti_102.1470.14	4.4462	0.2513	1819.62	1819.92	7275.1		2	1439.9	66.7	2	R.TSTDLDVDVDQPKEEK.K
	Hs283FLP_Ti_102.1483.14	4.0318	0.4481	1786.64	1786.85	4775.6		1	1112	67.6	2	K.GFVPAGESSSEAGGENYK.D
	HsF-IP-293-MG_Ti_102.222	4.3567	0.3366	1698.52	1698.8	5961.1		1	1617	80.8	7	K.DADECLLFGQEICK.N
	Hs283FLP_Ti_105.1567.15	4.0334	0.3604	2041.7	2040.14	6429		1	713.9	53.3	1	K.NGFCLNTRPGYECYCK.Q
	Hs283FLP_Ti_102.1907.19	3.9019	0.3297	1824.48	1824.91	4105.7		1	576.8	60	1	K.DSDDYAQLCNIPVTGR.R
	Hs283FLP_Ti_102.2997.29	5.5523	0.4632	2621.07	2620.79	4732.2		1	642.1	50	11	R.DALVDFSEQYTPEADPYFIQDR.F
	Hs283FLP_Ti_104.1672.16	3.9358	0.4819	2279.7	2280.34	6929		1	719.8	47.2	4	R.VQEGYTCDCFDGYHLDTAK.M
	Hs283FLP_Ti_103.2152.21	4.3156	0.4711	1748.55	1748.94	4905		1	919.2	71.4	4	K.PNYCTPLNTALNLEK.D

gi|13676857|ref|N	16	212	0.155	639	70021	5.7	U	heat shock 70kDa protein 2 [Homo sapiens]				
	HsF-IP-293-MG_Ti_102.174	2.6315	0.2566	1487.66	1488.59	3419.2		1	176.5	58.3	2	R.TTPSYVAFTDTER.L
	Hs293FLP-MG_Ti_202.217	3.2886	0.3043	1487.89	1488.59	4372.6		1	860.7	83.3	12	R.TTPSYVAFTDTER.L
	HsFLAG-Control_HeLa_NE	3.2444	0.2808	1487.89	1488.59	4634.5		1	570.4	66.7	57	R.TTPSYVAFTDTER.L
	HsHeLa_Control-MG_Ti_20	2.4813	0.2055	1488.47	1488.59	3249.8		1	121.1	50	1	R.TTPSYVAFTDTER.L
	HsHeLa_Control-MG_Ti_20	3.6044	0.4296	1489.1	1488.59	3675.9		1	589.8	75	9	R.TTPSYVAFTDTER.L
	HsFLAG-MOCK_300mM_T	3.2112	0.1491	2159.14	2157.39	6487.7		1	523.9	44.7	2	R.TTPSYVAFTDTERLIGDAAK.N
	Hs293FLP_TREX_Ti_103.1	3.1894	0.2192	1181.34	1181.33	4945.8		3	857.3	83.3	5	K.VQVEYKGETK.T
	HsHeLa_Control-MG_Ti_20	5.5061	0.3911	1661.88	1660.91	4282.5		1	1591.7	86.7	75	R.IINEPTAAAIAYGLDK.K
	HsFlag1P_Ti_105.2426.242	5.1147	0.1386	1787.95	1789.08	4898.2		1	1086.6	71.9	5	R.IINEPTAAAIAYGLDKK.G
*	HsFLAG-Control_HeLa_NE	4.6091	0.1001	2984.32	2985.23	10226		2	1524.2	32.7	1	R.TLSSSTQASIEIDSLYEGVDFYTSITR.A
	HsGST-MOCK_Ti_102.194	4.0503	0.2122	1481.42	1481.65	6150.3		2	1322.4	54.5	2	R.ARFEELNADLFR.G
	HsGST-MOCK_Ti_404.268	3.9815	0.2532	1481.49	1481.65	5240.4		1	1202.9	86.4	2	R.ARFEELNADLFR.G
	HsHeLa_Control-MG_Ti_10	4.2431	0.2761	1483.66	1481.65	4363.8		1	928.3	81.8	24	R.ARFEELNADLFR.G
	HsFLAG-Control_HeLa_S1(	3.8164	0.214	1254.28	1254.39	7085		1	1542.2	88.9	7	R.FEELNADLFR.G
	HsFLAG-Control_MG_293_	3.1449	0.1938	1082.22	1082.24	5278.9		5	835.3	87.5	7	K.LLQDFFNGK.E
	HsFLAG-MOCK_300mM_T	3.5405	0.2578	1568.26	1566.8	8502.8		1	1323.3	75	1	K.LLQDFFNGKELNK.S
gi|4826862|ref|NI	2	2	0.155	187	20659	10.3	U	nucleoside-diphosphate kinase 4 [Homo sapiens]				
*	Hs293FLP-MG_Ti_105.143	3.4179	0.2189	1284.79	1283.51	4534.9		1	880	77.3	1	R.TLVAVKPDGVQR.R
*	Hs293FLP-MG_Ti_304.138	3.0968	0.3867	1698.44	1698.89	8098.2		1	1065.5	56.2	1	R.AMIGHTDSAEAAPGTIR.G
gi|4826998|ref|NI	11	35	0.154	707	76150	9.4	U	splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated) [Hon				
*	HsFLAG-Control_293_Ti_2(	4.2244	0.372	1810.15	1809.03	3696.5		1	504.7	63.3	5	R.LFVGNLPADITEDEFK.R
*	HsFLAG-Control_HeLa_NE	3.1474	0.2683	1254.54	1253.4	4158.5		1	576.2	75	2	K.YGEPGEVFINK.G
*	HsFLAG-Control_293_Ti_2(	4.8003	0.4253	2639.96	2640.91	9649.3		1	1376.2	50	6	R.NLSPYVSNELLEEAFSQFGPIER.A
*	HsFLAG-Control_HeLa_NE	4.0997	0.3289	2642.23	2640.91	8669.7		1	1157.5	33	1	R.NLSPYVSNELLEEAFSQFGPIER.A
*	HsHeLa3_Ti_103.4375.437	4.7169	0.4149	2642.68	2640.91	8889.4		1	1350.5	50	4	R.NLSPYVSNELLEEAFSQFGPIER.A
*	HsFLAG-Control_293_Ti_1(	4.4459	0.2249	3598.96	3598.99	10027.8		4	581.1	21.8	4	R.CSEGVFLLTTTPRPVIVEPLEQLDDEDGLPEK.L
*	HsFLAG-Control_293_Ti_2(	3.1756	0.277	2135.27	2136.36	8622.2		1	439.8	41.7	1	R.PVIVEPLEQLDDEDGLPEK.L
*	HsGST-MOCK_Ti_103.118(	3.4426	0.3363	1572.67	1573.78	8317.7		1	949.7	68.2	1	R.RMEELHNQEMQK.R
*	HsFLAG-Control_293_Ti_2(	2.7436	0.2833	1341.61	1342.46	4825.8		4	281.2	50	1	R.FGQGGAGPVGGQGPR.G
*	HsFLAG-Control_HeLa_NE	4.3282	0.3946	1342.06	1342.46	6865.2		1	1473.6	75	9	R.FGQGGAGPVGGQGPR.G
*	HsFLAG-Control_293_Ti_2(	3.11	0.3301	1342.51	1342.46	7509.4		1	722.7	57.1	1	R.FGQGGAGPVGGQGPR.G
gi|4502099|ref|NI	7	23	0.154	298	32895	9.7	U	solute carrier family 25, member 5 [Homo sapiens]				
*	HsFLAG-Control_293_Ti_1(	3.3296	0.2947	1219.6	1220.41	9431		1	1058.7	62.5	6	K.DFLAGGVAAAISK.T
*	HsFLAG-Control_293_Ti_2(	4.1722	0.2789	1220.21	1220.41	6844.3		1	2272.7	87.5	5	K.DFLAGGVAAAISK.T
	HsFLAG-Control_293_Ti_2(	2.5345	0.1512	1136.47	1137.37	6396.6		1	520.4	66.7	3	K.LLLQVQHASK.Q
	HsFLAG-Control_293_Ti_2(	2.8322	0.1474	1446.65	1447.68	5163.2		1	536.7	63.6	2	R.YFPTQALNFAFK.D
	HsFLAG-Control_293_Ti_1(	3.4801	0.3843	1447.1	1447.68	4956.3		1	680.8	72.7	4	R.YFPTQALNFAFK.D
	HsFLAG-Control_293_Ti_2(	3.4134	0.2708	1447.39	1447.68	4739.5		1	896.4	86.4	2	R.YFPTQALNFAFK.D
*	HsFLAG-Control_MG_293_	2.8649	0.2453	1219.37	1220.37	8036.7		3	575.7	55	1	R.AAYFGIYDTAK.G
gi|21464101|ref|N	3	4	0.154	247	28303	4.9	U	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, gamma polyp				
*	HsHeLa3_Ti_103.5064.506	4.4654	0.305	2237.03	2236.53	6999.6		1	1691.9	43.1	1	K.ELEAVCQDVLSLLDNYLIK.N
*	HsHeLa3_Ti_103.5058.505	2.9923	0.1947	2238.08	2236.53	6423.7		1	899.4	52.8	1	K.ELEAVCQDVLSLLDNYLIK.N
*	HsFLAG-Control_HeLa_S1(	4.7093	0.4059	2131.54	2132.24	6878.9		1	1378.7	61.1	2	K.TAFDDAIAELDTLNEDSYK.D
gi|12667788|ref|N	24	75	0.153	1960	226530	5.6	U	myosin, heavy polypeptide 9, non-muscle [Homo sapiens]				
*	HsHeLa_Control-MG_Ti_10	5.1101	0.2353	1675.31	1673.87	5282.9		1	1214.6	78.6	6	K.NFINNPLAQADWAAK.K
*	HsFLAG-Control_Hela_Ti_1	4.0065	0.3395	1479.41	1479.72	8161.6		1	1474.1	75	2	K.VIQYLAYVASSHK.S
*	HsFLAG-MOCK_150mM_T	5.0454	0.3401	1487.6	1487.83	8285.6		1	2280	80.8	8	R.VISGVLQLGNIVFK.K
*	HsFLAG-MOCK_150mM_T	3.6062	0.3746	1615.84	1616	6821.1		1	967.3	64.3	1	R.VISGVLQLGNIVFKK.E

*	HsHeLa_Control_Ti_106.32	3.7069	0.2745	1574.83	1572.81	5305.9		1	1197.7	73.1	5	K.VSHLLGINVTDFTR.G
*	HsFLAG-Control_Hela_Ti_1	5.2973	0.3894	2033.92	2035.13	7879.5		1	1697.9	68.8	4	R.ELESQISELQEDLESER.A
*	Hs293FLP-MG_Ti_204.005	3.5393	0.1898	3021.45	3019.24	9337.3		1	1115.9	28.8	1	R.DLGEELEALKTELEDTLDSTAAQQELR.S
*	HsFLAG-Control_Hela_Ti_1	6.0207	0.3866	1920.51	1921.03	10202.6		1	3097	78.1	1	K.TELEDTLDSTAAQQELR.S
*	HsFLAG-MOCK_150mM_T	3.3436	0.186	1730.68	1730.87	5288.3		2	475	57.1	1	K.QTLENERGELANEVK.V
*	HsFLAG-MOCK_300mM_T	2.6797	0.1487	1311.81	1311.48	7657.2		3	703.9	63.6	1	K.VLLQGKGDSEHK.R
*	HsFLAG-MOCK_150mM_T	5.8352	0.4857	1946.68	1947.15	6967.4		1	2162	76.5	6	K.LQVELDNVTGLLSQSDSK.S
*	HsHeLa_Control-MG_Ti_20	5.1528	0.2831	2493.5	2494.63	10534.5		1	1317.8	52.5	3	K.DFSALESQLQDTQELLQEENR.Q
*	HsFLAG-MOCK_150mM_T	4.8836	0.3071	2494.08	2494.63	10742		1	2617.2	43.8	1	K.DFSALESQLQDTQELLQEENR.Q
*	HsFLAG-MOCK_150mM_T	5.9822	0.3374	2494.14	2494.63	9095.5		1	2119.1	62.5	12	K.DFSALESQLQDTQELLQEENR.Q
*	HsFLAG-MOCK_300mM_T	4.6889	0.2142	2208.9	2208.44	6022.9		2	1941.8	51.5	3	K.TRLQQELDDLLVDLDHQR.Q
*	HsFLAG-MOCK_150mM_T	2.7559	0.3581	1949.71	1951.14	8978.6		1	758.9	56.7	1	R.LQQELDDLLVDLDHQR.Q
	HsFLAG-Control_Hela_Ti_1	4.7548	0.4555	1962.12	1963.06	8836.7		1	1809.5	68.8	5	K.TQLEELEDELQATEDAK.L
*	HsFLAG-MOCK_150mM_T	2.6909	0.2741	1379.24	1379.48	6448		2	628.4	65	1	R.EMEAELEDERK.Q
*	HsFLAG-MOCK_150mM_T	3.8489	0.3172	1213.31	1213.29	7510.2		1	1451.4	80	1	K.DLEAHIDSANK.N
*	HsFLAG-MOCK_300mM_T	3.4733	0.3529	1717.02	1716.89	7924.2		1	849.5	53.6	1	R.ASREEILAQAKENEK.K
*	HsFLAG-MOCK_150mM_T	6.6273	0.4156	2473.76	2473.61	9757.6		1	2579	65	6	R.IAQLEEELEEEQGNTELINDR.L
*	HsFLAG-MOCK_150mM_T	4.5105	0.3057	1531.32	1531.66	8992.5		1	2112	79.2	2	K.IAQLEEQLDNETK.E
*	HsFLAG-MOCK_150mM_T	4.4938	0.1554	1489.64	1488.55	8355		1	1646.9	81.8	1	K.RQLEEAEEEAQR.A
*	HsFLAG-MOCK_150mM_T	4.7206	0.4722	1566.42	1566.64	9537.1		1	1743.6	73.1	2	R.ELEDATETADAMNR.E
gi|41327764|ref|N	3	3	0.153	359	39589	7.2	U	aldo-keto reductase family 7, member A2 [Homo sapiens]				
*	HsHeLa_Control-MG_Ti_20	3.7599	0.3185	3431.74	3433.74	7950.2		1	782.9	28.6	1	R.LQCPQVDLFYLHAPDHGTPVEETLHACQR.L
*	HsHeLa_Control-MG_Ti_20	4.5622	0.3951	1585.91	1585.84	5708		1	1290.6	78.6	1	R.FYAYNPLAGGLLTGK.Y
*	Hs293FLP_TREX_Ti_104.2	3.477	0.3636	1378.3	1378.49	7284.2		1	1143.4	80	1	R.FFGNSWAETYR.N
gi|4504809|ref|N	2	3	0.153	347	35879	9.2	U	jun B proto-oncogene [Homo sapiens]				
*	HsFLAG-MOCK_300mM_T	3.4873	0.4737	2227.7	2228.29	7899.9		1	605.4	37.5	2	R.GPGPEGGGGGGSYFSGQGSDTGASLK.L
*	HsHeLa3_Ti_102.2097.209	3.943	0.3451	2413.08	2413.48	7850.9		1	769.8	40.7	1	R.GGGSGGGAGGAGGGVTEEQEGFADGFVK.A
gi|4507185|ref|N	2	8	0.153	261	28048	8	U	sepiapterin reductase (7,8-dihydrobiopterin:NADP+ oxidoreductase) [Homo sapiens]				
*	HsFLAG-Control_HeLa_NE	4.2477	0.4008	2079.82	2079.53	6746.5		1	870	50	3	R.TLAPLLASLLSPGSVLVLSAR.N
*	HsFLAG-Control_HeLa_S1	6.2898	0.4431	1893.05	1893.19	8621.2		1	2748.4	75	5	R.VPADLGAEAGLQQLLGALR.E
gi|66933016|ref|N	5	9	0.152	514	55805	6.9	U	inosine monophosphate dehydrogenase 2 [Homo sapiens]				
*	HsHeLa_Control-MG_Ti_20	4.4733	0.3721	1822.13	1822.11	6360.3		1	1160.8	70	2	K.KYEQGFITDPVVLSPK.D
*	HsHeLa_Control-MG_Ti_20	3.8213	0.3891	1432.58	1431.56	7455.9		1	971.9	66.7	2	R.HGFCGIPITDTGR.M
*	HsHeLa_Control-MG_Ti_20	4.2236	0.4081	1892.28	1893.2	8406.1		1	1222.4	58.3	2	R.FGVPVIADGGIQNVGHIAK.A
*	HsHeLa_Control-MG_Ti_20	3.5115	0.3435	1159.34	1159.29	6595.2		1	1375.9	81.8	2	K.VAQGVSGAVQDK.G
*	HsHeLa_Control-MG_Ti_20	4.4766	0.4522	1917.37	1917.04	10041.2		1	1710.9	61.8	1	R.TSSAQVEGGVHSLHSYEK.R
gi|4506439|ref|N	4	15	0.151	425	47820	5	U	retinoblastoma binding protein 7 [Homo sapiens]				
	HsFLAG-Control_HeLa_NE	4.2739	0.3794	1472.49	1472.64	7189.3		1	1236.3	75	11	K.TPSSDVLVFDYTK.H
*	HsGST-MOCK_Ti_103.120	3.0017	0.3277	1791.4	1790.9	4904.7		1	630.3	60	1	K.HPAKPDPSGECNPDLR.L
	Hs293FLP_TREX_Ti_102.2	2.5042	0.1334	974.95	974.148	4357.2		7	580.5	78.6	1	K.TVALWDLR.N
*	HsGST-MOCK_Ti_102.191	4.9255	0.4001	2848.2	2849.04	6715.9		1	1416.4	34.6	2	K.IGEEQSAEDAEDGPPELLFIHGGHTAK.I
gi|7657649|ref|N	3	12	0.151	352	39595	5.2	U	tropomodulin 3 (ubiquitous) [Homo sapiens]				
*	HsFLAG-Control_Hela_Ti_1	5.4409	0.415	1934.99	1934.06	6207.5		1	1710.1	78.1	6	K.DLDEDELLGNLSETELK.Q
*	HsFLAG-Control_Hela_Ti_1	4.5361	0.4521	2326	2327.6	7553.5		1	1034.6	55	4	K.QLETVLDDLDPENALLPAGFR.Q
*	HsFLAG-Control_Hela_Ti_1	3.5087	0.3538	1722.88	1722.9	8482.4		1	745.9	53.6	2	K.ENDAHLVEVNLNNIK.N
gi|5031877|ref|N	6	15	0.15	586	66408	5.2	U	lamin B1 [Homo sapiens]				
*	HsFLAG-Control_293_Ti_2	3.4317	0.2513	1415.28	1415.59	9053.9		1	1240.2	72.7	1	K.AEHDQLLLNYAK.K
*	HsFLAG-Control_293_Ti_2	3.536	0.2419	1293.98	1294.45	7853.9		1	1283.7	80	1	K.LREYEAALNSK.D
*	HsFLAG-Control_293_Ti_2	3.2742	0.2515	1069.34	1069.27	6847.5		1	1359.8	93.8	1	K.LAQALHEMR.E

*	HsFLAG-Control_293_Ti_2	4.0552	0.4124	1499.12	1497.62	8414.6		1	1531.8	73.1	7	R.LSSEMNTSTVNSAR.E
*	HsFLAG-Control_293_Ti_2	4.8185	0.3536	2108.26	2109.32	9163.6		1	1919.9	68.8	3	R.DQMQQQLNDYEQLLDVK.L
*	HsFLAG-Control_293_Ti_1	3.5086	0.2444	2572.56	2569.92	7410.4		5	427.2	33.3	2	K.AGQTVTIWAANAGVTASPPTDLIWK.N
gi|46367787|ref|	8	17	0.149	636	70671	9.5	U	poly(A) binding protein, cytoplasmic 1 [Homo sapiens]				
	Hs283FLP_Ti_102.2047.20	5.1031	0.4609	1929.1	1930.08	6525.8		1	1508.8	68.8	4	R.SLGYAYVNFQQPADAER.A
	HsFLAG-Control_MG_293_	2.7317	0.2852	1267.36	1267.48	6619.4		2	691.1	70	1	R.ALDTMNFDVIK.G
	HsFlag1P_Ti_105.3641.364	3.1412	0.1714	1808.78	1808.01	8318		1	898.9	56.7	1	K.ALYDTFSAFGNILSCK.V
	Hs293FLP_TREX_Ti_104.2	2.9705	0.1917	1045.69	1046.17	7007.6		5	864	75	3	K.GFGFVSFER.H
*	Hs293FLP_TREX_Ti_102.2	3.1513	0.3725	1286.53	1285.44	8382.9		2	826.1	63.6	1	K.EFSPFGTITSAK.V
	Hs283FLP_Ti_106.2165.21	3.8984	0.424	1543.84	1543.89	2877.8		1	521.4	73.1	5	R.IVATKPLYVALAQR.K
	Hs283FLP_Ti_104.1603.16	3.028	0.1035	1031.54	1031.24	4323		1	1394.3	93.8	1	K.PLYVALAQR.K
	Hs283FLP_Ti_106.2067.20	4.1431	0.5246	1694.7	1694.93	7289.5		1	1770.6	76.7	1	R.SKVDEAVAVLQAHQAK.E
gi|23397427|ref|	5	6	0.149	623	69633	8.6	U	synaptotagmin binding, cytoplasmic RNA interacting protein [Homo sapiens]				
*	HsHeLa3_Ti_103.2372.237	3.2538	0.2468	2568.03	2567.81	7268.9		4	335.6	31.2	1	K.YGGPPPDSVYSGQQPSVGTEIFVGK.I
*	HsHeLa3_Ti_102.4035.403	3.4629	0.18	1596.57	1594.8	4357.6		9	804.3	75	1	R.DLFEDELVPLFEK.A
*	HsHeLa3_Ti_102.3367.336	2.882	0.0913	2657.92	2655.94	5716.4		1	431.2	37	1	K.VWGNVGTVEWADPIEDPDPEVMAK.V
*	HsHeLa3_Ti_103.2758.275	4.31	0.3052	1474.9	1474.65	6035.1		1	1579.2	87.5	2	R.NLANTVTEEILEK.A
*	HsFLAG-Control_HeLa_NE	2.7632	0.1794	2043.02	2043.28	12878.7		4	741.3	44.1	1	K.DLEGENIEIVFAKPPDQK.R
gi|19923142|ref|	9	40	0.148	876	97170	4.8	U	karyopherin beta 1 [Homo sapiens]				
*	HsFLAG-Control_HeLa_NE	3.6524	0.1169	1557.78	1557.74	8552.9		1	952	57.7	3	K.TVSPDRLELEAAQK.F
*	HsFLAG-Control_HeLa_S1	4.1744	0.3428	1659.92	1659.92	4484.8		1	830.3	71.4	10	R.AAVENLPTFLVELSR.V
*	HsFLAG-Control_HeLa_NE	3.2671	0.3052	1226.15	1226.38	4696		2	669.8	72.7	2	R.VLANPGNSQVAR.V
*	HsHeLa3_Ti_103.1471.147	2.2181	0.0899	799.73	799.989	6439.2		3	428.4	64.3	1	R.VAAGLQIK.N
*	HsFLAG-Control_HeLa_S1	4.0562	0.3448	2566.47	2566.74	8532.2		1	1388.4	52.4	3	K.ESTLEAIGYICQDIDPEQLQDK.S
*	HsFLAG-Control_HeLa_NE	5.2373	0.436	1606.44	1606.86	7304.9		1	1597.3	75	11	K.LAATNALLNSLEFTK.A
*	HsFLAG-Control_HeLa_NE	2.6397	0.0839	957.5	956.173	4543.4		1	964.5	87.5	1	R.VAALQNLVK.I
*	HsFLAG-Control_HeLa_S1	2.7132	0.2041	1760.03	1760.13	3989.2		4	507.5	60	1	K.GALQYLVPILTQTLTK.Q
*	HsFLAG-Control_HeLa_NE	6.2736	0.2997	2147.91	2148.42	12014		1	3095.1	69.4	8	K.YLEVVLNTLQQASQAQVDK.S
gi|89036402|ref|	7	159	0.148	229	25758	7.5	U	PREDICTED: similar to ubiquitin C isoform 5 [Homo sapiens]				
gi|89036412|ref|	7	106	0.128	266	29892	6.9	U	PREDICTED: similar to ubiquitin C isoform 10 [Homo sapiens]				
gi|89036410|ref|	7	159	0.148	229	25758	7.5	U	PREDICTED: similar to ubiquitin C isoform 9 [Homo sapiens]				
gi|89036408|ref|	7	265	0.089	381	42851	7.6	U	PREDICTED: similar to CG11624-PA, isoform A isoform 8 [Homo sapiens]				
gi|89036406|ref|	7	159	0.148	229	25758	7.5	U	PREDICTED: similar to ubiquitin C isoform 7 [Homo sapiens]				
gi|89036404|ref|	7	265	0.089	381	42851	7.6	U	PREDICTED: similar to CG11624-PA, isoform A isoform 6 [Homo sapiens]				
	Hs293FLP-MG_Ti_202.258	4.3083	0.411	1788.48	1788.99	4421.5		1	681.2	63.3	102	K.TITLEVEPSDTIENVK.A
	HsHeLa3_Ti_102.1529.152	2.7201	0.1339	1082.66	1082.2	2593.8		1	450.9	87.5	3	R.TLSDYNIQK.E
	Hs293FLP_TREX_Ti_105.1	2.0576	0.1817	1067.59	1068.26	3276.1		1	269.3	68.8	3	K.ESTLHLVLR.L
	HsFLAG-Control_MG_293_	3.1018	0.2925	1068.16	1068.26	4626.9		1	630.1	87.5	6	K.ESTLHLVLR.L
	HsFLAG-Control_HeLa_S1	2.918	0.1872	1068.33	1068.26	5493		2	625.2	81.2	24	K.ESTLHLVLR.L
	Hs293FLP_TREX_Ti_105.1	3.0039	0.2609	1068.5	1068.26	3971.6		1	573.1	87.5	18	K.ESTLHLVLR.L
	HsFLAG-Control_MG_293_	2.5598	0.2377	1068.52	1068.26	4043.5		2	291.4	68.8	3	K.ESTLHLVLR.L
gi|89037890|ref|	8	12	0.147	600	64322	7.4	U	PREDICTED: similar to Ig gamma-1 chain C region [Homo sapiens]				
	HsHeLa3_Ti_106.2298.229	2.9503	0.2269	1288.79	1288.46	3622.9		8	436.8	63.6	1	K.GPSVFPLAPCSR.S
	HsHeLa3_Ti_103.1746.174	2.5563	0.3299	1321.66	1322.47	7795.4		1	499.3	53.8	2	R.STSGGTAALGCLVK.D
	HsHeLa3_Ti_103.1754.175	3.6033	0.3401	1322.93	1322.47	8426.5		1	1064.8	65.4	1	R.STSGGTAALGCLVK.D
*	HsHeLa3_Ti_105.1295.129	3.4049	0.4566	1358.41	1356.44	7171.4		1	948.4	68.2	3	K.TPLGDTTHTCPR.C
	HsHeLa3_Ti_106.2848.285	3.5599	0.1238	1807.18	1809.12	6064.8		1	918.8	60	1	R.VVSVLTVLHQDWLNGK.E
	HsHeLa3_Ti_104.1455.145	2.1475	0.1794	838.63	839.023	2547.7		4	356.7	78.6	1	K.ALPAPIEK.T
	HsHeLa3_Ti_104.1648.164	2.7077	0.2801	1907.07	1906.16	3939.2		3	306.7	50	2	R.EPQVYTLPPSREEMTK.N

	HsHeLa3_Ti_103.1878.187	2.5117	0.1298	1161.73	1162.34	4608.6		9	333.8	66.7	1	K.NQVSLTCLVK.G
gi|27436969|ref|N	4	6	0.147	353	39287	8.6	U	potassium voltage-gated channel, shaker-related subfamily, beta member 2 isoform 2 [Ho				
gi|4504825|ref|NI	4	6	0.142	367	41000	9	U	potassium voltage-gated channel, shaker-related subfamily, beta member 2 isoform 1 [Ho				
	HsHeLa_Control-MG_Ti_10	3.7891	0.2983	1596.96	1596.87	6426.7		1	797.3	66.7	2	R.EKVEVQLPELFHK.I
	HsHeLa_Control-MG_Ti_10	2.8924	0.4575	1904.93	1905.23	5172		1	495.2	44.4	1	K.IGVGAMTWSPLACGIVSGK.Y
	HsHeLa_Control-MG_Ti_10	4.1189	0.24	2200.96	2202.51	6152.4		2	600.4	32.9	1	K.LSSSIIHEIDSILGNKPYSK.K
	HsHeLa_Control-MG_Ti_10	3.9108	0.3159	2203.94	2202.51	8779.1		1	1193	50	2	K.LSSSIIHEIDSILGNKPYSK.K
gi|5031569|ref|NI	3	14	0.146	376	42614	6.6	U	ARP1 actin-related protein 1 homolog A, centractin alpha [Homo sapiens]				
*	HsFLAG-Control_HeLa_S1	4.2272	0.3551	2534.87	2535.82	8689.8		1	763	45.2	2	K.DQLQTFSEEHPVLLTEAPLNPR.K
*	HsFLAG-Control_HeLa_NE	3.615	0.3851	1867.2	1868.05	5070.5		1	893.6	65.6	3	K.AQYYLPDGSTIEIGPSR.F
*	HsFLAG-Control_HeLa_S1	5.0607	0.3775	1685.92	1684.97	8231		1	1713.8	73.3	9	R.TLFSNIVLSGGSTLFK.G
gi|4757880|ref|NI	2	2	0.146	328	37155	6.8	U	BUB3 budding uninhibited by benzimidazoles 3 isoform a [Homo sapiens]				
gi|56550081|ref|N	2	2	0.147	326	36955	6.8	U	BUB3 budding uninhibited by benzimidazoles 3 isoform b [Homo sapiens]				
	HsGST-MOCK_Ti_103.215	4.1084	0.3337	3188.83	3189.44	9160.9		1	918.2	28.7	1	K.YQHTGAVLDCAFYDPTHAWSGGLDHQLK.M
	HsGST-MOCK_Ti_102.154	3.9301	0.3113	2277.59	2277.47	7783.1		1	1013.5	36.8	1	K.MHDLNTDQENLVGTHDAPIR.C
gi|8922498|ref|NI	2	11	0.146	261	29988	7.1	U	pyridoxine 5'-phosphate oxidase [Homo sapiens]				
*	HsHeLa_Control-MG_Ti_20	4.799	0.4432	2297.55	2298.56	10723.8		1	1296.5	50	10	K.ELDSNPFASLVFYWEPLNR.Q
*	Hs293FLP-MG_Ti_205.178	2.6978	0.1627	2343.83	2344.63	10466.7		2	715.7	44.4	1	R.KKNEELEQLYQDQEVPKPK.S
gi|4758516|ref|NI	2	3	0.146	240	26788	4.7	U	hepatoma-derived growth factor (high-mobility group protein 1-like) [Homo sapiens]				
*	HsGST-MOCK_Ti_302.280	3.0104	0.2846	1819.91	1821	6013.4		4	487.2	50	1	K.GFSEGLWEIENNPTVK.A
*	HsHeLa3_Ti_102.1462.146	4.6839	0.362	2046.65	2046.03	4126.3		1	724.5	61.1	2	K.SCVEEPEPEPEAAEGDGDK.K
gi|28875797|ref|N	2	3	0.145	248	26397	12.2	U	hypothetical protein LOC26097 [Homo sapiens]				
*	HsF-IP-293-MG_Ti_105.14	2.8631	0.1702	1784.86	1785.07	10069.8		2	1051	56.7	1	R.LAQQMENRPSVQAALK.L
*	HsF-IP-293-MG_Ti_104.23	3.3363	0.4054	2206.18	2207.29	7506.1		1	648.9	47.4	2	K.GHLDAELDAYMAQTDPETND.-
gi|4885539|ref|NI	2	8	0.145	227	24636	7.2	U	protein-L-isoaspartate (D-aspartate) O-methyltransferase [Homo sapiens]				
*	HsGST-MOCK_Ti_104.137	4.4803	0.3922	1478.62	1478.61	7635.5		1	1227.9	65.4	5	K.SGGASHSELIHNLR.K
*	HsFLAG-Control_293_Ti_2	5.0888	0.4555	2046.5	2044.37	4389.3		1	676.6	63.9	3	R.LILPVGPAGGNQMLEQYDK.L
gi|4885417|ref|NI	2	2	0.145	200	22407	5.4	U	huntingtin interacting protein 2 [Homo sapiens]				
*	HsFLAG-Control_HeLa_S1	2.9271	0.1828	1305.66	1303.5	7177.9		2	690.8	60	1	K.IPETYPFNPPK.V
*	HsFLAG-Control_HeLa_S1	3.1526	0.1694	1978.53	1977.23	7536.1		2	589.8	44.1	1	R.LWAHVYAGAPVSSPEYTK.K
gi|16117791|ref|N	2	3	0.145	110	12538	11.1	U	ribosomal protein L35a [Homo sapiens]				
	Hs293FLP_TREX_Ti_103.1	1.9829	0.1465	769.42	769.919	6471.7		3	518.2	75	1	K.AIFAGYK.R
*	Hs293FLP_TREX_Ti_102.1	2.6843	0.2877	1101.34	1102.19	7157.3		5	559.8	68.8	2	R.DETEFYLGK.R
gi|40288290|ref|N	2	3	0.144	236	26648	6.4	U	chloride intracellular channel 3 [Homo sapiens]				
*	HsFLAG-Control_HeLa_S1	3.2412	0.3822	1952.22	1951.18	4970.5		1	628.8	58.8	2	K.DFAPGSQLPILLYDSDAK.T
*	HsFLAG-Control_HeLa_S1	2.8223	0.1614	1856.57	1856.09	4733.5		5	284.7	46.7	1	K.NPVPAQDEALYQQLLR.A
gi|12751497|ref|N	1	2	0.144	229	24992	10	U	hypothetical protein LOC65265 [Homo sapiens]				
*	HsGST-MOCK_Ti_304.021	6.7239	0.5489	3664.76	3664.11	9339.3		1	2504.2	35.2	2	K.LAPEEVPLSAEAQAQQLAQELAWCVEQLELGLK.R
gi|29171734|ref|N	9	18	0.143	859	97208	9.2	U	eukaryotic translation initiation factor 2C, 2 [Homo sapiens]				
*	HsFLAG-Control_293_Ti_2	2.6513	0.1823	1347.31	1346.63	5070.8		7	439.4	54.5	1	K.NLYTAMPLPIGR.D
*	HsFLAG-Control_MG_293_	5.1938	0.5221	1744.04	1744.82	8988.3		1	1950.7	68.8	1	R.SFFTASEGCSNPLGGGR.E
*	Hs293FLP-MG_Ti_206.374	4.2695	0.4656	1794.45	1795.05	6315.1		1	1480.4	78.6	2	K.AQPVIEFVCEVLDFK.S
*	HsFLAG-Control_293_Ti_2	3.2352	0.2271	1660.36	1659.79	5558.7		2	491.7	53.8	2	K.SIEEQQKPLTDSQR.V
*	HsHeLa_Control-MG_Ti_20	6.0008	0.4766	3139.07	3139.42	9515.9		1	1847.7	35.6	2	R.RPASHQTFPLQQESGQTVECTVAQYFK.D
	Hs293FLP-MG_Ti_205.268	3.841	0.4209	1870.33	1871.11	5057.1		1	884.7	70	4	K.HTYLPLEVCNIVAGQR.C
*	HsFLAG-Control_Hela_Ti_1	2.84	0.3055	1299.77	1300.54	3510.1		7	379.6	63.6	1	R.VLQPPSILYGGR.N
	HsHeLa_Control-MG_Ti_10	2.2261	0.2133	1166.88	1167.31	5626.3		9	410	61.1	1	K.AVQVHQDTLR.T
	HsFLAG-Control_293_Ti_2	3.205	0.3047	1167.22	1167.31	5822.3		1	1125	88.9	4	K.AVQVHQDTLR.T

gi|61175215|ref|N	2	4	0.143	231	26860	8.1	U		hypothetical protein LOC139886 [Homo sapiens]			
*	Hs293FLP-MG_Ti_202.390	3.4757	0.3753	2868.26	2869.15	5751.7		1	479.5	38	2	R.IIPDSNYYFPTAEQEPGEVVDSLVGK.Q
	HsFLAG-Control_HeLa_NE	2.7657	0.1821	854.29	854.037	3938.9		1	651.2	91.7	2	K.PSVYFIK.F
gi|15082258|ref|N	2	3	0.142	183	20811	5.3	U		chromobox homolog 3 [Homo sapiens]			
gi|89038889|ref|X	2	3	0.142	183	20811	5.3	U		PREDICTED: similar to chromobox homolog 3 [Homo sapiens]			
gi|20544151|ref|N	2	3	0.142	183	20811	5.3	U		chromobox homolog 3 [Homo sapiens]			
	HsFLAG-Control_HeLa_NE	5.2192	0.2967	1663.64	1662.83	5417.6		1	1120.8	76.9	1	K.KVEEAEPEEFVVEK.V
	HsFlag1P_Ti_105.2805.280	4.1782	0.2869	1525.32	1525.71	8525		1	1987.3	86.4	2	K.CPQIVIAFYEER.L
gi|41872631|ref|N	19	44	0.141	2511	273424	6.4	U		fatty acid synthase [Homo sapiens]			
*	HsFLAG-Control_HeLa_S1	3.9759	0.3354	1917.94	1918.11	3853.7		1	514	59.4	3	K.EQGVTFPSGDIQEQLIR.S
*	HsFLAG-Control_HeLa_S1	3.2661	0.3135	2233.76	2234.51	6380.2		1	782.9	52.6	2	K.DTVTISGPQAPVFEFVEQLR.K
*	HsFLAG-Control_HeLa_S1	5.0648	0.4613	2475.51	2473.84	5467.5		1	667.5	47.7	3	R.LHLSGIDANPNALFPPVEFPAPR.G
*	HsFLAG-Control_HeLa_S1	3.0466	0.2352	1595.68	1594.94	5360.9		1	547.8	61.5	2	R.VLFPATGYLSIVWK.T
*	HsHeLa_Control-MG_Ti_20	3.6247	0.2555	2787.58	2787.32	5872.6		1	672	29	1	R.ALGLGVEQLPVVFEDVVLHQATILPK.T
*	HsFLAG-Control_HeLa_S1	5.7836	0.4099	2840.99	2842.18	7220.6		1	1279.8	36.5	4	R.LFDHPESPTPNPTEPLFLAQAEVYK.E
*	HsFLAG-Control_HeLa_S1	4.1345	0.4722	1870.36	1870.95	5933.9		1	650.2	60.7	2	K.FCFTPHTEEGCLSER.A
*	HsFLAG-Control_HeLa_S1	5.1333	0.4067	1779.12	1779.08	7692.6		1	2279.4	75	8	K.LPEDPLLSGLLDSPALK.A
*	HsFLAG-Control_HeLa_S1	4.252	0.1904	3722.99	3722.11	9423.4		2	547.6	22	1	R.GHPLGDIVAFLTSTEPQYGQGILSQDAWESLFSR.V
*	HsFLAG-Control_HeLa_S1	3.7502	0.2764	1469.81	1470.58	5798.3		1	1119.2	75	3	R.FPQLDSTSFANSR.D
*	HsFLAG-Control_HeLa_S1	4.0867	0.3734	1624.65	1623.93	7946.7		1	1600.1	71.4	3	K.VVVQVLAEEPEAVLK.G
*	HsFLAG-Control_HeLa_S1	4.8209	0.4715	2363.02	2363.77	9824.7		1	1809.2	54.8	1	K.SYIIAGGLGGFGLELAQWLIQR.G
*	HsFLAG-Control_HeLa_S1	4.6475	0.4147	2266.8	2265.7	5758.9		1	1184.3	54.5	2	R.GLIAEAAQLGPVGGVFNLAVVLR.D
*	HsFLAG-Control_HeLa_S1	2.787	0.1938	2266.76	2266.48	7218.9		2	522.3	44.4	1	R.DGLLENQTPEFFQDVCKPK.Y
*	HsFLAG-Control_HeLa_S1	3.4579	0.3357	1614.55	1614.76	9397.8		1	1452.5	69.2	1	K.EDGLAQQQTQLNLR.S
*	HsFLAG-Control_MG_293_	2.6526	0.2103	1427.03	1427.7	6604.9		2	662.8	62.5	1	R.SLLVNPEGPTLMR.L
*	HsFLAG-Control_HeLa_S1	5.0004	0.3548	2290.72	2291.36	7245.8		1	1004	50	4	K.TGGAYGEDLGADYNLSQVCDGK.V
*	HsFLAG-Control_HeLa_S1	3.6224	0.2703	2424.06	2423.77	5212.3		1	619.9	33	1	R.TLLEGSGLESIISIIHSSLAEPR.V
*	HsFLAG-Control_HeLa_S1	3.0978	0.3679	2425.03	2423.77	8878.8		2	381.7	31.8	1	R.TLLEGSGLESIISIIHSSLAEPR.V
gi|4557365|ref|N	12	31	0.14	1417	159000	7.5	U		Bloom syndrome protein [Homo sapiens]			
*	HsFLAG-Control_293_Ti_1	3.4312	0.2516	1621.88	1622.73	6823.7		1	768.2	60	2	K.TSSDNNVSVTNVSVAK.T
*	HsFLAG-Control_293_Ti_1	3.5998	0.3881	2539	2539.67	7856.7		1	785.8	45.2	1	K.DVNVTEDFSFSEPLPNTTNQQR.V
*	HsFLAG-Control_293_Ti_1	3.4232	0.2501	1258.75	1259.49	3579		1	652.7	80	1	K.SLLPDFLQTPK.E
*	HsFLAG-Control_293_Ti_1	4.2226	0.2872	1477.23	1477.62	9169.8		1	1604.6	75	2	K.EVVCTTQNTPTVK.K
*	HsFLAG-Control_293_Ti_1	2.191	0.1088	1477.26	1477.62	5285.1		1	311.1	54.2	1	K.EVVCTTQNTPTVK.K
*	HsFLAG-Control_293_Ti_1	2.549	0.1985	1402	1402.6	4577.5		1	594.3	72.7	1	K.SFVTPPQSHFVR.V
*	HsFLAG-Control_293_Ti_1	3.6357	0.3015	2833.42	2833.99	7453.4		1	584.2	37.5	3	K.TDCLPVSSTAQNINFSESIQNYTDK.S
*	HsFLAG-Control_293_Ti_1	5.2454	0.4739	2416.9	2417.78	4538.2		1	730.1	52.4	7	K.SLCYQLPACVSPGVTVVISPLR.S
*	HsFLAG-Control_293_Ti_1	3.0349	0.2215	1608.9	1608.83	3673		2	407.2	57.1	3	K.LTSLDIPATYLTGDK.T
*	HsFLAG-Control_293_Ti_1	4.9885	0.4808	2133.49	2134.36	9153.5		1	1664.9	64.7	4	R.IQLLAYFGENGFNPDFCK.K
*	HsFLAG-Control_293_Ti_1	4.6005	0.3569	2243.07	2244.33	6548.4		1	600.9	47.5	2	K.YSEWTSPAEDSSPGISLSSSR.G
*	HsFLAG-Control_293_Ti_1	4.7308	0.4882	2152.79	2153.22	12403.2		1	1458.4	47.7	4	K.SSSIIGSSSASHTSQATSGANSK.L
gi|4506587|ref|N	3	8	0.14	121	13569	5.1	U		replication protein A3, 14kDa [Homo sapiens]			
*	HsHeLa_Control-MG_Ti_10	4.1689	0.3134	2040.13	2040.33	5688.7		1	979.9	65.6	4	K.IIHDFPQFYPLGIVQHD.-
*	Hs293FLP_Ti_305.2973.29	4.6431	0.3836	2041.23	2040.33	4942.2		1	1228.9	71.9	2	K.IIHDFPQFYPLGIVQHD.-
*	HsHeLa_Control-MG_Ti_10	4.4009	0.2433	2042.71	2040.33	4570.3		8	660.6	39.1	2	K.IIHDFPQFYPLGIVQHD.-
gi|5454064|ref|N	6	11	0.139	669	69492	9.7	U		RNA binding motif protein 14 [Homo sapiens]			
*	HsFLAG-MOCK_300mM_T	2.7891	0.235	1556.81	1556.77	8606.3		2	691.9	57.7	1	R.AIEALHGHELRPGR.A
*	HsFlag1P_Ti_103.2238.223	5.8463	0.4734	1751.64	1752.93	6347.2		1	2334.2	86.7	3	K.IFVGNVSAACTSQELR.S
*	HsFlag1P_Ti_106.2176.217	3.9106	0.3764	1157.16	1157.31	6024.2		1	1210.2	81.8	2	K.KGPGLAVQSGDK.T

*	HsFlag1P_Ti_104.2101.210	3.7344	0.2227	1609.38	1609.82	5002.9		1	851.5	67.9	2	R.ASYVAPLTAQPATYR.A
*	HsFlag1P_Ti_105.1908.190	2.57	0.204	1219.61	1220.37	4634.8		1	772.9	81.8	2	R.AQPSVSLGAAYR.A
*	HsHeLa3_Ti_105.1607.160	3.6831	0.3266	2468.46	2466.63	8167.5		1	500.7	34.8	1	R.TQSSASLAASYAAQQHPQAAASYR.G
gi|23510338|ref|N	8	20	0.138	1058	117849	5.8	U	ubiquitin-activating enzyme E1 [Homo sapiens]				
gi|23510340|ref|N	8	20	0.138	1058	117849	5.8	U	ubiquitin-activating enzyme E1 [Homo sapiens]				
	HsFLAG-Control_HeLa_S1	3.6321	0.218	1909.54	1910.17	4656		1	535.1	52.9	2	K.SLVASLAEPDFVVTDFAK.F
	HsFLAG-Control_HeLa_S1	3.4288	0.341	1809.44	1810.02	6010.5		1	640.7	60	2	R.ALPAVQQNNLDEDLIR.K
	HsFLAG-Control_HeLa_S1	4.9245	0.3166	2602.68	2601.75	7958.6		1	1653	56.8	8	R.IYDDDFFQNLDGVANALDNVDAR.M
	Hs293FLP_TREX_Ti_105.1	3.106	0.1331	1244.57	1244.47	5933.5		1	951.3	77.3	1	R.KPLLESGTLGTK.G
	HsFLAG-Control_HeLa_S1	3.821	0.2784	2522.32	2522.77	4986.8		2	374.4	40.9	2	K.GNVQVVIPFLTESYSSSQDPPEK.S
	HsFLAG-Control_HeLa_S1	3.6143	0.4124	1624.67	1624.88	4112.2		1	708.9	67.9	2	R.LAGTQPLEVLEAVQR.S
	HsFLAG-Control_HeLa_S1	3.8377	0.3054	1933.83	1934.24	6524.2		1	809.5	52.9	1	R.AAVATFLQSVQVPEFTPK.S
	HsFLAG-Control_HeLa_S1	3.2224	0.1622	2279.6	2279.65	5067.5		1	630.9	47.5	2	K.NGFLNLALPFFGFSEPLAAPR.H
gi|89052386|ref|X	6	9	0.138	835	89356	9.5	U	PREDICTED: widely-interspaced zinc finger motifs isoform 1 [Homo sapiens]				
gi|89057269|ref|X	6	9	0.138	835	89356	9.5	U	PREDICTED: similar to widely-interspaced zinc finger motifs isoform 1 isoform 10 [Homo s				
	HsFLAG-Control_293_Ti_2	2.5955	0.1903	2320.77	2319.61	7485		1	379.5	35.7	1	R.QLGVAESESSGAPIDLLYELVK.Q
	Hs293FLP_Ti_304.1637.16	2.9303	0.274	1266.28	1265.45	8302.1		1	947.3	68.2	1	R.SPSDLHISPLAK.K
	HsHeLa_Control-MG_Ti_10	2.6106	0.2123	2334.64	2333.69	5539.5		2	227.4	28.3	1	R.ELSLTPITGAKPSATGYLGSVAAK.R
	Hs293FLP-MG_Ti_104.139	2.8918	0.3133	1696.01	1694.89	5191.5		1	711.2	55.9	3	R.AADGGERPLAASPPGTVK.A
	Hs293FLP-MG_Ti_203.369	3.5831	0.3743	2253.19	2254.47	9187.5		1	787.6	50	2	R.FCEVEFQGPLSIQEEWVR.H
	Hs293FLP-MG_Ti_202.001	2.7659	0.3465	2078.28	2077.17	5847.9		1	420.5	42.5	1	K.ADPPPEESQAPQAQTAAAEAP.-
gi|27545326|ref|N	4	5	0.138	385	44141	6.2	U	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily b,				
gi|55956801|ref|N	4	5	0.141	376	43158	5.7	U	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily b,				
	HsHeLa3_Ti_102.2147.214	2.5162	0.329	1548.83	1548.6	4062.2		1	376.5	61.5	1	K.ASEVEEILDGNDEK.Y
	HsHeLa3_Ti_102.2149.214	2.6418	0.1146	1548.96	1548.6	7845		1	790.7	61.5	2	K.ASEVEEILDGNDEK.Y
	HsHeLa3_Ti_103.3136.313	2.716	0.264	1921.94	1922.19	4260.6		1	377	50	1	K.TYAFSENPLPTVEIAIR.N
	HsHeLa3_Ti_102.4011.401	4.1184	0.3985	2539.73	2538.71	6253.4		1	654.2	45.2	1	R.NTGDADQWCPLLETLTDAEMEK.K
gi|4504483|ref|NI	1	2	0.138	218	24579	6.7	U	hypoxanthine phosphoribosyltransferase 1 [Homo sapiens]				
*	HsHeLa_Control-MG_Ti_20	4.943	0.3938	3436.62	3437.66	8052.3		1	792.1	26.7	2	R.SPGVVISDDEPGYDLDLFCIPNHYAEDLER.V
gi|4506629|ref|NI	4	10	0.138	159	17752	11.7	U	ribosomal protein L29 [Homo sapiens]				
	Hs293FLP_TREX_Ti_103.1	1.9567	0.2825	1377.42	1378.57	6296.3		1	579.3	53.6	1	K.AQAAAPASVPAQAPK.R
	HsFLAG-Control_293_Ti_2	4.4356	0.2747	1378.28	1378.57	3866.2		1	819.9	75	3	K.AQAAAPASVPAQAPK.R
	HsFLAG-MOCK_300mM_T	4.3009	0.3319	1378.49	1378.57	3446.4		4	647	67.9	4	K.AQAAAPASVPAQAPK.R
*	Hs293FLP_TREX_Ti_106.2	4.2122	0.4162	2161.61	2161.47	4704.1		1	559.4	50	2	K.AQAAAPASVPAQAPKRTQAPTK.A
gi|4506725|ref|NI	3	7	0.137	263	29598	10.2	U	ribosomal protein S4, X-linked X isoform [Homo sapiens]				
*	HsHeLa_Control-MG_Ti_10	4.0837	0.3446	1545.72	1543.9	6480.9		1	1123	77.3	4	K.LRECLPLIIFLR.N
	HsHeLa_Control-MG_Ti_20	2.6756	0.1698	1216.29	1216.39	3828.2		1	582.9	70	1	K.GIPHLVTHDAR.T
	HsGST-MOCK_Ti_105.142	3.3503	0.302	1507.79	1507.69	7678.8		1	887.3	66.7	2	R.ERHPGSFDVVHVK.D
gi|8393116|ref|NI	1	2	0.137	131	14711	5.1	U	chromatin accessibility complex 1 [Homo sapiens]				
*	HsFLAG-Control_HeLa_NE	3.8116	0.383	1873.43	1874.1	7814		2	578.5	47.1	2	K.SSPEVSSINQEALVLTAK.A
gi|21536286|ref|N	3	7	0.136	381	42644	5.6	U	brain creatine kinase [Homo sapiens]				
*	HsF-IP-293_Ti_202.0094.0	5.0972	0.4049	2520.34	2519.64	6448.9		1	1020	54.5	2	K.TDLNPDNLQGGDDLDPNYVLSSR.V
*	HsFLAG-Control_293_Ti_2	4.8649	0.484	1589.36	1587.77	11237.2		1	2354.5	73.3	3	K.LAVEALSSLDGDLAGR.Y
	Hs293FLP_TREX_Ti_106.2	3.6989	0.3438	1312.34	1312.61	6390.9		1	1267.6	79.2	2	K.PVSPLLLASGMAR.D
gi|88951236|ref|X	17	51	0.136	198	21115	9	U	PREDICTED: similar to eukaryotic translation elongation factor 1 alpha 2 isoform 30 [Hom				
	HsGST-MOCK_Ti_405.245	2.884	0.275	1314.28	1315.56	3797.5		1	422.1	63.6	2	R.EHALLAYTLGVK.Q
	Hs293FLP-MG_Ti_204.231	3.1474	0.3715	1314.52	1315.56	6113		1	627.9	63.6	1	R.EHALLAYTLGVK.Q
	HsFLAG-Control_HeLa_NE	3.8894	0.3764	1314.54	1315.56	7099.1		1	843.2	68.2	1	R.EHALLAYTLGVK.Q
	HsFLAG-Control_HeLa_S1	3.3633	0.3249	1314.54	1315.56	6442.6		1	682.8	63.6	1	R.EHALLAYTLGVK.Q

	HsHeLa3_Ti_105.2226.222	3.7276	0.3842	1314.65	1315.56	5432.8		1	771	68.2	6	R.EHALLAYTLGVK.Q
	HsGST-MOCK_Ti_405.244	3.0462	0.2235	1314.83	1315.56	6532.9		2	861.4	72.7	2	R.EHALLAYTLGVK.Q
	HsHeLa_Control-MG_Ti_10	3.4703	0.3478	1314.83	1315.56	5679.7		1	655	63.6	2	R.EHALLAYTLGVK.Q
	HsFLAG-Control_HeLa_S1	4.0957	0.3505	1315.1	1315.56	6796.4		1	1542.9	86.4	7	R.EHALLAYTLGVK.Q
	HsFLAG-Control_HeLa_S1	3.3605	0.3219	1315.28	1315.56	7637		1	1057.6	72.7	3	R.EHALLAYTLGVK.Q
	HsGST-MOCK_Ti_305.236	3.3426	0.261	1315.47	1315.56	3468.6		1	431.4	68.2	3	R.EHALLAYTLGVK.Q
	HsGST-MOCK_Ti_305.236	3.4506	0.2703	1315.48	1315.56	5538.1		1	959.1	81.8	7	R.EHALLAYTLGVK.Q
	HsFLAG-Control_HeLa_NE	3.1986	0.3053	1315.53	1315.56	6457.5		2	1086.8	77.3	2	R.EHALLAYTLGVK.Q
	HsFLAG-Control_HeLa_S1	3.6587	0.3109	1315.58	1315.56	6360.4		2	555.9	59.1	3	R.EHALLAYTLGVK.Q
	HsHeLa3_Ti_105.2218.221	3.3286	0.2525	1316.68	1315.56	6114.4		2	1130.5	81.8	2	R.EHALLAYTLGVK.Q
	HsHeLa_Control-MG_Ti_10	3.3203	0.2631	1316.86	1315.56	6340.9		1	1163.7	81.8	6	R.EHALLAYTLGVK.Q
	HsGST-MOCK_Ti_102.183	2.8304	0.2663	1317.2	1315.56	6447.2		1	1041.9	77.3	1	R.EHALLAYTLGVK.Q
	HsHeLa3_Ti_103.2430.243	3.7938	0.4396	1755.9	1755.95	7187.6		1	1037.6	57.1	2	K.PMCVESFSDYPPLGR.F
gi|20070130|ref|N	1	2	0.136	162	17699	7.5	U	basic transcription factor 3 [Homo sapiens]				
*	HsFLAG-Control_HeLa_S1	4.0459	0.3553	2400.74	2401.78	9186.9		1	1273	50	2	K.QLTEMLPSILNQLGADSLTSLR.R
gi|29837655|ref|N	3	3	0.135	421	46089	10	U	DNA polymerase delta interacting protein 3 isoform 1 [Homo sapiens]				
gi|30089919|ref|N	3	3	0.145	392	42895	9.9	U	DNA polymerase delta interacting protein 3 isoform 2 [Homo sapiens]				
	HsGST-MOCK_Ti_403.232	3.177	0.3722	1802.89	1803.03	6929.4		1	890.9	56.2	1	K.VVQNDAYTAPALPSSIR.T
	Hs293FLP-MG_Ti_202.300	2.5446	0.1748	2197.28	2196.5	5038.9		1	349.6	47.2	1	K.CNLHMNGNVITSDQPILLR.L
	HsFLAG-MOCK_300mM_T	2.7434	0.2133	2198.2	2198.4	3343.7		5	333.3	45	1	R.RVNSASSSNPPAEVDPDTILK.A
gi|28557745|ref|N	3	5	0.135	377	40140	8.2	U	zinc binding alcohol dehydrogenase, domain containing 2 [Homo sapiens]				
*	HsHeLa_Control-MG_Ti_10	4.2671	0.444	1818.68	1819.09	4020.8		1	1065.1	76.7	1	R.HFLDFQGSAIPQAMQK.L
*	HsHeLa_Control-MG_Ti_20	5.03	0.4762	2091.77	2091.5	8974.8		1	1402.9	52.6	3	R.LIVIGFISGYQTPTGLSPVK.A
*	HsHeLa_Control-MG_Ti_20	2.8554	0.3014	1698.41	1698.92	8255.2		1	619.6	50	1	K.SASVQGFFLNHYLSK.Y
gi|13786127|ref|N	2	4	0.135	356	37980	5.2	U	Cdc42 effector protein 4 [Homo sapiens]				
*	HsHeLa3_Ti_102.1325.132	4.2923	0.4059	1907.81	1907.9	6700.9		1	976.3	58.3	2	K.AGEPDGESLDEQPSSSSSK.R
*	HsHeLa3_Ti_105.2679.268	4.6388	0.4139	2829.73	2829.06	8656		1	1105.7	41.1	2	K.AGPDLPSLPSHALEDEGWAAAAPSPGSAR.S
gi|47419914|ref|N	6	20	0.134	471	53165	6.2	U	tryptophanyl-tRNA synthetase isoform a [Homo sapiens]				
gi|47419920|ref|N	6	20	0.147	430	48852	6.5	U	tryptophanyl-tRNA synthetase isoform b [Homo sapiens]				
gi|47419918|ref|N	6	20	0.147	430	48852	6.5	U	tryptophanyl-tRNA synthetase isoform b [Homo sapiens]				
gi|47419916|ref|N	6	20	0.134	471	53165	6.2	U	tryptophanyl-tRNA synthetase isoform a [Homo sapiens]				
	HsHeLa_Control-MG_Ti_20	1.8835	0.1233	972.55	973.12	2744.4		6	224.7	64.3	1	K.HVTFNQVK.G
	HsHeLa_Control-MG_Ti_20	4.6264	0.3732	2325.75	2326.66	9456.8		1	2258.9	42.5	1	K.ISFPAIQAAPSFSNSFPQIFR.D
	HsHeLa_Control-MG_Ti_10	3.6343	0.3525	2326.26	2326.66	3872.9		1	557.9	57.5	10	K.ISFPAIQAAPSFSNSFPQIFR.D
	Hs293FLP_Ti_305.3621.36	3.4553	0.3551	2327.3	2326.66	4076.9		1	494.7	47.5	4	K.ISFPAIQAAPSFSNSFPQIFR.D
	HsHeLa_Control-MG_Ti_20	4.2308	0.3991	1929.61	1928.24	7956.3		1	955.4	52.9	1	K.PALLHSTFFPALQGAQTK.M
	HsHeLa_Control-MG_Ti_20	4.6042	0.303	1801.61	1802.13	4684.2		1	1171.3	73.3	3	K.ALIEVLQPLIAEHQAR.R
gi|4503841|ref|N	5	9	0.133	609	69843	6.6	U	ATP-dependent DNA helicase II, 70 kDa subunit [Homo sapiens]				
*	HsFLAG-Control_HeLa_NE	4.0986	0.2902	2502.49	2502.43	8861.1		1	850	45.2	3	K.TEGDEEAEEEQEENLEASGDYK.Y
*	HsHeLa3_Ti_103.2486.248	4.2198	0.2374	1574.61	1574.77	7406.6		1	1792.5	73.1	1	K.NIYVLQELDNPGAK.R
	HsHeLa3_Ti_106.2591.259	2.527	0.1915	1401.9	1400.62	7822.8		1	687.5	63.6	1	K.KPGGFDISLFYR.D
	HsFLAG-Control_HeLa_S1	3.8349	0.3195	2133.35	2133.5	8492.6		1	1096.8	55.6	3	K.IQVTPPGFQLVFLPFADDK.R
	Hs293FLP_TREX_Ti_105.1	3.0738	0.2778	1705.15	1704.84	6138.4		1	602.1	53.8	1	R.SDSFENPVLQQHFR.N
gi|42476281|ref|N	2	3	0.133	294	31566	7.6	U	voltage-dependent anion channel 2 [Homo sapiens]				
gi|88955151|ref|X	2	3	0.133	293	31445	7.6	U	PREDICTED: similar to voltage-dependent anion channel 2 [Homo sapiens]				
gi|88953242|ref|X	2	3	0.133	293	31479	7.6	U	PREDICTED: similar to voltage-dependent anion channel 2 [Homo sapiens]				
	HsFLAG-Control_293_Ti_1	4.1304	0.4826	1908.18	1908.89	6745.2		1	1146.6	61.1	2	K.SCSGVEFSTSGSSNTDTGK.V
	HsFLAG-Control_293_Ti_1	3.2732	0.2801	2103.43	2104.41	6589.5		1	607.9	44.7	1	K.VNNSSLIGVGYTQTLRPGVK.L
gi|4506609|ref|N	2	5	0.133	196	23466	11.5	U	ribosomal protein L19 [Homo sapiens]				

*	Hs293FLP-MG_Ti_102.231	4.389	0.2864	1946.72	1944.07	5201.6		1	1189.1	71.9	4	K.VWLDPNETNEIANANSR.Q
	Hs293FLP_Ti_302.1160.11	3.1971	0.1637	987.53	987.101	2794.1		2	729.7	93.8	1	K.LLADQAEAR.R
gi|4504715|ref|N	6	9	0.132	644	70783	9.3	U	poly A binding protein, cytoplasmic 4 [Homo sapiens]				
	Hs283FLP_Ti_102.2047.20	5.1031	0.4609	1929.1	1930.08	6525.8		1	1508.8	68.8	4	R.SLGYAYVNFQQPADAER.A
	HsFLAG-Control_MG_293_	2.7317	0.2852	1267.36	1267.48	6619.4		2	691.1	70	1	R.ALDTMNFDVIK.G
	HsFlag1P_Ti_105.3641.364	3.1412	0.1714	1808.78	1808.01	8318		1	898.9	56.7	1	K.ALYDTFSAFGNILSCK.V
*	HsFlag1P_Ti_106.3058.305	3.5219	0.3437	2318.34	2319.49	8611.8		1	726.9	44.7	1	K.NFGEEVDDESLKELFSQFGK.T
*	Hs293FLP_TREX_Ti_102.2	2.7094	0.2559	1272.38	1271.41	8330.3		4	631.4	54.5	1	K.EFSPFGSITSAK.V
	Hs283FLP_Ti_104.1603.16	3.028	0.1035	1031.54	1031.24	4323		1	1394.3	93.8	1	K.PLYVALAQR.K
gi|8923557|ref|N	3	5	0.132	228	26749	5	U	chromosome 20 open reading frame 11 [Homo sapiens]				
*	HsHeLa_Control-MG_Ti_20	3.1981	0.1253	994.15	994.142	6134.3		2	1001.2	92.9	1	K.LNNLHVQR.A
*	HsHeLa_Control-MG_Ti_20	4.474	0.4016	2445.67	2446.77	7077.3		1	685.2	45.2	2	K.GQIQEAIALINSLHPELLDTNR.Y
*	HsHeLa_Control-MG_Ti_20	4.7467	0.2319	2448.45	2446.77	8805		3	1015.4	32.1	2	K.GQIQEAIALINSLHPELLDTNR.Y
gi|38027914|ref|N	1	2	0.131	160	17909	7.3	U	COP9 signalosome subunit 8 isoform 2 [Homo sapiens]				
gi|5729779|ref|N	1	2	0.1	209	23226	5.4	U	COP9 signalosome subunit 8 isoform 1 [Homo sapiens]				
	HsFLAG-Control_HeLa_S1	3.2632	0.2383	2314.11	2314.69	5857.8		9	348.6	37.5	2	K.FIPLSEPAPVPPIPNEQQLAR.L
gi|19923466|ref|N	27	108	0.13	2752	299676	12.1	U	splicing coactivator subunit SRm300 [Homo sapiens]				
*	HsHeLa_Control-MG_Ti_10	3.7296	0.2251	1734.95	1734.87	6728.7		1	1043.6	76.9	1	R.RGERPDYKGEEELR.R
*	HsFLAG-Control_HeLa_NE	4.1622	0.4481	2019.49	2020.12	7757.3		1	1717.5	63.9	3	R.AAFGISDSYVDGSSFDPQR.R
*	HsFLAG-Control_HeLa_NE	3.9907	0.4222	1720.01	1720.92	4695.7		1	651.2	62.5	12	R.SSTGPEPPAPTPLLAER.H
*	HsHeLa_Control-MG_Ti_20	6.4117	0.4968	2853.17	2854.11	8201.6		1	2762.3	42.6	2	R.HGGSPQPLATTPLSQEPVNPPSEASPTR.D
*	HsHeLa_Control-MG_Ti_10	5.8867	0.4397	2095.41	2094.3	5176.4		1	1484.7	68.4	4	K.SKDSLVQSCPGSLSLCAGVK.S
*	HsHeLa_Control-MG_Ti_10	4.0887	0.3388	1879.31	1879.05	3729.9		1	653.5	61.8	1	K.DSLVQSCPGSLSLCAGVK.S
*	HsFLAG-Control_HeLa_NE	3.2816	0.3755	1884.88	1885.08	4204.1		1	330	50	1	K.SSTPPGESYFGVSSLQLK.G
*	HsFLAG-MOCK_300mM_T	4.8751	0.4684	2274.91	2276.38	3989.5		1	800.3	60	16	R.FQSDSSSYPTVDSNSLLGQSR.L
*	HsHeLa_Control-MG_Ti_20	3.7357	0.2909	1980.48	1981.26	9257.7		1	1028.4	59.4	3	K.FSPFPVQDRPESSLVFK.D
*	HsHeLa_Control-MG_Ti_20	3.5585	0.3918	1825.81	1826.01	6183.6		1	818.7	59.4	4	K.SEEPAGQILSHLSSELK.E
*	HsFLAG-Control_HeLa_NE	5.4207	0.4448	1618.55	1617.67	9486.5		1	2136.8	73.3	9	R.SSGHSSSELSPDAVEK.A
*	HsHeLa_Control-MG_Ti_10	4.1344	0.4108	1903.9	1903.01	4163.2		1	1000	67.6	4	R.SGSSQELDVKPSASPQER.S
*	HsHeLa_Control-MG_Ti_10	3.3388	0.2372	1371.78	1371.49	4395.2		1	748.6	75	2	R.RSPSVSSPEPAEK.S
*	HsF-IP-293-MG_Ti_103.17	4.5098	0.4684	1416.18	1415.65	8336.5		1	1487.5	71.4	5	R.IPAASAAAMNLASAR.T
*	HsF-IP-293-MG_Ti_103.17	3.3097	0.1893	1428.39	1426.61	2956.8		2	383.6	65.4	6	R.TPAIPTAVNLADSR.T
*	HsFLAG-Control_MG_293_	4.2501	0.482	1344.15	1342.56	6855.4		1	1692.4	80.8	2	R.TPAAAAAMNLASPR.T
*	HsFLAG-Control_HeLa_NE	3.1932	0.3883	1239.35	1239.42	3910.8		1	747.9	75	6	R.TPTAPAVNLAGAR.T
*	HsHeLa_Control-MG_Ti_10	5.2768	0.4278	2560.34	2560.82	4348		1	378.7	38.5	3	R.TPAALAALSLTGSGTPPTAANYPSSSR.T
*	HsFLAG-Control_293_Ti_2	2.3416	0.2745	1378.29	1379.56	2964.5		8	121.4	50	1	R.TPQAPASANLVGPR.S
*	HsFLAG-Control_HeLa_NE	3.2321	0.1769	1379.13	1379.56	4301.7		1	654.5	65.4	6	R.TPQAPASANLVGPR.S
*	HsFLAG-Control_293_Ti_2	3.4918	0.2611	1379.37	1379.56	4099.5		1	866.1	73.1	5	R.TPQAPASANLVGPR.S
*	HsHeLa_Control-MG_Ti_20	3.0351	0.4454	1351.59	1352.49	2938.7		1	162.3	53.8	1	R.SAHATAPVNIAGSR.T
*	HsFLAG-Control_HeLa_NE	3.467	0.3351	1351.66	1352.49	5229.2		1	486.9	61.5	3	R.SAHATAPVNIAGSR.T
*	HsHeLa_Control-MG_Ti_20	2.8964	0.2917	1352.24	1352.49	6836.4		2	866.3	65.4	2	R.SAHATAPVNIAGSR.T
*	HsFLAG-Control_HeLa_NE	3.4	0.3969	1354.58	1352.49	5588.4		2	683.5	65.4	3	R.SAHATAPVNIAGSR.T
*	HsFLAG-Control_HeLa_NE	2.0336	0.1842	1300.61	1301.49	3633.4		1	172.7	53.8	1	R.TAAALAPASLTSAR.M
*	HsGST-MOCK_Ti_305.194	3.323	0.2237	1385.9	1386.61	6279.5		1	1346.6	80.8	2	R.MAPALSGANLTSPR.V
gi|33598968|ref|N	9	12	0.13	1349	153670	7.8	U	LIM domain only 7 [Homo sapiens]				
*	HsHeLa3_Ti_103.2494.249	4.9648	0.4812	2684.11	2684.96	3733.1		1	581.9	50	2	R.VTTEIQLPSQSPVEEQSPASLSSLR.S
*	HsFLAG-MOCK_300mM_T	3.7162	0.4527	2584.22	2584.8	3947.9		1	431.4	42	1	R.TPNNVVSTPAPSPDASQLASSLSSQK.E
*	HsFLAG-MOCK_300mM_T	4.2345	0.3421	3253.25	3251.49	5886.7		1	1099.8	30.8	2	K.EVAATEEDVTRLPSPTSPFSSLSQDQAATSK.A
*	HsFLAG-MOCK_150mM_T	2.8325	0.2955	2748.5	2749.01	4975.7		1	301.7	34	1	R.SQFFEQGSSDSVVPDLPVPTISAPSR.W

*	HsFLAG-MOCK_300mM_T	4.7523	0.2652	1732.6	1731.86	8766.9	1	2406.3	87.5	1	R.KWEQQLQEEQEQK.R
*	HsFLAG-MOCK_300mM_T	3.0306	0.2061	1360.74	1359.44	3769.2	2	615.1	77.3	1	R.RGESLDNLDSPR.S
*	HsHeLa3_Ti_104.1267.126	2.8311	0.2468	1411.67	1411.56	2607	1	405.7	71.4	1	R.NPSSSVPPPSAGSVK.T
*	HsHeLa3_Ti_103.1222.122	4.302	0.4128	1505.31	1505.63	6634.7	1	825.3	60.7	2	K.TSTTGVATTQSPTPR.S
*	HsFLAG-MOCK_300mM_T	2.9061	0.1352	1501.24	1498.65	5891.1	1	810.5	68.2	1	K.RICSYCNNILGK.G
gi|4505775|ref|N	3	7	0.13	361	39959	9.4	U	solute carrier family 25 member 3 isoform b precursor [Homo sapiens]			
gi|47132595|ref|N	3	7	0.13	361	39959	9.4	U	solute carrier family 25 member 3 isoform b precursor [Homo sapiens]			
	HsFLAG-Control_293_Ti_1	3.6474	0.4172	2911.74	2912.33	9164.8	1	450.6	30.8	1	K.YYALCGFGGVLSCGLTHTAVVPLDLVK.C
	HsFLAG-Control_MG_293_	2.2798	0.1689	1036.39	1037.2	9729.6	2	804.7	78.6	1	K.FGFYEVFK.V
	HsFLAG-Control_293_Ti_2	3.0263	0.2404	1362.04	1362.53	4524.2	2	503.4	68.2	5	R.IQTQPGYANTLR.D
gi|38016127|ref|N	3	5	0.129	425	48063	10.1	U	RNA binding motif protein 34 [Homo sapiens]			
*	HsFLAG-MOCK_300mM_T	4.109	0.393	2312.71	2313.74	4751.1	1	612.9	50	2	R.LASLFSSLEPQIQPVYVPVPK.Q
*	Hs293FLP_TREX_Ti_104.1	4.1765	0.2288	2460.1	2458.6	6234.4	1	558.2	31.2	2	K.RNEEEESTSQIERPLSQEPAK.K
*	Hs293FLP_TREX_Ti_103.1	3.6095	0.2518	1449.38	1449.66	6017.3	1	1147.8	79.2	1	R.TVFVGNLPVTCNK.K
gi|13129094|ref|N	2	3	0.129	232	25858	9.7	U	hypothetical protein LOC79074 [Homo sapiens]			
*	HsHeLa3_Ti_104.2701.270	4.7352	0.4302	1967.62	1967.23	6414.4	1	1232.7	65.6	2	K.DSLTDLYVQHAIPLPQR.D
*	HsHeLa3_Ti_105.1568.156	1.9594	0.2226	1279.46	1280.51	5344.2	3	270.9	50	1	K.SPPLSPVGTTPVK.L
gi|15431290|ref|N	2	8	0.129	178	20252	9.6	U	ribosomal protein L11 [Homo sapiens]			
*	HsGST-MOCK_Ti_303.233	4.2803	0.4469	1547.41	1547.79	7785	1	1670.1	76.9	7	K.VLEQLTGQTPVFSK.A
*	Hs293FLP_TREX_Ti_102.1	3.104	0.1158	976.32	976.161	4034.8	1	893.7	87.5	1	K.YDGIILPGK.-
gi|11056044|ref|N	2	7	0.128	289	32660	5.9	U	pyrophosphatase (inorganic) 1 [Homo sapiens]			
*	HsHeLa_Control-MG_Ti_20	4.3674	0.3909	1864.47	1865.1	7572.6	1	1442.1	70	6	K.GQYISPFHDIPIYADK.D
*	HsHeLa_Control_Ti_102.22	3.8269	0.3661	2288.78	2289.46	7045.7	1	601	42.5	1	K.VIAINVDDPDAANYNDINDVK.R
gi|4506607|ref|N	2	3	0.128	188	21634	11.7	U	ribosomal protein L18 [Homo sapiens]			
*	Hs293FLP_TREX_Ti_103.1	2.287	0.2994	1345.53	1346.52	3613.1	1	162.5	50	1	K.TAVVVGTITDDVR.V
*	Hs293FLP_TREX_Ti_103.1	3.6837	0.2883	1117.54	1117.26	6808.6	1	1391.4	85	2	K.GCGTVLLSGPR.K
gi|5901928|ref|N	4	22	0.127	551	59209	7.4	U	cleavage and polyadenylation specific factor 6, 68 kD subunit [Homo sapiens]			
*	HsFLAG-MOCK_300mM_T	2.5187	0.2747	1749.75	1749.93	4092.7	2	430.5	53.6	1	K.RELHGQNPVVTPCNK.Q
*	HsHeLa3_Ti_103.2731.273	4.5426	0.4991	1667.74	1666.84	7141.6	1	1784.2	80.8	2	R.TPLSEAEFEEIMNR.N
*	HsHeLa3_Ti_104.5107.510	6.0854	0.5146	2453.66	2453.75	7072.2	1	2162.8	62.5	15	R.AVSDASAGDYGSAIETLVTAISLIK.Q
*	HsHeLa3_Ti_104.2532.253	4.5392	0.4281	1801.8	1800.03	8603.6	1	1242.7	60	4	K.VLISSLQDCLHGIESK.S
gi|5032027|ref|N	3	14	0.127	425	47656	4.9	U	retinoblastoma binding protein 4 [Homo sapiens]			
*	HsHeLa3_Ti_106.3462.346	4.332	0.4903	3826.87	3828.38	9837.1	1	1070.3	25	2	K.NTPFLYDLVMTHALEWPSLTAQWLPDVTRPEGK.D
	HsFLAG-Control_HeLa_NE	4.2739	0.3794	1472.49	1472.64	7189.3	1	1236.3	75	11	K.TPSSDVLVFDYTK.H
	Hs293FLP_TREX_Ti_102.2	2.5042	0.1334	974.95	974.148	4357.2	7	580.5	78.6	1	K.TVALWDLR.N
gi|4506753|ref|N	5	7	0.125	456	50228	6.4	U	TATA binding protein interacting protein 49 kDa [Homo sapiens]			
	HsFLAG-Control_MG_293_	2.3175	0.2976	1080.45	1081.3	8451.9	1	551.2	54.5	1	R.AVLLAGPPGTGK.T
	HsFLAG-Control_MG_293_	3.2797	0.2057	1081.42	1081.3	6728.2	1	1272.9	77.3	1	R.AVLLAGPPGTGK.T
	HsHeLa3_Ti_103.3108.310	3.9209	0.3233	1387.08	1386.63	9725.9	1	2035.2	76.9	1	K.TALALAIAQELGSK.V
	HsHeLa3_Ti_103.2559.255	3.9498	0.2317	1943.91	1944.22	4524.1	1	892.6	68.8	2	K.VPFCPMVGSEVYSTEIK.K
	HsFLAG-Control_HeLa_NE	3.1477	0.2634	1532.41	1531.84	5514.4	2	539.4	57.7	2	R.YSVQLLTPANLLAK.I
gi|18702323|ref|N	1	4	0.125	96	10855	7.5	U	dynein, cytoplasmic, light polypeptide 2B [Homo sapiens]			
gi|7661822|ref|N	1	4	0.125	96	10922	7.2	U	Roadblock-1 [Homo sapiens]			
gi|29570775|ref|N	1	4	0.19	63	7342	7.3	U	cytoplasmic dynein light chain 2A isoform b [Homo sapiens]			
	HsFLAG-Control_HeLa_S1	3.9839	0.385	1447.69	1447.59	6036.8	1	1256.2	86.4	4	R.DIDPQNDLTFLR.I
gi|58761546|ref|N	6	9	0.124	852	92903	6.5	U	amine oxidase (flavin containing) domain 2 isoform b [Homo sapiens]			
*	HsHeLa3_Ti_105.2238.223	4.8338	0.3754	1385.7	1384.66	6890.5	1	1921.9	82.1	3	K.VIIIGSGVSGLAAAR.Q
*	HsHeLa3_Ti_103.4319.431	4.0875	0.4156	2422.09	2421.83	9844	1	1434.6	45.8	2	K.GNYVADLGAMVVTGLGGNPMAVVSK.Q
*	HsHeLa3_Ti_102.2047.204	3.398	0.2879	1920.79	1919.1	2961.4	1	425.8	59.4	1	K.LQELEANPPSDVYLSSR.D

*	HsHeLa3_Ti_106.2730.273	2.5302	0.2885	2179.03	2178.41	6087.8		1	478.8	44.7	1	R.VFWDPSVNLFGHVGSTTASR.G
*	HsHeLa3_Ti_106.2247.224	2.698	0.2665	1571.14	1569.8	4783.1		1	833.4	71.4	1	R.NYPATVHGALLSGLR.E
*	HsHeLa3_Ti_103.3016.301	2.5621	0.0965	1596.41	1596.89	7905.7		3	584.1	50	1	R.IADQFLGAMYTLPR.Q
gi|34335134|ref|N	2	4	0.124	322	35541	5.5	U	SEC13-like 1 isoform b [Homo sapiens]				
gi|34335136|ref|N	2	4	0.123	325	35857	5.6	U	SEC13-like 1 isoform a [Homo sapiens]				
	HsFLAG-Control_HeLa_S1	3.6888	0.323	2390.33	2390.58	6419.4		1	907.3	50	1	R.DVAWAPSIGLPTSTIASCSQDGR.V
	HsFLAG-Control_HeLa_NE	5.2187	0.4522	1706.96	1706.72	7325.7		1	1473.7	68.8	3	K.GQGSVSASVTEGQQNEQ.-
gi|16753233|ref|N	16	53	0.123	2541	269665	6	U	talin 1 [Homo sapiens]				
*	HsFLAG-Control_HeLa_NE	3.7117	0.3129	1545.47	1544.66	8635.9		1	1214.8	69.2	2	R.DDILNGSHPVSFDK.A
*	HsFLAG-Control_HeLa_S1	4.9148	0.4172	2122.44	2123.46	10097.7		1	1244.1	52.5	3	K.LLAALLEDEGGSGRPLLQAAK.G
*	HsFLAG-Control_HeLa_S1	4.6597	0.432	2140.94	2141.4	7474.3		1	1237	60.5	2	K.VVAPTISSPVCQEQLVEAGR.L
*	HsFLAG-Control_HeLa_NE	5.2899	0.4584	2092.56	2092.4	8103.8		1	1109.1	50	3	R.GVGAAATAVTQALNELLQHVK.A
*	HsFLAG-Control_HeLa_NE	3.5675	0.4032	1995.58	1996.19	7514.8		1	687.1	42.5	3	K.QAAASATQTIAAAQHAASTPK.A
*	HsFLAG-Control_HeLa_S1	3.1706	0.3174	1458.37	1456.65	5064.5		1	421.3	53.8	1	K.ASAGPQPLLVQSCK.A
*	HsFLAG-Control_HeLa_S1	4.1006	0.2778	1494.21	1493.79	4503.6		2	894	73.1	3	K.AVAEQIPLLVQGVR.G
*	HsFLAG-Control_HeLa_S1	4.5858	0.4133	2575.16	2574.85	9362.9		1	823.2	38	2	K.AVSSAIAQLLGEVAQGNENYAGIAAR.D
*	HsFLAG-Control_HeLa_S1	5.5864	0.445	2470.28	2470.78	6479.3		1	1041	47.9	4	R.GVAALTSDPAVQAIVLDTASDVLDK.A
*	HsFLAG-Control_HeLa_NE	6.2256	0.5571	2027.31	2028.23	8780.8		1	2510.4	71.1	8	R.LNEAAAGLNQAATELVQASR.G
*	HsFLAG-Control_HeLa_S1	5.0704	0.3514	1522.55	1522.78	9707		1	2092.3	76.9	1	K.TLAESALQLLYTAK.E
*	HsFLAG-Control_HeLa_S1	4.524	0.4502	2249.08	2250.38	6286.7		1	847.9	52.5	4	K.SNTSPEELGPLANQLTSDYGR.L
*	HsFLAG-Control_HeLa_S1	3.3526	0.2723	1244.15	1244.39	8203.5		1	1322.7	77.3	2	K.VLVQNAAGSQEK.L
*	HsFLAG-Control_HeLa_NE	5.206	0.3432	2197.8	2196.51	6584.8		1	1104.4	54.8	8	K.LGAASLGAEDPETQVVLINAVK.D
*	HsFLAG-Control_HeLa_S1	6.3389	0.4424	3053.58	3053.35	9687.7		1	2097.7	32.8	1	K.GTEWVDPEDPTVIAENELLGAAAAIEAAAK.K
*	HsFLAG-Control_HeLa_S1	3.8387	0.2756	1937.11	1937.07	7567.3		1	1248.7	59.4	6	K.EADESLNFEEQILEAAK.S
gi|17998551|ref|N	3	3	0.123	405	46276	5.5	U	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 12 [Homo sapiens]				
*	HsFLAG-Control_Hela_Ti_1	4.4746	0.2968	1979.78	1980.31	9301.9		1	1303.7	58.8	1	K.DAINAETVLVLVNAVYFK.A
*	HsFLAG-Control_Hela_Ti_1	2.9063	0.1356	1677.94	1676.91	4034.6		6	389	50	1	R.ADLTGISPSPNLYLSK.I
*	HsFLAG-Control_Hela_Ti_1	3.5322	0.2506	2028.06	2025.32	6484.9		1	641.1	53.3	1	R.SWVEFNANHPFLFFIR.H
gi|89058472|ref|X	37	129	0.123	106	11497	4.6	U	PREDICTED: similar to Ig kappa chain V-II region RPMI 6410 precursor [Homo sapiens]				
gi|89066978|ref|X	37	129	0.102	127	13922	4.6	U	PREDICTED: similar to Ig kappa chain V-II region Cum [Homo sapiens]				
gi|89062133|ref|X	37	129	0.103	126	13837	8	U	PREDICTED: similar to Ig kappa chain V-II region RPMI 6410 precursor [Homo sapiens]				
gi|89059101|ref|X	37	129	0.123	106	11497	4.6	U	PREDICTED: similar to Ig kappa chain V-II region RPMI 6410 precursor [Homo sapiens]				
	HsF-IP-293-MG_Ti_102.164	2.4822	0.3036	1303.36	1304.4	4962.6		1	426.2	58.3	1	R.FSGSGSGTDFTLK.I
	Hs293FLP-MG_Ti_302.148	2.4021	0.2196	1303.37	1304.4	5772		1	565.4	62.5	1	R.FSGSGSGTDFTLK.I
	HsF-IP-293_Ti_102.1532.1	2.4622	0.1828	1303.41	1304.4	5967.2		1	498.8	58.3	1	R.FSGSGSGTDFTLK.I
	HsFLAG-MOCK_300mM_T	2.6432	0.155	1303.41	1304.4	5549.6		4	386.7	54.2	4	R.FSGSGSGTDFTLK.I
	HsFLAG-Control_HeLa_S1	2.454	0.1032	1303.47	1304.4	8068.6		2	599.5	54.2	1	R.FSGSGSGTDFTLK.I
	HsHeLa_Control-MG_Ti_20	2.7908	0.3	1303.47	1304.4	4785		1	375.7	54.2	2	R.FSGSGSGTDFTLK.I
	HsFLAG-Control_HeLa_NE	2.4076	0.0967	1303.51	1304.4	8365.7		1	649.2	58.3	2	R.FSGSGSGTDFTLK.I
	HsFLAG-Control_Hela_Ti_1	2.4787	0.2146	1303.53	1304.4	6955.7		1	460	54.2	2	R.FSGSGSGTDFTLK.I
	HsFLAG-Control_HeLa_NE	2.4885	0.2399	1303.53	1304.4	6545		1	428.6	54.2	2	R.FSGSGSGTDFTLK.I
	HsFLAG-Control_HeLa_S1	2.3958	0.1668	1303.53	1304.4	6705.5		1	555.3	58.3	2	R.FSGSGSGTDFTLK.I
	HsFLAG-Control_HeLa_S1	2.2885	0.1132	1303.54	1304.4	7477.6		3	423.3	50	1	R.FSGSGSGTDFTLK.I
	HsFLAG-Control_293_Ti_1	2.3873	0.1671	1303.57	1304.4	5554.1		1	304.9	50	1	R.FSGSGSGTDFTLK.I
	HsFLAG-MOCK_150mM_T	2.1994	0.2202	1303.62	1304.4	5494.2		3	375.8	58.3	2	R.FSGSGSGTDFTLK.I
	Hs293FLP-MG_Ti_102.191	2.6432	0.2729	1303.66	1304.4	5482.3		1	513.4	62.5	3	R.FSGSGSGTDFTLK.I
	HsFLAG-Control_HeLa_NE	2.8651	0.1896	1303.69	1304.4	7306.2		1	623.7	62.5	2	R.FSGSGSGTDFTLK.I
	HsFLAG-Control_Hela_Ti_1	3.6589	0.3434	1303.7	1304.4	7750.8		1	1082.8	70.8	2	R.FSGSGSGTDFTLK.I
	HsFLAG-Control_HeLa_NE	2.3983	0.2314	1303.71	1304.4	7335.3		1	530.1	58.3	1	R.FSGSGSGTDFTLK.I

	Hs293FLP_Ti_302.1695.16	2.6276	0.2038	1303.72	1304.4	5302		2	335.2	54.2	2	R.FSGSGSGTDFTLK.I
	Hs293FLP-MG_Ti_202.206	3.8724	0.374	1304.24	1304.4	7809.5		1	1687.6	83.3	4	R.FSGSGSGTDFTLK.I
	HsFLAG-Control_HeLa_S1(	3.8098	0.3479	1304.24	1304.4	7119.9		1	1544	83.3	2	R.FSGSGSGTDFTLK.I
	HsF-IP-293-MG_Ti_102.164	3.4709	0.3064	1304.27	1304.4	7647.3		2	914.9	66.7	2	R.FSGSGSGTDFTLK.I
	HsFLAG-Control_293_Ti_1(	3.3066	0.3009	1304.27	1304.4	7234.8		2	881.8	66.7	2	R.FSGSGSGTDFTLK.I
	HsFLAG-Control_HeLa_NE	4.0584	0.3569	1304.28	1304.4	7412.3		1	1790.4	87.5	38	R.FSGSGSGTDFTLK.I
	HsFLAG-Control_293_Ti_2(	3.5765	0.3136	1304.29	1304.4	7784.8		1	1303.4	75	2	R.FSGSGSGTDFTLK.I
	HsHeLa-FLAG-IP_S100_Ti_	4.2429	0.3528	1304.31	1304.4	7675.1		1	1241.6	75	12	R.FSGSGSGTDFTLK.I
	HsFLAG-Control_HeLa_S1(	3.9044	0.3713	1304.34	1304.4	7345.3		1	1783.2	87.5	3	R.FSGSGSGTDFTLK.I
	HsFLAG-Control_HeLa_S1(	3.9647	0.3938	1304.38	1304.4	7559.8		1	2084	91.7	8	R.FSGSGSGTDFTLK.I
	HsFLAG-Control_HeLa_NE	3.9064	0.3229	1304.41	1304.4	8364.8		1	1413.2	75	2	R.FSGSGSGTDFTLK.I
	HsFLAG-Control_HeLa_NE	3.9037	0.3447	1304.43	1304.4	7714.9		1	1286.6	75	2	R.FSGSGSGTDFTLK.I
	Hs293FLP_TREX_Ti_102.1	3.716	0.3385	1304.44	1304.4	7098.2		1	1625.6	83.3	5	R.FSGSGSGTDFTLK.I
	HsFLAG-Control_293_Ti_2(	2.237	0.082	1304.46	1304.4	6614.7		1	376.4	50	2	R.FSGSGSGTDFTLK.I
	HsFLAG-MOCK_150mM_T	3.8755	0.3973	1304.47	1304.4	7824		1	1389.9	79.2	2	R.FSGSGSGTDFTLK.I
	HsHeLa_Control-MG_Ti_20	4.0816	0.3492	1304.51	1304.4	8679.7		1	1676.5	83.3	2	R.FSGSGSGTDFTLK.I
	HsHeLa_Control-MG_Ti_10	3.5662	0.332	1304.8	1304.4	6938.2		1	1435	79.2	2	R.FSGSGSGTDFTLK.I
	Hs293FLP_Ti_302.1690.16	3.5838	0.3123	1305.25	1304.4	6880.5		1	992	70.8	2	R.FSGSGSGTDFTLK.I
	Hs293FLP-MG_Ti_302.148	3.3516	0.3642	1306	1304.4	6959.5		1	1004.3	70.8	2	R.FSGSGSGTDFTLK.I
	HsHeLa_Control_Ti_103.19	3.9922	0.2916	1306.15	1304.4	7658.2		1	980.5	70.8	3	R.FSGSGSGTDFTLK.I
gi|13129018|ref|N	1	2	0.122	188	21008	5.1	U	hypothetical protein LOC79017 [Homo sapiens]				
*	HsFLAG-Control_Hela_Ti_1	3.5986	0.3985	2623.83	2624.82	9037.5		1	492.2	34.1	2	K.DVTGPDEESFLYFAYGSNLLTER.I
gi|4502847|ref|NI	1	5	0.122	172	18648	9.5	U	cold inducible RNA binding protein [Homo sapiens]				
*	HsFLAG-Control_293_Ti_2(	5.1098	0.3943	2345.8	2346.6	8380.9		1	1073.7	47.5	5	K.LFVGGLSFDTNEQSLEQVFSK.Y
gi|56676335|ref|N	19	42	0.121	2472	274464	5.5	U	RAP1 interacting factor 1 [Homo sapiens]				
*	HsFLAG-Control_HeLa_NE	4.4513	0.2794	1719.79	1718.94	6757.9		1	1128.5	66.7	2	K.ITSELSEANALELLSK.L
*	HsFLAG-Control_HeLa_NE	4.8938	0.3149	1912.55	1911.17	10147.3		1	2535.1	71.9	3	R.SGSFINSLLQLEELGFR.S
*	HsFlag1P_Ti_104.3553.355	3.0881	0.2791	1891.53	1892.13	5946.8		1	876.5	62.5	1	K.SLIDNFALNPDILCSAK.R
*	HsFLAG-Control_HeLa_NE	2.6491	0.1673	1218.5	1218.31	6493.6		1	718.3	66.7	2	K.GASSPYGAPGTPR.M
*	HsFlag1P_Ti_105.2915.291	3.6183	0.3018	1649.03	1649.93	7743.6		1	1272.1	64.3	1	K.SLESIVKSEVFPVSK.T
*	HsFLAG-Control_HeLa_NE	3.5255	0.2736	2594.1	2594.84	10254.3		1	967	29.3	1	K.FDGSENRPFSPSPLNNISSTVTVK.N
*	HsFlag1P_Ti_104.2337.233	4.8446	0.246	1679.5	1679.93	9881.5		1	2425.9	80.8	2	K.NNQETMIKTDFLPK.A
*	HsFLAG-Control_HeLa_NE	3.705	0.2878	1642.14	1642.89	9906.6		1	1332.8	69.2	2	K.LIAEQTLQENLIEK.G
*	HsFlag1P_Ti_105.2397.239	5.8448	0.306	2408.15	2408.71	3961.4		1	941.8	46.2	2	K.LIAEQTLQENLIEKGSNLHEK.T
*	HsHeLa3_Ti_102.1194.119	4.448	0.4226	1594.44	1593.65	7780.8		1	1804.2	78.6	2	K.TLGETSANAETEQNK.K
*	HsHeLa_Control_Ti_102.11	4.0342	0.3196	1521.6	1521.54	5676.5		1	1273.1	83.3	3	K.SNESVDIQDQEEK.V
*	Hs293FLP-MG_Ti_202.318	3.1234	0.3759	1973.66	1974.18	5142.8		1	540.7	53.1	1	K.YAEYSFTSLPVPESNLR.T
*	HsFLAG-Control_HeLa_NE	3.0752	0.4028	1793.3	1793.88	6871.1		1	702.8	53.3	1	K.EDNDTINDSLIVSETK.S
*	HsFLAG-Control_HeLa_NE	4.5111	0.3668	3560.89	3562.65	10471.5		1	910.2	23.5	1	K.LNAQTEISEQTAAGELDGGNDVSDLHSSEETNTK.M
*	HsFlag1P_Ti_106.2730.273	4.0126	0.2922	1647.37	1646.89	5345.8		1	1339	75	2	R.CVWSPLASPSTSILK.R
*	HsFLAG-Control_HeLa_NE	3.0723	0.2762	1491.97	1489.58	5231.2		1	463.6	66.7	3	K.RSQEDEISSPVNK.V
*	HsFlag1P_Ti_103.2953.295	4.4926	0.2738	1733.84	1733.96	7384.5		1	1523.1	71.4	2	K.TRGLEEIPVFDISEK.T
*	HsFlag1P_Ti_106.3244.324	3.8869	0.3012	2735.95	2737.12	3569.2		1	369.5	39.6	2	K.SLSPDEERLVSDIIDPVALEIPLSK.N
*	HsFLAG-Control_HeLa_NE	4.9507	0.3774	1822.54	1823.18	6233		1	1590.3	71.9	9	R.LVSDIIDPVALEIPLSK.N
gi|31317212|ref|N	9	30	0.121	1169	128399	6.1	U	ankyrin repeat and FYVE domain containing 1 isoform 1 [Homo sapiens]				
	HsHeLa_Control-MG_Ti_20	3.3643	0.3022	2113.77	2112.38	11749.5		1	978.7	50	1	R.LLAIVADLYEQEQYSDLK.I
*	Hs293FLP_Ti_303.1441.14	3.9883	0.3486	1914.96	1914.99	4721.7		1	630.6	58.8	2	R.GSHTDAPDTATGNCLLQR.A
*	HsHeLa_Control-MG_Ti_20	6.0613	0.3553	3081.21	3082.48	8176.4		1	1417.4	33	5	R.HGLANLTAELLQQGANPNLQTEEALPLPK.E
*	HsHeLa_Control-MG_Ti_20	4.9873	0.4544	2080.91	2081.38	5050.8		1	1289.8	66.7	2	K.ANALHATNNLQIIPDFSLK.D

*	HsHeLa_Control-MG_Ti_20	5.0395	0.4164	2377.87	2378.73	6033.4		1	1152.7	59.5	4	K.GNPPLWLALANNLEDIASTLVR.H
*	HsHeLa_Control-MG_Ti_20	3.738	0.295	2379.03	2378.73	8179.2		2	1079	34.5	2	K.GNPPLWLALANNLEDIASTLVR.H
*	HsF-IP-293-MG_Ti_106.32	4.0174	0.3079	2379.56	2378.73	4634.4		1	471.3	47.6	3	K.GNPPLWLALANNLEDIASTLVR.H
*	HsHeLa_Control-MG_Ti_20	2.5544	0.131	1819.37	1818.17	8727.7		3	534.9	46.9	1	K.LTPLHLAVQAGSEIIVR.N
*	Hs293FLP-MG_Ti_203.274	4.0292	0.3904	2093.47	2094.34	7900		1	922.9	52.8	10	R.LGVNNNQGVNIFNYQVATK.Q
gi|4507349|ref|N	7	15	0.121	1083	109944	9.9	U	TBP-associated factor 4 [Homo sapiens]				
*	HsFLAG-Control_HeLa_NE	4.5618	0.4136	3064.88	3064.43	10786.2		1	819.2	23.4	2	R.SPGVQPQLVLGGAAQTASLGTATAVQTGTPQR.T
*	HsFLAG-Control_HeLa_NE	3.8289	0.3985	1733.76	1733.02	4783		1	642.5	60.7	3	R.ELNSSPQPYLVPFLK.R
*	HsHeLa_Control_Ti_104.33	3.8756	0.3074	2567.09	2565.97	3214.2		2	238.7	36	1	K.TAATVTSALQPPVLSLTQPTQVGVGK.Q
*	HsF-IP-293_Ti_103.1354.1	3.1534	0.3328	1286.7	1287.46	7926.9		1	1109	61.5	1	K.ALSAVSAQAAAAQK.N
*	HsFLAG-Control_HeLa_NE	4.4688	0.4256	1488.23	1488.73	8068.7		1	1497.3	76.9	3	R.ILATNSELVGTLTR.S
*	HsFlag1P_Ti_106.2568.256	5.2603	0.4196	1806.53	1807.02	8918.1		1	1595.6	67.9	3	R.SCKDETFLLQAPLQR.R
*	HsFlag1P_Ti_105.2385.23	5.4379	0.3169	1729.63	1729.97	7850.5		1	2003	78.6	2	R.LQNLVEKISETAQQK.N
gi|5174751|ref|N	3	4	0.121	454	48755	5.1	U	Yes-associated protein 1, 65 kD [Homo sapiens]				
*	HsHeLa3_Ti_104.1472.147	2.3354	0.23	1213.69	1214.43	3307.8		2	177.8	60	1	K.TANVPQTVPMR.L
*	HsHeLa3_Ti_105.1430.14	3.5901	0.5183	1782.38	1781.92	6839.1		1	812	52.9	2	R.QASTDAGTAGALTPQHVR.A
*	HsHeLa3_Ti_103.2083.208	3.671	0.1972	2758.86	2757.99	7463.6		1	566	36	1	R.SQLPTLEQDGGTQNPVSSPGMSQELR.T
gi|4826659|ref|N	2	5	0.121	272	30629	6	U	F-actin capping protein beta subunit [Homo sapiens]				
*	HsHeLa3_Ti_104.0004.000	3.1681	0.1929	2786.1	2785.13	2519.6		1	266.8	37.5	4	K.NLSDLIDLVPSLCEDLLSSVDQPLK.I
*	HsFLAG-Control_Hela_Ti_1	2.0139	0.1515	895.51	895.988	7755.4		3	516.5	71.4	1	R.SVQTFADK.S
gi|4826774|ref|N	1	2	0.121	165	17887	7.5	U	interferon, alpha-inducible protein (clone IFI-15K) [Homo sapiens]				
*	HsFLAG-Control_HeLa_S1	5.7164	0.5347	1951.53	1951.31	6453.5		1	1017.8	57.9	2	R.VPLASQGLGPGSTVLLVVDK.C
gi|4557493|ref|N	4	9	0.12	577	60959	6.8	U	cleavage stimulation factor subunit 2 [Homo sapiens]				
	HsFLAG-Control_HeLa_NE	3.3227	0.2498	1924.14	1925.15	3386.9		1	449.3	59.4	5	R.SVFVGNIPYEATEEQLK.D
*	HsFLAG-Control_HeLa_NE	3.8239	0.2987	1452.62	1452.65	5509.9		1	1006.8	75	1	K.DIFSEVGPVVSFR.L
*	HsFLAG-Control_HeLa_NE	3.6446	0.2198	2833.74	2833.08	6800.3		1	501.6	33.3	2	K.SLGTGAPVIESPYGETISPEDAPESISK.A
*	HsFLAG-Control_HeLa_NE	3.1341	0.1627	1302.37	1302.4	8388.3		1	1312.6	80	1	K.LCVQNSPQEAR.N
gi|21362046|ref|N	7	32	0.12	541	60540	5.2	U	hypothetical protein LOC79596 [Homo sapiens]				
*	HsHeLa_Control_Ti_102.17	3.4306	0.2668	1442.47	1442.49	5100.3		1	1058.5	80	2	K.EYEDEIDCLQK.E
*	HsHeLa_Control_Ti_102.30	5.075	0.4006	1898.99	1899.11	7952.9		1	1827.3	71.9	12	K.TILDPLTLVQGNQNEDK.H
*	Hs293FLP-MG_Ti_103.173	2.1943	0.2152	934.62	935.111	6169.5		7	553	62.5	1	R.FAVAALQSK.V
*	Hs283FLP_Ti_103.1514.15	2.7865	0.1439	934.63	935.111	7336.2		3	793	68.8	1	R.FAVAALQSK.V
*	Hs283FLP_Ti_103.1519.15	3.2354	0.0957	935.31	935.111	4564.6		1	1089.6	87.5	2	R.FAVAALQSK.V
*	Hs283FLP_Ti_102.2246.22	5.2062	0.3298	1550.59	1550.75	7656.2		1	2253	87.5	8	K.YIEELESQVAQLK.N
*	Hs283FLP_Ti_102.2026.20	5.0276	0.4255	1747.48	1747.82	7435.8		1	2379.7	82.1	6	K.LVFDDFCDSSNVSNK.D
gi|5579478|ref|N	2	4	0.12	393	43439	6.6	U	mitogen-activated protein kinase kinase 1 [Homo sapiens]				
*	HsFLAG-Control_HeLa_S1	5.5847	0.3819	3151.89	3150.47	9837.1		1	1351.9	29.2	2	K.KPTPIQLNPAPDGSAVNGTSSAETNLEALQK.K
*	HsFLAG-Control_HeLa_S1	4.9271	0.3301	1828.41	1828.08	7567.9		1	1618	70	2	K.LPSGVFSLEFQDFVNK.C
gi|5031857|ref|N	3	5	0.12	332	36689	8.3	U	lactate dehydrogenase A [Homo sapiens]				
*	HsHeLa3_Ti_106.3572.357	2.5321	0.3822	2114.97	2113.43	6648.1		1	626.8	47.4	1	K.GYTSWAIGLSVADLAESIMK.N
*	HsHeLa3_Ti_102.1395.139	2.9409	0.2052	1135.34	1135.22	6368.6		1	1264.7	88.9	2	K.VTLTSEEEAR.L
*	HsHeLa3_Ti_103.1902.190	2.1672	0.2706	1118.68	1119.26	5673.6		2	579.3	66.7	2	K.SADTLWGIQK.E
gi|4506743|ref|N	2	6	0.12	208	24205	10.3	U	ribosomal protein S8 [Homo sapiens]				
*	HsGST-MOCK_Ti_104.122	3.7308	0.2795	1348.4	1348.55	6741.5		1	1062.7	77.3	4	R.KYELGRPAANTK.I
*	Hs293FLP_TREX_Ti_102.1	4.4424	0.3308	1507.08	1507.68	7888.5		1	1342.7	70.8	2	K.ISSLLEEQFQQGK.L
gi|11321591|ref|N	2	2	0.12	209	24034	7.8	U	high-mobility group box 2 [Homo sapiens]				
	HsHeLa3_Ti_104.2319.231	2.6019	0.1928	1498.04	1497.68	7096.5		1	627.9	59.1	1	K.MSSYAFFVQTCR.E
*	HsHeLa3_Ti_104.1492.149	2.9763	0.2375	1314.68	1312.42	3592.6		1	453.6	66.7	1	K.SEHPGLSIGDTAK.K
gi|4758950|ref|N	2	4	0.12	216	23743	9.4	U	peptidylprolyl isomerase B precursor [Homo sapiens]				

*	Hs293FLP_TREX_Ti_102.2	3.5418	0.3318	1365.16	1365.53	6911		1	1236.6	75	2	K.TVDNFVALATGEK.G
*	Hs293FLP_TREX_Ti_102.2	4.0442	0.4084	1458.21	1458.61	8683.7		1	1392.4	70.8	2	K.DTNGSQFFITTVK.T
gi|14741936|ref|X	1	2	0.12	92	10678	8.1	U	PREDICTED: small nuclear ribonucleoprotein polypeptide E-like 1 [Homo sapiens]				
gi|89030198|ref|X	1	2	0.12	92	10678	8.1	U	PREDICTED: similar to small nuclear ribonucleoprotein E [Homo sapiens]				
gi|4507129|ref|N	1	2	0.12	92	10804	9.4	U	small nuclear ribonucleoprotein polypeptide E [Homo sapiens]				
	HsFLAG-Control_293_Ti_2	3.277	0.2676	1330.35	1330.68	5047.3		3	705	75	2	K.VMVQPINLIFR.Y
gi|5453629|ref|N	3	14	0.118	406	44820	5.2	U	dynactin 2 [Homo sapiens]				
*	HsFLAG-Control_HeLa_NE	3.5946	0.1828	1670.45	1668.89	7538.1		1	1335.3	73.1	2	R.LLHEVQELTTEVEK.I
*	HsFLAG-Control_HeLa_NE	4.8657	0.4234	1865.09	1866.12	7373.8		1	1096.8	55.6	11	K.LLGPDAAINLTDPDGALAK.R
*	HsFLAG-Control_HeLa_S1	3.6673	0.294	1601.59	1599.83	9271.3		1	1513.3	67.9	1	K.VSALDLAVLDQVEAR.L
gi|5803036|ref|N	2	3	0.118	305	30841	9.3	U	heterogeneous nuclear ribonucleoprotein A0 [Homo sapiens]				
*	Hs293FLP-MG_Ti_203.286	4.6456	0.3853	1691.39	1691.93	9889.5		1	2468.7	76.7	2	K.LFIGGLNVQTSESGLR.G
*	Hs293FLP-MG_Ti_202.353	3.5145	0.3107	2181.29	2179.35	9941.2		2	655.6	42.1	1	K.GDVAEGDLIEHFSQFGTVEK.A
gi|18379349|ref|N	3	5	0.117	393	41920	6.3	U	vesicle amine transport protein 1 [Homo sapiens]				
*	HsHeLa3_Ti_102.1218.121	3.0104	0.3851	1656.99	1656.74	5980.7		1	907.8	59.4	1	R.EVAEAATGEDASSPPPK.T
*	HsFLAG-Control_HeLa_S1	3.6606	0.3075	1443.8	1443.69	3355.8		1	780.3	71.4	2	R.PAAPPAPGPGQLTLR.L
*	HsHeLa3_Ti_104.2521.252	3.0713	0.3222	1465.68	1464.76	5577.4		1	921.6	65.4	2	K.VVTYGMANLLTGPK.R
gi|5174447|ref|N	3	5	0.117	317	35077	7.7	U	guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1 [Homo sapiens]				
*	HsFLAG-Control_MG_293_	3.6847	0.3488	1367.57	1367.55	6727.3		1	1527.2	81.8	3	R.YWLCAATGPSIK.I
*	HsFLAG-Control_293_Ti_2	4.4339	0.4001	1789.52	1790.06	9041.2		1	1774.9	70	1	K.IIVDELKQEVISTSSK.A
*	Hs293FLP_TREX_Ti_105.1	2.756	0.1176	1060.28	1060.24	4620.3		6	897.2	81.2	1	R.VWQVTIGTR.-
gi|6005926|ref|N	6	17	0.116	475	53501	9.1	U	U2 (RNU2) small nuclear RNA auxiliary factor 2 isoform a [Homo sapiens]				
gi|60279268|ref|N	6	17	0.117	471	53121	9.1	U	U2 (RNU2) small nuclear RNA auxiliary factor 2 isoform b [Homo sapiens]				
	HsHeLa_Control-MG_Ti_20	4.9019	0.4649	2133.65	2134.44	5556.7		1	766.5	52.5	11	R.LGGLTQAPGNPVLAVQINQDK.N
	HsHeLa3_Ti_104.2343.234	5.0824	0.5003	2133.99	2134.44	4187		1	828.7	60	1	R.LGGLTQAPGNPVLAVQINQDK.N
	HsHeLa3_Ti_104.2335.233	5.1467	0.1884	2136.64	2134.44	8078.6		1	1767	40	2	R.LGGLTQAPGNPVLAVQINQDK.N
	HsHeLa3_Ti_104.2987.298	2.9821	0.1317	1045.11	1044.2	4810		2	968.6	92.9	1	K.NFAFLEFR.S
	HsFLAG-Control_HeLa_NE	3.2017	0.2066	1806.87	1807.06	4510		1	357.5	46.7	1	K.LFIGGLPNYLNDDQVK.E
	Hs293FLP_TREX_Ti_103.2	2.6443	0.2136	1105.08	1105.32	5602.4		1	925.3	77.8	1	K.ELLTSFGPLK.A
gi|38327552|ref|N	3	12	0.116	466	52164	5.5	U	Ras-GTPase-activating protein SH3-domain-binding protein [Homo sapiens]				
gi|5031703|ref|N	3	12	0.116	466	52164	5.5	U	Ras-GTPase-activating protein SH3-domain-binding protein [Homo sapiens]				
	HsFLAG-Control_HeLa_NE	3.4501	0.2299	1886.5	1886.03	8245.8		4	551.2	47.1	2	K.SSSPAPADIAQTVQEDLR.T
	HsFLAG-Control_HeLa_S1	2.9522	0.4059	1879.87	1880.24	4242.5		5	261.8	47.2	1	K.NLPPSGAVPVTGIPPHVVK.V
	HsFLAG-Control_HeLa_NE	4.8609	0.39	1938.62	1939.18	8312.2		1	1629.3	65.6	9	K.LPNFGFVVFDDSEPVQK.V
gi|46877102|ref|N	2	7	0.116	251	27372	6.3	U	upstream stimulatory factor 1 isoform 2 [Homo sapiens]				
gi|6005934|ref|N	2	7	0.094	310	33538	5.5	U	upstream stimulatory factor 1 isoform 1 [Homo sapiens]				
	HsHeLa3_Ti_104.2457.245	3.9063	0.2217	1217.48	1215.44	6496.8		1	1282.8	88.9	3	K.INNWIVQLSK.I
	HsFLAG-Control_HeLa_NE	3.819	0.2914	2200.25	2199.42	9538		1	890.1	47.2	4	R.LSEELQGLDQLQLDNDVLR.Q
gi|25470886|ref|N	4	6	0.115	407	43383	8.6	U	DAZ associated protein 1 isoform b [Homo sapiens]				
gi|25470890|ref|N	4	6	0.124	378	40530	8.3	U	DAZ associated protein 1 isoform a [Homo sapiens]				
	HsHeLa3_Ti_103.3307.330	3.1596	0.1301	1928.18	1926.16	6253.2		1	593.5	53.3	1	R.SYFSQYGEVVDCVIMK.D
	HsHeLa3_Ti_106.2150.215	3.7959	0.321	1799.97	1799.99	3129.2		1	495	70	2	K.IFVGGIPHNCGETELR.E
	HsHeLa3_Ti_104.1385.138	2.3466	0.1491	1513.69	1514.6	5122.5		1	370.6	53.6	1	K.SQAPGQPGASQWGSR.V
	HsHeLa3_Ti_104.1383.138	3.6957	0.4679	1514.7	1514.6	4148.1		1	826.3	78.6	2	K.SQAPGQPGASQWGSR.V
gi|5453597|ref|N	2	5	0.115	286	32923	5.7	U	F-actin capping protein alpha-1 subunit [Homo sapiens]				
*	HsHeLa_Control-MG_Ti_20	2.9681	0.2561	2089.59	2090.3	4298.7		1	496.8	55.9	3	K.FITHAPPGEFNEVFNDVR.L
*	HsHeLa3_Ti_105.2747.274	2.8857	0.3662	1572.62	1571.9	3103.2		1	483.7	67.9	2	K.FTITPPTAQVVGVLK.I
gi|5031755|ref|N	4	6	0.114	633	70943	8.1	U	heterogeneous nuclear ribonucleoprotein R [Homo sapiens]				
*	HsHeLa3_Ti_103.2578.257	4.0533	0.3852	2508.12	2508.79	5277.2		1	652	45.8	2	K.YGGPPPDSVYSGVQPGIGTEVFVGK.I

*	HsHeLa3_Ti_104.2797.279	2.6213	0.1567	1941.83	1942.18	7854.4		4	522.1	43.8	1	K.VTEGLVDVILYHQPDDK.K
*	HsHeLa3_Ti_103.3139.313	4.1473	0.3156	1461.63	1461.65	6486.2		1	1394.1	75	2	R.NLATTVTEEILEK.S
*	HsFLAG-Control_HeLa_NE	4.0783	0.3025	1909.63	1910.17	8819.9		1	1060.6	56.2	1	K.EIEGEEIEIVLAKPPDK.K
gi|26051237|ref|N	4	6	0.114	507	55436	7	U	nucleoporin 54kDa [Homo sapiens]				
*	HsHeLa3_Ti_104.2713.271	3.7815	0.3388	1436.7	1436.61	8139.4		1	1315.1	77.3	1	K.WNQLQAFWGTGK.G
*	HsFLAG-Control_HeLa_NE	2.8121	0.2398	1630.49	1630.84	10259.7		9	594.1	46.7	1	K.VLGGNQTLTVNVEGTK.T
*	HsFLAG-Control_HeLa_NE	4.6732	0.314	1503.4	1503.69	6698.1		1	1749.4	87.5	1	R.LDIISEDISELQK.N
*	HsFLAG-Control_HeLa_NE	5.3532	0.4318	1903.66	1903.14	9229.7		1	2625.5	78.1	3	R.VQLDTIQGELNAPTQFK.G
gi|7662238|ref|NP	10	25	0.113	1341	151887	6.4	U	apoptotic chromatin condensation inducer 1 [Homo sapiens]				
*	HsFLAG-Control_HeLa_NE	5.13	0.3828	2118.76	2119.12	4990.2		1	889.6	61.1	5	K.LSEGSQPAEEEEDQETPSR.N
*	Hs293FLP-MG_Ti_202.309	2.5669	0.2528	2421.61	2422.74	5792.2		2	301.3	36.4	1	K.ASLVALPEQTASEEETPPPLLTK.E
*	HsHeLa3_Ti_105.2864.286	3.2343	0.2643	1721.83	1722.08	4936.1		1	786	63.3	2	R.SAQPLPLKIEELALAK.G
*	Hs293FLP_Ti_303.1397.13	4.8522	0.3481	3340.55	3340.46	4417.5		1	894.9	34.5	2	K.KCEAEEEAEPPAATQPQTSETQTSHLPESER.I
*	Hs293FLP-MG_Ti_205.171	3.0111	0.2716	1303.57	1304.53	5545		1	545.5	63.6	2	K.KPSISITTESLK.S
*	Hs293FLP-MG_Ti_205.171	3.4831	0.2651	1304.58	1304.53	7657		1	1482.9	81.8	2	K.KPSISITTESLK.S
*	HsFLAG-Control_HeLa_NE	3.5023	0.2143	1305.41	1304.53	8039.7		1	1059.4	72.7	5	K.KPSISITTESLK.S
*	HsHeLa_Control-MG_Ti_20	5.0039	0.3987	2561.4	2560.87	6627.6		1	901.1	35.9	2	K.SLIPDIKPLAGQEAVVDLHADDSR.I
*	Hs293FLP_Ti_304.1483.14	2.7314	0.2211	1105.4	1104.29	3459		3	600.6	77.8	1	K.KVTLGDTLTR.R
*	HsHeLa_Control-MG_Ti_20	3.9141	0.24	2105.78	2104.42	5172.6		1	513.8	50	3	K.AAPCIYWLPLTDSQIVQK.E
gi|9506671|ref|NP	3	4	0.113	524	56876	6.3	U	hypothetical protein LOC54502 [Homo sapiens]				
*	HsHeLa3_Ti_103.3308.330	4.4128	0.4763	2010.01	2009.33	3937		1	1038.2	71.1	2	K.VPEGVAGAPNEAALLALMER.T
*	HsHeLa3_Ti_104.1808.180	3.4568	0.3008	1399.18	1398.48	4407.2		1	964.6	81.8	1	K.SFGQFNPGCVER.V
*	HsHeLa3_Ti_106.2836.283	3.4428	0.2525	2694.06	2695.13	3459.7		1	401.5	42.3	1	R.IPTAGIYGASYVPFAAPATATIATLQK.N
gi|38146107|ref|N	3	5	0.113	434	50560	11.3	U	hypothetical protein LOC65117 isoform a [Homo sapiens]				
gi|38146113|ref|N	3	5	0.131	375	43805	11.4	U	hypothetical protein LOC65117 isoform b [Homo sapiens]				
gi|38146109|ref|N	3	5	0.243	202	22395	8.8	U	hypothetical protein LOC65117 isoform c [Homo sapiens]				
	HsHeLa3_Ti_103.2646.264	4.1692	0.3333	2279.78	2278.63	2721.2		1	687.7	57.1	2	K.ALAETGIAVPSYYNPAAVNPMK.F
	HsHeLa3_Ti_102.1345.134	4.5783	0.5474	1792.62	1792.73	5882		1	1340.9	73.3	2	K.SEDEAGCSSVDEESYK.T
	HsHeLa3_Ti_104.1980.198	3.2869	0.2801	1144.39	1144.35	4555.5		1	666.5	75	1	R.GMGLGFTSSMR.G
gi|4504011|ref|NP	1	2	0.113	274	30727	6	U	glutamate-cysteine ligase regulatory protein [Homo sapiens]				
*	HsFLAG-Control_HeLa_S1	4.3063	0.2547	3649.64	3650.13	7926.5		1	1088.7	28.3	2	K.ELLSEASFQEALQESIPDIQAHEWVPLWLLR.Y
gi|38570081|ref|N	2	2	0.112	483	51617	8.5	U	CUG triplet repeat, RNA-binding protein 1 isoform 2 [Homo sapiens]				
gi|71164871|ref|N	2	2	0.111	486	52063	8.5	U	CUG triplet repeat, RNA-binding protein 1 isoform 3 [Homo sapiens]				
gi|5729794|ref|NP	2	2	0.112	482	51546	8.5	U	CUG triplet repeat, RNA-binding protein 1 isoform 1 [Homo sapiens]				
	HsFLAG-MOCK_300mM_T	2.8778	0.2283	2017.08	2016.38	6072.8		2	623.7	50	1	K.VLPGMHHPIQMKPADSEK.N
	HsHeLa3_Ti_105.4915.491	4.6947	0.3951	4040.86	4041.59	8682.3		1	565	19.3	1	K.EGPEGANLFIYHLPQEFGDQDLLQMFMPFGNVVSAK.V
gi|5032179|ref|NP	5	15	0.111	835	88550	5.8	U	tripartite motif-containing 28 protein [Homo sapiens]				
*	HsFLAG-MOCK_300mM_T	5.3421	0.4575	3601.47	3600.81	10268.4		1	1448.3	26.4	2	K.RSTAPSAAASASASAAASSPAGGGAEALELLEHCGVCR.E
*	Hs293FLP_TREX_Ti_104.2	3.2793	0.232	1520.58	1521.63	8758.4		1	1215.6	72.7	1	K.DHQYQFLEDAVR.N
*	HsFLAG-Control_HeLa_NE	4.5835	0.4054	1659.6	1659.88	6411.8		1	1452.2	75	7	R.LDLDLTADSQPPVFK.V
*	HsFLAG-Control_HeLa_NE	3.6295	0.3484	1953.92	1954.19	3183.3		1	426.9	59.4	3	K.VFPGSTTEDYNLIVIER.G
*	HsFLAG-Control_HeLa_NE	3.4373	0.2478	1200.56	1200.38	7045.9		1	1346.7	80	2	K.ADVQSIIGLQR.F
gi|10835051|ref|N	5	7	0.111	748	85473	6.7	U	cysteinyl-tRNA synthetase isoform b [Homo sapiens]				
gi|62240994|ref|N	5	7	0.112	738	84472	6.4	U	cysteinyl-tRNA synthetase isoform d [Homo sapiens]				
gi|62240992|ref|N	5	7	0.1	831	94638	6.8	U	cysteinyl-tRNA synthetase isoform c [Homo sapiens]				
gi|21269877|ref|N	5	7	0.114	726	82846	7	U	cysteinyl-tRNA synthetase isoform a [Homo sapiens]				
	HsGST-MOCK_Ti_305.359	3.1838	0.2234	1754.58	1753.01	9058.5		1	852.4	56.7	1	K.RPEAAQLLEDVQAALK.P

	HsGST-MOCK_Ti_302.513	5.5714	0.4179	2602.14	2602.78	7353.1		1	934	47.7	2	K.DLLSDWLDSTLGCDVTDNSIFSK.L
	HsGST-MOCK_Ti_302.305	3.3564	0.3508	1651.7	1651.9	2893.4		1	650.9	76.9	2	R.VSEYVPEIVNFVQK.I
	HsGST-MOCK_Ti_302.240	4.7413	0.4708	2096.04	2096.23	11015.6		1	1383.8	55.9	1	K.DTLDYSSNTMESALQYEK.F
	HsGST-MOCK_Ti_303.322	3.9041	0.3458	1354.22	1354.59	8426.8		1	1524	81.8	1	K.VPEILQLSDALR.D
gi|5803111|ref|N	2	5	0.111	306	34820	10.1	U	EBNA1 binding protein 2 [Homo sapiens]				
*	HsGST-MOCK_Ti_303.269	3.9638	0.3063	2189.88	2190.46	6493.2		4	399.3	38.1	1	R.LDVTLGPVPEIGGSEAPAPQNK.D
*	Hs293FLP_TREX_Ti_103.2	3.9253	0.3586	1238.56	1237.49	6999.6		1	1667.3	90.9	4	R.QAQAAVLAVLPR.L
gi|16753225|ref|N	2	3	0.111	216	23503	10.9	U	ribosomal protein L14 [Homo sapiens]				
gi|89036208|ref|X	2	3	0.113	213	23259	10.9	U	PREDICTED: similar to 60S ribosomal protein L14 (CAG-ISL 7) isoform 2 [Homo sapiens]				
gi|89036206|ref|X	2	3	0.113	213	23259	10.9	U	PREDICTED: similar to 60S ribosomal protein L14 (CAG-ISL 7) isoform 1 [Homo sapiens]				
	Hs293FLP_TREX_Ti_106.2	2.4976	0.2643	1232.4	1233.41	5263.4		1	504.7	59.1	2	R.VAYVSFGPHAGK.L
	HsGST-MOCK_Ti_303.278	3.8399	0.1938	1355.94	1355.58	7630.6		1	1324.7	77.3	1	K.LVAIVDVIDQNR.A
gi|5902034|ref|N	4	9	0.11	501	55828	4.8	U	periodic tryptophan protein 1 [Homo sapiens]				
*	Hs293FLP_TREX_Ti_104.1	4.0701	0.4053	1110.46	1110.26	7547.5		1	1446	85	2	K.PAASLAVHTDK.V
*	HsHeLa_Control_Ti_105.33	4.8811	0.3779	2410.98	2410.69	4059.6		1	880.2	60	4	K.VQTLQFHPFEAQTLISGSYDK.S
*	Hs293FLP-MG_Ti_204.305	4.4243	0.2617	2411.32	2410.69	8176.3		2	983.2	36.2	2	K.VQTLQFHPFEAQTLISGSYDK.S
*	HsHeLa_Control-MG_Ti_10	3.6917	0.3842	2655.26	2655.97	6872.9		1	573.1	40.9	1	K.MGVLFCSSCCPDLPFIYAFGGQK.E
gi|38195084|ref|N	4	11	0.11	347	39899	5.7	U	HMT1 hnRNP methyltransferase-like 2 isoform 2 [Homo sapiens]				
gi|38195089|ref|N	4	11	0.105	361	41486	5.5	U	HMT1 hnRNP methyltransferase-like 2 isoform 1 [Homo sapiens]				
gi|38195087|ref|N	4	11	0.111	343	39572	5.7	U	HMT1 hnRNP methyltransferase-like 2 isoform 3 [Homo sapiens]				
	HsHeLa_Control-MG_Ti_20	3.1231	0.157	1351.94	1351.63	9671.8		1	1128.2	68.2	3	K.ANKLDHVVTIIK.G
	Hs293FLP-MG_Ti_105.169	2.001	0.2222	1037.68	1038.28	4984.2		4	483.3	68.8	1	K.LDHVVTIIK.G
	Hs283FLP_Ti_102.1854.18	3.7094	0.397	1252.42	1252.41	6498.8		1	1258	80	1	R.ATLYVTAIEDR.Q
	Hs293FLP-MG_Ti_204.189	3.4565	0.3179	1725.55	1725.86	5574		1	681.6	60.7	6	R.TGFSTSPESPYTHWK.Q
gi|18375501|ref|N	2	2	0.11	318	35554	8.1	U	APEX nuclease [Homo sapiens]				
gi|18375505|ref|N	2	2	0.11	318	35554	8.1	U	APEX nuclease [Homo sapiens]				
gi|18375503|ref|N	2	2	0.11	318	35554	8.1	U	APEX nuclease [Homo sapiens]				
	HsHeLa3_Ti_103.3834.383	3.193	0.3535	1849.38	1849.1	4756.6		2	386.6	46.9	1	R.QGFGELLQAVPLADSFR.H
	HsHeLa3_Ti_104.3683.368	3.7628	0.3371	2094.92	2093.39	5623.7		1	728.6	55.9	1	R.LDYFLLSHSLLPALCDSK.I
gi|15149463|ref|N	5	9	0.109	558	64256	7	U	caldesmon 1 isoform 4 [Homo sapiens]				
gi|4826657|ref|N	5	9	0.113	538	62663	6.4	U	caldesmon 1 isoform 2 [Homo sapiens]				
gi|44680105|ref|N	5	9	0.077	793	93231	5.7	U	caldesmon 1 isoform 1 [Homo sapiens]				
gi|15149467|ref|N	5	9	0.108	564	65707	6.6	U	caldesmon 1 isoform 3 [Homo sapiens]				
gi|15149465|ref|N	5	9	0.115	532	61213	6.7	U	caldesmon 1 isoform 5 [Homo sapiens]				
	HsHeLa3_Ti_102.1921.192	4.5587	0.4607	2100.1	2099.17	5170.3		1	952	61.1	2	K.TTTTNTQVEGDDEAAFLER.L
	HsHeLa3_Ti_106.1616.161	2.1403	0.2184	1042.97	1042.18	4921.2		2	429.1	61.1	1	K.STHQAAIVSK.I
	HsHeLa3_Ti_102.1634.163	3.2871	0.2817	1339.63	1340.47	5594.5		1	550.9	68.2	2	R.LEQYTSAIEGTK.S
	HsHeLa3_Ti_102.1642.164	3.6935	0.3559	1342.46	1340.47	6539.5		1	1785.9	90.9	2	R.LEQYTSAIEGTK.S
	HsHeLa3_Ti_106.2056.205	3.4862	0.3861	1992.65	1992.28	4297.5		1	540.4	50	2	K.SAKPTKPAASDLPVPAEGVR.N
gi|42544123|ref|N	4	7	0.109	548	59712	9.5	U	splicing factor 1 isoform 3 [Homo sapiens]				
gi|42544130|ref|N	4	7	0.094	639	68330	9	U	splicing factor 1 isoform 1 [Homo sapiens]				
gi|42544125|ref|N	4	7	0.094	638	68633	9.2	U	splicing factor 1 isoform 2 [Homo sapiens]				
	HsGST-MOCK_Ti_104.232	5.16	0.4663	2936.8	2937.39	6633.5		1	1035.5	32	2	R.HNLITEMVALNPDFKPPADYKPPATR.V
	HsHeLa3_Ti_104.4416.441	4.2831	0.4293	2401.38	2401.83	4214.1		1	508.7	50	2	K.VMIPQDEYPEINFVGLLIGPR.G
	HsHeLa3_Ti_104.4415.441	5.3868	0.3658	2402.04	2401.83	8056.7		1	2362.9	46.2	2	K.VMIPQDEYPEINFVGLLIGPR.G
	HsFLAG-MOCK_300mM_T	3.0595	0.1822	1475.52	1474.57	3067.1		4	464.7	70.8	1	K.FQRPGDPQSAQDK.A
gi|55769533|ref|N	2	4	0.109	340	36568	5.4	U	PRKC, apoptosis, WT1, regulator [Homo sapiens]				
*	HsHeLa3_Ti_102.2575.257	3.2391	0.4333	2611.03	2611.7	2987.8		1	254.8	39.1	2	R.STGVVNIPAAECLDEYEDDEAGQK.E
*	HsHeLa3_Ti_102.1235.123	3.2795	0.3497	1384.37	1384.4	4816.6		1	626.6	66.7	2	K.STTSVSEEDVSSR.Y

gi|14110428|ref|N	3	3	0.109	303	33299	5.2	U		heterogeneous nuclear ribonucleoprotein C isoform a [Homo sapiens]			
gi|4758544|ref|N	3	3	0.114	290	31966	5.2	U		heterogeneous nuclear ribonucleoprotein C isoform b [Homo sapiens]			
	HsFLAG-Control_293_Ti_2	2.7732	0.1694	1317.84	1317.62	6993.2		2	960.6	68.2	1	R.VFIGNLNTLVVK.K
	HsFlag1P_Ti_104.2693.269	2.6483	0.2296	1331.24	1330.49	6067.9		1	957.4	75	1	K.GFAFVQYVNER.N
	Hs293FLP_TREX_Ti_102.2	2.5539	0.1185	1160.75	1160.31	5951.6		3	739.4	77.8	1	K.VDSLLENLEK.M
gi|5729842|ref|N	1	6	0.109	184	20720	5.5	U		glyoxalase I [Homo sapiens]			
*	Hs293FLP-MG_Ti_202.465	4.4177	0.3852	2303.54	2304.61	5570.4		1	919.2	57.9	6	K.GLAFIQDPDGYWIEILNPNK.M
gi|4506765|ref|N	2	9	0.109	101	11728	6.1	U		S100 calcium-binding protein A4 [Homo sapiens]			
gi|9845516|ref|N	2	9	0.109	101	11728	6.1	U		S100 calcium-binding protein A4 [Homo sapiens]			
	HsHeLa3_Ti_105.1908.190	2.9994	0.1538	1247.58	1248.48	6317.4		1	781.2	75	4	K.ALDVMVSTFHK.Y
	HsHeLa3_Ti_105.1902.190	3.4107	0.1998	1249.28	1248.48	5493.9		3	831.6	70	5	K.ALDVMVSTFHK.Y
gi|4507943|ref|N	9	19	0.107	1071	123386	6.1	U		exportin 1 [Homo sapiens]			
*	HsFLAG-Control_HeLa_S1	3.8223	0.3896	2027.74	2028.27	10134		1	1304.2	58.8	4	K.LLSEEVFDFSSGQITQVK.S
*	HsFLAG-Control_HeLa_NE	2.4926	0.1104	1068.42	1069.16	7554.3		2	576.8	68.8	1	K.DTDSINLYK.N
*	HsHeLa3_Ti_104.4383.438	2.8706	0.3523	2149.48	2149.51	3938.3		1	276.8	44.1	2	K.YMLLPNQVWDSIIQQATK.N
*	HsFLAG-Control_HeLa_S1	2.8304	0.241	1295.78	1294.54	3769.9		2	526.5	72.7	1	K.AVGHPFVIQLGR.I
*	HsFLAG-Control_HeLa_S1	4.0348	0.3307	2888.56	2888.29	8589.2		1	638.5	36	2	K.ISTSLNPGNPVNNQIFLQEYVANLLK.S
*	HsFLAG-Control_HeLa_S1	4.5173	0.372	2889.92	2888.29	7184.4		1	1011.3	32	1	K.ISTSLNPGNPVNNQIFLQEYVANLLK.S
*	HsFLAG-Control_HeLa_NE	5.05	0.3574	2890.19	2888.29	8918		1	1186.4	31	2	K.ISTSLNPGNPVNNQIFLQEYVANLLK.S
*	HsFLAG-Control_HeLa_S1	4.2437	0.4038	1910.59	1911.25	5552.5		1	1315.4	68.8	4	K.LFVTGLFSLNQDIPAFK.E
*	HsFLAG-Control_HeLa_NE	3.2129	0.3799	1758.56	1758.84	7592.1		2	404.6	50	2	K.EFAGEDTSDLFLEER.E
gi|50301238|ref|N	3	5	0.107	522	56257	8.5	U		glutathione reductase [Homo sapiens]			
*	HsGST-MOCK_Ti_302.349	3.2355	0.3051	2574.28	2574.78	9367.2		1	652.2	40.9	1	R.SFDSMISTNCTEELENAGVEVLK.F
*	HsFLAG-Control_MG_293_	3.4896	0.2904	1153.48	1153.41	5050.9		1	1294	90.9	2	K.ALLTPVAIAAGR.K
*	HsGST-MOCK_Ti_403.282	4.0271	0.3228	2315.69	2316.53	5959.4		1	585.8	45	2	K.ADFDNTVAIHPTSSEELVTLR.-
gi|6005854|ref|N	2	3	0.107	299	33296	9.8	U		prohibitin 2 [Homo sapiens]			
*	HsFLAG-Control_293_Ti_1	2.9523	0.3272	1724.55	1725.04	8437.1		4	476.7	50	1	R.IPWFQYPIIYDIR.A
*	HsFLAG-Control_293_Ti_1	3.5051	0.3526	2227.97	2226.49	9925.7		1	449.2	38.9	2	R.IYLTADNLVLNLQDESFTR.G
gi|23503295|ref|N	1	2	0.107	215	24942	5.6	U		casein kinase 2, beta polypeptide [Homo sapiens]			
*	HsHeLa3_Ti_103.3422.342	3.497	0.2913	2563.71	2562.97	4788.6		1	499.1	45.5	2	R.VYCENQPMLPIGLSDIPGEAMVK.L
gi|40806162|ref|N	3	4	0.106	461	52788	7.1	U		thyroid hormone receptor, beta [Homo sapiens]			
*	HsFLAG-MOCK_300mM_T	4.0243	0.2164	2250.48	2248.66	4131.5		1	625.9	58.8	2	K.KLPMFCELPCEDQIILLK.G
*	HsFLAG-MOCK_300mM_T	3.9912	0.3357	2424.26	2424.69	3066.4		2	342.7	47.6	1	R.AAVRYDPESETLTLNGEMAVTR.G
	HsFLAG-MOCK_300mM_T	2.6738	0.2103	1004.24	1003.13	3533.9		1	786.1	93.8	1	R.MIGACHASR.F
gi|15055539|ref|N	2	4	0.106	293	31324	10.2	U		ribosomal protein S2 [Homo sapiens]			
	HsHeLa_Control-MG_Ti_20	3.6692	0.4069	2154.67	2154.47	6937.1		1	459.9	44.4	1	K.ESEIIDFFLGASLKDEVLK.I
	Hs293FLP_TREX_Ti_105.2	3.4138	0.1797	1466.25	1464.62	8412.7		1	927.3	68.2	3	K.SPYQEFTDHLVK.T
gi|4504345|ref|N	3	10	0.106	142	15258	8.7	U		alpha 2 globin [Homo sapiens]			
gi|4504347|ref|N	3	10	0.106	142	15258	8.7	U		alpha 1 globin [Homo sapiens]			
	HsFLAG-MOCK_150mM_T	3.3017	0.1978	1530.32	1530.64	7524.9		1	1185.1	64.3	7	K.VGAHAGEYGAEALER.M
	HsGST-MOCK_Ti_404.184	2.9652	0.082	1530.53	1530.64	8670.6		1	1094.4	60.7	2	K.VGAHAGEYGAEALER.M
	HsGST-MOCK_Ti_101.072	3.6361	0.1261	1532.12	1530.64	8551.5		1	1862.9	50	1	K.VGAHAGEYGAEALER.M
gi|42476164|ref|N	4	7	0.105	743	76472	6.8	U		POU domain, class 2, transcription factor 1 [Homo sapiens]			
*	HsFLAG-Control_HeLa_NE	3.0907	0.2226	1883.61	1883.15	7464.4		3	490.6	44.1	2	R.TIAATPIQTLPQSQSTPK.R
	HsHeLa3_Ti_103.2220.222	3.7662	0.3966	1395.15	1394.63	5454		1	1009.5	73.1	2	K.LGFTQGDVGLAMGK.L
*	HsHeLa3_Ti_102.2975.297	3.0625	0.4101	3105.94	3105.3	5976.1		1	341.6	29.3	1	K.WLNDAENLSSDSSLSSPSALNSPGIEGLSR.R
*	HsHeLa3_Ti_106.1907.190	4.2148	0.4522	1586.76	1585.76	7118.6		1	1424.2	73.3	2	K.RINPPSSGGTSSSPIK.A
gi|4757810|ref|N	4	7	0.105	553	59751	9.1	U		ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit precursor [Homo			
gi|50345984|ref|N	4	7	0.105	553	59751	9.1	U		ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit precursor [Homo			

gi|50345982|ref|N	4	7	0.115	503	54494	8.2	U	ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit isoform b [Homo			
	HsFLAG-Control_MG_293_	3.59	0.2178	1317.68	1317.53	8740.2	2	1264	72.7	1	K.TSIAIDTIINQK.R
	Hs293FLP_TREX_Ti_106.2	3.1754	0.2634	1288.24	1288.49	7431.3	1	1570.8	90	2	K.HALIIYDDLSK.Q
	HsFLAG-Control_293_Ti_2	2.8034	0.2668	1554.32	1554.7	5716	1	689	66.7	1	R.EAYPGDVFYLHSR.L
	HsFLAG-Control_293_Ti_2	5.2945	0.505	2339.23	2339.57	7680	1	1709	59.5	3	R.EVAAFAQFGSDLDAATQQLLSR.G
gi|4826686|ref|N	6	14	0.104	740	82432	7.2	U	DEAD (Asp-Glu-Ala-Asp) box polypeptide 1 [Homo sapiens]			
*	HsHeLa3_Ti_104.2656.265	3.3356	0.3618	2139.08	2139.46	8378.7	1	710.8	47.2	2	K.ALIVEPSRELAEQTLNNIK.Q
*	HsHeLa3_Ti_103.4476.447	3.8987	0.2447	2373.13	2373.62	8466.3	1	1053.4	35	1	R.FLVLDEADGLLSQGYSDFINR.M
*	HsHeLa_Control-MG_Ti_20	3.8098	0.2379	2374.59	2373.62	7057	1	735.5	47.5	1	R.FLVLDEADGLLSQGYSDFINR.M
*	HsHeLa3_Ti_103.4470.447	5.6952	0.4996	2374.74	2373.62	7496.9	1	2080	67.5	8	R.FLVLDEADGLLSQGYSDFINR.M
*	HsHeLa3_Ti_104.3015.301	3.7647	0.3309	2080.81	2080.39	3328.2	1	493.7	55.6	1	R.GIDIHGVPYVINVTLPDEK.Q
*	HsHeLa3_Ti_106.2808.281	4.8597	0.4674	2135.21	2135.43	5487.5	1	1119.2	61.8	1	K.EAQTSFLHLGYLPNQLFR.T
gi|6005802|ref|N	1	3	0.104	134	15097	7.1	U	proline rich 4 (lacrimal) [Homo sapiens]			
*	HsFLAG-Control_293_Ti_2	4.0174	0.4045	1602.8	1602.79	7361.4	1	1402.2	73.1	3	R.FPSVSLQEASSFFR.R
gi|61175258|ref|N	1	3	0.104	125	14116	8.3	U	hypothetical protein LOC388753 [Homo sapiens]			
*	HsFLAG-MOCK_300mM_T	3.5485	0.3518	1584.27	1584.69	6294.5	1	741.7	62.5	3	R.SSFESSCPQQWIK.Y
gi|50659095|ref|N	6	9	0.103	783	87344	9.3	U	DEAD (Asp-Glu-Ala-Asp) box polypeptide 21 [Homo sapiens]			
*	HsFLAG-Control_HeLa_NE	3.0186	0.1514	1712.78	1712.81	7077.7	1	1152.2	67.9	1	K.NEEPSEEEIDAPKPK.K
	HsFLAG-Control_HeLa_NE	3.5754	0.2599	1669.63	1669.83	4427.2	1	858.2	71.4	2	K.EGAFSNFPISEETIK.L
*	HsFLAG-Control_HeLa_NE	3.1048	0.3125	1221.49	1221.49	4549.8	1	783.1	80	1	R.GVTFLFPIQAK.T
*	HsFLAG-Control_HeLa_NE	4.0264	0.2829	1165.55	1165.42	7913.2	1	1609.6	80	3	R.APQVLVLAPTR.E
*	HsFLAG-Control_HeLa_NE	2.9057	0.2191	2009.22	2010.18	6036.1	1	445.2	44.1	1	K.LSVACFYGGTPYGGQFER.M
*	HsGST-MOCK_Ti_305.200	3.6705	0.336	1195.95	1196.43	5497.4	2	882.7	80	1	K.TAITVEHLAIK.C
gi|40538736|ref|N	3	5	0.103	620	67257	6.8	U	RAN binding protein 10 [Homo sapiens]			
	HsHeLa_Control-MG_Ti_20	2.8666	0.2447	1939.44	1938.2	7390.7	1	634.5	53.1	1	R.ATHPIPAACGIYYFEVK.I
*	HsHeLa_Control-MG_Ti_20	3.7476	0.392	1475.25	1472.65	8032.9	1	891.9	66.7	2	K.VQGTVHCFPISAR.L
*	HsHeLa_Control-MG_Ti_20	4.4535	0.3274	3351.72	3351.3	10770.3	1	985.2	23.5	2	K.YPAPSSSSSSSSSSSSSPSSVNYSESNSTDSTK.S
gi|45505149|ref|N	2	2	0.103	428	47629	8.2	U	nuclear factor I/C isoform 1 [Homo sapiens]			
gi|45505151|ref|N	2	2	0.088	499	54682	8.5	U	nuclear factor I/C isoform 2 [Homo sapiens]			
	HsHeLa3_Ti_105.3106.310	3.0393	0.3258	1488.36	1488.69	6397.6	1	853.1	72.7	1	R.AFAYTWFNLQAR.K
	HsHeLa3_Ti_106.2770.277	4.0557	0.2858	3284.69	3284.65	5583	1	678.5	27.4	1	R.TPVVTGTGPNFSLGELQGHLAYDLNPASTGLR.R
gi|14141193|ref|N	2	4	0.103	194	22591	10.7	U	ribosomal protein S9 [Homo sapiens]			
*	HsHeLa_Control-MG_Ti_20	3.7725	0.2026	1189.66	1189.4	5500.8	3	936.7	83.3	3	R.RLFEGNALLR.R
*	HsHeLa_Control-MG_Ti_20	2.5899	0.1884	1003.8	1004.09	5968.7	3	630.3	72.2	1	R.SPYGGGRPGR.V
gi|68508957|ref|N	2	3	0.102	566	62393	6.6	U	carboxylesterase 1 isoform c precursor [Homo sapiens]			
gi|68508967|ref|N	2	3	0.102	568	62592	6.6	U	carboxylesterase 1 isoform a precursor [Homo sapiens]			
gi|68508965|ref|N	2	3	0.102	567	62521	6.6	U	carboxylesterase 1 isoform b precursor [Homo sapiens]			
	HsHeLa_Control-MG_Ti_20	5.6553	0.2625	3791.42	3792.24	11343.9	1	769.9	20.3	1	R.WVQDNIASFGGNPGSVTIFGESAGGESVSVLVLSPLAK.N
	HsHeLa_Control-MG_Ti_20	5.0858	0.4591	2151.57	2150.44	8052.2	1	1589.3	63.2	2	K.TVIGDHGDELFSVFGAPFLK.E
gi|32189394|ref|N	4	4	0.102	529	56560	5.4	U	ATP synthase, H+ transporting, mitochondrial F1 complex, beta subunit precursor [Homo			
*	Hs293FLP_TREX_Ti_102.2	2.4944	0.1619	1088.38	1089.32	5472.3	1	602	72.2	1	K.VVDLLAPYAK.G
*	HsFLAG-Control_MG_293_	1.947	0.1464	975.48	976.164	7656.4	4	796.2	70	1	K.IGLFGGAGVGK.T
*	HsFLAG-Control_293_Ti_2	3.6924	0.3095	1436.36	1436.61	8831.5	1	1628	76.9	1	R.FTQAGSEVSALLGR.I
*	HsHeLa_Control_Ti_102.30	2.9661	0.2161	1990.5	1989.23	3844.9	2	357	44.4	1	R.AIAELGIYPAVDPLDSTSR.I
gi|5031977|ref|N	2	3	0.102	491	55521	7.2	U	pre-B-cell colony enhancing factor 1 isoform a [Homo sapiens]			
gi|89031848|ref|X	2	3	0.1	499	56177	7.8	U	PREDICTED: similar to Nicotinamide phosphoribosyltransferase (NAmPRTase) (Nampt)			
gi|89030888|ref|X	2	3	0.095	527	59154	8	U	PREDICTED: similar to Nicotinamide phosphoribosyltransferase (NAmPRTase) (Nampt)			

	HsFLAG-Control_HeLa_S1	3.7378	0.2569	2235.52	2236.57	8713.6		1	628.2	42.5	1	R.STQAPLIIRPDSGNPLDTVLK.V
	HsHeLa_Control-MG_Ti_20	6.6016	0.4987	3209.17	3209.54	9602.2		1	1443.8	30.4	2	R.TPAGNFVTLEEGKGDLEEYGQDLLHTVFK.N
gi|4506649|ref|N	6	11	0.102	403	46109	10.2	U	ribosomal protein L3 isoform a [Homo sapiens]				
gi|76496472|ref|	6	11	0.116	354	40152	10.2	U	ribosomal protein L3 isoform b [Homo sapiens]				
	Hs293FLP_TREX_Ti_106.2	2.3195	0.2147	983.54	984.146	4112.9		4	418.9	81.2	1	R.HGSLGFLPR.K
	Hs293FLP_TREX_Ti_106.2	3.322	0.3199	984.42	984.146	5846.2		1	1191.5	93.8	2	R.HGSLGFLPR.K
	Hs293FLP_TREX_Ti_103.1	4.236	0.4254	1434.16	1436.53	8938		1	1867.9	81.8	2	K.TVFAEHISDECK.R
	Hs293FLP_TREX_Ti_103.1	2.9559	0.1247	892.25	892.086	4286.8		1	829.5	92.9	2	K.IGQGYLIK.D
	Hs293FLP_TREX_Ti_102.1	3.205	0.3377	1342.31	1343.35	3790.1		1	292.5	59.1	2	K.NNASTDYDLSDK.S
	Hs293FLP_TREX_Ti_102.1	3.8602	0.2146	1343.15	1343.35	6180.1		1	1059.2	77.3	2	K.NNASTDYDLSDK.S
gi|50053872|ref|	2	2	0.102	246	28661	10.5	U	ribosomal protein L7-like 1 [Homo sapiens]				
*	HsGST-MOCK_Ti_104.168	2.9759	0.2343	1447.25	1446.61	4711.2		1	510.2	70	1	K.RLESFLHDSWR.Q
*	HsGST-MOCK_Ti_105.152	3.4805	0.3773	1645.48	1645.94	6112.8		1	713.8	65.4	1	R.RLEVKPHALELPDK.H
gi|21362060|ref|	1	2	0.102	147	15015	7.8	U	hypothetical protein LOC84326 [Homo sapiens]				
*	HsGST-MOCK_Ti_302.277	4.2119	0.2979	1759.18	1759.92	4269		1	1171.1	71.4	2	R.AFPLAEWQPSDVDQR.C
gi|21237805|ref|	9	14	0.101	1214	132879	5.7	U	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin c2 isoform a [				
gi|21237808|ref|	9	14	0.109	1130	124841	5.6	U	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin c2 isoform b [				
	HsHeLa3_Ti_102.2101.210	3.1833	0.4706	1792.66	1792.9	4719.4		1	827.9	67.9	1	K.YYEAADTVTQFDNVR.L
	HsHeLa3_Ti_103.1310.131	2.0753	0.1061	1160.63	1161.3	3370.7		1	331.5	72.2	1	K.YIQAEPPTNK.S
	HsHeLa3_Ti_106.3770.377	5.1666	0.334	2152.22	2152.5	7770.2		1	1778.3	66.7	3	K.SLSSLVVQLLQFQEEVFGK.H
	HsHeLa3_Ti_106.1751.175	1.9468	0.2579	966.58	967.113	4466.8		1	449.7	68.8	1	K.HVSNAPLTK.L
	HsHeLa3_Ti_103.1911.191	2.5713	0.3068	1553.68	1553.68	3453.2		1	333	62.5	1	R.LNPQEYLTSTACR.R
	HsHeLa3_Ti_104.2471.247	3.7585	0.261	1433.7	1432.59	6393.3		1	1149	80	1	R.TQDECILHFLR.L
	HsHeLa3_Ti_103.1014.101	2.8107	0.2608	1347.53	1347.42	6864.1		1	651.8	66.7	2	R.EGGGAIEEEAKEK.T
	HsFLAG-Control_HeLa_NE	4.5416	0.4429	1886.84	1886.11	8225.2		1	1305.3	55	2	R.DIGEGNLSTAAAAALAAAAVK.A
	HsHeLa3_Ti_105.3182.318	3.4996	0.1814	1333.68	1332.64	6963.5		1	1092.7	72.7	2	K.SLVALLVETQMK.K
gi|55741671|ref|	7	7	0.101	1083	121837	6.5	U	hypothetical protein LOC22998 [Homo sapiens]				
*	HsHeLa3_Ti_106.3310.331	2.6342	0.2379	2366.7	2366.81	7186.2		1	495.5	35.7	1	R.TGLENGILLCELLNAIKPGLVK.K
*	HsHeLa3_Ti_106.3315.331	4.2575	0.3902	2369.15	2366.81	6518.4		1	858.5	33.3	1	R.TGLENGILLCELLNAIKPGLVK.K
*	HsHeLa3_Ti_104.2505.250	3.0686	0.2554	2117.05	2116.31	7205.9		1	606.4	50	1	R.SHSTEPNLSSFLNDPNPMK.Y
*	HsHeLa3_Ti_105.1551.155	2.7276	0.3386	1614.07	1613.81	3662.2		1	370	57.1	1	K.KPNSVPQELAATTEK.T
*	HsHeLa3_Ti_104.1765.176	4.0862	0.4417	2088.93	2089.27	4464.6		1	639.2	55.6	1	K.GNIELASSEPQHFTTTVTR.C
*	HsHeLa3_Ti_104.2677.267	3.2932	0.4721	1894.87	1895.13	7462		1	759.7	53.1	1	R.CSPTVAFVEFPSSPQLK.N
*	HsHeLa3_Ti_105.1524.152	3.9384	0.4273	1626.82	1625.78	6598.2		1	945	59.4	1	K.GSLTEGALAHSGNPVSK.G
gi|4503519|ref|N	3	9	0.101	357	37564	5.4	U	eukaryotic translation initiation factor 3, subunit 5 epsilon, 47kDa [Homo sapiens]				
*	HsFLAG-Control_HeLa_NE	4.9136	0.477	1658.95	1658.85	10183.2		1	2197.5	68.8	2	R.VIGLSSDLQQVGGASAR.I
	HsFLAG-Control_HeLa_NE	3.67	0.3155	2052.44	2051.3	11247.3		1	1369.2	36.1	1	R.IQDALSTVLQYAEDVLSGK.V
	HsFLAG-Control_HeLa_NE	5.9137	0.4821	2052.76	2051.3	5460.1		1	1351.8	69.4	6	R.IQDALSTVLQYAEDVLSGK.V
gi|20149592|ref|	2	4	0.1	350	38452	5.1	U	serine/threonine kinase receptor associated protein [Homo sapiens]				
*	HsFLAG-Control_HeLa_NE	4.2539	0.3899	2004.66	2003.13	10655.7		1	1229	52.9	1	K.TVDFTQDSNYLLTGGQDK.L
	Hs293FLP_TREX_Ti_104.1	3.3001	0.3785	1798.72	1799.98	5338		1	565	53.1	3	K.SFEAPATINSASLHPEK.E
gi|56549119|ref|	5	6	0.099	866	97652	7.6	U	dynamin 2 isoform 3 [Homo sapiens]				
gi|56549121|ref|	5	6	0.099	870	98064	7.5	U	dynamin 2 isoform 1 [Homo sapiens]				
	HsFLAG-Control_HeLa_NE	4.5386	0.3037	2985.18	2985.29	10809.7		1	1241.8	26.8	1	K.LQDAFSSIGQSCHLDLPQIAVVGGQSAGK.S
	HsFLAG-Control_HeLa_NE	3.9422	0.4425	2093.86	2094.5	7982.5		1	1211.1	55.6	1	R.VYSPHVLNLTLIDLPGITK.V
	HsFLAG-MOCK_300mM_T	2.6045	0.2686	1338.12	1338.51	7841.8		8	493.4	55	1	K.TLNQQLTNHIR.E
	HsFLAG-Control_HeLa_NE	3.6789	0.3978	1622.48	1622.9	4048.4		1	657.7	67.9	2	R.TGLFTPDLAFEAIVK.K
	HsFLAG-Control_HeLa_NE	4.4893	0.2918	1349.35	1349.57	6618.3		1	1459	81.8	1	R.NLVDSYVAIINK.S
gi|18201905|ref|	4	7	0.099	558	63147	8.3	U	glucose phosphate isomerase [Homo sapiens]				

*	Hs293FLP_TREX_Ti_105.2	4.162	0.3554	1603.35	1603.82	6138		1	1023.7	69.2	3	R.VWYVSNIDGTHIAK.T
*	Hs293FLP_TREX_Ti_105.1	2.8339	0.179	1219.45	1219.38	4150.4		1	832.6	80	1	K.HFVALSTNTTK.V
*	HsHeLa3_Ti_105.4384.438	2.8672	0.3245	1704.81	1705.07	6651.6		1	771.2	57.1	1	K.ILLANFLAQTEALMR.G
*	Hs293FLP_TREX_Ti_105.1	3.4316	0.2472	1710.03	1709.94	5756		2	723.7	60.7	2	K.VFEGNRPTNSIVFTK.L
gi|6912478|ref|N	3	9	0.099	536	60030	5	U		karyopherin alpha 6 [Homo sapiens]			
*	HsFLAG-Control_HeLa_S1	5.0836	0.4385	2091.18	2091.46	8310.2		1	1197.8	58.8	4	R.DYVLNCSILNPLLTLLTK.S
	HsFLAG-Control_HeLa_S1	2.9294	0.2836	2340.3	2337.81	8146.2		1	578.2	40	1	R.AQIQAVIDANIFPVLIEILQK.A
	Hs293FLP-MG_Ti_306.280	5.0537	0.1983	1555.66	1552.86	10035.6		1	2847.9	84.6	4	K.IVQVALNGLENILR.L
gi|88951232|ref|X	5	21	0.099	262	28060	8.9	U		PREDICTED: similar to eukaryotic translation elongation factor 1 alpha 1 isoform 27 [Hom			
gi|88951276|ref|X	5	21	0.099	262	28060	8.9	U		PREDICTED: similar to eukaryotic translation elongation factor 1 alpha 1 isoform 50 [Hom			
gi|88951274|ref|X	5	21	0.099	262	28060	8.9	U		PREDICTED: similar to eukaryotic translation elongation factor 1 alpha 1 isoform 49 [Hom			
gi|88951270|ref|X	5	21	0.099	262	28060	8.9	U		PREDICTED: similar to eukaryotic translation elongation factor 1 alpha 1 isoform 47 [Hom			
gi|88951268|ref|X	5	21	0.134	194	20771	9.1	U		PREDICTED: similar to eukaryotic translation elongation factor 1 alpha 1 isoform 46 [Hom			
gi|88951266|ref|X	5	21	0.099	262	28060	8.9	U		PREDICTED: similar to eukaryotic translation elongation factor 1 alpha 1 isoform 45 [Hom			
gi|88951264|ref|X	5	21	0.099	262	28060	8.9	U		PREDICTED: similar to eukaryotic translation elongation factor 1 alpha 1 isoform 44 [Hom			
gi|88951262|ref|X	5	21	0.099	262	28060	8.9	U		PREDICTED: similar to eukaryotic translation elongation factor 1 alpha 1 isoform 43 [Hom			
gi|88951258|ref|X	5	21	0.099	262	28060	8.9	U		PREDICTED: similar to eukaryotic translation elongation factor 1 alpha 1 isoform 41 [Hom			
gi|88951252|ref|X	5	21	0.099	262	28060	8.9	U		PREDICTED: similar to eukaryotic translation elongation factor 1 alpha 1 isoform 38 [Hom			
gi|88951250|ref|X	5	21	0.099	262	28060	8.9	U		PREDICTED: similar to eukaryotic translation elongation factor 1 alpha 1 isoform 37 [Hom			
gi|88951248|ref|X	5	21	0.099	262	28060	8.9	U		PREDICTED: similar to eukaryotic translation elongation factor 1 alpha 1 isoform 36 [Hom			
gi|88951244|ref|X	5	21	0.099	262	28060	8.9	U		PREDICTED: similar to eukaryotic translation elongation factor 1 alpha 1 isoform 34 [Hom			
gi|88951242|ref|X	5	21	0.099	262	28060	8.9	U		PREDICTED: similar to eukaryotic translation elongation factor 1 alpha 1 isoform 33 [Hom			
gi|88951240|ref|X	5	21	0.099	262	28060	8.9	U		PREDICTED: similar to eukaryotic translation elongation factor 1 alpha 1 isoform 32 [Hom			
gi|88951238|ref|X	5	21	0.099	262	28060	8.9	U		PREDICTED: similar to eukaryotic translation elongation factor 1 alpha 1 isoform 31 [Hom			
gi|88951234|ref|X	5	21	0.099	262	28060	8.9	U		PREDICTED: similar to eukaryotic translation elongation factor 1 alpha 1 isoform 29 [Hom			
	Hs293FLP_Ti_306.2670.26	3.2917	0.2924	1342.8	1342.62	4781.3		1	708	75	11	K.PLRLPLQDVYK.I
	HsHeLa_Control_Ti_106.31	3.1476	0.2914	1342.85	1342.62	5204.3		1	841.7	75	4	K.PLRLPLQDVYK.I
	HsHeLa3_Ti_106.2360.236	4.1661	0.2161	1343.33	1342.62	6881.1		1	1536.8	60	2	K.PLRLPLQDVYK.I
	HsGST-MOCK_Ti_102.184	4.1506	0.2292	1343.6	1342.62	6531.1		1	1475	57.5	2	K.PLRLPLQDVYK.I
	HsHeLa3_Ti_103.2430.243	3.7938	0.4396	1755.9	1755.95	7187.6		1	1037.6	57.1	2	K.PMCVESFSDYPPLGR.F
gi|37544743|ref|X	1	3	0.099	101	11741	11.3	U		PREDICTED: similar to 60S ribosomal protein L35 [Homo sapiens]			
gi|89057079|ref|X	1	3	0.074	136	15556	10.6	U		PREDICTED: similar to 60S ribosomal protein L35 [Homo sapiens]			
gi|89050566|ref|X	1	3	0.074	136	15556	10.6	U		PREDICTED: similar to 60S ribosomal protein L35 [Homo sapiens]			
gi|89037172|ref|X	1	3	0.099	101	11741	11.3	U		PREDICTED: similar to 60S ribosomal protein L35 [Homo sapiens]			
gi|6005860|ref|N	1	3	0.081	123	14551	11	U		ribosomal protein L35 [Homo sapiens]			
	Hs293FLP_TREX_Ti_103.1	3.0717	0.1459	1144.44	1144.36	7306		1	1149.6	83.3	3	R.VLTVINQTQK.E
gi|7661744|ref|N	2	11	0.098	419	48162	6.7	U		basic leucine zipper and W2 domains 2 [Homo sapiens]			
*	HsFLAG-Control_HeLa_NE	5.7814	0.484	1960.15	1959.12	7956		1	2839.8	77.8	10	R.DTLVQGLNEAGDDLEAVAK.F
*	HsFLAG-Control_HeLa_S1	2.6974	0.2002	2434.31	2434.84	11354.7		1	635.7	38.1	1	K.QYAPLLAVFSSQGQSELILLQK.V
gi|4557497|ref|N	2	3	0.098	440	47535	6.8	U		C-terminal binding protein 1 isoform 1 [Homo sapiens]			
gi|61743967|ref|N	2	3	0.1	429	46405	6.6	U		C-terminal binding protein 1 isoform 2 [Homo sapiens]			
	Hs293FLP-MG_Ti_203.516	3.8546	0.2794	3517.25	3518.84	6015.1		1	429.9	22.7	2	K.SAGDLGIAVCNVPAASVEETADSTLCHILNLYR.R
	HsFLAG-MOCK_300mM_T	3.0572	0.0847	1057.75	1057.24	7465.3		1	1550.7	88.9	1	K.ALAQALKEGR.I
gi|5730023|ref|N	4	8	0.097	463	51157	5.6	U		RuvB-like 2 [Homo sapiens]			
*	HsHeLa3_Ti_104.1464.146	2.6336	0.3445	1111.62	1112.32	5785.7		1	485.3	59.1	2	R.AVLIAGQPGTGK.T
*	HsHeLa3_Ti_104.1461.146	3.7679	0.2357	1112.52	1112.32	4927.6		2	852.9	72.7	3	R.AVLIAGQPGTGK.T
*	HsFLAG-Control_HeLa_S1	2.9598	0.3216	1684.25	1684.89	8236.7		1	1138.7	63.3	1	R.TQGFLALFSGDTGEIK.S
*	HsHeLa3_Ti_105.2384.238	3.2062	0.4093	1871.07	1870.07	4656.5		1	648.5	56.2	2	R.GTSYQSPHGIPIDLLDR.L
gi|24308093|ref|N	3	6	0.097	463	50526	9.4	U		hypothetical protein LOC26065 [Homo sapiens]			

*	HsFLAG-Control_293_Ti_2	4.5575	0.4344	2101.86	2102.35	7439.5		1	787.5	50	2	R.YEGILYTIDTENSTVALAK.V
*	HsFLAG-Control_MG_293_	3.8295	0.3189	1455.59	1455.65	8263.2		1	1009.9	65.4	1	R.SPVSTRPLPSASQK.A
*	HsFLAG-Control_MG_293_	3.4417	0.413	1489.84	1490.49	5615.3		1	706.5	72.7	3	K.SFFDNISCDDNR.E
gi|22202633|ref|N	1	2	0.097	154	17328	6.3	U		prefoldin 5 isoform alpha [Homo sapiens]			
gi|22202637|ref|N	1	2	0.138	109	12379	6.8	U		prefoldin 5 isoform gamma [Homo sapiens]			
	HsFLAG-Control_HeLa_S1	3.7727	0.3779	1484.96	1485.72	10459		1	957.7	57.1	2	K.IQQLTALGAAQATAK.A
gi|21327701|ref|N	3	11	0.096	592	61830	8	U		TBP-associated factor 15 isoform 1 [Homo sapiens]			
gi|4507353|ref|NI	3	11	0.097	589	61558	8	U		TBP-associated factor 15 isoform 2 [Homo sapiens]			
	HsFLAG-Control_HeLa_NE	4.602	0.3782	3624.43	3624.72	9071.2		1	704.3	22.7	4	R.TDADSESDNSDNNTIFVQGLGEGVSTDQVGEFFK.Q
	HsFLAG-Control_HeLa_S1	3.1093	0.3568	1420.76	1421.5	8011.9		1	1098.8	65.4	3	K.GEATVSFDDPPSAK.A
	HsFLAG-Control_HeLa_NE	2.937	0.2157	1023.19	1023.13	5824.6		1	1015.2	87.5	4	K.AAIDWFDGK.E
gi|56676330|ref|N	3	4	0.096	553	61207	9.7	U		HP1-BP74 [Homo sapiens]			
*	HsHeLa3_Ti_106.2579.257	4.8978	0.4184	1559.85	1559.89	6267.8		1	1522	78.6	2	K.ALPLIVGAQLIHADK.L
*	HsHeLa3_Ti_104.2687.268	3.182	0.4533	1604.7	1602.83	3818.5		1	491.3	64.3	1	K.TIPSWATLSASQLAR.A
*	HsHeLa3_Ti_106.3828.383	3.8208	0.1724	2392.12	2390.86	11401.8		2	1096.1	31.8	1	K.PLLGGSLMEYAILSAIAAMNEPK.T
gi|4885073|ref|NI	1	2	0.096	271	29233	8.4	U		activating transcription factor 1 [Homo sapiens]			
*	HsHeLa3_Ti_103.2583.258	4.0143	0.4203	2679.64	2679.06	4767		1	453	40	2	R.TTPSATSLPQTVVMTSPVTLTSQTTK.T
gi|4505117|ref|NI	1	2	0.095	411	43255	10	U		methyl-CpG binding domain protein 2 isoform 1 [Homo sapiens]			
*	HsHeLa3_Ti_104.4020.402	4.4745	0.3293	3723.27	3722.1	4985.5		1	470.4	21.1	2	K.GLQGVGPGSNDETLLSAVASALHTSSAPITGQVSAAVEK.N
gi|11321601|ref|N	4	7	0.094	784	85596	7.6	U		phosphofructokinase, platelet [Homo sapiens]			
*	HsFLAG-Control_HeLa_S1	3.9443	0.373	2119.78	2120.33	8282.2		1	803.6	45	2	K.EIGWTDVGGWTGQGGSILGTK.R
*	Hs293FLP-MG_Ti_202.386	3.5387	0.2824	2677.58	2678.75	9303.7		1	917.5	42.9	3	R.NESCSENYTTDFIYQLYSEEGK.G
*	HsFLAG-Control_HeLa_S1	3.4535	0.2031	1414.92	1414.69	7277.5		1	935.7	68.2	1	K.RNVIFQPVAELK.K
*	HsFLAG-Control_HeLa_S1	4.1065	0.3746	2104.67	2105.23	4337.9		1	689.3	58.3	1	K.ASYDVSDSGQLEHVQPWSV.-
gi|51093863|ref|N	4	7	0.094	746	84138	6.2	U		hypothetical protein LOC64855 [Homo sapiens]			
*	HsFLAG-Control_HeLa_S1	3.3622	0.2413	1750.67	1749.92	7879.5		1	940.3	60.7	2	R.IVFSGNLFQHQEDSK.K
*	HsFLAG-Control_HeLa_NE	4.1383	0.1429	2334.54	2334.67	6563.4		7	503.4	38.1	2	K.ILTSVDQYLELIGNSLPGTTAK.S
*	HsFLAG-Control_HeLa_S1	3.5187	0.1431	1485.84	1485.85	6768.5		7	694.6	58.3	1	R.EALLQISIPFLLK.K
*	HsFLAG-Control_HeLa_S1	3.3144	0.3531	1968.61	1969.25	7533.5		1	575	44.7	2	K.AAPEASSPPASPLQHLLPGK.A
gi|28557709|ref|N	2	5	0.094	318	34839	6.4	U		phosphoribosyl pyrophosphate synthetase 1-like 1 [Homo sapiens]			
gi|4506127|ref|NI	2	5	0.094	318	34834	7	U		phosphoribosyl pyrophosphate synthetase 1 [Homo sapiens]			
	HsHeLa_Control-MG_Ti_10	3.5118	0.206	1435.57	1434.55	8101.5		7	1235.4	70.8	1	K.IFSGSSHQDLSQK.I
	HsHeLa_Control-MG_Ti_10	4.617	0.2185	1803.17	1803.11	6525		1	1667.7	75	4	R.VYAILTHGIFSGPAISR.I
gi|41149143|ref|X	3	6	0.094	203	23619	10.9	U		PREDICTED: similar to ribosomal protein L13a isoform 1 [Homo sapiens]			
gi|89037072|ref|X	3	6	0.107	178	20680	10.9	U		PREDICTED: similar to ribosomal protein L13a isoform 3 [Homo sapiens]			
gi|89037070|ref|X	3	6	0.094	203	23443	10.8	U		PREDICTED: similar to ribosomal protein L13a isoform 1 [Homo sapiens]			
gi|89037068|ref|X	3	6	0.105	181	21017	10.9	U		PREDICTED: similar to ribosomal protein L13a isoform 2 [Homo sapiens]			
gi|89035384|ref|X	3	6	0.094	203	23299	10.3	U		PREDICTED: similar to ribosomal protein L13a isoform 7 [Homo sapiens]			
gi|89035382|ref|X	3	6	0.094	203	23299	10.3	U		PREDICTED: similar to ribosomal protein L13a isoform 6 [Homo sapiens]			
gi|89035380|ref|X	3	6	0.094	203	23299	10.3	U		PREDICTED: similar to ribosomal protein L13a isoform 5 [Homo sapiens]			
gi|89035378|ref|X	3	6	0.111	171	20142	10.5	U		PREDICTED: similar to ribosomal protein L13a isoform 4 [Homo sapiens]			
gi|89035375|ref|X	3	6	0.105	181	20847	10.4	U		PREDICTED: similar to ribosomal protein L13a isoform 3 [Homo sapiens]			
gi|89035373|ref|X	3	6	0.221	86	10191	10.3	U		PREDICTED: similar to ribosomal protein L13a isoform 2 [Homo sapiens]			
gi|89033544|ref|X	3	6	0.134	142	16773	10.8	U		PREDICTED: similar to ribosomal protein L13a isoform 3 [Homo sapiens]			
gi|89033542|ref|X	3	6	0.105	181	21167	11.1	U		PREDICTED: similar to ribosomal protein L13a isoform 2 [Homo sapiens]			
gi|89033540|ref|X	3	6	0.094	203	23619	10.9	U		PREDICTED: similar to ribosomal protein L13a isoform 1 [Homo sapiens]			
gi|89031570|ref|X	3	6	0.094	203	23619	10.9	U		PREDICTED: similar to ribosomal protein L13a isoform 5 [Homo sapiens]			

gi|89031568|ref|X	3	6	0.134	142	16773	10.8	U		PREDICTED: similar to ribosomal protein L13a isoform 4 [Homo sapiens]			
gi|89031566|ref|X	3	6	0.107	178	20803	10.9	U		PREDICTED: similar to ribosomal protein L13a isoform 3 [Homo sapiens]			
gi|89031563|ref|X	3	6	0.105	181	21167	11.1	U		PREDICTED: similar to ribosomal protein L13a isoform 2 [Homo sapiens]			
gi|6912634|ref|N	3	6	0.094	203	23577	10.9	U		ribosomal protein L13a [Homo sapiens]			
gi|41202038|ref|X	3	6	0.094	203	23299	10.3	U		PREDICTED: similar to ribosomal protein L13a isoform 1 [Homo sapiens]			
	Hs293FLP_TREX_Ti_104.1	2.0082	0.187	939.32	940.09	3739.2		3	444.9	71.4	2	R.LAHEVGWK.Y
	Hs293FLP_TREX_Ti_102.1	2.8214	0.2948	1252.35	1253.4	8080.1		1	709.3	65	2	K.YQAVTATLEEK.R
	Hs293FLP_TREX_Ti_103.1	3.1521	0.3144	1254.43	1253.4	3965.1		1	1007.4	90	2	K.YQAVTATLEEK.R
gi|18104948|ref|N	1	6	0.094	160	18565	10.5	U		ribosomal protein L21 [Homo sapiens]			
gi|89057392|ref|X	1	6	0.094	160	18592	10.2	U		PREDICTED: similar to ribosomal protein L21 isoform 1 [Homo sapiens]			
gi|89042532|ref|X	1	6	0.128	117	13398	10.1	U		PREDICTED: similar to ribosomal protein L21 isoform 1 [Homo sapiens]			
gi|89040203|ref|X	1	6	0.094	160	18593	10.5	U		PREDICTED: similar to ribosomal protein L21 isoform 1 [Homo sapiens]			
gi|89034571|ref|X	1	6	0.094	160	18521	10.5	U		PREDICTED: similar to 60S ribosomal protein L21 [Homo sapiens]			
gi|89031623|ref|X	1	6	0.094	160	18565	10.5	U		PREDICTED: similar to ribosomal protein L21 isoform 1 [Homo sapiens]			
gi|89026818|ref|X	1	6	0.094	160	18595	10.5	U		PREDICTED: similar to 60S ribosomal protein L21 [Homo sapiens]			
gi|89025818|ref|X	1	6	0.094	160	18595	10.5	U		PREDICTED: similar to 60S ribosomal protein L21 [Homo sapiens]			
gi|88952736|ref|X	1	6	0.094	160	18535	10.5	U		PREDICTED: similar to 60S ribosomal protein L21 [Homo sapiens]			
gi|88943726|ref|X	1	6	0.094	160	18535	10.5	U		PREDICTED: similar to 60S ribosomal protein L21 [Homo sapiens]			
gi|51466076|ref|X	1	6	0.094	160	18595	10.5	U		PREDICTED: similar to 60S ribosomal protein L21 [Homo sapiens]			
gi|41200850|ref|X	1	6	0.094	160	18521	10.5	U		PREDICTED: similar to 60S ribosomal protein L21 [Homo sapiens]			
gi|41150972|ref|X	1	6	0.094	160	18592	10.2	U		PREDICTED: similar to ribosomal protein L21 isoform 1 [Homo sapiens]			
	Hs293FLP_TREX_Ti_106.2	5.4706	0.3631	1641.57	1641.91	7689.9		1	2235.5	78.6	6	R.VYNVTQHAVGIVVNK.Q
gi|42542379|ref|N	5	9	0.093	904	102335	11.8	U		serine/arginine repetitive matrix 1 [Homo sapiens]			
*	Hs293FLP-MG_Ti_205.265	3.3765	0.1373	1439.77	1440.77	8182.1		3	1082.6	72.7	2	K.VNLEVIKPWITK.R
*	Hs293FLP-MG_Ti_202.213	2.9095	0.338	1605.7	1605.74	6940.6		2	544.7	50	1	K.EPSVQEATSTSDILK.V
*	Hs293FLP_Ti_306.1975.19	3.2735	0.3247	1223.53	1222.39	5825.4		3	628.1	70	3	K.RESPSPAPKPR.K
*	HsHeLa_Control-MG_Ti_20	3.2833	0.3081	1224.72	1224.36	5423.6		1	680.8	72.7	2	R.APQTSSSPPPVR.R
*	Hs293FLP-MG_Ti_202.407	4.0261	0.1468	3117.34	3116.54	6980.9		1	860.4	25.8	1	K.AVAAAAAAAVTPAAIAAATTTLAQEEPVAAPEPK.K
gi|4508047|ref|N	4	6	0.093	572	61277	6.7	U		zyxin [Homo sapiens]			
gi|58530845|ref|N	4	6	0.093	572	61277	6.7	U		zyxin [Homo sapiens]			
	HsHeLa3_Ti_105.1100.110	2.1549	0.3396	1076.74	1077.23	6559.5		5	397.8	50	1	R.GPPASSPAPAPK.F
	HsHeLa_Control-MG_Ti_20	2.639	0.3169	1516.45	1516.61	3971.7		2	312.3	53.3	2	K.FSPGAPGGSGSQPNQK.L
	HsHeLa_Control-MG_Ti_20	4.2708	0.2946	2597.85	2598.83	7212.3		1	1317.6	37.5	2	K.LGHPEALSAGTGSPQPPSFTYAQQR.E
	HsFLAG-Control_Hela_Ti_1	2.7854	0.1973	2599.91	2598.83	11079.1		1	613.8	33.3	1	K.LGHPEALSAGTGSPQPPSFTYAQQR.E
gi|4503765|ref|N	5	10	0.092	632	71175	7.4	U		fragile X mental retardation 1 [Homo sapiens]			
*	Hs293FLP_TREX_Ti_104.1	2.7158	0.1747	1198.35	1198.41	4598.7		1	773.9	77.8	2	K.IKLDVPEDLR.Q
*	Hs293FLP_TREX_Ti_105.1	2.5106	0.1804	1075.36	1076.24	7323.1		2	556.4	71.4	1	R.FHEQFIVR.E
*	Hs293FLP_TREX_Ti_103.1	3.0298	0.1665	1088.24	1088.21	6847.6		4	923.7	81.2	1	R.VRIEAENEK.N
*	Hs293FLP_TREX_Ti_103.1	3.7532	0.3236	1479.32	1477.53	7569.3		1	1301.9	79.2	2	K.ENSTHFSQPNSTK.V
*	Hs293FLP_TREX_Ti_105.1	5.0958	0.4143	1842.52	1842.14	7050.9		1	1760	70.6	4	R.VLVASSVVAGESQKPELK.A
gi|8659574|ref|N	4	7	0.092	575	61521	5.6	U		transcription factor binding to IGHM enhancer 3 [Homo sapiens]			
*	HsHeLa3_Ti_104.2299.229	4.5652	0.4722	2515.85	2516.77	3888.6		1	624	46.2	2	R.SSLPISLQATPATPATLSASSSAGGSR.T
*	HsHeLa3_Ti_105.1272.127	2.243	0.1893	1194.56	1195.32	7058.6		8	418.7	61.1	2	K.VQTHLENPTR.Y
*	HsHeLa3_Ti_105.1286.128	2.8853	0.2648	1196.66	1195.32	8577.1		2	1249	83.3	1	K.VQTHLENPTR.Y
*	HsHeLa3_Ti_102.2011.201	4.4611	0.3894	1530.71	1529.73	5993.4		1	1320.6	73.3	2	R.AASDPLLSSVSPAVSK.A
gi|24797086|ref|N	6	12	0.091	1115	125545	4.9	U		RAN binding protein 5 [Homo sapiens]			
*	HsFLAG-Control_HeLa_S1	3.4409	0.2846	1843.9	1842.96	7125.7		1	824	60	2	R.NLIDEDGNNQWPEGLK.F
*	HsFLAG-Control_HeLa_S1	4.3402	0.4261	1571.23	1569.76	6209.4		1	979	69.2	5	K.FLFDSVSSQNVGLR.E

*	HsFLAG-Control_HeLa_S1	4.0526	0.1947	3087.41	3087.51	10489.9		1	927.9	28	1	R.EAALHIFWNFPGIFGNQQQHYLDVIK.R
*	HsFLAG-Control_HeLa_S1	4.2314	0.3061	1830.68	1831.13	7357.8		1	988.6	53.1	2	R.ATAAFILANEHNVALFK.H
*	HsFLAG-Control_HeLa_S1	3.0789	0.3771	2104.24	2103.38	10318.9		1	656.6	39.5	1	K.LVLEQVVTSIASVADTAEEK.F
*	HsFLAG-Control_HeLa_S1	2.1634	0.2185	1037.72	1038.19	6121.9		9	404.5	62.5	1	K.HIVENAVQK.E
gi|27501446|ref|N	1	2	0.091	198	22092	5.3	U	density-regulated protein [Homo sapiens]				
*	HsHeLa3_Ti_102.1259.125	3.7731	0.3368	1850.45	1849.86	6244.3		1	680.6	52.9	2	K.QEAGISEGQGTAGEEEEK.K
gi|4507149|ref|N	1	4	0.091	154	15936	6.1	U	superoxide dismutase 1, soluble [Homo sapiens]				
*	Hs293FLP_TREX_Ti_102.2	3.8877	0.3597	1501.81	1502.67	6118.4		4	980	65.4	4	K.GDGPVQGIINFEQK.E
gi|16418385|ref|N	1	2	0.09	212	22741	9.7	U	mediator of RNA polymerase II transcription subunit MED8 isoform 2 [Homo sapiens]				
gi|WM4	1	2	0.065	291	31872	5.4	U	MEDIATOR_Med8 (WT) [Homo sapiens]				
gi|Med8_S82D	1	2	0.065	291	31900	5.3	U	MEDIATOR_Med8 S82D Mutant [Homo sapiens]				
gi|Med8_S82A	1	2	0.065	291	31856	5.4	U	MEDIATOR_Med8 S82A Mutant [Homo sapiens]				
gi|MM1	1	2	0.065	291	31900	5.4	U	MEDIATOR_Med8 (BC box L166P-C170F double mutant) [Homo sapiens]				
gi|LP1	1	2	0.065	291	31830	5.4	U	MEDIATOR_Med8 (BC box L166A single mutant) [Homo sapiens]				
gi|48762706|ref|N	1	2	0.071	268	29080	7.5	U	mediator of RNA polymerase II transcription subunit MED8 isoform 4 [Homo sapiens]				
gi|48762704|ref|N	1	2	0.106	179	19002	9.1	U	mediator of RNA polymerase II transcription subunit MED8 isoform 1 [Homo sapiens]				
gi|48762702|ref|N	1	2	0.063	301	32819	9.1	U	mediator of RNA polymerase II transcription subunit MED8 isoform 3 [Homo sapiens]				
gi|42490747|ref|N	1	2	0.106	179	19002	9.1	U	mediator of RNA polymerase II transcription subunit MED8 isoform 1 [Homo sapiens]				
gi|21717644|gb|A	1	2	0.071	268	29080	7.5	U	MEDIATOR_MED8 {mediator of RNA polymerase II transcription subunit MED8} [Homo s				
	HsFLAG-Control_HeLa_NE	4.3625	0.5082	1966.56	1966.2	7636.7		1	866.8	52.8	2	K.QTFNPTDTNALVAAVAFGK.G
gi|4507357|ref|N	1	5	0.09	199	22391	8.2	U	transgelin 2 [Homo sapiens]				
gi|89028870|ref|X	1	5	0.14	129	14618	5.5	U	PREDICTED: similar to Transgelin-2 [Homo sapiens]				
gi|89028241|ref|X	1	5	0.14	129	14618	5.5	U	PREDICTED: similar to Transgelin-2 [Homo sapiens]				
	Hs293FLP_Ti_302.3943.39	4.0285	0.3719	2103.74	2101.32	5927.8		1	746.1	55.9	5	R.YGINTTDIFQTVDLWEGK.N
gi|41393554|ref|N	5	10	0.089	371	43728	9.9	U	LUC7-like isoform b [Homo sapiens]				
gi|8922297|ref|N	5	10	0.102	325	38405	10	U	LUC7-like isoform a [Homo sapiens]				
	Hs293FLP_Ti_303.1279.12	2.8366	0.2292	1167.66	1168.29	4978		1	557.6	66.7	1	K.VHELNEEIGK.L
	HsHeLa_Control-MG_Ti_20	2.9432	0.147	1168.12	1168.29	5296.9		1	676.8	77.8	1	K.VHELNEEIGK.L
	Hs293FLP_Ti_303.1278.12	3.1115	0.1986	1170.57	1168.29	4706.3		1	711	83.3	1	K.VHELNEEIGK.L
	HsHeLa_Control_Ti_102.10	3.6501	0.2978	1578.35	1575.63	7585.8		1	1320.6	71.4	4	K.AEQLGAEGNVDESQK.I
	HsHeLa_Control-MG_Ti_10	1.9477	0.1266	844.78	844.946	3744.8		1	350.9	64.3	3	R.LADHFGGK.L
gi|4506133|ref|N	2	4	0.089	369	40926	7.4	U	phosphoribosyl pyrophosphate synthetase-associated protein 2 [Homo sapiens]				
*	HsHeLa_Control-MG_Ti_10	4.1299	0.1403	2082.97	2083.35	3443.2		3	598.1	56.2	2	R.ASPFLLQYIQEEIPDYR.N
*	HsHeLa_Control-MG_Ti_10	3.9264	0.3904	1717.3	1716.01	5671.6		1	841.1	63.3	2	K.IFVMATHGLLSSDAPR.R
gi|4504035|ref|N	3	6	0.088	693	76715	6.9	U	guanine monophosphate synthetase [Homo sapiens]				
*	HsFLAG-Control_HeLa_NE	4.1261	0.4107	2179.78	2180.55	5649.3		1	670.9	52.8	3	R.ELFVQSEIFPLETPAFAIK.E
*	HsGST-MOCK_Ti_103.125	3.1643	0.1185	1404.67	1404.56	9299.4		6	841.3	68.2	1	R.KRESQSVEEALK.K
*	HsFLAG-Control_HeLa_S1	4.5022	0.3609	3247.75	3246.81	9158.6		1	755.6	25	2	R.VVYIFGPPVKEPPTDVTPTFLTTGVLSTLR.Q
gi|4504901|ref|N	2	3	0.088	521	57887	5	U	karyopherin alpha 4 [Homo sapiens]				
*	HsFLAG-Control_HeLa_NE	4.2584	0.2927	3014.98	3014.28	11991.7		1	1045.2	26.8	1	R.VQNTSLEAIVQNASSDNQGIQLSAVQAAR.K
*	Hs293FLP-MG_Ti_306.324	4.3078	0.2327	1812.49	1812.12	7584.7		1	1820.7	68.8	2	K.DAQVVQVVLDGLSNILK.M
gi|57527756|ref|N	3	8	0.088	454	51103	5.9	U	odorant response abnormal 4 [Homo sapiens]				
*	HsFLAG-Control_MG_293_	5.094	0.3807	1594.88	1595.8	7301.2		1	1167.7	67.9	6	K.AFVSGLLIGQCSSQK.D
*	HsHeLa_Control-MG_Ti_20	3.1661	0.3411	1420.45	1420.48	5013.8		1	893.3	70.8	1	R.GNTQATSHSFDVR.V
*	HsHeLa_Control-MG_Ti_20	2.997	0.1827	1411.7	1409.63	10693		1	1466.5	72.7	1	R.VLTQLLLNSDHR.S
gi|4557663|ref|N	2	6	0.088	339	39222	5.4	U	immunoglobulin binding protein 1 [Homo sapiens]				
*	HsFLAG-Control_HeLa_S1	4.3824	0.2596	1478.06	1477.57	8756.3		1	2429.8	87.5	5	R.NEDLEEIASTDLK.Y
	HsFLAG-Control_HeLa_S1	4.0416	0.3672	2063.65	2061.29	11506.7		1	1153.9	56.2	1	R.WIDISLEEIESIDQEIK.I
gi|13027644|ref|N	2	2	0.088	240	24614	11.2	U	small nuclear ribonucleoprotein polypeptide N [Homo sapiens]				

gi|4507135|ref|N		2	2	0.088	240	24614	11.2	U		small nuclear ribonucleoprotein polypeptide N [Homo sapiens]			
gi|4507125|ref|N		2	2	0.091	231	23656	10.9	U		small nuclear ribonucleoprotein polypeptide B/B' isoform B [Homo sapiens]			
gi|38150007|ref|N		2	2	0.088	240	24610	11.2	U		small nuclear ribonucleoprotein polypeptide B/B' isoform B' [Homo sapiens]			
gi|13027650|ref|N		2	2	0.088	240	24614	11.2	U		small nuclear ribonucleoprotein polypeptide N [Homo sapiens]			
gi|13027648|ref|N		2	2	0.088	240	24614	11.2	U		small nuclear ribonucleoprotein polypeptide N [Homo sapiens]			
gi|13027646|ref|N		2	2	0.088	240	24614	11.2	U		small nuclear ribonucleoprotein polypeptide N [Homo sapiens]			
	HsFLAG-MOCK_300mM_T		3.5787	0.2807	1724.48	1723.87	5651		5	789.2	66.7	1	K.HMNLILCDCDEFR.K
	Hs293FLP_TREX_Ti_106.2		3.19	0.0979	883.31	883.166	3985.4		3	898.1	92.9	1	R.VLGLVLLR.G
gi|21361794|ref|N		8	20	0.085	1230	136375	5.8	U		TIP120 protein [Homo sapiens]			
*	HsFLAG-Control_HeLa_S1		3.7805	0.3154	2047.35	2048.35	6164.5		1	757.3	52.9	4	K.VIRPLDQPSSFDATPYIK.D
*	HsFLAG-Control_HeLa_S1		3.5762	0.1391	2049.78	2048.35	10857.6		2	1127.2	36.8	1	K.VIRPLDQPSSFDATPYIK.D
*	HsFLAG-Control_MG_293_		3.5793	0.1971	1084.38	1084.35	7870.9		1	1465.6	80	2	K.ALTLIAGSPLK.I
*	HsHeLa3_Ti_104.2157.215		2.4669	0.2012	1084.64	1084.35	4401.6		1	308.5	65	2	K.ALTLIAGSPLK.I
*	HsHeLa3_Ti_104.4347.434		5.0224	0.2699	1484.75	1484.78	6569.5		1	1514.8	80.8	2	K.ISGSILNELIGLVR.S
*	HsFLAG-Control_HeLa_S1		5.3632	0.4071	3281.89	3281.73	8884.7		1	1152.5	28.3	2	K.SAASYALGSISVGNLPEYLPFVLQEITSQPK.R
*	HsFLAG-Control_HeLa_S1		2.6307	0.2115	1939.51	1939.27	10510.4		2	529.1	41.2	1	R.VALVTFNSAAHNKPSLIR.D
*	HsFLAG-Control_MG_293_		3.7971	0.2705	1328.17	1326.58	6453.3		7	915.1	70.8	6	R.AVAALLTIPEAEK.S
gi|14702169|ref|N		3	29	0.085	516	57371	7.5	U		plasminogen activator, tissue type isoform 3 precursor [Homo sapiens]			
gi|4505861|ref|N		3	29	0.078	562	62917	7.8	U		plasminogen activator, tissue type isoform 1 preproprotein [Homo sapiens]			
	Hs283FLP_Ti_103.1571.15		5.1155	0.4286	1618.68	1618.83	5099.4		1	1424.8	80	9	K.VYTAQNPSAQALGLGK.H
	HsFLAG-MOCK_150mM_T		5.4732	0.3467	2030.74	2029.17	7621.3		1	1708.6	71.9	16	K.EFDDDTYDNDIALLQLK.S
	Hs283FLP_Ti_104.1529.15		3.296	0.2476	1336.68	1336.45	4606.8		1	849.3	80	4	K.HEALSPFYSER.L
gi|6598323|ref|N		2	15	0.085	445	50663	6.5	U		GDP dissociation inhibitor 2 [Homo sapiens]			
*	HsHeLa3_Ti_103.4651.465		3.6292	0.4274	1981.07	1981.27	6432.6		1	944.7	55.6	1	K.VPSTEAEALASSLMGLFEK.R
	HsF-IP-293_Ti_206.2734.27		5.4817	0.4503	2142.55	2142.46	4270.1		1	1265.1	72.2	14	K.SPYLYPLYGLGELPQGFAR.L
gi|7661920|ref|N		2	16	0.085	411	46871	6.7	U		DEAD (Asp-Glu-Ala-Asp) box polypeptide 48 [Homo sapiens]			
	HsFLAG-Control_HeLa_NE		4.3475	0.477	1828.66	1829.07	5470.9		1	956.4	66.7	13	R.GIYAYGFEKPSAIQQR.A
*	HsFLAG-Control_HeLa_NE		4.6352	0.3398	2140.59	2141.43	8355.3		1	1132.1	52.8	3	R.GLDVPQVSLIINYDLPNNR.E
gi|16117787|ref|N		1	2	0.085	117	13293	11.5	U		ribosomal protein L34 [Homo sapiens]			
gi|89036972|ref|X		1	2	0.08	125	14515	11.4	U		PREDICTED: similar to ribosomal protein L34 [Homo sapiens]			
gi|89036654|ref|X		1	2	0.185	54	6255	10.9	U		PREDICTED: similar to ribosomal protein L34 [Homo sapiens]			
gi|16117789|ref|N		1	2	0.085	117	13293	11.5	U		ribosomal protein L34 [Homo sapiens]			
	Hs293FLP_TREX_Ti_105.1		2.7934	0.1153	1154.47	1154.27	6736.8		2	925.4	77.8	2	R.RLSYNTASNK.T
gi|4501955|ref|N		6	13	0.084	1014	113135	8.9	U		poly (ADP-ribose) polymerase family, member 1 [Homo sapiens]			
*	HsFLAG-MOCK_300mM_T		2.641	0.2797	1518.03	1517.64	6375.6		5	565.4	53.8	1	K.RKGDEVDGVDEVAK.K
*	HsFLAG-Control_HeLa_NE		4.5279	0.4527	1626.42	1625.77	8552.4		1	1614.3	71.4	3	R.VVSEDFLQDVSASTK.S
*	HsHeLa3_Ti_106.3211.321		4.7637	0.385	2141.53	2139.5	8082.5		1	1448.2	58.3	1	K.SLQELFLAHILSPWGAEVK.A
*	HsFLAG-MOCK_300mM_T		5.269	0.4014	3187.55	3187.71	7744.3		1	1316.4	31.2	3	K.SLQELFLAHILSPWGAEVKAEPVEVVAPR.G
*	HsFLAG-Control_HeLa_NE		3.6979	0.313	1497.57	1495.72	7590.1		1	902	65.4	2	K.KPPLLNNADSVQAK.V
*	HsFLAG-Control_HeLa_NE		4.3031	0.4379	1378.21	1378.57	7118.4		1	1449.6	79.2	3	R.TTNFAGILSQGLR.I
gi|20149598|ref|N		1	2	0.084	287	31282	9.5	U		solute carrier family 25 (mitochondrial carrier; dicarboxylate transporter), member 10 [Hom			
*	HsFLAG-Control_293_Ti_1		4.2424	0.4268	2300.66	2299.68	8676.2		1	862.5	43.5	2	K.VLLGSVSGLAGGFVGTPADLVNVR.M
gi|21237802|ref|N		6	8	0.083	1105	122721	5.8	U		SWI/SNF-related matrix-associated actin-dependent regulator of chromatin c1 [Homo sap			
*	HsHeLa3_Ti_103.2356.235		3.1964	0.2631	1781.13	1780.93	7535.3		1	1130.1	64.3	1	K.FWESPETVSQLDSVR.V
*	HsHeLa3_Ti_105.5166.516		5.3508	0.3779	2079.05	2078.42	9016.1		1	1853	61.1	2	K.TLAGLVVQLLQFQEDAFGK.H
*	HsHeLa3_Ti_106.2704.270		4.1818	0.2695	2613.55	2615.01	4303.6		1	449.2	45.2	1	K.TLVQNNCLTRPNIYLIPDIDLK.L
	HsHeLa3_Ti_103.1911.191		2.5713	0.3068	1553.68	1553.68	3453.2		1	333	62.5	1	R.LNPQEYLTSTACR.R
	HsHeLa3_Ti_104.2471.247		3.7585	0.261	1433.7	1432.59	6393.3		1	1149	80	1	R.TQDECILHFLR.L
	HsHeLa3_Ti_105.3182.318		3.4996	0.1814	1333.68	1332.64	6963.5		1	1092.7	72.7	2	K.SLVALLVETQMK.K

gi|13699868|ref|N	4	4	0.083	935	101531	7.2	U	methylenetetrahydrofolate dehydrogenase 1 [Homo sapiens]				
*	Hs293FLP-MG_Ti_203.446	3.7734	0.261	4302.21	4302.74	11348.7		1	827.5	19.7	1	K.YITSLNEDSTVHGFLVQLPLDSENSINTEEVINAIAPEK.D
*	HsFLAG-Control_MG_293_	3.8475	0.3875	1631.71	1631.91	7371.7		1	1187.4	63.3	1	K.YVVVTGITPTPLGEGK.S
*	HsFLAG-Control_293_Ti_2	3.9385	0.2652	1097.64	1098.29	8215		1	1875.2	85	1	K.GALALAQAVQR.A
*	HsGST-MOCK_Ti_104.126	2.8019	0.104	1391.2	1391.53	9959.2		1	784	59.1	1	K.THLSLSHNPEQK.G
gi|89034039|ref|X	3	4	0.083	747	85105	4.9	U	PREDICTED: similar to heterogeneous nuclear ribonucleoprotein U [Homo sapiens]				
gi|89034820|ref|X	3	4	0.069	904	101753	5.4	U	PREDICTED: similar to heterogeneous nuclear ribonucleoprotein U [Homo sapiens]				
	HsHeLa_Control-MG_Ti_20	4.723	0.3876	3932.16	3932.39	8144.6		1	925.4	25.8	2	K.NCVVELNFGQKEEPFFPPPEEFVFIHAVPVEER.V
	HsFlag1P_Ti_103.2987.29	2.9094	0.2917	1609.37	1608.85	9675.2		1	948.6	61.5	1	R.YNVLGAETVLNQMR.M
	HsGST-MOCK_Ti_305.201	4.7112	0.3938	1733.66	1733.93	10768.6		1	2558.6	78.6	1	K.SRDLLVQQASQCLSK.L
gi|5031677|ref|N	3	5	0.083	699	78061	6.7	U	dynamin 1-like protein isoform 3 [Homo sapiens]				
gi|6996007|ref|N	3	5	0.082	710	79456	6.9	U	dynamin 1-like protein isoform 2 [Homo sapiens]				
gi|6996005|ref|N	3	5	0.079	736	81891	6.8	U	dynamin 1-like protein isoform 1 [Homo sapiens]				
	HsFLAG-Control_HeLa_S1	4.4319	0.479	2437.89	2438.7	9416.6		1	1497.8	54.8	2	R.INVLAAQYQSLLNSYGEPVDDK.S
	HsFLAG-Control_HeLa_NE	5.4745	0.4867	2211.6	2212.55	9695.5		1	1720.4	60	2	R.TLESVDPLGGLNTIDILTAIR.N
	HsFLAG-Control_HeLa_S1	4.2475	0.4259	1557.39	1557.84	5940.3		1	739.6	64.3	1	K.GHAVNLLDVPVPVAR.K
gi|58761486|ref|N	6	21	0.083	544	60463	6.5	U	chaperonin containing TCP1, subunit 3 isoform b [Homo sapiens]				
gi|63162572|ref|N	6	21	0.083	545	60534	6.5	U	chaperonin containing TCP1, subunit 3 isoform a [Homo sapiens]				
	Hs293FLP_TREX_Ti_104.1	2.2961	0.1026	1120.5	1121.28	3931.9		6	264.6	61.1	1	R.EIQVQHPAAK.S
	HsFLAG-Control_HeLa_NE	2.8479	0.207	1120.68	1121.28	5081.4		2	544.8	72.2	2	R.EIQVQHPAAK.S
	HsFLAG-Control_HeLa_S1	2.9787	0.1096	1121.72	1121.28	7302		1	829.2	77.8	3	R.EIQVQHPAAK.S
	HsFLAG-Control_HeLa_S1	3.5163	0.1443	1431.36	1429.62	6655.5		1	954.9	70.8	4	K.IPGGIIEDSCVLR.G
	HsFLAG-Control_HeLa_S1	4.196	0.2605	1167.39	1167.39	7385.7		2	1954.6	90	10	R.AVAQALEVIPR.T
	HsFLAG-Control_MG_293_	2.9597	0.1284	1187.73	1186.44	11238.3		1	1627.4	80	1	K.TAVETAVLLLR.I
gi|15149476|ref|N	3	7	0.082	660	75379	6.7	U	arginyl-tRNA synthetase [Homo sapiens]				
*	HsFLAG-Control_HeLa_S1	3.7339	0.3463	2153.72	2153.44	6359		1	982.6	52.6	3	K.AAYPDLENPPLLVTPSQQAK.F
*	HsFLAG-Control_HeLa_S1	2.8322	0.2124	2200.59	2200.54	6792.9		1	455.6	41.7	1	K.FPDYLTVSPPIGDLQVFYK.E
*	HsFLAG-Control_293_Ti_1	3.5265	0.321	1643.4	1644.02	2855.3		1	926.6	78.6	3	K.IVFVPGCSIPLTIVK.S
gi|11968003|ref|N	2	4	0.082	392	44935	6.6	U	5-azacytidine induced 2 [Homo sapiens]				
*	Hs293FLP_Ti_304.1445.14	4.0811	0.3709	1584	1583.75	6824		1	919.1	60.7	3	K.ALCHTTSSPLPGDVK.V
*	Hs293FLP_Ti_303.1433.14	3.2012	0.3763	1956.74	1956	3467.6		1	292	50	1	R.SIPNDGTCFQEHSSYGR.N
gi|32189380|ref|N	4	13	0.082	380	42151	5.6	U	nucleoporin 43kDa [Homo sapiens]				
gi|38605733|ref|N	4	13	0.082	380	42151	5.6	U	nucleoporin 43kDa [Homo sapiens]				
	HsFLAG-Control_HeLa_NE	5.0199	0.4905	1862.41	1862.05	8213.9		1	1457.1	62.5	6	R.TIDNADSSTLHAVTFLR.T
	HsFLAG-MOCK_300mM_T	4.6247	0.4296	3357.46	3356.8	8247.1		1	1186.1	28.3	1	R.TIDNADSSTLHAVTFLRTPEILTVNSIGQLK.I
	HsFLAG-Control_HeLa_NE	3.1638	0.4179	1512.72	1513.78	5929		1	496	61.5	2	R.TPEILTVNSIGQLK.I
	HsFLAG-Control_HeLa_NE	3.9637	0.3671	1513.02	1513.78	7659.5		1	948.9	65.4	4	R.TPEILTVNSIGQLK.I
gi|4885063|ref|N	2	4	0.082	364	39456	6.9	U	fructose-bisphosphate aldolase C [Homo sapiens]				
*	HsHeLa3_Ti_103.2146.214	4.0318	0.1664	2273.72	2274.45	4600.5		1	432	45.5	2	K.GVVPLAGTDGETTTQGLDGLSER.C
	HsHeLa3_Ti_103.1446.144	2.1033	0.1778	763.77	763.955	6992.1		2	713.3	75	2	K.VLAAVYK.A
gi|35493987|ref|N	4	6	0.082	158	18007	8.7	U	ubiquitin-conjugating enzyme E2I [Homo sapiens]				
gi|4507785|ref|N	4	6	0.082	158	18007	8.7	U	ubiquitin-conjugating enzyme E2I [Homo sapiens]				
gi|35494003|ref|N	4	6	0.082	158	18007	8.7	U	ubiquitin-conjugating enzyme E2I [Homo sapiens]				
gi|35493996|ref|N	4	6	0.082	158	18007	8.7	U	ubiquitin-conjugating enzyme E2I [Homo sapiens]				
	HsFLAG-MOCK_300mM_T	3.7213	0.344	1444.26	1443.69	4589.7		1	740.7	75	2	R.KDHPFGFVAVPTK.N
	HsHeLa3_Ti_105.2036.203	2.1339	0.3223	1314.58	1315.51	3497.4		1	405.8	63.6	1	K.DHPFGFVAVPTK.N
	HsGST-MOCK_Ti_405.234	2.2882	0.1911	1315.53	1315.51	3335		4	327.8	59.1	1	K.DHPFGFVAVPTK.N
	HsHeLa3_Ti_105.2035.203	2.96	0.3667	1315.7	1315.51	3483.2		1	566.8	72.7	2	K.DHPFGFVAVPTK.N

gi|40254898|ref|N		6	12	0.081	1165	130277	7.8	U		hypothetical protein LOC54790 [Homo sapiens]			
*	HsFlag1P_Ti_102.1975.197	5.655	0.4745	2414.59	2415.46	7608.6			1	989.5	47.8	1	K.LASGEEFCSGSSSNLQAPGGSSER.Y
*	HsHeLa_Control-MG_Ti_10	2.9576	0.3319	2424.07	2424.59	4882.5			1	451.4	44.7	1	K.NKEEILQTFPHPQSNNDQQR.E
*	HsFlag1P_Ti_105.2681.268	2.7248	0.2163	1329.66	1329.55	7073.1			1	1001.6	75	2	K.SIIETMEQHLK.Q
*	Hs293FLP-MG_Ti_103.162	3.7288	0.3712	2473.97	2474.6	5045.2			1	410.7	40.9	1	R.QTTAAELDSHTPALEQQTTSSEK.T
*	HsHeLa_Control_Ti_106.31	4.8952	0.3221	1736.8	1734.95	5655.3			1	1639.4	80	6	K.RTAASVLNNFIESPSK.L
*	HsFlag1P_Ti_103.2781.278	3.4165	0.2424	1578.13	1578.76	6943.8			1	987.3	60.7	1	R.TAASVLNNFIESPSK.L
gi|24308127|ref|N		4	8	0.081	793	91080	7.2	U		DnaJ (Hsp40) homolog, subfamily C, member 10 [Homo sapiens]			
*	HsHeLa_Control-MG_Ti_20	3.1486	0.2846	1438.32	1438.54	7253.2			1	757	66.7	1	K.NPNNPNAHGDFLK.I
*	HsFLAG-Control_293_Ti_2	3.8774	0.4579	2075.94	2075.24	6976.1			1	920	59.4	2	R.YDFGIYDDDPEIITLER.R
*	HsFLAG-Control_293_Ti_2	3.3401	0.1685	1336.29	1335.54	9838.7			3	1231.8	72.7	1	K.NSILFLNSLDAK.E
*	HsFLAG-Control_293_Ti_2	4.1403	0.259	2465.51	2465.81	5535.4			1	541	42.9	4	R.IWGLGFLPQVSTDLTPQTFSEK.V
gi|4502801|ref|NI		2	2	0.081	421	44969	7.5	U		regulator of chromosome condensation 1 [Homo sapiens]			
*	HsHeLa3_Ti_103.2715.271	2.6525	0.2545	1639.82	1639.01	7515.7			2	751.5	57.1	1	K.SMVPVQVQLDVPVVK.V
*	HsHeLa3_Ti_105.2023.202	2.7806	0.2671	1839.68	1838.08	6009.9			1	413.4	41.7	1	R.LPAVSSVACGASVGYAVTK.D
gi|14150147|ref|N		1	2	0.081	211	23338	8.9	U		syndesmos [Homo sapiens]			
*	HsFLAG-MOCK_300mM_T	3.15	0.4962	1756.25	1757	6663			1	714.1	56.2	2	R.VGGFPNFLSNAFVSTAK.C
gi|4503297|ref|NI		6	9	0.08	1279	142069	6.6	U		DEAH (Asp-Glu-Ala-His) box polypeptide 9 isoform 1 [Homo sapiens]			
*	Hs293FLP_TREX_Ti_102.2	2.7751	0.1767	1026.09	1026.18	5912.3			2	1059.9	92.9	1	R.DFVNYLVR.I
*	Hs293FLP_TREX_Ti_103.1	3.3973	0.3654	1289.21	1289.48	6302.8			1	1251	77.3	1	K.LAAQSCALSLVR.Q
*	Hs293FLP-MG_Ti_206.028	4.1024	0.2963	4329.45	4329.94	6369.7			2	466.1	20.4	1	K.VNLSQDLEHQLQNIIQELNLEILPPPEDPSVPVALNIGK.L
*	HsHeLa_Control-MG_Ti_20	3.4244	0.2824	2051.25	2051.26	5498.6			1	628.4	59.4	4	K.TTQVPQFILDDFIQNDR.A
*	HsFLAG-Control_HeLa_NE	2.9093	0.1242	1088.14	1088.25	7477.5			1	1086.7	83.3	1	R.RISAVSVAER.V
*	Hs293FLP-MG_Ti_202.283	3.9397	0.251	1742.61	1742.88	6773.9			1	1576.1	70	1	R.ELDALDANDELTPLGR.I
gi|4505621|ref|NI		1	2	0.08	187	21057	7.5	U		prostatic binding protein [Homo sapiens]			
*	Hs293FLP_TREX_Ti_105.2	3.0242	0.3376	1689.19	1689.95	5086.1			1	717	64.3	2	K.LYTLVLTDPDAPSRK.D
gi|15187164|ref|N		1	2	0.08	138	14246	5.5	U		lacritin precursor [Homo sapiens]			
*	HsFlag1P_Ti_103.2350.235	3.5288	0.1826	1187.24	1187.42	6501.6			2	1527.1	85	2	K.SILLTEQALAK.A
gi|61837501|ref|N		3	4	0.079	781	82893	5.6	U		sine oculis homeobox homolog 4 [Homo sapiens]			
*	HsHeLa3_Ti_104.3451.345	2.8802	0.1714	1476.75	1475.73	3279.8			1	594.8	77.3	1	R.FLWSLPQSDLLR.G
*	HsHeLa3_Ti_102.3262.326	3.7403	0.4786	2485.52	2485.78	8049.8			1	736.2	41.3	2	K.MSSNIVSNGISMTDILGSTSQDVK.E
*	HsHeLa3_Ti_104.3157.316	3.4384	0.2235	2636.72	2637.05	4197.4			1	331.2	36	1	K.VFLSSLAPSAVVYTVPNTGQTIGSVK.Q
gi|24432016|ref|N		2	6	0.079	471	52050	8	U		pre-mRNA cleavage factor I, 59 kDa subunit [Homo sapiens]			
*	HsHeLa3_Ti_104.2313.231	3.005	0.2277	1355.41	1355.58	5001.2			5	656.7	63.6	1	K.TPAILYTYSGLR.N
*	HsHeLa3_Ti_105.5110.511	5.3394	0.4581	2437.88	2437.75	6636.8			1	1459.6	52.1	5	K.AVSGASAGDYSDAIETLLTAIAVIK.Q
gi|38044288|ref|N		3	6	0.078	731	80641	5.8	U		gelsolin isoform b [Homo sapiens]			
gi|4504165|ref|NI		3	6	0.073	782	85697	6.3	U		gelsolin isoform a [Homo sapiens]			
	HsFLAG-Control_Hela_Ti_1	2.7419	0.1592	1831.44	1831.08	5078.8			1	449.7	53.1	2	K.QTQVSVLPEGGETPLFK.Q
	HsFLAG-Control_Hela_Ti_1	3.9275	0.3704	1838.53	1839.01	6971.1			1	884.3	55.9	1	K.TPSAAYLWVGTGASEAEK.T
	HsFLAG-Control_HeLa_S1	4.6507	0.432	2273.32	2273.46	5838.2			1	1059.5	57.1	3	R.AQPVQVAEGSEPDGFWEALGGK.A
gi|68563515|ref|N		2	4	0.078	579	64136	8.3	U		hypothetical protein LOC448834 [Homo sapiens]			
*	HsFLAG-Control_293_Ti_1	4.273	0.375	2505.86	2504.56	9219			1	891.3	45	3	R.FSTQCQYQGSYSSCGPQFQSR.A
*	HsFLAG-Control_Hela_Ti_1	2.6643	0.3013	2790.87	2790.9	8983.5			1	394	30.4	1	R.TSFSPCVPQCQTQGSYGSFTEQHR.S
gi|4507847|ref|NI		2	4	0.078	346	36955	5.1	U		upstream stimulatory factor 2 isoform 1 [Homo sapiens]			
gi|46877105|ref|N		2	4	0.097	279	30570	5.2	U		upstream stimulatory factor 2 isoform 2 [Homo sapiens]			
	HsHeLa3_Ti_104.2457.245	3.9063	0.2217	1217.48	1215.44	6496.8			1	1282.8	88.9	3	K.INNWIVQLSK.I
	HsHeLa3_Ti_105.1582.158	3.5081	0.3069	1940.52	1940.14	5651.3			1	634.4	53.1	1	R.AQLQQHNLEMVGEGTRQ.-
gi|88942850|ref|X		2	3	0.078	294	32601	4.8	U		PREDICTED: similar to 40S ribosomal protein SA (p40) (34/67 kDa laminin receptor) (Co			

gi|89036252|ref|X	2	3	0.078	295	32744	4.5	U	PREDICTED: similar to 40S ribosomal protein SA (p40) (34/67 kDa laminin receptor) (Col			
gi|88951517|ref|X	2	3	0.078	294	32601	4.8	U	PREDICTED: similar to 40S ribosomal protein SA (p40) (34/67 kDa laminin receptor) (Col			
gi|88951515|ref|X	2	3	0.078	294	32601	4.8	U	PREDICTED: similar to 40S ribosomal protein SA (p40) (34/67 kDa laminin receptor) (Col			
gi|88951513|ref|X	2	3	0.078	294	32601	4.8	U	PREDICTED: similar to 40S ribosomal protein SA (p40) (34/67 kDa laminin receptor) (Col			
gi|88951511|ref|X	2	3	0.078	294	32601	4.8	U	PREDICTED: similar to 40S ribosomal protein SA (p40) (34/67 kDa laminin receptor) (Col			
gi|88951507|ref|X	2	3	0.078	294	32601	4.8	U	PREDICTED: similar to 40S ribosomal protein SA (p40) (34/67 kDa laminin receptor) (Col			
gi|88951505|ref|X	2	3	0.078	294	32601	4.8	U	PREDICTED: similar to 40S ribosomal protein SA (p40) (34/67 kDa laminin receptor) (Col			
gi|88942860|ref|X	2	3	0.078	294	32601	4.8	U	PREDICTED: similar to 40S ribosomal protein SA (p40) (34/67 kDa laminin receptor) (Col			
gi|88942858|ref|X	2	3	0.078	294	32601	4.8	U	PREDICTED: similar to 40S ribosomal protein SA (p40) (34/67 kDa laminin receptor) (Col			
gi|88942856|ref|X	2	3	0.078	294	32601	4.8	U	PREDICTED: similar to 40S ribosomal protein SA (p40) (34/67 kDa laminin receptor) (Col			
gi|88942854|ref|X	2	3	0.078	294	32601	4.8	U	PREDICTED: similar to 40S ribosomal protein SA (p40) (34/67 kDa laminin receptor) (Col			
	Hs293FLP_TREX_Ti_102.2	3.1804	0.1068	1136.19	1136.33	3788.9	2	847.8	83.3	1	K.SDGIYIINLK.R
	HsFLAG-Control_MG_293_	4.1115	0.3213	1204.29	1204.37	7835.3	1	1714.7	83.3	2	K.FAAATGATPIAGR.F
gi|4505185|ref|N	1	6	0.078	115	12476	7.9	U	macrophage migration inhibitory factor (glycosylation-inhibiting factor) [Homo sapiens]			
*	Hs293FLP_TREX_Ti_104.2	3.5441	0.1792	1045.32	1045.23	4540.1	1	1074.5	93.8	6	K.LLCGLLAER.L
gi|58530840|ref|N	12	25	0.077	2871	331774	6.8	U	desmoplakin isoform I [Homo sapiens]			
gi|58530842|ref|N	12	25	0.097	2272	260116	7	U	desmoplakin isoform II [Homo sapiens]			
	HsFLAG-Control_Hela_Ti_1	3.7795	0.304	1842.98	1843.04	10605.4	1	1486.2	64.3	2	K.SAIYQLEEEYENLLK.A
	HsFLAG-Control_HeLa_S1	2.9961	0.1606	1273.26	1272.45	6219.4	2	891.2	80	2	R.QLQNIIQATSR.E
	HsFLAG-Control_Hela_Ti_1	4.1787	0.4713	2386.68	2387.56	9872.2	1	887.1	44.7	1	K.ENAAYFQFFEEAQSTEAYLK.G
	HsFLAG-Control_Hela_Ti_1	2.9956	0.425	1717.41	1717.92	7983.6	1	739.5	60	1	K.NLPLADQGSSHHITVK.I
	HsFLAG-Control_Hela_Ti_1	3.05	0.2374	1857.17	1858.06	9934	4	699.2	46.9	1	K.SVQNDSQAIAEVLNQLK.D
	HsFLAG-Control_Hela_Ti_1	3.9404	0.4311	2138.51	2139.34	10148.2	1	888	50	1	K.LENINGVTDGYLNSLCTVR.A
	HsFLAG-Control_Hela_Ti_1	5.0684	0.4567	2434.4	2434.67	8275.5	1	1180.1	52.5	2	K.AQQIHSQTSQQYPLYDLDLGK.F
	HsFLAG-Control_293_Ti_1	4.7702	0.4362	2482.73	2482.83	12718	1	1681	50	3	K.DYELQLASYTSGLETLLNIPIK.R
	HsFLAG-Control_Hela_Ti_1	4.731	0.4141	2254.64	2254.63	8552.9	1	919	45.2	2	R.LLEAQIASGGVVDPVNSVFLPK.D
	HsHeLa3_Ti_103.3755.375	2.6849	0.1403	2385.37	2384.67	6480.9	3	417	38.1	1	R.AVTGYNDPETGNIISLFQAMNK.E
	HsFLAG-Control_HeLa_S1	4.371	0.2559	2160.73	2160.25	8171.1	1	770.3	47.2	4	R.GYFNEELSEILSDPSDDTK.G
	HsFLAG-Control_Hela_Ti_1	4.5616	0.4676	2029.48	2030.24	9966.6	1	1840.6	65.6	5	K.GFFDPNTEENLTYLQLK.E
gi|22027538|ref|N	3	6	0.077	868	96023	6.5	U	programmed cell death 6 interacting protein [Homo sapiens]			
*	HsFLAG-Control_HeLa_S1	3.7045	0.228	3409.4	3410.84	6797.7	2	434.5	22	1	R.EATTLANGVLASLNLPAAIEDVSGDTVPQSILTK.S
*	HsFLAG-Control_HeLa_S1	4.6625	0.3441	1728.63	1728.98	7060.6	1	1995	76.7	2	R.SVIEQGGIQTVDQLIK.E
*	HsFLAG-Control_HeLa_S1	4.8948	0.499	1895.9	1896.15	7597.1	1	1729.5	68.8	3	K.NLATAYDNFVELVANLK.E
gi|28212272|ref|N	2	2	0.077	636	69438	7.3	U	hypothetical protein LOC161424 [Homo sapiens]			
*	HsFLAG-Control_HeLa_NE	4.4208	0.3336	1630.49	1629.89	6423.1	1	1179.8	71.4	1	R.TLLQVLGGTILESER.A
*	HsFLAG-Control_HeLa_NE	5.7145	0.4057	3358.44	3359.85	6801.1	1	918.7	28	1	R.SLGALTGPQLLSLAQSPAGSHVLDAILTSPSVTR.K
gi|7657015|ref|N	3	4	0.077	505	55210	7.2	U	hypothetical protein LOC51493 [Homo sapiens]			
*	HsFLAG-Control_MG_293_	3.3957	0.264	1385.29	1386.5	10073.2	1	1157	75	2	R.SYNDELQFLEK.I
*	HsFLAG-Control_MG_293_	3.1328	0.249	1090.78	1091.31	4943.3	1	796.1	72.7	1	R.GGGVGGFLPAMK.Q
*	HsHeLa3_Ti_105.2179.217	3.4567	0.2256	1642.8	1640.9	6215	1	1044.5	63.3	1	R.GLGHQVATDALVAMEK.A
gi|33469922|ref|N	3	3	0.076	543	60643	6.3	U	minichromosome maintenance protein 7 isoform 2 [Homo sapiens]			
gi|33469968|ref|N	3	3	0.057	719	81308	6.5	U	minichromosome maintenance protein 7 isoform 1 [Homo sapiens]			
	HsFLAG-Control_HeLa_S1	3.0362	0.2881	1553.51	1551.87	5892.8	1	812.7	64.3	1	K.ALLLLLVGGVDQSPR.G
	HsFLAG-Control_MG_293_	2.9509	0.218	1188.33	1188.37	7492	1	1469.5	75	1	R.GSSGVGLTAAVLR.D
	HsHeLa_Control-MG_Ti_20	2.7134	0.1683	1475.5	1474.7	6884	1	680.1	58.3	1	R.TQRPADVIFATVR.E
gi|5174529|ref|N	2	3	0.076	395	43661	6.5	U	methionine adenosyltransferase II, alpha [Homo sapiens]			
*	HsFLAG-Control_MG_293_	2.7446	0.1402	1809.88	1807.96	6744.5	1	373	46.4	1	K.YLDEDTIYHLQPSGR.F
*	HsFLAG-Control_MG_293_	4.2203	0.3116	1445.48	1445.62	7492.1	1	1834.1	78.6	2	R.FVIGGPQGDAGLTGR.K
gi|4885403|ref|N	11	22	0.075	1938	198471	7.3	U	host cell factor C1 (VP16-accessory protein) [Homo sapiens]			

*	HsFLAG-Control_HeLa_NE	2.5478	0.3359	1158.51	1159.33	5521.4		1	534.8	65	1	R.LGHSFSLVGNK.C
*	HsFLAG-Control_HeLa_NE	2.6021	0.1402	1264.04	1264.38	6867.7		1	751.2	70	1	R.ESHTAVVYTEK.D
*	HsHeLa3_Ti_106.1832.183	2.7788	0.3763	1129.5	1129.26	5104.7		1	523.1	65	5	R.SLHSATTIGNK.M
*	HsHeLa3_Ti_104.2276.227	2.564	0.1791	1813.26	1813.06	4843.8		7	268.7	42.9	1	K.DLWYLETEKPPPPAR.V
*	HsFLAG-Control_HeLa_NE	4.257	0.4319	1598.94	1597.85	2957.6		3	325.2	56.2	5	K.SPISVPGGSALISNLGK.V
*	HsFLAG-Control_HeLa_NE	3.9996	0.4386	1636.68	1636.89	9739.5		1	1591.5	66.7	2	K.IATGHGQQGVTQVVLK.G
*	HsHeLa3_Ti_105.2251.225	2.6215	0.2337	1345.46	1345.58	8858.5		2	661.6	54.2	1	R.SPAFVQLAPLSSK.V
*	HsFLAG-Control_HeLa_NE	3.8013	0.2432	1345.88	1345.58	9628.7		2	1288.7	66.7	2	R.SPAFVQLAPLSSK.V
*	HsFLAG-MOCK_300mM_T	2.6673	0.2537	1268.68	1269.42	4144.1		1	300.6	63.6	1	R.HSHAVSTAAMTR.S
*	HsFLAG-Control_HeLa_NE	3.7321	0.3673	2915.42	2915.36	7513.1		1	672.6	25	1	K.LQAAATLTEVANGIESLGVKPDLPPPPSK.A
*	HsFLAG-Control_HeLa_NE	3.0056	0.201	1263.59	1263.44	9892.6		1	1241.1	80	2	K.KQELQPGTAYK.F
gi|4758556|ref|N	2	3	0.075	683	77529	9.5	U	PRP3 pre-mRNA processing factor 3 homolog [Homo sapiens]				
*	HsHeLa3_Ti_106.2619.261	4.0079	0.2659	2118.95	2119.44	8259.1		1	811.1	47.4	1	K.RVLGFSEPTVVTAALNCVGK.G
*	HsHeLa3_Ti_105.2842.284	4.1952	0.1268	3330.64	3330.69	5792.3		1	729.3	26.7	2	K.TPSSSQPERLPIGNTIQPSQAATFMNDAIEK.A
gi|24430160|ref|	2	3	0.075	389	44173	7.5	U	proteasome 26S ATPase subunit 6 [Homo sapiens]				
*	HsFLAG-Control_HeLa_S1	3.1322	0.1686	1441.79	1441.71	5301.7		1	953.7	73.1	1	K.ALQSVGQIVGEVLK.Q
*	HsFLAG-Control_HeLa_S1	3.9217	0.3011	1800.18	1799.08	4754.5		1	634.5	64.3	2	R.EVIELPLTNPELFQR.V
gi|4506691|ref|N	1	6	0.075	146	16445	10.2	U	ribosomal protein S16 [Homo sapiens]				
gi|89057335|ref|	1	6	0.075	146	16412	10	U	PREDICTED: similar to 40S ribosomal protein S16 isoform 6 [Homo sapiens]				
gi|89057333|ref|	1	6	0.075	146	16412	10	U	PREDICTED: similar to 40S ribosomal protein S16 isoform 5 [Homo sapiens]				
gi|89057331|ref|	1	6	0.075	146	16412	10	U	PREDICTED: similar to 40S ribosomal protein S16 isoform 4 [Homo sapiens]				
gi|89052405|ref|	1	6	0.075	146	16412	10	U	PREDICTED: similar to 40S ribosomal protein S16 isoform 3 [Homo sapiens]				
gi|89052403|ref|	1	6	0.075	146	16412	10	U	PREDICTED: similar to 40S ribosomal protein S16 isoform 2 [Homo sapiens]				
gi|88946111|ref|	1	6	0.085	129	14346	9.8	U	PREDICTED: similar to 40S ribosomal protein S16 isoform 4 [Homo sapiens]				
gi|88946109|ref|	1	6	0.075	146	16448	9.8	U	PREDICTED: similar to 40S ribosomal protein S16 isoform 3 [Homo sapiens]				
gi|88942427|ref|	1	6	0.085	129	14346	9.8	U	PREDICTED: similar to 40S ribosomal protein S16 isoform 2 [Homo sapiens]				
gi|88942425|ref|	1	6	0.075	146	16448	9.8	U	PREDICTED: similar to 40S ribosomal protein S16 isoform 1 [Homo sapiens]				
gi|51493358|ref|	1	6	0.075	146	16412	10	U	PREDICTED: similar to 40S ribosomal protein S16 isoform 1 [Homo sapiens]				
	Hs293FLP_TREX_Ti_105.2	3.6945	0.3515	1188.38	1188.37	5581.1		1	995.5	75	6	K.GPLQSVQVFGR.K
gi|15553127|ref|	5	10	0.074	917	102380	6.1	U	hexokinase 2 [Homo sapiens]				
*	HsHeLa3_Ti_106.1874.187	2.7795	0.2992	1223.64	1224.4	4854.6		4	479.5	58.3	2	K.GLGATTHPTAAVK.M
*	HsHeLa3_Ti_106.1875.187	3.0395	0.2543	1224.03	1224.4	6365.5		1	1076.4	75	1	K.GLGATTHPTAAVK.M
*	HsHeLa3_Ti_104.2899.289	4.2086	0.3748	1532.84	1532.75	9906.9		1	1746.1	67.9	2	R.SASLCAATLAAVLQR.I
	HsHeLa3_Ti_103.3107.310	5.2043	0.3815	1498.67	1496.66	7210.9		1	2027.1	80.8	3	K.GDFLALDLGGTNFR.V
*	HsHeLa3_Ti_104.4323.432	3.4035	0.2413	2900.68	2899.28	3540.2		1	247.3	34	2	K.GVSLPLGFTFSFPCQQNSLDESILLK.W
gi|20070260|ref|	2	2	0.074	580	65697	6.1	U	cofactor of BRCA1 [Homo sapiens]				
gi|89030627|ref|	2	2	0.074	579	65326	5.8	U	PREDICTED: similar to cofactor of BRCA1 [Homo sapiens]				
	HsFLAG-Control_HeLa_NE	3.802	0.3065	3294.78	3293.75	8988.4		1	600.6	22.4	1	K.AIEQFQTENGVLLPSLQSALPFLDLHGTPR.L
	HsFLAG-Control_HeLa_NE	2.5966	0.111	1287.41	1287.41	4908.6		2	632.9	66.7	1	K.ALEPTGQSGEAVK.E
gi|4503735|ref|N	3	4	0.074	553	56788	8.6	U	forkhead box C1 [Homo sapiens]				
*	HsHeLa3_Ti_104.1443.144	2.4082	0.3215	1346.51	1347.51	5772.9		1	392.7	54.5	1	R.AYGPYTPQPQPK.D
*	HsHeLa3_Ti_104.1445.144	3.478	0.3435	1348.55	1347.51	4054.9		1	583	72.7	2	R.AYGPYTPQPQPK.D
*	HsHeLa3_Ti_105.2091.209	2.623	0.3911	2733.72	2734.99	9229.7		1	822	37.5	1	K.TENGTCPSPPQPLSPAAALGSGSAAAVPK.I
gi|14141170|ref|	3	7	0.073	668	75023	9.7	U	metastasis-associated protein 2 [Homo sapiens]				
*	HsFLAG-Control_HeLa_NE	3.7852	0.3314	2110.17	2110.29	8535.4		1	832.4	50	1	R.VGDYVYFENSSSNPYLVR.R
*	HsFLAG-Control_HeLa_NE	4.3773	0.4145	1551.63	1550.62	9493.1		2	882.4	57.1	4	R.DISSSLNSLADSNAR.E
*	HsFLAG-Control_HeLa_NE	3.083	0.3131	1654.92	1653.92	4428.4		3	385.9	53.3	2	K.LNPADAPNPVVFVATK.D
gi|13128860|ref|	2	2	0.073	482	55103	5.5	U	histone deacetylase 1 [Homo sapiens]				
	HsHeLa3_Ti_104.1499.149	2.5627	0.0945	1428.9	1427.57	6387.6		4	437.4	54.5	1	R.SIRPDNMSEYSK.Q

*	HsHeLa3_Ti_103.2998.299		4.4707	0.2773	2515.2	2514.79	4745.4		1	661.9	47.7	1	K.VMEMFQPSAVVLQCGSDSLSGDR.L
gi|42657272|ref|X		1	2	0.073	124	13614	10.1	U	PREDICTED: similar to 40S ribosomal protein S25 [Homo sapiens]				
gi|88988836|ref|X		1	2	0.073	124	13615	10	U	PREDICTED: similar to 40S ribosomal protein S25 [Homo sapiens]				
gi|4506707|ref|N		1	2	0.072	125	13742	10.1	U	ribosomal protein S25 [Homo sapiens]				
	Hs293FLP_TREX_Ti_102.2		3.5568	0.2179	1076.41	1076.28	6849.2		6	1143.9	87.5	2	K.LNNLVLFDK.A
gi|4759196|ref|N		3	5	0.072	1142	126500	6.4	U	symplekin [Homo sapiens]				
*	HsFLAG-Control_HeLa_NE		3.8073	0.504	1839.02	1839.18	6730.2		1	1182.2	65.6	2	K.VVLEAPLITESALEVVR.K
*	HsFLAG-Control_HeLa_NE		5.1041	0.2405	3308.92	3309.75	13148.2		1	1307.1	25.8	1	R.LLGTQHGEGNSALSPLNPGELLIALHNIDSVK.C
*	HsFLAG-Control_HeLa_NE		3.6879	0.356	3460.12	3460.91	5997.8		5	290.2	18.8	2	K.EAPAGPLEEDDLEPLTLAPAPAPRPPQDLIGLR.L
gi|33519426|ref|N		1	5	0.072	499	54604	6.5	U	thioredoxin reductase 1 [Homo sapiens]				
gi|33519432|ref|N		1	5	0.072	499	54604	6.5	U	thioredoxin reductase 1 [Homo sapiens]				
gi|33519430|ref|N		1	5	0.072	499	54604	6.5	U	thioredoxin reductase 1 [Homo sapiens]				
gi|33519428|ref|N		1	5	0.072	499	54604	6.5	U	thioredoxin reductase 1 [Homo sapiens]				
	HsGST-MOCK_Ti_403.499		6.1725	0.4345	3971.6	3972.48	6307.1		1	913.5	25.7	5	K.IPVTDEEQTNVPYIYAIGDILEDKVELTPVAIQAGR.L
gi|21361547|ref|N		2	3	0.072	461	49974	4.8	U	ribonuclease/angiogenin inhibitor [Homo sapiens]				
gi|42822874|ref|N		2	3	0.072	461	49974	4.8	U	ribonuclease/angiogenin inhibitor [Homo sapiens]				
gi|42822872|ref|N		2	3	0.072	461	49974	4.8	U	ribonuclease/angiogenin inhibitor [Homo sapiens]				
gi|42822870|ref|N		2	3	0.072	461	49974	4.8	U	ribonuclease/angiogenin inhibitor [Homo sapiens]				
gi|42822868|ref|N		2	3	0.072	461	49974	4.8	U	ribonuclease/angiogenin inhibitor [Homo sapiens]				
gi|42822866|ref|N		2	3	0.072	461	49974	4.8	U	ribonuclease/angiogenin inhibitor [Homo sapiens]				
gi|42822864|ref|N		2	3	0.072	461	49974	4.8	U	ribonuclease/angiogenin inhibitor [Homo sapiens]				
gi|42794608|ref|N		2	3	0.072	461	49974	4.8	U	ribonuclease/angiogenin inhibitor [Homo sapiens]				
	HsFLAG-Control_HeLa_S1		3.0873	0.3173	1210.42	1210.42	7806.4		1	1229.2	80	2	R.VNPALAELNLR.S
	Hs293FLP-MG_Ti_202.467		3.4251	0.259	2417.03	2416.66	9331.6		9	502.8	35.7	1	R.ELDLSNNCLGDAGILQLVESVR.Q
gi|63252913|ref|N		2	6	0.072	348	38499	6.2	U	gelsolin-like capping protein [Homo sapiens]				
*	HsFLAG-Control_HeLa_NE		2.7225	0.2183	1319.52	1318.34	6728.8		2	502.9	59.1	1	K.EGNPEEDLTADK.A
*	HsFLAG-Control_HeLa_NE		4.2956	0.3567	1390.89	1390.58	6579.1		1	1281.7	83.3	5	R.QAALQVAEGFISR.M
gi|88953910|ref|X		7	13	0.07	2354	265615	6.2	U	PREDICTED: hypothetical protein LOC57683 [Homo sapiens]				
gi|88959048|ref|X		7	13	0.07	2354	265615	6.2	U	PREDICTED: hypothetical protein LOC57683 [Homo sapiens]				
	Hs293FLP-MG_Ti_204.255		3.5083	0.2348	2712.2	2712.07	6429.8		1	674.4	29.2	1	K.SVFETSLDSDVPLQAATHKPEVIVK.E
	HsF-IP-293-MG_Ti_105.16		3.5474	0.39	2229.1	2229.45	4544.6		1	717.2	50	1	K.TSLDSGVPHYSVTEPQVAVNK.I
	Hs293FLP-MG_Ti_202.405		4.535	0.3762	2424.58	2422.78	6746.1		1	962.1	52.4	6	K.GYVPSDSEIIYVSNIPLQSVIK.Q
	Hs283FLP_Ti_106.2520.25		4.3933	0.2318	2839.6	2837.16	7704		1	820.1	30	1	K.LGDFDVSYASHIPVQFVFTDQSSVPVK.E
	Hs283FLP_Ti_103.3724.37		3.7457	0.2539	3695.02	3694.21	6792.4		2	412.6	22	1	K.VVLVDLVPGDSDYEVISDDIPLQLVTDPPQLTVK.D
	Hs293FLP-MG_Ti_202.004		5.1022	0.4431	1589.66	1589.62	9269.8		1	1871.7	70	2	K.SCQSSASAVDFGASSK.S
	Hs293FLP-MG_Ti_203.222		3.3773	0.3637	2233.87	2234.34	9218.8		1	549.3	42.1	1	R.YGFNSHQGTSDSSLFLEESK.V
gi|12056468|ref|N		5	19	0.07	745	81745	6.1	U	junction plakoglobin [Homo sapiens]				
gi|4504811|ref|N		5	19	0.07	745	81745	6.1	U	junction plakoglobin [Homo sapiens]				
	HsFLAG-Control_Hela_Ti_1		3.701	0.0831	1450.59	1450.72	4773.4		1	766.6	77.3	2	K.LLNQPNQWPLVK.A
	HsFLAG-Control_293_Ti_1		3.2337	0.3304	2158.16	2156.46	9620.9		3	402.6	36.8	4	R.NLALCPANHAPLQEAAVIPR.L
	HsFLAG-Control_Hela_Ti_1		4.3959	0.4513	2347.65	2348.75	6641.8		1	634.5	44.7	6	R.LNTIPLFVQLLYSSVENIQR.V
	HsFLAG-Control_HeLa_S1		4.6279	0.2776	2349.62	2348.75	8343.6		1	1284.8	40.8	3	R.LNTIPLFVQLLYSSVENIQR.V
	HsFLAG-Control_293_Ti_1		5.257	0.4227	2350.36	2348.75	7476		1	1219.6	57.9	4	R.LNTIPLFVQLLYSSVENIQR.V
gi|46411166|ref|N		2	2	0.07	388	41817	8.9	U	muscleblind-like 1 isoform c [Homo sapiens]				
*	HsHeLa3_Ti_103.2827.282		6.8135	0.509	2606.37	2607.9	9899.6		1	2411.9	53.8	1	K.AAQYQVNQAAAAQAAATAAAMTQSAVK.S
*	HsHeLa3_Ti_103.2814.281		5.9053	0.4002	2609.53	2607.9	8250.7		1	2650.4	40.4	1	K.AAQYQVNQAAAAQAAATAAAMTQSAVK.S
gi|4502337|ref|N		1	2	0.07	298	34259	6.1	U	alpha-2-glycoprotein 1, zinc [Homo sapiens]				
*	HsFLAG-Control_293_Ti_1		2.7744	0.1316	2404.87	2404.69	8648.6		3	337.6	35	2	K.HVEDVPAFQALGSLNDLQFFR.Y
gi|15718687|ref|N		2	2	0.07	243	26688	9.7	U	ribosomal protein S3 [Homo sapiens]				

*	Hs293FLP_TREX_Ti_102.1		1.9952	0.158	896.37	897.062	6718.7		3	715.4	78.6	1	K.FVADGIFK.A
*	Hs293FLP_TREX_Ti_105.2		3.1769	0.1801	1030.43	1030.25	6214.3		4	1475.8	87.5	1	R.TEIIILATR.T
gi|24475847|ref|N		3	4	0.069	642	71729	5.5	U	influenza virus NS1A binding protein isoform a [Homo sapiens]				
	HsHeLa_Control-MG_Ti_10		3.4971	0.3366	2433.84	2434.71	6692.8		1	821	47.4	1	K.VDAYIQEHLLQISEEEEFLK.L
*	HsHeLa_Control-MG_Ti_10		3.5137	0.2104	1399.49	1397.57	4715.8		2	1096.8	79.2	2	K.LYIVGGSDPYGQK.G
*	HsHeLa_Control-MG_Ti_10		3.0251	0.2602	1331.58	1331.52	6272.2		1	1130.9	80	1	K.LWTSCAPLNIR.R
gi|5730041|ref|N		1	2	0.069	333	37805	5.2	U	suppressor of G2 allele of SKP1 [Homo sapiens]				
*	HsFLAG-Control_HeLa_NE		4.3775	0.2063	2615.51	2615.85	6763.3		1	605.9	43.2	2	R.FFQSFSDALIDEDPQAALEELTK.A
gi|16945970|ref|N		1	2	0.069	333	37653	9.2	U	PC4 and SFRS1 interacting protein 1 isoform 1 [Homo sapiens]				
gi|19923653|ref|N		1	2	0.043	530	60103	9.1	U	PC4 and SFRS1 interacting protein 1 isoform 2 [Homo sapiens]				
	HsGST-MOCK_Ti_105.165		4.9197	0.1624	2532.32	2531.83	8572.3		1	1780.6	40.9	2	K.GYPHWPARVDEVPDGAVKPPTNK.L
gi|31795538|ref|N		1	2	0.069	202	22710	9	U	replication factor C 3 isoform 2 [Homo sapiens]				
gi|4506489|ref|N		1	2	0.039	356	40556	8.3	U	replication factor C 3 isoform 1 [Homo sapiens]				
	HsFLAG-Control_HeLa_NE		4.3984	0.367	1589.66	1590.69	10077.3		1	1528.9	69.2	2	K.TVAQSQQLETNSQR.D
gi|4503401|ref|N		4	18	0.068	1049	113716	5	U	desmoglein 1 preproprotein [Homo sapiens]				
*	HsFLAG-Control_Hela_Ti_1		3.8013	0.3012	1664.31	1663.75	6676.3		1	1095.4	76.9	2	K.IHSDCAANQQVTYR.I
*	HsFLAG-Control_Hela_Ti_1		4.632	0.4144	2046.26	2046.37	4735.3		1	621.3	55.6	13	R.ISGVGIDQPPYGIFVINQK.T
*	HsFLAG-Control_293_Ti_1		3.202	0.2501	1714.27	1714.73	7006.1		1	497.4	50	1	R.DGGADGMSAECECNIK.I
*	HsFLAG-Control_Hela_Ti_1		4.0782	0.2014	2241.96	2242.62	8232.5		2	621.1	38.1	2	K.ASAISVTVLNVIEGPVFRPGSK.T
gi|4507955|ref|N		2	3	0.068	414	44713	6.3	U	YY1 transcription factor [Homo sapiens]				
*	HsFLAG-MOCK_300mM_T		2.6861	0.2564	1664.74	1664.73	5359.8		4	455.8	44.7	1	K.SYLSGGAGAAGGGGADPGNK.K
*	HsFLAG-MOCK_300mM_T		2.3945	0.1499	907.78	907.06	3902.5		9	345.5	64.3	2	K.SHILTHAK.A
gi|42716280|ref|N		5	5	0.067	1268	141439	6.9	U	high density lipoprotein binding protein [Homo sapiens]				
gi|4885409|ref|N		5	5	0.067	1268	141439	6.9	U	high density lipoprotein binding protein [Homo sapiens]				
	HsFLAG-Control_HeLa_NE		3.5857	0.364	1780.34	1780.88	5153.9		1	900.3	66.7	1	K.VATLNSEEESDPPTYK.D
	HsFLAG-Control_HeLa_S1		2.6343	0.2116	1726.67	1725.99	9811.9		4	574.3	46.4	1	K.ASVITQVFHVPLEER.K
	HsFLAG-Control_HeLa_NE		4.0746	0.3689	1616.45	1615.87	7436.3		1	1490.9	76.9	1	K.FPEVIINFPDPAQK.S
	HsFLAG-Control_HeLa_NE		3.4846	0.3414	1915.69	1916.14	7532.9		1	507	47.1	1	K.IDLPAENSNSETIIITGK.R
	HsGST-MOCK_Ti_403.527		3.1772	0.2301	2485.84	2485.81	8624.7		1	387.5	35.7	1	K.ELEALIQNLDNVVEDSMLVDPK.H
gi|89052285|ref|X		3	4	0.067	1278	138244	8.4	U	PREDICTED: hypothetical protein LOC57662 [Homo sapiens]				
gi|89057109|ref|X		3	4	0.067	1278	138244	8.4	U	PREDICTED: similar to Protein KIAA1543 [Homo sapiens]				
	HsHeLa_Control-MG_Ti_20		3.7825	0.2666	3033.82	3035.38	4472.8		1	671.7	34.3	1	R.TPTQPPPEPGDLPTIEEALQIIHSAEPR.L
	Hs293FLP_Ti_303.1450.14		3.6608	0.2009	3639.05	3637.72	5461.8		1	538.7	24.3	1	R.EASGEAEAEAEEADSGPVPGGERPAGEGQGEPTSRPK.A
	HsHeLa_Control-MG_Ti_20		3.6083	0.3409	2255.98	2256.48	5475		1	300.8	42.5	2	K.AVTFSPDLGPVPHEGLGEYNR.A
gi|32454741|ref|N		2	4	0.067	418	46441	8.7	U	serine (or cysteine) proteinase inhibitor, clade H, member 1 precursor [Homo sapiens]				
*	HsHeLa_Control-MG_Ti_20		3.8521	0.3996	1661.35	1660.82	5838.7		1	884.6	67.9	2	R.LYGPSSVSFADDFVR.S
*	HsHeLa_Control-MG_Ti_20		3.636	0.3578	1638.79	1638.95	6587.4		1	896.7	70.8	2	K.LFYADHPFIFLVR.D
gi|14251215|ref|N		2	2	0.066	457	50792	8.6	U	Kruppel-like factor 5 [Homo sapiens]				
*	HsHeLa3_Ti_106.2472.247		2.7041	0.3756	2130.33	2129.46	5213.9		1	685.4	55.3	1	R.LGPVPQPPAPQDEPVFAQLK.P
*	HsHeLa3_Ti_105.1355.135		2.958	0.1919	966.64	966.128	3834.9		1	728.6	83.3	1	K.PVLGAANPAR.D
gi|7706377|ref|N		2	3	0.066	335	37014	8.2	U	ankyrin repeat and SOCS box-containing protein 1 [Homo sapiens]				
*	Hs293FLP-MG_Ti_206.378		4.7261	0.3356	2388.73	2389.72	8858.7		1	1861	38.1	1	R.HGCEAAFVSLLVEFGANLNLVK.W
*	Hs293FLP-MG_Ti_206.377		5.4207	0.4564	2389.09	2389.72	8643.7		1	1883.8	57.1	2	R.HGCEAAFVSLLVEFGANLNLVK.W
gi|75709200|ref|N		1	2	0.066	197	22025	8.4	U	glutathione peroxidase 4 [Homo sapiens]				
*	HsGST-MOCK_Ti_305.216		3.8646	0.1564	1560.88	1561.84	6328.8		1	1050.9	75	2	K.RYGPMEEPLVIEK.D
gi|4506623|ref|N		2	3	0.066	136	15798	10.6	U	ribosomal protein L27 [Homo sapiens]				
*	Hs293FLP_TREX_Ti_102.1		2.1674	0.1684	1049.46	1050.2	3629		2	354.9	62.5	2	R.YSVDIPLDK.T
*	Hs293FLP_TREX_Ti_102.1		2.5686	0.1696	1050.43	1050.2	4358.1		2	582.9	75	1	R.YSVDIPLDK.T

gi|18379328|ref|N	3	3	0.065	647	70724	9.5	U	WW domain-containing adapter with a coiled-coil region isoform 1 [Homo sapiens]				
gi|18379332|ref|N	3	3	0.077	544	59505	9.5	U	WW domain-containing adapter with a coiled-coil region isoform 3 [Homo sapiens]				
gi|18379330|ref|N	3	3	0.07	602	65483	9.4	U	WW domain-containing adapter with a coiled-coil region isoform 2 [Homo sapiens]				
	HsFLAG-Control_HeLa_NE	3.3603	0.348	2630.45	2632.07	6613		1	429.9	35.4	1	R.ISTPQTNTVPIKPLISTPPVSSQPK.V
	HsFLAG-Control_HeLa_NE	4.4957	0.3471	2631.59	2632.07	9110.5		1	1105	30.2	1	R.ISTPQTNTVPIKPLISTPPVSSQPK.V
	HsFLAG-Control_HeLa_NE	4.3141	0.486	1742.45	1742.88	8753.8		1	971.6	56.2	1	K.QGPVSQSATQQPVTADK.Q
gi|37595750|ref|N	2	5	0.065	615	70703	9.4	U	lamin B receptor [Homo sapiens]				
gi|37595752|ref|N	2	5	0.065	615	70703	9.4	U	lamin B receptor [Homo sapiens]				
	HsFLAG-Control_293_Ti_1	3.2754	0.2786	2468.99	2469.84	3952.9		3	224	37.5	2	K.DPSLLNFPPPLPALYELWETR.V
	HsFLAG-Control_293_Ti_2	4.9234	0.3489	2031.88	2031.19	8575.9		1	1304.4	61.1	3	R.NDLSPASSGNAVYDFFIGR.E
gi|4505623|ref|NF	2	2	0.065	430	46626	7	U	pre-B-cell leukemia transcription factor 1 [Homo sapiens]				
*	HsHeLa3_Ti_104.3172.317	2.7626	0.2032	1304.43	1304.54	5964.5		1	823.2	70	1	K.PALFNVLCEIK.E
	HsHeLa3_Ti_104.3057.305	2.6581	0.347	2127.08	2127.35	11015.6		1	775	46.9	1	K.YEQACNEFTTHVMNLLR.E
gi|55770900|ref|N	2	3	0.065	353	41401	9.9	U	BRIX [Homo sapiens]				
*	Hs293FLP_TREX_Ti_103.1	3.3731	0.2047	1240.41	1240.36	3648.4		1	804.6	85	2	K.RNEIDAEPPAK.R
*	Hs293FLP_TREX_Ti_106.2	2.7159	0.1342	1466.15	1464.75	8137		2	911.3	72.7	1	K.PIEIQWVKPEPK.V
gi|21361741|ref|N	1	2	0.065	307	33879	6.3	U	hypothetical protein LOC51534 [Homo sapiens]				
*	HsFLAG-Control_HeLa_S1	4.519	0.3815	2185.8	2186.38	8391.4		1	1103.1	52.6	2	K.YAGSALQYEDVSTAVQNLQK.A
gi|4502027|ref|NF	6	30	0.064	609	69367	6.3	U	albumin precursor [Homo sapiens]				
*	HsFLAG-Control_293_Ti_1	2.7549	0.2713	1372.22	1372.41	7505.4		1	651.3	63.6	1	K.AAFTECCQAADK.A
*	HsFLAG-Control_HeLa_S1	3.4004	0.3166	1445.84	1444.5	8946.2		1	972.5	68.2	2	K.YICENQDSISSK.L
	HsFLAG-Control_293_Ti_1	3.3407	0.256	1641.11	1640.92	6425.6		1	835.2	64.3	14	K.KVPQVSTPTLVEVSR.N
	HsGST-MOCK_Ti_304.202	2.7217	0.3551	1511.61	1512.75	3525.1		1	258.4	57.7	2	K.VPQVSTPTLVEVSR.N
	HsGST-MOCK_Ti_304.203	3.5901	0.321	1512.02	1512.75	6656.5		1	1019.8	69.2	2	K.VPQVSTPTLVEVSR.N
	HsFLAG-Control_HeLa_NE	3.6048	0.3135	1514.08	1512.75	6985.6		2	883.4	61.5	9	K.VPQVSTPTLVEVSR.N
gi|45593130|ref|N	2	2	0.064	549	61993	9.2	U	guanine nucleotide binding protein-like 3 isoform 1 [Homo sapiens]				
gi|45643129|ref|N	2	2	0.065	537	60540	8.8	U	guanine nucleotide binding protein-like 3 isoform 2 [Homo sapiens]				
gi|45643127|ref|N	2	2	0.065	537	60540	8.8	U	guanine nucleotide binding protein-like 3 isoform 2 [Homo sapiens]				
	HsFLAG-Control_MG_293_	3.2488	0.1771	1087.34	1087.31	4104.8		1	945.4	90	1	R.VGVIGFPNVGK.S
	HsHeLa3_Ti_104.3737.373	2.763	0.2092	2530.82	2530.92	6961.2		2	425.6	30.4	1	K.QITIIDSPSFIVSPLNSSSALALR.S
gi|4557641|ref|NF	2	2	0.064	488	55325	5.8	U	histone deacetylase 2 [Homo sapiens]				
	HsHeLa3_Ti_104.1499.149	2.5627	0.0945	1428.9	1427.57	6387.6		4	437.4	54.5	1	R.SIRPDNMSEYSK.Q
*	HsHeLa3_Ti_106.2102.210	5.3751	0.3969	2234.85	2235.49	6588.3		1	1716.8	69.4	1	K.LHISPSNMTNQNTPEYMEK.I
gi|4759100|ref|NF	3	4	0.064	484	53542	10.5	U	splicing factor p54 [Homo sapiens]				
*	HsFLAG-Control_HeLa_NE	4.4647	0.3518	1785.55	1785.09	3810.9		1	910.8	68.8	2	R.ALIVVPYAEGVIPDEAK.A
*	HsFLAG-Control_HeLa_NE	3.7824	0.2871	1406.81	1406.67	6176.2		1	780.9	65.4	1	K.LNHVAAGLVSPSLK.S
*	HsHeLa3_Ti_106.2116.211	3.1504	0.2486	1407.08	1406.67	6277.5		1	693.1	61.5	1	K.LNHVAAGLVSPSLK.S
gi|39780588|ref|N	3	3	0.063	804	91810	7.4	U	hypothetical protein LOC55720 [Homo sapiens]				
*	HsHeLa3_Ti_104.3360.336	3.8809	0.2961	2536.36	2535.86	4672.4		1	608.2	43.2	1	R.AYLFAHAVDFVPSEENNLVGTLK.I
*	HsHeLa3_Ti_105.1495.149	2.5703	0.2989	1373.6	1373.51	5779.4		8	491.8	58.3	1	R.ASPLFSQHTAADK.H
*	HsHeLa3_Ti_103.3462.346	3.0107	0.4114	1890.83	1891.18	3934.6		1	304.5	53.6	1	K.WTYDPYVPEPVPWLK.S
gi|61835148|ref|N	3	4	0.063	621	69721	6.2	U	fragile X mental retardation-related protein 1 isoform a [Homo sapiens]				
gi|61835164|ref|N	3	4	0.072	539	60792	6.4	U	fragile X mental retardation-related protein 1 isoform b [Homo sapiens]				
	Hs293FLP_TREX_Ti_102.2	3.334	0.1584	1575.49	1575.69	4008.2		1	400.8	62.5	1	R.ANDQEPCGWWLAK.V
	HsFlag1P_Ti_105.2429.243	4.0286	0.3644	1949.66	1949.17	6222		1	924.9	64.7	1	R.KVPGVTAIELDEDTGTFR.I
	Hs293FLP_TREX_Ti_102.1	2.1428	0.1072	943.49	944.116	6968.5		3	643.7	71.4	2	K.VIQEIVDK.S
gi|12383062|ref|N	2	2	0.063	622	68935	7.2	U	likely ortholog of kinesin light chain 2 [Homo sapiens]				
gi|89077469|ref|X	2	2	0.061	638	70717	6.6	U	PREDICTED: similar to likely ortholog of kinesin light chain 2 [Homo sapiens]				
	HsHeLa3_Ti_103.2304.230	2.8705	0.3639	2106.58	2106.34	5987.1		1	405.8	42.5	1	R.ALLAPLVAPEAGEAEPGSQER.C

	HsHeLa3_Ti_105.2863.286	2.823	0.2582	1868.62	1868.14	7389.6		1	1027	64.7	1	K.DHPAVAATLNNLAVLYGK.R
gi|41327730|ref|N	1	5	0.063	270	29500	7	U	calponin 2 isoform b [Homo sapiens]				
gi|4758018|ref|NI	1	5	0.055	309	33697	7.3	U	calponin 2 isoform a [Homo sapiens]				
	HsFLAG-Control_HeLa_NE	5.2958	0.4527	1863.87	1863.12	7842		1	1815.3	71.9	5	R.TWIEGLTGLSIGPDFQK.G
gi|4504555|ref|NI	5	6	0.062	1262	144480	6.1	U	isoleucine-tRNA synthetase [Homo sapiens]				
gi|7770072|ref|NI	5	6	0.062	1262	144480	6.1	U	isoleucine-tRNA synthetase [Homo sapiens]				
	HsFLAG-Control_293_Ti_2	2.8556	0.1396	2175.17	2172.31	6973.3		8	292.9	36.1	1	R.EFEDAFPADFIAEGIDQTR.G
	HsFLAG-Control_MG_293_	2.8072	0.2087	1527.24	1527.76	8460.4		1	656.7	53.6	1	K.NVIVNGLVLASDGQK.M
	HsFLAG-Control_293_Ti_2	3.786	0.2887	1491.02	1491.73	7364.6		1	963.9	66.7	2	K.EIVVIHQDPEALK.D
	HsFLAG-Control_MG_293_	2.6878	0.215	1399.79	1399.63	5574.6		1	468.2	62.5	1	K.APLKPYPVSPSDK.V
	HsFLAG-Control_293_Ti_2	3.6098	0.2428	2120	2119.38	10401.6		5	546.8	44.1	1	K.LFLNETQTQEITEDIPVK.T
gi|48762920|ref|N	2	3	0.062	780	85018	7.5	U	liver phosphofructokinase isoform b [Homo sapiens]				
gi|50346005|ref|N	2	3	0.058	827	90203	7.8	U	liver phosphofructokinase isoform a [Homo sapiens]				
	Hs293FLP-MG_Ti_205.353	4.9445	0.3446	3105.73	3104.46	10971.1		1	1149.4	26.7	1	R.AAAYNLVQHGITNLCVIGGDGSLTGANIFR.S
	HsFLAG-Control_HeLa_S1	4.7241	0.391	1910.02	1909.11	10812.1		1	1135.1	52.9	2	R.TNVLGHLQQGGAPTPFDR.N
gi|55956788|ref|N	5	9	0.062	710	76615	4.7	U	nucleolin [Homo sapiens]				
*	Hs293FLP_TREX_Ti_105.2	3.0164	0.2915	1563.45	1563.79	5454.2		1	887.2	71.4	2	K.SAPELKTGISDVFAK.N
*	Hs293FLP_TREX_Ti_103.1	2.9153	0.2358	1177.43	1177.39	5286.9		1	916	88.9	1	K.VFGNEIKLEK.P
*	Hs293FLP_TREX_Ti_102.1	2.4024	0.2492	1178.52	1179.27	2110.6		3	162.5	61.1	1	K.EVFEDAAEIR.L
*	Hs293FLP_TREX_Ti_102.1	3.5063	0.2046	1179.36	1179.27	4829.7		1	1007	88.9	2	K.EVFEDAAEIR.L
*	Hs293FLP_TREX_Ti_104.1	3.0568	0.2184	1058.29	1058.27	6465.5		2	1156.9	87.5	3	K.VTLDWAKPK.G
gi|31657101|ref|N	2	2	0.062	520	58846	6.1	U	WD repeat domain 23 isoform 2 [Homo sapiens]				
gi|31657103|ref|N	2	2	0.059	546	61670	6.4	U	WD repeat domain 23 isoform 1 [Homo sapiens]				
	HsGST-MOCK_Ti_305.286	3.2676	0.1417	2169.04	2169.4	5406.3		1	545.9	50	1	R.VISHFLPNDLGFTDSYSQK.A
	HsGST-MOCK_Ti_305.293	4.09	0.3559	1443.12	1442.74	6993.5		1	1442.2	79.2	1	K.VVVYDLLSGHIVK.K
gi|4506331|ref|NI	1	7	0.062	145	16386	6.7	U	6-pyruvoyltetrahydropterin synthase [Homo sapiens]				
*	HsFLAG-Control_MG_293_	2.2407	0.1768	987.54	988.258	3988.1		1	482.7	68.8	7	K.VLPVGVLYK.V
gi|4505101|ref|NI	2	2	0.061	749	84052	9.6	U	microtubule-associated protein 7 [Homo sapiens]				
*	HsHeLa_Control-MG_Ti_20	2.211	0.348	989.49	990.147	2882.4		1	300.5	75	1	R.IIHGTASYK.K
*	HsGST-MOCK_Ti_105.155	3.7001	0.0881	3615.67	3615.95	6316.6		1	623.1	24.3	1	K.GALTGGTEVSALPCTTNAPGNGKPVGSPHVVTSHQSK.V
gi|34485722|ref|N	2	3	0.061	521	57811	4.9	U	karyopherin alpha 3 [Homo sapiens]				
*	Hs293FLP-MG_Ti_302.165	2.732	0.2108	2039.14	2038.09	6191.3		1	498.4	50	1	R.NVPQEESLEDSDVDADFK.A
*	Hs293FLP-MG_Ti_305.156	4.0623	0.3624	1759.22	1758.93	7535.4		1	1150.4	69.2	2	K.IEVLQQHENEDIYK.L
gi|16905517|ref|N	1	3	0.061	262	31301	11.3	U	FUS interacting protein (serine-arginine rich) 1 isoform 2 [Homo sapiens]				
gi|88952702|ref|X	1	3	0.151	106	12581	9.4	U	PREDICTED: similar to FUS interacting protein (serine-arginine rich) 1 [Homo sapiens]				
gi|88944399|ref|X	1	3	0.232	69	8329	9.4	U	PREDICTED: similar to FUS interacting protein (serine-arginine rich) 1 isoform 10 [Homo				
gi|88944397|ref|X	1	3	0.061	262	31301	11.3	U	PREDICTED: similar to FUS-interacting serine-arginine-rich protein 1 (TLS-associated pro				
gi|88944395|ref|X	1	3	0.232	69	8329	9.4	U	PREDICTED: similar to FUS interacting protein (serine-arginine rich) 1 isoform 9 [Homo sa				
gi|88944389|ref|X	1	3	0.087	183	22222	10.3	U	PREDICTED: similar to FUS interacting protein (serine-arginine rich) 1 isoform 6 [Homo sa				
gi|88944257|ref|X	1	3	0.092	173	21000	10.5	U	PREDICTED: similar to FUS interacting protein (serine-arginine rich) 1 isoform 4 [Homo sa				
gi|88944255|ref|X	1	3	0.232	69	8329	9.4	U	PREDICTED: similar to FUS interacting protein (serine-arginine rich) 1 isoform 3 [Homo sa				
gi|88944253|ref|X	1	3	0.232	69	8329	9.4	U	PREDICTED: similar to FUS interacting protein (serine-arginine rich) 1 isoform 2 [Homo sa				
gi|5730079|ref|NI	1	3	0.087	183	22222	10.3	U	FUS interacting protein (serine-arginine rich) 1 isoform 1 [Homo sapiens]				
	HsFLAG-Control_HeLa_NE	3.3069	0.2737	1919	1918.2	5915.8		1	829.5	56.7	3	R.YGPIVDVYVPLDFYTR.R
gi|14277700|ref|N	1	2	0.061	132	14515	7.2	U	ribosomal protein S12 [Homo sapiens]				
gi|89034991|ref|X	1	2	0.061	132	14598	6.9	U	PREDICTED: similar to ribosomal protein S12 [Homo sapiens]				
gi|88955046|ref|X	1	2	0.061	132	14502	6.8	U	PREDICTED: similar to ribosomal protein S12 [Homo sapiens]				
gi|88953190|ref|X	1	2	0.061	132	14501	7.2	U	PREDICTED: similar to ribosomal protein S12 [Homo sapiens]				

gi|51468838|ref|X	1	2	0.061	132	14598	6.9	U	PREDICTED: similar to ribosomal protein S12 [Homo sapiens]				
	Hs293FLP_TREX_Ti_102.2	2.1502	0.0925	1042.38	1043.16	7478.7		1	895.4	78.6	2	K.DVIEEYFK.C
gi|50658082|ref|N	3	5	0.06	597	69752	5.7	U	centrosomal protein 70 kDa [Homo sapiens]				
*	Hs283FLP_Ti_103.1176.11	2.58	0.1816	1078.43	1078.21	4357.9		2	604.2	77.8	1	K.SKIDALSSEK.L
*	Hs283FLP_Ti_105.2971.29	3.5739	0.1743	1484.85	1484.78	3732.9		4	755.7	79.2	3	K.TLSAELVPWLNLK.K
*	Hs283FLP_Ti_104.2351.23	3.9724	0.3912	1478.58	1477.7	3056.8		2	540.9	70.8	1	K.LFDVPSLNGVYPR.M
gi|40556376|ref|N	2	6	0.06	553	60547	9.2	U	cytokine-like nuclear factor n-pac [Homo sapiens]				
*	Hs293FLP-MG_Ti_205.267	4.2458	0.3543	1706.65	1707.03	8497.6		1	1511.2	65.6	5	K.DLVLGPSGVLQGIRPGK.C
*	HsHeLa_Control-MG_Ti_20	2.5839	0.2054	1985.2	1986.24	9993.8		1	720.9	53.3	1	K.CQNILQGNFKPDFYLK.Y
gi|5454096|ref|NI	2	3	0.06	487	55630	5.1	U	serine/threonine kinase 4 [Homo sapiens]				
*	Hs293FLP-MG_Ti_202.460	3.2892	0.3539	1776.26	1777.02	7185.8		1	1034.5	56.7	2	K.TLTEDEIATILQSTLK.G
*	HsHeLa_Control-MG_Ti_20	2.5846	0.2356	1482.63	1482.73	9273.7		1	640.2	54.2	1	R.ATATQLLQHPFVR.S
gi|73486658|ref|N	2	3	0.06	430	47518	9	U	aspartate aminotransferase 2 precursor [Homo sapiens]				
*	Hs293FLP_TREX_Ti_104.1	2.8438	0.2459	1451.24	1450.68	7317.6		1	1182	69.2	1	R.FVTVQTISGTGALR.I
*	Hs293FLP_TREX_Ti_103.2	4.1146	0.25	1269.4	1268.5	7896.3		1	1490.1	81.8	2	R.IAAAILNTPDLR.K
gi|54607053|ref|N	8	16	0.059	2671	292708	7.4	U	GCN1 general control of amino-acid synthesis 1-like 1 [Homo sapiens]				
*	HsFLAG-Control_HeLa_S1	3.7369	0.2039	1443.85	1441.63	5689.8		1	789.1	69.2	1	K.NLLHSLQSSGIGSK.A
*	HsFLAG-Control_HeLa_S1	4.6561	0.4493	1914.43	1913.18	7307.8		1	1875.6	69.4	3	K.VLPLEALVTDAGEVTEAGK.A
*	HsFLAG-Control_HeLa_S1	3.9187	0.3901	2023.55	2022.4	10550.1		1	1250.5	52.8	2	R.VLPQLISTITASVQNPALR.L
*	HsFLAG-Control_HeLa_S1	4.5137	0.3915	2238.37	2238.63	9501.6		1	1620.5	57.5	3	R.LQELDGELEAALGLLDIILAK.N
*	HsFLAG-Control_293_Ti_1	4.118	0.0935	2316.5	2315.76	5146.5		1	801.7	55	3	K.NPSGLTQYIPVLVDSFLPLLK.S
*	HsFLAG-Control_HeLa_S1	3.7862	0.2491	2117.62	2117.5	5375.5		1	787.7	55	1	K.GEPGAAPLSAPAFSLVFPFLK.M
*	HsFLAG-Control_HeLa_S1	3.4723	0.2196	2121.43	2119.47	6998		1	538	47.4	2	R.NPEILAIAPVLLDALTDPSR.K
*	HsFLAG-Control_HeLa_S1	3.6865	0.2137	2450.18	2449.72	7148.9		1	513.2	38.1	1	R.LFNDSSPVVLEESWDALNAITK.K
gi|4507659|ref|NI	8	10	0.059	2349	265598	5.1	U	translocated promoter region (to activated MET oncogene) [Homo sapiens]				
*	HsHeLa3_Ti_104.2324.232	3.1553	0.2307	1829	1827.05	6885.8		1	717.8	57.1	1	K.ELLHSQNTWLNTELK.T
*	HsHeLa3_Ti_105.2923.292	2.5393	0.283	2835.24	2836.26	3454.5		1	198.9	29.6	1	R.ILLSQTTGVAIPLHASSLDDVSLASTPK.R
*	HsHeLa3_Ti_105.2922.292	3.9948	0.3113	2836.07	2836.26	7233.1		1	1261.6	32.4	1	R.ILLSQTTGVAIPLHASSLDDVSLASTPK.R
*	HsHeLa3_Ti_104.4460.446	5.5743	0.4546	2026.04	2025.36	10623.9		1	2145	67.6	2	R.GQNLLLTNLQTIQGILER.S
*	HsFLAG-Control_HeLa_NE	4.7791	0.34	1774.9	1773.94	7699.6		1	1448.4	71.4	1	R.NLQEQTVQLQSELSR.L
*	HsFLAG-MOCK_300mM_T	3.9037	0.2974	1396.22	1394.66	6149.4		1	1136.9	75	2	K.IAHLAGVKDQLTK.E
*	HsHeLa3_Ti_106.2055.205	3.1085	0.1071	2366.39	2366.67	3726.9		1	284.2	43.5	1	R.GIASTSDPPTANIKPTPVVSTPSK.V
*	HsHeLa3_Ti_102.1650.165	4.5734	0.4692	2486.58	2487.47	6687.7		1	764.4	43.8	1	R.AADSQNSGEGNTGAAESSFSQEVSR.E
gi|55956916|ref|N	4	5	0.059	1108	127062	8.9	U	myosin IE [Homo sapiens]				
	HsFLAG-Control_Hela_Ti_1	3.0802	0.3693	1842.83	1844.12	8212.9		1	1014.4	56.2	1	K.DIILQSNPLLEAFGNAK.T
*	HsFLAG-Control_Hela_Ti_1	3.9928	0.4105	1728.61	1728.86	8450.1		1	1176	63.3	1	K.YFEIQFSPGGEPDGGK.I
*	HsFLAG-Control_Hela_Ti_1	4.2006	0.1627	1208.48	1208.49	6118		4	1165.8	77.3	2	K.VLQVSIGPGLPK.N
*	HsFLAG-Control_Hela_Ti_1	3.8786	0.4989	2172.73	2174.25	4440.7		1	401.1	50	1	R.NTTQNTGYSSGTQNANYPVR.A
gi|21071052|ref|N	4	4	0.059	1009	113928	8.6	U	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin a3 [Homo sap				
gi|21071054|ref|N	4	4	0.059	1009	113928	8.6	U	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin a3 [Homo sap				
	HsHeLa3_Ti_103.2008.200	2.9061	0.1546	1872.99	1872.11	6532.5		3	532.7	46.7	1	R.YYTGVVNNNEMVALQR.D
	HsHeLa3_Ti_103.2623.262	2.8686	0.2511	1482.46	1481.61	5571		2	566.9	61.5	1	K.TLGFNLESGWGSGR.A
	HsHeLa3_Ti_104.4928.492	2.7424	0.1012	1223.42	1222.47	7561.8		8	798.8	66.7	1	K.DLWSLLSFLK.L
	HsHeLa3_Ti_106.3456.345	4.2761	0.4414	2266.03	2265.62	6270.4		1	851.8	50	1	R.YFNEGTVLAHYADVLGLLLR.L
gi|34996483|ref|N	3	4	0.059	749	79423	9	U	hypothetical protein LOC132660 [Homo sapiens]				
*	HsHeLa3_Ti_105.1234.123	2.8377	0.2457	1300.18	1299.47	6875.5		2	664.7	63.6	1	K.LGNQTLKPDGQK.L
*	HsHeLa3_Ti_104.1231.123	1.9286	0.2304	1000.55	1001.17	3954		9	204	55.6	1	R.TPTSGPVITK.L
*	HsHeLa3_Ti_106.2386.238	4.5329	0.3915	2214.05	2213.5	9344.6		1	630.3	38.1	2	K.LSSQISDLLTRPTPALNSGGGK.L
gi|17402904|ref|N	1	2	0.059	272	28235	6.3	U	homolog of yeast mRNA transport regulator 3 [Homo sapiens]				

*	HsHeLa3_Ti_104.1416.141	3.1186	0.3246	1309.68	1309.43	5699.8		4	633.9	53.3	2	R.GGGPAGAGGEAPAALR.G
gi|62460633|ref|N	4	10	0.058	1271	140519	8.3	U	RNA-binding motif protein 16 [Homo sapiens]				
	HsFLAG-Control_HeLa_NE	3.7821	0.31	1331.71	1331.6	7308		1	1695.9	86.4	3	K.VPGLYVIDSIVR.Q
*	HsFLAG-Control_HeLa_NE	4.8537	0.4183	3232.46	3230.65	5369		1	776.8	28	4	K.DVGFGSLVIPGGSVASNLATSALPAGNVFNAPTK.Q
*	HsFLAG-MOCK_300mM_T	2.939	0.1697	1804.94	1803.97	5335.2		3	555.1	56.7	2	K.VPHLIDHQISSGENTR.S
*	HsFLAG-Control_HeLa_NE	3.8685	0.2474	1421.53	1420.52	8191.2		1	1309.8	72.7	1	R.VFDYFEGATSQR.K
gi|15559211|ref|N	4	5	0.058	1097	121888	6.7	U	RE1-silencing transcription factor [Homo sapiens]				
*	HsFLAG-MOCK_150mM_T	3.551	0.4293	2763.81	2765.05	4713.3		1	621	44	1	R.SLELSVVEPQPVFEASGAPDIYSSNK.D
*	HsFLAG-MOCK_150mM_T	4.7158	0.4622	1658.29	1658.68	6816.5		1	1580	73.3	2	K.ARESGSSTAEEGDFSK.G
*	HsFLAG-MOCK_150mM_T	3.4432	0.2576	1376.51	1376.42	4999.9		3	696	77.3	1	K.ENLREEASGDQK.L
*	HsFLAG-MOCK_150mM_T	3.0112	0.3269	1289.53	1289.36	5426.5		1	883.4	77.8	1	K.GDFVCIFCDR.S
gi|45446743|ref|N	2	3	0.058	938	102975	7	U	DEAD box polypeptide 42 protein [Homo sapiens]				
gi|45446747|ref|N	2	3	0.058	938	102975	7	U	DEAD box polypeptide 42 protein [Homo sapiens]				
	HsHeLa3_Ti_103.3692.369	3.1505	0.2662	1607.94	1607.87	6751.7		1	846.9	66.7	1	K.ELLDLAMQNAWFR.K
	HsHeLa3_Ti_104.1751.175	4.6343	0.3776	3814.33	3814.98	5569		1	570.4	21.2	2	K.AGSSAAGASGWTSAGSLNSVPTNSAQQGHNSPDSPVTSAAK.G
gi|25777602|ref|N	3	3	0.058	908	100200	5.2	U	proteasome 26S non-ATPase subunit 2 [Homo sapiens]				
*	HsFLAG-Control_293_Ti_2	3.8151	0.189	2217.97	2219.42	8423.6		2	1035.5	33	1	K.APVQPQQSPAAAPGGTDEKPSGK.E
*	HsFLAG-Control_MG_293_	3.5779	0.3401	1474.35	1474.67	11789.1		1	1126	57.1	1	K.SGALLACGIVNSGVR.N
*	HsFLAG-Control_HeLa_S1	4.074	0.3087	1453.31	1453.68	7761.1		1	1252.6	67.9	1	R.VGQAVDVVGQAGKPK.T
gi|45439306|ref|N	2	5	0.058	501	57136	6.5	U	aspartyl-tRNA synthetase [Homo sapiens]				
*	Hs293FLP_TREX_Ti_103.2	3.7597	0.222	1162.02	1161.39	8345.9		1	1584.3	83.3	3	K.IYVISLAEPR.L
*	HsFLAG-Control_293_Ti_2	5.3771	0.3845	1963.57	1962.21	10130.2		1	2402.1	66.7	2	K.IISAASEGGANVFTVSYFK.N
gi|11321607|ref|N	2	2	0.058	432	48551	6.1	U	thyroid hormone receptor interactor 13 [Homo sapiens]				
*	HsFLAG-Control_HeLa_S1	3.2197	0.2863	1446.45	1446.64	7165.6		1	1090.7	75	1	R.NVQSVSIIDTELK.V
*	HsFLAG-Control_HeLa_S1	3.2064	0.2886	1175.52	1175.42	5586.3		1	1105.4	77.3	1	R.VVLLHGPPGTGK.T
gi|22027651|ref|N	3	3	0.057	949	104637	5.1	U	adaptor-related protein complex 1 beta 1 subunit isoform a [Homo sapiens]				
gi|22027653|ref|N	3	3	0.057	942	103921	5.1	U	adaptor-related protein complex 1 beta 1 subunit isoform b [Homo sapiens]				
	HsGST-MOCK_Ti_403.148	2.1831	0.0929	889.49	889.039	5749		3	411.2	75	1	K.YFTTTKK.G
	HsFLAG-Control_HeLa_S1	4.4884	0.3089	1570.99	1569.84	6416.5		1	1202.6	71.4	1	R.LASQANIAQVLAELK.E
	HsFLAG-Control_HeLa_S1	3.6245	0.1112	3617.86	3618.03	11471.7		3	726.2	21.8	1	R.IDNADELLESFLEGFHDESTQVQLQLLTAIVK.L
gi|4557495|ref|N	2	4	0.057	717	82922	8.1	U	cleavage stimulation factor subunit 3 isoform 1 [Homo sapiens]				
*	HsFLAG-Control_HeLa_NE	5.5941	0.4046	1738.87	1739.02	6922.7		1	2018.9	80	3	R.FLAFESNIGDLASILK.V
*	HsFLAG-Control_HeLa_NE	3.5518	0.4149	2436.72	2437.75	10100.5		1	797.8	37.5	1	R.IITGGAPELAVEGNGPVESNAVLTK.A
gi|41146847|ref|X	2	4	0.057	581	62543	9.4	U	PREDICTED: hypothetical protein LOC57606 isoform 1 [Homo sapiens]				
gi|88979579|ref|X	2	4	0.07	469	51384	8.8	U	PREDICTED: hypothetical protein LOC57606 isoform 9 [Homo sapiens]				
gi|88979572|ref|X	2	4	0.057	581	62543	9.4	U	PREDICTED: hypothetical protein LOC57606 isoform 6 [Homo sapiens]				
gi|88974131|ref|X	2	4	0.07	469	51384	8.8	U	PREDICTED: hypothetical protein LOC57606 isoform 3 [Homo sapiens]				
	HsFLAG-Control_293_Ti_2	3.7649	0.2917	1497.7	1497.65	7257.8		2	867.4	56.2	3	R.SGAVQGAGSLGPGSPVR.A
	HsFLAG-Control_MG_293_	2.7314	0.262	1737.89	1738.94	6181.8		4	371.1	46.7	1	R.LSLQGHPTDLQTSNVK.N
gi|23510379|ref|N	3	7	0.056	890	101310	5	U	transportin 1 [Homo sapiens]				
gi|23510381|ref|N	3	7	0.056	890	101310	5	U	transportin 1 [Homo sapiens]				
	HsFLAG-Control_HeLa_NE	4.4075	0.3855	2473.57	2473.83	3927		1	538.9	52.6	5	K.LEQLNQYPDFNNYLIFVLTK.L
	HsFLAG-Control_HeLa_S1	3.6736	0.4336	1676.07	1675.8	8464.3		1	1361.4	67.9	1	K.SECLNNIGDSSPLIR.A
	HsFLAG-Control_HeLa_S1	2.6286	0.2264	1804.74	1805.04	8689.3		1	790.6	53.6	1	R.YAHWVVSQPPDTYLK.P
gi|55749689|ref|N	3	5	0.056	891	97792	4.6	U	hypothetical protein LOC22870 [Homo sapiens]				
*	HsFLAG-Control_293_Ti_1	4.9045	0.4333	2293.14	2291.65	11341.8		1	1436.4	52.5	1	R.LYGFLQSTGSLNPLLASFFSK.V
*	HsFLAG-Control_293_Ti_2	3.2374	0.1526	1130.41	1130.29	7306.9		1	1398.8	85	3	R.VAGALVQNTEK.G

*	HsFLAG-Control_293_Ti_2	4.3508	0.4974	1826.95	1827.9	6213.9		1	986.2	64.7	1	R.SQDPTPPSAPQEATEGSK.V
gi|5901922|ref|N	1	3	0.056	378	44468	5.2	U	CDC37 homolog [Homo sapiens]				
*	HsFLAG-Control_Hela_Ti_1	4.5639	0.4852	2270.05	2270.54	6735.3		1	938.6	52.5	3	R.LGPGGLDPVEVYESLPEELQK.C
gi|5454004|ref|N	1	2	0.056	391	44156	6.3	U	D4, zinc and double PHD fingers family 2 [Homo sapiens]				
*	HsHeLa3_Ti_102.3546.354	3.7567	0.3617	2643.22	2642.7	7647.3		1	1127.1	50	2	R.ILEPDDFLDDLDDEDYEEDTPK.R
gi|4759098|ref|N	1	2	0.056	288	33666	11.2	U	splicing factor, arginine/serine-rich 10 (transformer 2 homolog, Drosophila) [Homo sapiens				
*	HsFLAG-Control_HeLa_NE	3.9566	0.4379	1811.86	1811.99	7379.7		1	1140.2	60	2	K.YGPIADVSIVYDQQSR.R
gi|27735029|ref|N	2	3	0.056	216	25091	6.7	U	MOB1, Mps One Binder kinase activator-like 1A [Homo sapiens]				
gi|8922671|ref|N	2	3	0.056	216	25008	7.2	U	Mob4B protein [Homo sapiens]				
	HsFLAG-Control_HeLa_NE	2.7304	0.2531	1225.65	1226.34	4974.6		6	247.7	50	2	K.HAEATLGSGNLR.M
	HsFLAG-Control_HeLa_NE	3.0957	0.3354	1227.11	1226.34	6901		1	990.7	72.7	1	K.HAEATLGSGNLR.M
gi|4759172|ref|N	4	6	0.055	1148	128875	8.3	U	splicing factor, arginine/serine-rich 2, interacting protein [Homo sapiens]				
*	HsHeLa_Control-MG_Ti_10	4.0644	0.4703	2464.56	2464.61	5336.4		1	728.3	47.8	2	R.VGSSSSESCAQDLPVLVGEEGEVK.K
*	HsHeLa_Control-MG_Ti_10	2.1431	0.1471	996.7	997.139	4111.6		3	433.2	71.4	1	K.THIEQIQK.H
*	HsHeLa_Control_Ti_102.13	3.4151	0.2593	1642.78	1640.66	5686.9		1	900.7	60.7	1	K.NDIHLDADDPNSADK.H
*	HsHeLa_Control-MG_Ti_20	4.3994	0.4727	1626.07	1626.72	5100.8		1	1250.3	80	2	R.KPLSGNSNSSGSESFK.F
gi|34101286|ref|N	4	10	0.055	1074	117012	9	U	zinc finger RNA binding protein [Homo sapiens]				
*	HsHeLa3_Ti_103.1378.137	3.2702	0.3547	1860.03	1859.95	6472.8		1	640.9	53.1	1	K.AGYSQGATQYTQAQQTR.Q
*	HsHeLa3_Ti_103.1268.126	2.245	0.2286	1124.54	1125.23	5454.8		1	394.8	66.7	2	K.ISCAGPQTYK.E
*	HsHeLa3_Ti_105.1952.195	3.7302	0.2574	1602.04	1601.85	6117		5	692	57.7	2	R.NVNLVLLCSEKPSK.T
*	HsHeLa3_Ti_104.4803.480	4.3782	0.3917	2136.17	2136.47	4403.8		1	1111.3	70.6	5	R.VPTWSDFPSWAMELLVEK.A
gi|19913410|ref|N	2	3	0.055	893	99327	5.5	U	major vault protein [Homo sapiens]				
gi|19913412|ref|N	2	3	0.055	893	99327	5.5	U	major vault protein [Homo sapiens]				
	HsFLAG-Control_Hela_Ti_1	3.079	0.2855	1932.77	1932.14	6640.2		1	550.1	50	1	R.QAIPLDENEGIYVQDVK.T
	HsHeLa_Control-MG_Ti_20	4.8192	0.4571	3121.49	3121.44	7939.4		1	805.9	26.6	2	R.VASGPSPGEGISPQSAQAPQAPGDNHVVPVLR.-
gi|24762225|ref|N	2	3	0.055	381	41542	6.3	U	homeobox protein Meis2 isoform f [Homo sapiens]				
gi|9910356|ref|N	2	3	0.07	302	32836	6	U	homeobox protein Meis2 isoform e [Homo sapiens]				
gi|57863281|ref|N	2	3	0.05	421	46175	5.3	U	Meis1, myeloid ecotropic viral integration site 1 homolog 3 isoform 1 [Homo sapiens]				
gi|57863279|ref|N	2	3	0.059	358	39052	5	U	Meis1, myeloid ecotropic viral integration site 1 homolog 3 isoform 2 [Homo sapiens]				
gi|4505151|ref|N	2	3	0.054	390	43016	6.3	U	Meis1 homolog [Homo sapiens]				
gi|27502383|ref|N	2	3	0.069	306	33598	5.6	U	homeobox protein Meis2 isoform h [Homo sapiens]				
gi|27502381|ref|N	2	3	0.054	388	42272	6.2	U	homeobox protein Meis2 isoform g [Homo sapiens]				
gi|24762250|ref|N	2	3	0.045	470	51060	6.5	U	homeobox protein Meis2 isoform d [Homo sapiens]				
gi|24762246|ref|N	2	3	0.053	394	43061	6.2	U	homeobox protein Meis2 isoform b [Homo sapiens]				
gi|24762244|ref|N	2	3	0.052	401	43791	6.2	U	homeobox protein Meis2 isoform a [Homo sapiens]				
gi|24762241|ref|N	2	3	0.044	477	51790	6.4	U	homeobox protein Meis2 isoform c [Homo sapiens]				
	HsHeLa3_Ti_104.4967.496	4.2091	0.1825	2400.28	2399.81	6531.6		2	1113.2	37.5	1	K.PLFSSNPELDNLMIQAIQVLR.F
	HsHeLa3_Ti_105.4866.486	2.677	0.1092	2400.96	2399.81	7217.2		7	451.3	40	2	K.PLFSSNPELDNLMIQAIQVLR.F
gi|8923114|ref|N	1	2	0.055	271	31312	4.9	U	OTU domain, ubiquitin aldehyde binding 1 [Homo sapiens]				
*	HsFLAG-Control_HeLa_S1	4.1174	0.3082	1725.42	1724.96	9140.5		3	1250.7	60.7	2	R.IQQEIAVQNPLVSER.L
gi|14149627|ref|N	2	3	0.054	952	109297	5.2	U	ubiquitin specific protease 15 [Homo sapiens]				
*	HsHeLa_Control-MG_Ti_20	5.109	0.356	3552.4	3554.86	3625		1	413.7	28.4	1	R.FAPQFSGYQQQDCQELLAFLLDGLHEDLNR.I
*	HsHeLa_Control-MG_Ti_20	4.9155	0.4804	2142.67	2143.45	4688.7		1	1015.2	62.5	2	K.IGNILDLCTALSALSGIPADK.M
gi|44955910|ref|N	4	5	0.054	911	99854	8.2	U	E2F transcription factor 7 [Homo sapiens]				
*	Hs293FLP_Ti_302.4544.45	3.2685	0.193	1648.48	1648	5574.9		1	834.4	64.3	1	R.LYDIANVLTSLALIK.K
*	HsHeLa_Control-MG_Ti_20	3.753	0.4369	1333.52	1333.4	5891.7		1	1088	81.8	2	R.HGSFNTVQASER.I
*	HsFLAG-MOCK_300mM_T	3.9564	0.4383	2360.05	2360.68	4277.2		1	519.2	45.2	1	R.SHSVVQQPESPVYVGHPVSVVK.L
*	HsHeLa_Control-MG_Ti_20	4.8851	0.4022	2361.1	2360.68	8797.1		1	2236.6	44	1	R.SHSVVQQPESPVYVGHPVSVVK.L
gi|4557843|ref|N	2	6	0.054	616	65323	9.3	U	regulatory factor X, 5 [Homo sapiens]				

gi|71040090|ref|N	2	6	0.054	616	65323	9.3	U	regulatory factor X, 5 [Homo sapiens]				
	HsFLAG-MOCK_300mM_T	4.6545	0.373	1796.31	1795.99	4177.4		1	1009	67.6	3	K.RTAEVPVSEASGQAPPAK.A
	HsFLAG-Control_HeLa_NE	4.4403	0.383	1388.54	1388.52	7376.7		1	1451.6	75	3	K.GAVLAQGQGDGTVSK.G
gi|51599156|ref|N	6	12	0.053	1912	218003	5.9	U	chromodomain helicase DNA binding protein 4 [Homo sapiens]				
	HsHeLa3_Ti_106.3111.311	4.4414	0.4161	1901.51	1901.22	3706		1	749.4	68.8	3	K.GPFLVSAPLSTIINWER.E
*	HsHeLa3_Ti_102.3199.319	3.6713	0.3572	2479.06	2479.59	6380		1	1041.8	52.5	2	R.NQDETEDTELQGMNEYLSSFK.V
*	HsHeLa3_Ti_102.1610.161	4.4474	0.4	2304.88	2304.39	6650.6		1	945.1	52.4	2	K.STAPETAIECTQAPAPASEDEK.V
*	HsHeLa3_Ti_104.1941.194	4.1784	0.3933	2206.84	2206.45	4365.5		1	465.9	50	1	R.AAYLNMSEDPSHPSMALNTR.F
	HsHeLa3_Ti_106.1736.173	3.3318	0.2573	850.94	850.008	6119.2		3	1098.6	92.9	2	K.PANAVLHK.V
*	HsFLAG-Control_HeLa_NE	3.2172	0.245	1422.2	1422.54	8020.4		4	888.3	62.5	2	R.APEPTPQQVAQQQ.-
gi|8923609|ref|NI	2	7	0.053	608	68183	6.3	U	nuclear protein localization 4 [Homo sapiens]				
*	HsFLAG-Control_HeLa_NE	5.2272	0.4691	2023.49	2024.24	6554.6		1	1165	64.7	5	K.VFGAPNVVEDEIDQYLSK.Q
*	HsFLAG-Control_HeLa_NE	4.0536	0.4589	1678.85	1678.79	4632.6		1	767	69.2	2	K.ESSSEQYVPDVFYK.D
gi|54873624|ref|N	2	2	0.053	585	64990	8.9	U	CDA02 protein [Homo sapiens]				
*	HsFLAG-Control_HeLa_S1	2.8996	0.2381	2381.64	2380.54	10052.5		1	941.9	44.7	1	R.NVNNEVHFFENNNFNTIANK.L
*	HsFLAG-Control_HeLa_S1	3.1871	0.1467	1215.5	1215.44	7187.2		3	699.7	65	1	K.VATAYRPPALR.N
gi|28144916|ref|N	1	2	0.053	246	28383	8.7	U	hypothetical protein LOC55957 [Homo sapiens]				
*	HsHeLa3_Ti_103.3855.385	3.1663	0.2226	1544.35	1544.76	6184.4		1	931.3	70.8	2	R.NQLDAVLQCLLEK.S
gi|7657351|ref|NI	4	9	0.052	1328	148850	9.2	U	MYB binding protein 1a [Homo sapiens]				
*	HsFLAG-Control_HeLa_NE	3.7018	0.1768	2485.63	2484.9	6375.4		1	379.4	35.7	1	K.ADLNIILSSPEQLELFLLAQQK.V
*	HsFLAG-MOCK_300mM_T	4.675	0.4117	2105.27	2105.4	11604		1	2156.9	61.1	6	R.EAVSSAFFSLLQTLSTQFK.Q
*	HsFLAG-Control_MG_293_	3.2406	0.2771	1317.4	1317.53	7418.4		1	998.8	72.7	1	R.VYSTALSSFLTK.R
*	HsFLAG-MOCK_300mM_T	2.9346	0.3434	1522.92	1522.7	5449		4	368.5	53.3	1	K.SPAPGAPTRSPSTPAK.S
gi|62460637|ref|N	3	5	0.052	1081	118715	5	U	importin 4 [Homo sapiens]				
*	HsFLAG-Control_HeLa_S1	4.5743	0.3224	2180.24	2179.52	7484.4		1	1296.7	55.3	2	R.LLNETLGEVGSPGLLFYSLR.T
*	HsFLAG-Control_HeLa_S1	3.5223	0.339	2110.46	2110.42	7179.1		1	706.7	50	2	R.EDLQPVQIQSLETLGVLAR.A
*	HsFLAG-Control_293_Ti_2	2.5996	0.1102	1852.9	1852.14	10830.4		1	762	46.9	1	R.LLPVLLSTAQEADPEVR.S
gi|4505541|ref|NI	3	6	0.052	962	107907	4.9	U	vesicle docking protein p115 [Homo sapiens]				
*	HsFLAG-Control_HeLa_NE	2.7143	0.2965	1743.51	1742.92	10027.8		2	778.8	53.6	1	R.QSEDLGSQFTEIFIK.Q
*	HsFLAG-Control_HeLa_NE	4.8926	0.4486	1810.43	1810.87	10329.8		1	1819.2	61.8	4	K.SSQTSGTNEQSSAIVSAR.D
*	HsFLAG-Control_HeLa_NE	3.3277	0.2573	1877.68	1878.04	12381.8		1	895.7	46.9	1	K.EQLDSSNSTIAILQTEK.D
gi|21618338|ref|N	2	2	0.052	769	87981	6.3	U	signal transducer and activator of transcription 3 isoform 2 [Homo sapiens]				
gi|47458820|ref|N	2	2	0.055	722	83126	7.1	U	signal transducer and activator of transcription 3 isoform 3 [Homo sapiens]				
gi|21618340|ref|N	2	2	0.052	770	88068	6.3	U	signal transducer and activator of transcription 3 isoform 1 [Homo sapiens]				
	HsFLAG-Control_HeLa_S1	3.1737	0.3482	1762.79	1761.98	7979		1	781.4	57.7	1	R.FLQESNVLYQHNLR.R
	HsFLAG-Control_HeLa_S1	3.9232	0.3264	2576.87	2577.86	6369.9		1	706.8	29	1	R.LLQTAATAAQQGGQANHPTAAVVTEK.Q
gi|7657581|ref|NI	2	2	0.052	675	74176	8.6	U	solute carrier family 25, member 13 (citrin) [Homo sapiens]				
*	HsFLAG-Control_MG_293_	3.0117	0.2113	1509.65	1507.69	8475.8		1	1030.7	70.8	1	R.YLNIFGESQPNPK.T
*	HsFLAG-Control_293_Ti_2	3.537	0.3869	2107.39	2106.47	7904.9		1	868.6	45.2	1	R.FGLGSVAGAVGATAVYPIDLVK.T
gi|13376212|ref|N	1	2	0.052	404	44863	4.8	U	ubiquitin-activating enzyme E1-domain containing 1 isoform 1 [Homo sapiens]				
gi|38327032|ref|N	1	2	0.06	348	38537	4.8	U	ubiquitin-activating enzyme E1-domain containing 1 isoform 2 [Homo sapiens]				
	HsFLAG-Control_HeLa_S1	3.8331	0.2657	2216.63	2216.54	5578.8		1	445.5	47.5	2	K.NFSGPVPDLPEGITVAYTIPK.K
gi|28872796|ref|N	1	2	0.052	345	36106	8.3	U	CCAAT/enhancer binding protein beta [Homo sapiens]				
*	HsHeLa3_Ti_105.1474.147	5.3614	0.4639	1757.83	1757.95	7692.1		1	2227.8	73.5	2	K.APPTACYAGAAPAPSQVK.S
gi|31652240|ref|N	4	5	0.051	1505	164312	6	U	CCAAT displacement protein isoform a [Homo sapiens]				
	HsHeLa3_Ti_103.3667.366	3.0465	0.3286	2174.18	2173.56	3975.5		1	355.4	44.7	1	R.LIDVPDPVPALDLGQQLQLK.V
	HsHeLa3_Ti_105.2219.221	3.925	0.2782	2132.02	2131.35	8069.1		1	1393.9	61.1	2	K.LRENSASQISQLEQQLSAK.N
*	HsFLAG-Control_HeLa_NE	3.4874	0.3624	2091.79	2091.41	8456.8		1	775.5	47.4	1	R.LFGETILGLTQGSVSDLLAR.P
*	HsHeLa3_Ti_106.2583.258	4.0843	0.3866	1859.93	1858.11	7604.4		1	1055.9	61.8	1	R.RPSSLQSLFGLPEAAGAR.D

gi|4503539|ref|N	2	3	0.051	907	102362	7.1	U	eukaryotic translation initiation factor 4 gamma, 2 [Homo sapiens]			
*	HsHeLa3_Ti_104.3801.380	3.7227	0.2962	3148.39	3147.57	10132.5	1	904.8	25.8	1	K.MDRDPLGGLADMFGQMPGSGIGTGPGVIQDR.F
*	HsFLAG-Control_HeLa_NE	2.9762	0.1548	1579.52	1579.84	6408.2	1	603.2	57.1	2	R.TQTPPLGQTPQLGLK.T
gi|55770844|ref|N	2	4	0.051	906	100071	6.3	U	catenin, alpha 1 [Homo sapiens]			
*	HsFLAG-Control_HeLa_NE	3.9668	0.4152	3202.99	3202.5	7777.7	1	1275.7	32.1	3	R.VLTDAVDDITSIDDFLAVSENHILEDVNK.C
	HsFLAG-Control_HeLa_NE	2.7217	0.1492	1821.7	1819.92	11683.5	2	797.6	46.9	1	R.TSVQTEDDQLIAGQSAR.A
gi|21361114|ref|N	1	3	0.051	314	34062	9.9	U	solute carrier family 25 (mitochondrial carrier; oxoglutarate carrier), member 11 [Homo sa			
*	HsFLAG-Control_293_Ti_2	5.3125	0.5082	1637.01	1636.85	10456.6	1	2856	80	3	R.AVVVNAAQLASYSQSK.Q
gi|23510448|ref|N	3	11	0.05	734	82286	8.4	U	minichromosome maintenance deficient protein 5 [Homo sapiens]			
*	HsFLAG-Control_293_Ti_2	3.4591	0.2131	1417.4	1417.69	3512.4	1	688.5	79.2	2	R.LAALPNVYEVISK.S
*	HsFLAG-Control_MG_293_	4.1649	0.2926	1165.27	1165.34	7055.3	1	1924.6	90	4	K.AIACLLFGGSR.K
*	HsFLAG-Control_MG_293_	3.8953	0.2758	1352.77	1352.5	9044.5	1	932.4	62.5	5	R.CSVLAAANSVFGR.W
gi|4502563|ref|N	1	2	0.05	700	80007	5	U	calpain 2, large subunit [Homo sapiens]			
*	Hs293FLP-MG_Ti_203.449	4.107	0.3322	3977.12	3977.39	8334.2	7	401.5	18.4	2	K.YLNQDYEALRNECLEAGTLFQDPSFPAIPSALGFK.E
gi|4885225|ref|N	2	7	0.05	656	68478	9.3	U	Ewing sarcoma breakpoint region 1 isoform EWS [Homo sapiens]			
gi|7669490|ref|N	2	7	0.057	583	61287	9.1	U	Ewing sarcoma breakpoint region 1 isoform EWS-b [Homo sapiens]			
	HsFLAG-Control_HeLa_NE	3.7839	0.3421	1451.15	1451.53	5493	1	1086.3	73.1	5	K.GDATVSYEDPPTAK.A
	HsFLAG-MOCK_300mM_T	4.9716	0.4413	2235.2	2236.3	4457.2	1	1175.9	72.2	2	R.AGDWQCPNPGCGNQNFAWR.T
gi|24308207|ref|N	2	3	0.05	583	63473	8.3	U	leucine rich repeat containing 47 [Homo sapiens]			
*	HsFLAG-Control_HeLa_S1	4.0547	0.4624	1773.97	1773.09	6591.4	1	886.3	58.8	2	R.NALGPGLSPELGPLPALR.V
*	HsFLAG-Control_HeLa_NE	3.1391	0.2206	1184.66	1184.34	6524.9	1	800.8	75	1	R.TAATLATHELR.A
gi|4506013|ref|N	1	2	0.05	360	41564	4.9	U	protein phosphatase 1, regulatory subunit 7 [Homo sapiens]			
*	HsFLAG-Control_HeLa_S1	4.0427	0.4459	1991.76	1992.28	10280.7	1	1207.2	55.9	2	R.AIENIDTLTNLESLFLGK.N
gi|33469917|ref|N	3	3	0.049	863	96558	6.7	U	minichromosome maintenance protein 4 [Homo sapiens]			
gi|33469919|ref|N	3	3	0.049	863	96558	6.7	U	minichromosome maintenance protein 4 [Homo sapiens]			
	HsHeLa3_Ti_105.1162.116	2.5732	0.1297	1101.09	1100.22	6283.9	2	720	83.3	1	R.QRPDLGSAQK.G
	HsHeLa3_Ti_104.4224.422	2.674	0.1353	2142.38	2142.48	7065.2	1	507.9	44.4	1	R.NLNPEDIDQLITISGMVIR.T
	Hs293FLP_TREX_Ti_102.2	2.9899	0.3402	1366.31	1366.51	5282.7	1	733.1	66.7	1	R.ALADDDFLTVTGK.T
gi|68509926|ref|N	2	3	0.049	795	90933	7.5	U	DEAH (Asp-Glu-Ala-His) box polypeptide 15 [Homo sapiens]			
*	HsHeLa3_Ti_106.1510.151	2.5837	0.0999	1046.49	1045.15	5670.7	1	878.2	93.8	2	K.RGVACTQPR.R
*	HsHeLa_Control-MG_Ti_20	4.1102	0.2318	3550.04	3552.02	7324.7	3	382.3	21.6	1	K.DNQVVQLHPSTVLDHKPEWVLYNEFVLTTK.N
gi|4758410|ref|N	3	6	0.049	673	74128	6.1	U	fragile X mental retardation syndrome related protein 2 [Homo sapiens]			
*	Hs293FLP_TREX_Ti_102.2	2.891	0.219	1617.68	1617.73	3406.5	3	382.1	62.5	1	R.ANEQEPCGWWLAR.V
*	Hs293FLP_TREX_Ti_106.2	3.4958	0.3492	1321.62	1320.58	7004.8	1	1218.5	77.3	3	R.LRPVNPNPLATK.G
	Hs293FLP_TREX_Ti_102.1	2.1428	0.1072	943.49	944.116	6968.5	3	643.7	71.4	2	K.VIQEIVDK.S
gi|18379334|ref|N	1	7	0.049	305	34208	11.8	U	RNA-binding protein S1, serine-rich domain [Homo sapiens]			
gi|6857826|ref|N	1	7	0.049	305	34208	11.8	U	RNA-binding protein S1, serine-rich domain [Homo sapiens]			
	HsFLAG-Control_HeLa_NE	4.7284	0.4565	1761.18	1761.84	7184.3	1	1917.5	78.6	7	K.GYAYVEFENPDEAEK.A
gi|8922491|ref|N	1	2	0.049	247	27951	9.7	U	transmembrane protein 33 [Homo sapiens]			
*	HsFLAG-Control_MG_293_	4.4062	0.3988	1214.24	1214.45	9738	1	2157.6	86.4	2	R.ALLANALTSALR.L
gi|89038202|ref|X	5	6	0.048	1563	169040	6	U	PREDICTED: MAX dimerization protein 5 isoform 4 [Homo sapiens]			
gi|89038899|ref|X	5	6	0.048	1563	169040	6	U	PREDICTED: similar to MAX-interacting protein isoform 8 [Homo sapiens]			
	HsFlag1P_Ti_104.2463.246	2.7234	0.1207	1490.31	1490.74	5338.9	6	600.5	60.7	1	K.TTGITTPVASVAFPK.S
	HsF-IP-293-MG_Ti_102.24	4.0219	0.3815	2396.96	2397.52	9038.1	1	1357	55	2	K.TCQENSDVFQQEQGISDLLGK.S
	HsF-IP-293-MG_Ti_103.19	2.838	0.2575	1288.42	1288.49	5452.6	1	804.6	72.7	1	R.ISNPSAFSIVPR.R
	HsFLAG-Control_HeLa_NE	2.8288	0.0956	1523.65	1523.64	9297.1	1	787.9	57.7	1	R.AFSEIQGLTDQADK.L
	Hs293FLP_TREX_Ti_104.2	2.581	0.2606	1388.51	1388.65	6845.5	2	625.2	58.3	1	R.VTLGPTQVFLANK.D
gi|4503251|ref|N	2	3	0.048	770	82588	5.7	U	disabled homolog 2 [Homo sapiens]			

*	HsHeLa3_Ti_106.1794.179	3.0735	0.3185	1361.49	1360.51	6327.8		1	1067.9	77.3	2	K.TGVIEHEHPVNK.I
*	HsHeLa3_Ti_102.3090.309	3.2848	0.4544	2668.96	2669.89	4377.8		1	403.4	41.7	1	K.SGVDQMDLFGDMSTPPDLNSPTESK.D
gi|33667028|ref|N	1	2	0.048	587	61099	8.8	U	interferon regulatory factor 2 binding protein 2 [Homo sapiens]				
*	HsHeLa3_Ti_104.2212.221	5.0015	0.417	2494.84	2495.75	9275		1	1543.3	46.3	2	R.AAASLAAVSGTAAASLGSAQPTDLGAHK.R
gi|13540586|ref|N	1	2	0.048	518	57341	5.2	U	hypothetical protein LOC81556 [Homo sapiens]				
gi|89039134|ref|X	1	2	0.052	483	53627	5.2	U	PREDICTED: similar to CG4785-PA [Homo sapiens]				
	HsFLAG-Control_HeLa_NE	2.9165	0.2075	2582.14	2579.56	9486		1	776.1	39.6	2	K.EGDEVGTGITDDNEDENSANQIAGK.I
gi|4503747|ref|N	7	16	0.047	2602	278193	5.7	U	filamin B, beta (actin binding protein 278) [Homo sapiens]				
	HsHeLa_Control-MG_Ti_20	4.0112	0.3224	1227.4	1227.53	5098.2		1	1284	90	3	R.LIALLEVLSQK.R
*	HsHeLa3_Ti_105.3086.308	4.5288	0.4415	2048.91	2049.29	4010.1		1	771.9	68.8	4	K.IPYLPITNFNQNWQDGK.A
*	HsHeLa3_Ti_104.1868.186	2.9744	0.2222	1905.81	1906.04	6323.2		1	618.3	50	1	K.SPFVVQVGEACNPNACR.A
*	HsFLAG-Control_HeLa_S1	3.8963	0.3687	2099.99	2098.28	8233.5		1	1083.7	55.9	1	K.DFLDGVYAFEYYPSTPGR.Y
*	HsFLAG-Control_HeLa_S1	3.1392	0.3426	1769.74	1768.02	9302.6		5	583.6	46.9	1	K.APLNVQFNSPLPGDAVK.D
*	HsHeLa_Control-MG_Ti_20	3.5012	0.3731	2548.67	2548.86	5244.9		1	544.6	40	4	K.VTASGPGLSSYGVPASLPVDFAIDAR.D
*	HsFLAG-Control_HeLa_S1	3.0305	0.3228	1645.9	1645.86	8978.6		1	858.9	56.7	2	R.APSVATVGSICDLNLK.I
gi|61744475|ref|N	2	4	0.047	661	71123	5	U	solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2 is				
gi|65506891|ref|N	2	4	0.049	630	67994	5	U	solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2 is				
gi|61744483|ref|N	2	4	0.059	529	57945	5.3	U	solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2 is				
gi|61744481|ref|N	2	4	0.055	568	61816	5.2	U	solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2 is				
gi|61744479|ref|N	2	4	0.052	599	64873	5.1	U	solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2 is				
gi|61744477|ref|N	2	4	0.049	631	68101	5	U	solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2 is				
	HsHeLa_Control-MG_Ti_20	3.9866	0.3746	1867.22	1868.1	10204		1	1100	50	2	R.IGDLQAFQGHGAGNLAGLK.G
	HsHeLa_Control-MG_Ti_20	3.3859	0.2748	1373.36	1372.69	5781.7		1	753.6	68.2	2	R.LLTSFLPAQLLR.L
gi|4505257|ref|N	2	5	0.047	577	67820	6.4	U	moesin [Homo sapiens]				
*	HsHeLa3_Ti_103.4003.400	3.0576	0.4331	2083.1	2083.26	10433		1	1283.2	59.4	2	K.FYPEDVSEELIQDITQR.L
	Hs293FLP_TREX_Ti_103.2	3.2866	0.3333	1182.58	1183.35	5407.2		1	745.5	72.2	3	K.APDFVFYAPR.L
gi|15420883|gb|A	2	2	0.047	557	59909	8.2	U	neuralized [Mus musculus]				
*	HsFLAG-Control_293_Ti_2	4.0718	0.4605	1819.28	1819.11	9498.3		1	1438.1	63.3	1	R.TVDPLWALVDVYGLTR.G
*	HsFLAG-Control_MG_293_	3.0796	0.3122	1120.81	1121.34	5164.7		1	977	88.9	1	R.ILGSTIMTER.G
gi|21735596|ref|N	2	4	0.047	469	51735	5.2	U	programmed cell death 4 isoform 1 [Homo sapiens]				
gi|21735598|ref|N	2	4	0.048	458	50576	5.5	U	programmed cell death 4 isoform 2 [Homo sapiens]				
	HsFLAG-Control_HeLa_NE	3.1274	0.2416	1240.01	1240.4	4818		1	767.4	80	1	K.DLPELALDTPR.A
	HsFLAG-Control_HeLa_NE	3.7957	0.1344	1200.36	1200.43	5287.8		1	1441.6	90	3	R.APQLVGQFIAR.A
gi|51475836|ref|X	3	6	0.046	762	86115	8.7	U	PREDICTED: dpy-19-like 1 [Homo sapiens]				
gi|89026863|ref|X	3	6	0.046	762	86157	8.7	U	PREDICTED: similar to dpy-19-like 1, like [Homo sapiens]				
gi|89025889|ref|X	3	6	0.046	762	86115	8.7	U	PREDICTED: similar to dpy-19-like 1, like [Homo sapiens]				
	HsFLAG-Control_MG_293_	3.6327	0.2883	1404.61	1404.69	4494.9		1	893.5	81.8	3	K.LTEYPLVINTLK.R
	HsFLAG-Control_293_Ti_1	2.6211	0.2074	1771.87	1772.06	8368.2		1	576.4	57.7	1	R.FNLYPEVILASWYR.I
	HsFLAG-Control_MG_293_	2.8069	0.1811	1058.27	1058.27	6299.7		1	1025.1	87.5	2	K.TPLCNLLVK.D
gi|54607120|ref|N	2	10	0.046	710	78182	8.1	U	lactotransferrin [Homo sapiens]				
gi|88967530|ref|X	2	10	0.064	512	56162	6.8	U	PREDICTED: similar to lactotransferrin [Homo sapiens]				
	HsFLAG-Control_293_Ti_1	4.2475	0.4482	2089.01	2089.36	8589.3		1	1422.8	58.3	5	R.IDSGLYLGSGYFTAIQNLR.K
	HsFLAG-Control_Hela_Ti_1	3.9714	0.3525	1537.34	1537.8	7809.3		1	1181.9	69.2	5	K.YLGPQYVAGITNLK.K
gi|8922358|ref|N	1	2	0.046	546	64441	10.5	U	PRP38 pre-mRNA processing factor 38 (yeast) domain containing B [Homo sapiens]				
*	HsGST-MOCK_Ti_304.014	3.1302	0.4013	3104.09	3105.29	5211.7		1	319	35.4	2	R.YTQPPTDLWDWFESFLDDEEDLDVK.A
gi|20373175|ref|N	2	2	0.046	328	35197	8.5	U	musashi 2 isoform a [Homo sapiens]				
gi|25121993|ref|N	2	2	0.06	251	28421	8.5	U	musashi 2 isoform b [Homo sapiens]				
	HsHeLa3_Ti_103.2903.290	2.2833	0.3164	1558.62	1558.73	5044.9		1	329.7	46.4	1	R.GFGFVTFADPASVDK.V
	HsHeLa3_Ti_103.2896.289	4.1432	0.324	1559.04	1558.73	5748.4		1	1297.4	75	1	R.GFGFVTFADPASVDK.V

gi|57864582|ref|N		8	28	0.045	2850	282389	10	U	hornerin [Homo sapiens]				
	HsFLAG-MOCK_300mM_T	3.2709	0.3643	1562.01	1562.61	9018.9			1	1055.5	60	1	R.GRHGSGSGQSPGHGQR.G
	HsFLAG-Control_HeLa_NE	5.3604	0.4902	1585.75	1585.63	9758.4			1	2397.6	76.7	12	R.GPYESGSGHSSGLGHR.E
	Hs293FLP_Ti_304.1486.14	5.2148	0.5014	2351.04	2350.34	5289.1			1	932.2	52.2	6	R.HGSGSGQSSSYSPYGSGSGWSSSR.G
	HsFLAG-MOCK_300mM_T	4.6562	0.3482	2726.9	2726.67	7906.9			1	1043.6	30.6	2	R.SGQSSRGEQHGSSSGSSSSYGQHGSGSR.Q
	HsFLAG-Control_Hela_Ti_1	4.6769	0.4669	2122.77	2124.06	8984.4			1	1127	50	2	R.GEQHGSSSGSSSSYGQHGSGSR.Q
	HsFLAG-Control_Hela_Ti_1	5.8706	0.5712	2319.72	2320.31	9109.1			1	1687.8	56.5	2	R.HGSGSGQSSSYGPYGSGSGWSSSR.G
*	HsHeLa_Control-MG_Ti_10	3.568	0.4411	1860.7	1860.82	7441.1			1	677.9	50	2	R.HGSGSGHSSSHGQHGSGSGR.S
*	HsFLAG-MOCK_300mM_T	3.6793	0.3664	1861.27	1860.82	5469.9			1	720.5	36.8	1	R.HGSGSGHSSSHGQHGSGSGR.S
gi|8922328|ref|NI		1	2	0.045	420	46896	8.5	U	RNA binding motif protein 22 [Homo sapiens]				
*	HsHeLa3_Ti_103.3523.352	4.2623	0.4413	2293.24	2292.57	5858.5			1	951.8	55.6	2	K.NVCQTCLLDLEYGLPIQVR.D
gi|41349454|ref|N		1	3	0.045	382	43810	9.4	U	proline arginine-rich end leucine-rich repeat protein precursor [Homo sapiens]				
gi|4506041|ref|NI		1	3	0.045	382	43810	9.4	U	proline arginine-rich end leucine-rich repeat protein precursor [Homo sapiens]				
	HsFLAG-MOCK_300mM_T	4.1358	0.4369	2138.78	2138.19	5069.9			1	1011.8	68.8	3	R.ECYCPPDFPSALYCDSR.N
gi|29826335|ref|N		1	2	0.045	333	38388	5.8	U	eukaryotic translation initiation factor 2 beta [Homo sapiens]				
*	HsFLAG-Control_HeLa_NE	4.0476	0.3648	1757.61	1757.81	7695.9			1	1307.6	64.3	2	K.DASDDLDDLNFFNQK.K
gi|5729953|ref|NI		1	6	0.045	331	38243	5.4	U	nuclear distribution gene C homolog (A. nidulans) [Homo sapiens]				
*	HsFLAG-Control_HeLa_S1	4.0566	0.3709	1648.45	1646.84	5541.3			1	973.5	71.4	6	K.GQPAIIDGELYNEVK.V
gi|4758012|ref|NI		4	7	0.044	1675	191613	5.7	U	clathrin heavy chain 1 [Homo sapiens]				
*	HsFLAG-Control_HeLa_S1	4.1581	0.2614	1946.47	1946.26	5209.8			1	491.3	47.1	2	K.LHIIEVGTPPTGNQPFPK.K
*	HsFLAG-Control_HeLa_S1	3.6923	0.3285	1971.84	1972.21	8087.9			2	769.9	50	3	R.LASTLVHLGEYQAAVDGAR.K
*	HsFLAG-Control_HeLa_S1	3.5128	0.3552	2355.95	2356.55	9593.2			1	529.5	42.1	1	K.SVNESLNNLFITEEDYQALR.T
*	HsFLAG-Control_HeLa_S1	3.0898	0.2564	1943.32	1944.07	9704.9			1	1032.1	56.2	1	R.TSIDAYDNFDNISLAQR.L
gi|44888822|ref|N		4	4	0.044	1424	152587	7.3	U	hypothetical protein LOC23248 [Homo sapiens]				
*	HsFLAG-Control_HeLa_NE	3.9971	0.2877	1487.41	1487.73	4456			3	681.1	65.4	1	K.VEITPESILSALSK.T
*	HsHeLa3_Ti_106.2224.222	2.8868	0.3006	2337.57	2337.59	7626.8			1	424.2	31.8	1	R.SLFSPQNTLAAPTGHPPTSGVEK.V
*	HsHeLa3_Ti_106.1740.174	1.8122	0.1203	871.58	871.971	3924.4			6	349.3	71.4	1	K.HFGQAPSK.G
*	HsHeLa3_Ti_104.2560.256	2.5279	0.171	1840.94	1840.04	3203			1	417	56.2	1	R.DAPTHLPSVDLSNPFTK.E
gi|5454158|ref|NI		2	2	0.044	1264	140476	7.6	U	valyl-tRNA synthetase [Homo sapiens]				
*	Hs293FLP_Ti_303.4554.45	4.5357	0.3384	3908.54	3906.38	5953.8			1	476.5	22.1	1	K.SLGNVIDPLDVIYGISLQGLHNQLLNSNLDPSEVEK.A
*	HsFLAG-Control_HeLa_S1	2.7304	0.1891	1970.56	1968.13	7086.8			1	509.3	47.2	1	K.GFVPSPTSQPGGHESLVDR.W
gi|47519639|ref|N		3	3	0.044	1152	121005	5.4	U	microtubule-associated protein 4 isoform 1 [Homo sapiens]				
	HsGST-MOCK_Ti_403.534	3.1499	0.3909	2225.89	2227.43	12411.9			1	1110.4	45	1	R.DFIATLEAEAFDDVVGETVGK.T
	HsFLAG-Control_293_Ti_2	3.0293	0.1831	1359.21	1358.54	5934.8			2	731	66.7	1	K.KPTSAKPSSTTPR.L
	HsFLAG-Control_MG_293_	3.3953	0.2262	1591.53	1591.81	8606.9			1	799.6	53.1	1	K.VGSLDNVGHLPAGGAVK.T
gi|7662128|ref|NI		2	6	0.044	697	78292	7.6	U	zinc finger and BTB domain containing 24 [Homo sapiens]				
*	Hs283FLP_Ti_102.2429.24	4.3289	0.3732	1451.79	1450.68	6503.8			1	1389.5	75	2	K.STEQILATAQFLK.V
*	Hs293FLP_Ti_302.1183.11	5.597	0.5292	1836.56	1834.85	5861.5			1	1629.2	76.5	4	K.HASDASSISGSSNTEEVR.N
gi|39812378|ref|N		2	2	0.044	729	77847	6.8	U	RAN binding protein 9 [Homo sapiens]				
*	HsF-IP-293_Ti_206.2204.2	3.4053	0.3292	1784.62	1785.01	6501.6			1	1283.3	71.4	1	K.RLYPAVDEQETPLPR.S
	HsHeLa_Control-MG_Ti_20	2.8666	0.2447	1939.44	1938.2	7390.7			1	634.5	53.1	1	R.ATHPIPAACGIYYFEVK.I
gi|4506445|ref|NI		1	3	0.044	366	40940	8.2	U	RNA binding motif protein 4 [Homo sapiens]				
*	HsFLAG-Control_HeLa_NE	5.0186	0.5016	1856.22	1856.99	8869.5			1	1844	70	3	R.VADLTEQYNEQYGAVR.T
gi|56119128|ref|N		7	10	0.043	2302	262345	6.7	U	chromodomain helicase DNA binding protein 8 [Homo sapiens]				
*	HsHeLa3_Ti_106.2047.204	2.2823	0.1782	1006.69	1007.22	3985.8			2	459.2	72.2	1	R.HVVLGSLPGK.I
*	HsHeLa3_Ti_104.2239.223	2.4777	0.2401	1567.89	1568.86	5755.9			6	311.4	50	2	K.IVLQGNQLAALTQAK.N
*	HsHeLa3_Ti_104.2231.223	4.1616	0.4324	1569.35	1568.86	6933.5			1	1277.6	67.9	2	K.IVLQGNQLAALTQAK.N
*	HsHeLa3_Ti_105.1806.180	5.1475	0.4056	2110.82	2111.32	6217			1	738.4	45.5	2	K.VLSASEVAALSSPASSAPHSGGK.T

*	HsHeLa3_Ti_103.2990.299	2.9067	0.1666	2518.31	2518.78	5515.4		5	321.4	36.4	1	R.LPPAAGDEPPDPNLFIEPITEER.A
*	HsHeLa3_Ti_105.1887.188	3.2383	0.0853	1420.66	1420.66	3923.1		1	588.2	66.7	1	R.LALCQPPGPELPK.W
*	HsHeLa3_Ti_105.1674.167	2.7816	0.2067	1592.6	1591.85	6057.1		3	573.6	53.6	1	R.TASPLPLRPDAPVEK.S
gi|13435359|ref|N	3	8	0.043	1140	126988	5.3	U	damage-specific DNA binding protein 1 [Homo sapiens]				
gi|89034790|ref|X	3	8	0.043	1140	126968	5.3	U	PREDICTED: similar to DNA damage binding protein 1 (Damage-specific DNA binding pro				
gi|89034784|ref|X	3	8	0.046	1057	117226	5.3	U	PREDICTED: similar to DNA damage binding protein 1 (Damage-specific DNA binding pro				
gi|89034782|ref|X	3	8	0.043	1140	126968	5.3	U	PREDICTED: similar to DNA damage binding protein 1 (Damage-specific DNA binding pro				
	HsGST-MOCK_Ti_304.299	3.9632	0.3293	2421.08	2421.65	6515.8		1	730.9	50	5	K.FLYGCQAPTICFVYQDPQGR.H
	HsFLAG-Control_MG_293_	2.6227	0.1108	1100.14	1099.4	6090.7		3	858.5	77.8	1	K.YLAIAPPIIK.Q
	HsGST-MOCK_Ti_305.325	3.8728	0.2811	2180.59	2181.56	4450.6		1	354.6	44.4	2	R.SVLLLAYKPMEGNFEEIAR.D
gi|4504341|ref|NI	1	2	0.043	419	49513	5.7	U	histone acetyltransferase 1 isoform a [Homo sapiens]				
gi|74319831|ref|N	1	2	0.054	334	39786	5.9	U	histone acetyltransferase 1 isoform b [Homo sapiens]				
	HsFLAG-Control_HeLa_S1	4.7497	0.3453	2090.1	2090.29	4344.3		1	686.4	61.8	2	R.YYTEFPTVLDITAEDPSK.S
gi|57164942|ref|N	4	5	0.042	2032	225493	7.8	U	colonic and hepatic tumor over-expressed protein isoform a [Homo sapiens]				
gi|57222563|ref|N	4	5	0.044	1972	218524	8.1	U	colonic and hepatic tumor over-expressed protein isoform b [Homo sapiens]				
	HsFLAG-Control_HeLa_NE	3.5088	0.0996	3948.49	3948.15	8579.5		1	501.7	20.3	1	K.LEQQQSAGGDAEGGGDDGDEVPQIDAYELLEAVEILSK.L
	HsFLAG-Control_HeLa_NE	3.3585	0.2353	1542.98	1541.83	4584.7		7	519.2	61.5	1	K.FIQPNIGELPTALK.G
	HsFlag1P_Ti_106.2742.274	2.7419	0.3412	2203.65	2204.49	8377.5		1	405.5	36.8	2	R.NAALNTIVTVYNVHGDQVFK.L
	HsFLAG-Control_HeLa_NE	3.8112	0.3892	1625.66	1625.9	6583.5		1	1227.9	69.2	1	K.LDDIFEPVLIPEPK.I
gi|13435361|ref|N	2	4	0.041	894	99987	5.4	U	desmocollin 1 isoform Dsc1a preproprotein [Homo sapiens]				
gi|4826702|ref|NI	2	4	0.044	840	93835	5.5	U	desmocollin 1 isoform Dsc1b preproprotein [Homo sapiens]				
	HsFLAG-Control_Hela_Ti_1	3.9112	0.5415	3070.08	3069.48	6856.9		1	753.7	40.4	3	K.YEQFALYGYATTADGYAPEYPLPLIIK.I
	HsFLAG-Control_Hela_Ti_1	2.7442	0.1988	1189.1	1189.4	8718.7		4	854.9	72.2	1	K.ILQQIPDHPK.H
gi|4502885|ref|NI	2	5	0.041	490	58572	9.5	U	CDC-like kinase 3 isoform hclk3 [Homo sapiens]				
gi|89030229|ref|X	2	5	0.1	201	22662	9	U	PREDICTED: similar to Dual specificity protein kinase CLK3 (CDC-like kinase 3) [Homo sa				
gi|89029200|ref|X	2	5	0.1	201	22662	9	U	PREDICTED: similar to Dual specificity protein kinase CLK3 (CDC-like kinase 3) [Homo sa				
	Hs293FLP-MG_Ti_205.444	5.464	0.3728	2225.28	2226.58	8684.3		1	2130.8	44.7	1	R.ITLAEALLHPFFAGLTPEER.S
	HsHeLa_Control-MG_Ti_20	4.3958	0.4224	2225.81	2226.58	6127.4		1	785.7	52.6	4	R.ITLAEALLHPFFAGLTPEER.S
gi|48255889|ref|N	1	2	0.04	528	59425	4.4	U	protein kinase C substrate 80K-H isoform 1 [Homo sapiens]				
gi|48255891|ref|N	1	2	0.04	525	59178	4.4	U	protein kinase C substrate 80K-H isoform 2 [Homo sapiens]				
	HsHeLa3_Ti_105.2714.271	3.6775	0.3745	2168.95	2169.36	7148		1	754.5	47.5	2	K.LGGSPTSLGTWGSWIGPDHDK.F
gi|4506567|ref|NI	1	2	0.04	476	54844	6.6	U	RNA (guanine-7-) methyltransferase [Homo sapiens]				
*	HsHeLa3_Ti_104.3271.327	3.0164	0.1349	2069.99	2070.35	5224.9		3	388.7	44.4	2	R.LSPGGYFIGTTPNSFELIR.R
gi|88942360|ref|X	1	2	0.04	328	34023	10.8	U	PREDICTED: similar to 60S ribosomal protein L10 (QM protein) (Tumor suppressor QM) (				
gi|88945316|ref|X	1	2	0.04	328	34023	10.8	U	PREDICTED: similar to 60S ribosomal protein L10 (QM protein) (Tumor suppressor QM) (				
	Hs293FLP_TREX_Ti_102.1	4.2826	0.3349	1561.21	1561.69	6583.9		1	1604.4	83.3	2	K.FNADEFEYVVAEK.Q
gi|4506145|ref|NI	1	10	0.04	247	26558	6.5	U	protease, serine, 1 preproprotein [Homo sapiens]				
	HsF-IP-293_Ti_103.1872.1	3.5732	0.1014	1175.32	1175.43	3489.8		2	534.4	83.3	10	K.TLNNDIMLIK.L
gi|31657094|ref|N	3	4	0.039	1124	124199	8.1	U	anillin, actin binding protein (scraps homolog, Drosophila) [Homo sapiens]				
*	HsHeLa3_Ti_104.3855.385	4.9569	0.4829	2363.93	2363.56	7029		1	1353.1	57.5	2	R.LANLAATICSWEDDVNHSFAK.Q
*	HsHeLa3_Ti_105.1487.148	2.6388	0.1755	1590.83	1590.77	3225.8		2	334.2	57.1	1	K.STLSQTVPSKGELSR.E
*	HsHeLa3_Ti_104.1876.187	1.8572	0.1112	829.66	829.071	5944.4		8	391.5	64.3	1	R.LLLIATGK.R
gi|68131557|ref|N	2	2	0.039	1053	112966	6.3	U	ankyrin repeat domain 28 [Homo sapiens]				
*	HsFLAG-Control_Hela_Ti_1	4.4028	0.4314	1988.57	1989.29	8399.4		1	876.4	52.8	1	R.NLINATNAALQTPLHVAAR.N
*	HsFLAG-Control_Hela_Ti_1	2.9846	0.2631	2220.65	2219.42	8774.2		3	426.8	35.7	1	K.GASVLAVDENGYTPALACAPNK.D
gi|14327896|ref|N	1	4	0.039	433	48337	7.5	U	cyclin B1 [Homo sapiens]				
*	HsFLAG-Control_HeLa_NE	3.7217	0.3723	1811.57	1812.12	6509.5		1	591	53.1	4	K.ISTLPQLNSALVQDLAK.A
gi|6912618|ref|NI	1	4	0.039	361	40877	6.6	U	glutaminyl-peptide cyclotransferase precursor [Homo sapiens]				

*	Hs283FLP_Ti_103.2343.23	4.3738	0.2998	1493.68	1493.7	5516.8		1	890.2	69.2	4	R.SFSNIISTLNPTAK.R
gi|5730104|ref|N	1	2	0.039	335	37490	5.3	U		thioredoxin-like [Homo sapiens]			
*	HsFLAG-Control_HeLa_S1	3.5616	0.3294	1578.45	1578.85	4337.7		1	816.8	75	2	K.YEISSVPTFLFFK.N
gi|4505587|ref|N	1	3	0.039	231	25734	6.8	U		platelet-activating factor acetylhydrolase, isoform Ib, gamma subunit 29kDa [Homo sapien			
*	Hs293FLP_TREX_Ti_106.2	3.2964	0.1482	966.33	966.255	5556.8		2	1070.3	75	3	R.VVVLGLLPR.G
gi|19923217|ref|N	6	7	0.038	3256	358747	9.4	U		antigen identified by monoclonal antibody Ki-67 [Homo sapiens]			
*	HsHeLa3_Ti_103.1203.120	4.4426	0.4022	1633.89	1633.76	6292.4		1	1205.7	73.1	2	K.TPVQYSQQQNSPQK.H
*	HsFLAG-MOCK_300mM_T	3.1931	0.3957	2429.96	2430.63	6483.8		1	616.8	40.9	1	R.NRTPAKVEDAADSATKPENLSSK.T
*	HsGST-MOCK_Ti_106.235	4.4736	0.2203	2316.26	2315.59	6335.1		1	1025.7	39.5	1	K.RRPQTPKEEAQALEDLTGFK.E
*	HsFLAG-Control_HeLa_NE	2.8965	0.1653	1786.45	1785.95	6292.1		1	667.5	56.2	1	K.ELFQTPGHTEEAVAAGK.T
*	HsGST-MOCK_Ti_104.120	2.7273	0.2547	1394.69	1395.62	4828.5		7	399.5	58.3	1	K.AMHTPKPAVGEEK.D
*	HsGST-MOCK_Ti_403.369	4.1765	0.3733	3759.4	3760.02	7184.7		1	932.9	26.4	1	K.AQPLEDLASFQELSQTPGHTEELANGAADSFTSAPK.Q
gi|13128864|ref|N	2	12	0.038	1215	131419	5.3	U		histone deacetylase 6 [Homo sapiens]			
*	HsFLAG-MOCK_300mM_T	4.3553	0.3636	2462.67	2463.76	5703.9		1	995	50	3	R.SAQASVSCALEALEPFWEVLVR.S
*	HsFLAG-MOCK_300mM_T	4.8978	0.3845	2604.65	2606.04	7455.1		1	1423.2	54.3	9	R.LVLPIAYEFNPELVLVSAGFDAAR.G
gi|55741709|ref|N	3	5	0.038	843	100186	6.3	U		RNA binding motif protein 25 [Homo sapiens]			
*	HsFLAG-Control_HeLa_NE	3.7814	0.3914	2034.01	2034.06	4666.5		1	419.5	47.1	2	R.EYSSELNAPSQESDSHPR.K
*	HsHeLa3_Ti_104.1155.115	2.1151	0.2416	1355.83	1356.48	5374.6		1	298.3	50	1	K.LGASNSPGQPNSVK.R
*	HsHeLa3_Ti_104.1152.115	3.0933	0.1931	1357.79	1356.48	4666.4		2	458.1	61.5	2	K.LGASNSPGQPNSVK.R
gi|29570791|ref|N	1	2	0.038	391	45144	7.7	U		casein kinase II alpha 1 subunit isoform a [Homo sapiens]			
gi|4503095|ref|N	1	2	0.038	391	45144	7.7	U		casein kinase II alpha 1 subunit isoform a [Homo sapiens]			
	HsHeLa3_Ti_105.2070.207	4.1466	0.3744	1732.65	1732.93	5729.2		1	1069.8	67.9	2	R.TPALVFEHVNNTDFK.Q
gi|8922673|ref|N	1	5	0.038	372	42244	5.9	U		parvin, alpha [Homo sapiens]			
*	HsFLAG-Control_HeLa_NE	4.8583	0.3329	1608.33	1607.76	7155.6		1	1588.2	80.8	5	K.DLAEDLYDGQVLQK.L
gi|39725634|ref|N	3	5	0.037	1019	116465	9.1	U		la related protein isoform 1 [Homo sapiens]			
gi|61102725|ref|N	3	5	0.035	1096	123510	8.8	U		la related protein isoform 2 [Homo sapiens]			
	HsFLAG-Control_293_Ti_2	3.2409	0.4042	1713.31	1713.97	6327.8		1	951.3	66.7	1	R.AVTPVPTKTEEVSNLK.T
	HsFLAG-Control_293_Ti_2	3.0877	0.2784	1596.32	1594.83	8028		3	460.9	46.2	2	R.LGIGQSQEMNTLFR.F
	HsFLAG-Control_MG_293_	3.1893	0.3483	1058.29	1058.19	6720.4		1	1170	92.9	2	R.YGLECLFR.Y
gi|4506749|ref|N	2	2	0.037	792	90070	7.1	U		ribonucleoside-diphosphate reductase M1 chain [Homo sapiens]			
*	HsHeLa_Control-MG_Ti_10	2.6598	0.172	1696.1	1695.02	6870.7		4	555.2	50	1	R.VLSGEFQIVNPHLLK.D
*	HsFLAG-Control_HeLa_S1	4.0655	0.3196	1571.77	1571.82	9533		1	1053.9	61.5	1	R.TRPAANPIQFTLNK.E
gi|76150623|ref|N	3	5	0.037	808	88973	9.2	U		nucleolar protein 1, 120kDa [Homo sapiens]			
gi|76150625|ref|N	3	5	0.037	808	88973	9.2	U		nucleolar protein 1, 120kDa [Homo sapiens]			
	Hs293FLP_TREX_Ti_105.1	3.6586	0.2934	1546.45	1546.72	6906.5		1	793.1	61.5	2	R.LGVTNTIISHYDGR.Q
	Hs293FLP_TREX_Ti_105.1	4.4856	0.2947	1547.15	1546.72	4617		3	697.2	46.2	1	R.LGVTNTIISHYDGR.Q
	Hs293FLP_TREX_Ti_102.1	4.1147	0.379	1627.28	1626.68	8821		1	1118.2	60	2	K.TQASSSFQDSSQPAGK.A
gi|42519916|ref|N	1	2	0.037	673	71277	5.2	U		forkhead box O3A [Homo sapiens]			
gi|4503739|ref|N	1	2	0.037	673	71277	5.2	U		forkhead box O3A [Homo sapiens]			
	HsHeLa3_Ti_105.2870.287	3.655	0.5066	2456.38	2457.66	5312.5		2	405.8	35.4	2	K.GSGLGSPTSSFNSTVFGPSSLNSLR.Q
gi|23397696|ref|N	1	4	0.037	537	59059	5.8	U		copine I [Homo sapiens]			
gi|4503013|ref|N	1	4	0.037	537	59059	5.8	U		copine I [Homo sapiens]			
gi|23397708|ref|N	1	4	0.037	537	59059	5.8	U		copine I [Homo sapiens]			
gi|23397706|ref|N	1	4	0.037	537	59059	5.8	U		copine I [Homo sapiens]			
gi|23397704|ref|N	1	4	0.037	537	59059	5.8	U		copine I [Homo sapiens]			
gi|23397702|ref|N	1	4	0.037	537	59059	5.8	U		copine I [Homo sapiens]			
gi|23397700|ref|N	1	4	0.037	537	59059	5.8	U		copine I [Homo sapiens]			
gi|23397698|ref|N	1	4	0.037	537	59059	5.8	U		copine I [Homo sapiens]			

	HsHeLa_Control-MG_Ti_20	4.4433	0.3523	2236.63	2236.57	7224.3		1	697.7	47.4	4	R.EALAQTVLAEVPTQLVSYFR.A
gi|5032093|ref|N	1	2	0.037	541	56598	5.5	U	solute carrier family 1 (neutral amino acid transporter), member 5 [Homo sapiens]				
*	HsFLAG-Control_293_Ti_2	2.9041	0.1963	2160.63	2159.49	6383		2	446.4	42.1	2	K.SELPLDPLPVPTEEGNPLLK.H
gi|71774083|ref|N	1	3	0.037	454	50565	5.4	U	myc proto-oncogene protein [Homo sapiens]				
*	HsGST-MOCK_Ti_305.298	4.035	0.3358	1840.7	1842.07	6768		1	1247.2	62.5	3	R.SGLCSPSYVAVTPFSLR.G
gi|10835203|ref|N	1	2	0.037	404	42803	6.1	U	advanced glycosylation end product-specific receptor isoform 1 precursor [Homo sapiens]				
*	HsGST-MOCK_Ti_403.218	2.9314	0.1527	1528.49	1526.69	5025.9		1	892.9	75	2	K.VLSPQGGGPWDSVAR.V
gi|89061564|ref|X	1	4	0.037	377	41540	8.3	U	PREDICTED: similar to Ig gamma-2 chain C region [Homo sapiens]				
	HsHeLa3_Ti_104.2172.217	4.4668	0.3679	1678.47	1678.84	6616.4		1	1547.6	80.8	4	K.FNWYVDGVEVHNAK.T
gi|33350932|ref|N	11	23	0.036	4646	532412	6.4	U	dynein, cytoplasmic, heavy polypeptide 1 [Homo sapiens]				
*	HsFLAG-Control_HeLa_S1	3.8227	0.4903	2348.72	2349.68	8010.9		1	975.9	50	1	K.LVPLLLEDGGEAPAALEAALEEK.S
*	HsFLAG-Control_HeLa_S1	4.1587	0.32	2349.33	2349.68	8720.5		1	1208.1	36.4	1	K.LVPLLLEDGGEAPAALEAALEEK.S
*	HsHeLa3_Ti_103.4032.403	5.6195	0.3853	2349.88	2349.68	8342.9		1	1750.9	39.8	2	K.LVPLLLEDGGEAPAALEAALEEK.S
*	HsHeLa3_Ti_103.4027.402	2.7563	0.4848	2349.9	2349.68	6514.8		1	439	38.6	1	K.LVPLLLEDGGEAPAALEAALEEK.S
*	HsHeLa3_Ti_103.4014.401	5.177	0.4585	2448.11	2446.86	7354		1	1567.2	56.8	3	R.ALPDMEVVGLNFSSATTPELLLK.T
*	HsHeLa3_Ti_106.3146.314	3.5248	0.2261	2125.88	2124.53	4909.3		1	757.7	52.8	1	R.GIFEALRPLETLPVEGLIR.I
*	HsFLAG-Control_HeLa_S1	3.7232	0.2171	2789.12	2789.2	5608.2		5	644.4	30.7	1	K.VFYEEELDVPLVLFNEVLDHVLR.I
*	HsFLAG-Control_HeLa_S1	3.2294	0.2387	2266.6	2266.51	6515.9		1	485.8	42.1	1	R.ENFIPTIVNFSAEEISDAIR.E
*	HsHeLa3_Ti_103.3655.365	2.9754	0.2347	2329.72	2330.66	3826		2	328	42.1	1	R.YPLIIDPSGQATEFIMNEYK.D
*	HsHeLa3_Ti_103.3915.391	5.3178	0.3968	2601.18	2599.95	6965.9		1	895.5	45.5	10	R.FGNPLLVQDVESYDPVLNPVLNR.E
*	HsFLAG-Control_HeLa_S1	3.4602	0.2813	1800.51	1799.12	6637		2	511.3	46.9	1	K.LSLSNAISTALPLTQLR.W
gi|21396489|ref|N	1	2	0.036	959	106489	6.4	U	protease, serine, 15 [Homo sapiens]				
*	HsHeLa_Control-MG_Ti_20	4.9091	0.2211	3874.6	3875.24	8889.6		1	1088.8	25.7	2	R.GYQGDPSSALLELLDPEQNANFLDHYLDVPVDLSK.V
gi|38372901|ref|N	1	2	0.036	785	80693	7.3	U	Sp1 transcription factor [Homo sapiens]				
*	HsFLAG-Control_HeLa_NE	6.1241	0.4065	2815.76	2816.01	10401.5		1	1854.2	34.3	2	R.VSGLQGSDALNIQQNQTSGGSLQAGQQK.E
gi|4505293|ref|N	1	2	0.036	700	78764	6.9	U	MYB-related protein B [Homo sapiens]				
*	HsHeLa3_Ti_103.2802.280	4.0557	0.2455	2395.15	2393.74	6887.8		1	851.4	47.9	2	R.GELIPISPSTEVGGSGIGTPPSVLK.R
gi|11321603|ref|N	2	2	0.036	557	64406	7.4	U	TNF receptor-associated factor 5 [Homo sapiens]				
gi|77404348|ref|N	2	2	0.036	557	64406	7.4	U	TNF receptor-associated factor 5 [Homo sapiens]				
gi|22027627|ref|N	2	2	0.036	557	64406	7.4	U	TNF receptor-associated factor 5 [Homo sapiens]				
	HsGST-MOCK_Ti_104.110	3.3636	0.3046	1333.5	1333.45	8087.1		3	899.5	70	1	R.NLQQHEHSALR.E
	HsGST-MOCK_Ti_105.109	2.5848	0.2344	1116.9	1115.24	7453.8		2	708	75	1	K.HDTHINIHK.A
gi|4557809|ref|N	1	2	0.036	439	48535	7	U	ornithine aminotransferase precursor [Homo sapiens]				
*	Hs283FLP_Ti_102.3218.32	3.7255	0.438	1953.57	1954.14	4720.7		1	797.5	66.7	2	R.AFYNNVLGEYEEYITK.L
gi|21361809|ref|N	1	3	0.036	390	42142	9.9	U	RNA binding motif protein, X-linked-like 1 [Homo sapiens]				
gi|8850217|ref|N	1	3	0.036	392	42784	10.3	U	testes-specific heterogenous nuclear ribonucleoprotein G-T [Homo sapiens]				
gi|56699409|ref|N	1	3	0.036	391	42332	10.1	U	RNA binding motif protein, X-linked [Homo sapiens]				
	HsFLAG-MOCK_300mM_T	4.7701	0.4184	1488.48	1487.65	6161.6		1	1359.2	76.9	3	R.GFAFVTFESPADAK.D
gi|4506017|ref|N	1	2	0.036	309	35594	5.5	U	protein phosphatase 2, catalytic subunit, alpha isoform [Homo sapiens]				
gi|57222565|ref|N	1	2	0.036	309	35575	5.4	U	protein phosphatase 2, catalytic subunit, beta isoform [Homo sapiens]				
gi|4758952|ref|N	1	2	0.036	309	35575	5.4	U	protein phosphatase 2, catalytic subunit, beta isoform [Homo sapiens]				
	HsFLAG-Control_HeLa_NE	3.1503	0.3341	1341.56	1341.51	7159.9		1	815.8	65	2	K.YSFLQFDPAPR.R
gi|21361659|ref|N	2	6	0.035	1041	115963	4.8	U	importin 9 [Homo sapiens]				
*	HsFLAG-Control_HeLa_S1	4.2509	0.2812	1942.75	1941.23	7967.6		1	757.5	50	5	K.EALVDTLTGILSPVQEVR.A
*	HsFLAG-Control_HeLa_S1	3.9977	0.3359	2253.72	2254.19	4272.6		1	629.9	64.7	1	K.YEEDYYEDDEEDDPDALK.D
gi|24497620|ref|N	1	2	0.035	627	70730	8.6	U	signal recognition particle 68kDa [Homo sapiens]				
*	HsHeLa3_Ti_105.0314.031	2.8868	0.1631	2569.97	2570	6180.9		4	469.6	38.1	2	R.LYDIILQNLVELLQLPGLEEDK.A
gi|19923399|ref|N	1	2	0.035	482	54121	5.6	U	Ras-GTPase activating protein SH3 domain-binding protein 2 isoform a [Homo sapiens]				

gi|45359849|ref|N	1	2	0.035	482	54121	5.6	U	Ras-GTPase activating protein SH3 domain-binding protein 2 isoform a [Homo sapiens]			
gi|45359846|ref|N	1	2	0.038	449	50817	5.4	U	Ras-GTPase activating protein SH3 domain-binding protein 2 isoform b [Homo sapiens]			
	HsFLAG-Control_HeLa_NE	3.9927	0.4429	1967.93	1967.19	8005.9	1	954.1	59.4	2	K.LPNFGFVVFDDSEPVQR.I
gi|4507835|ref|N	1	2	0.035	480	52222	7.2	U	uridine monophosphate synthase [Homo sapiens]			
*	HsFLAG-Control_HeLa_S1	4.8871	0.4739	1763.75	1764.08	5520.5	1	1365.8	71.9	2	R.AALGPLVTGLYDVQAFK.F
gi|48526509|ref|N	1	2	0.035	456	50465	9.4	U	translocase of inner mitochondrial membrane 50 homolog [Homo sapiens]			
*	HsFLAG-Control_293_Ti_2	4.1501	0.3322	1913.35	1913.14	7467.8	1	1046	63.3	2	K.IPDEFDNDPILVQQLR.R
gi|61743954|ref|N	12	53	0.034	5890	629114	6.1	U	AHNAK nucleoprotein isoform 1 [Homo sapiens]			
*	HsFLAG-Control_HeLa_NE	4.1252	0.4048	1638.18	1638.78	6493.9	1	761.7	52.9	1	R.AGAISASGPELQGAGHSK.L
*	HsFLAG-Control_HeLa_NE	2.9202	0.2033	1599.37	1599.78	3764.3	2	401.6	53.1	1	R.GGVQVPAVDISSSLGGR.A
*	HsFLAG-MOCK_300mM_T	3.2106	0.1933	1365.53	1364.5	6745.6	1	859.7	66.7	2	K.FGVSTGREGQTPK.A
	HsFLAG-Control_HeLa_NE	3.8693	0.3255	1268.06	1268.41	6260.3	2	1082.3	77.3	12	K.AEGPEVDVNLPK.A
*	HsFLAG-Control_HeLa_NE	3.6878	0.3269	1701.06	1699.85	3881.4	1	546.8	60	3	K.IDVTAPDVSIEEPEGK.L
*	HsFLAG-Control_HeLa_NE	3.77	0.2296	1655.71	1655.8	3871.6	1	739.9	66.7	1	K.VDIEAPDVSLEGPEGK.L
	HsFLAG-Control_HeLa_NE	3.7626	0.3116	1671.08	1669.83	3357.6	1	709.4	70	9	K.VDVEVPDVSLEGPEGK.L
	HsHeLa_Control-MG_Ti_20	3.1529	0.3187	2625.77	2626.84	7108.5	1	460.6	35.4	2	K.LEGDLTGPSVGVEVPDVELECPDAK.L
	HsFLAG-Control_HeLa_NE	2.7765	0.1796	1159.34	1157.35	4239.9	1	521.5	75	8	K.VKGDVDVSLPK.L
	HsFLAG-Control_HeLa_NE	3.5873	0.3784	1682.41	1682.83	3362.1	1	561.9	66.7	12	K.VDVDVPDVNIEGPDAK.L
*	HsHeLa3_Ti_104.3117.311	4.8118	0.3117	2182.97	2184.5	4493.6	1	828.8	60	1	K.TPSFGISAPQVSIPDVNVNLK.G
*	HsHeLa3_Ti_102.2107.210	2.7722	0.203	1734.85	1733.83	5301.8	1	514.8	50	1	K.ASLGSLEGEAEAEASSPK.G
gi|53759103|ref|N	2	2	0.034	1037	119938	5.2	U	importin 8 [Homo sapiens]			
*	HsFLAG-Control_MG_293_	3.1005	0.2828	1333.18	1333.61	8711.1	1	1185.4	77.3	1	K.TYAVGIQQVLLK.I
*	Hs293FLP-MG_Ti_202.456	3.7017	0.3651	2538.42	2538.81	6338.3	1	711	45.5	1	K.FDIFEDYASPTTAAQTLLYTAAK.K
gi|42560244|ref|N	2	4	0.034	754	88617	10.3	U	peptidyl-prolyl isomerase G (cyclophilin G) [Homo sapiens]			
*	HsHeLa_Control-MG_Ti_20	3.5267	0.3553	1408.76	1408.47	8809.8	1	1421.1	72.7	2	K.SKGQENDHVHEK.N
*	Hs293FLP-MG_Ti_203.120	3.9368	0.2937	1592.49	1592.62	7762.8	1	1465.4	73.1	2	K.KFDHESSPGTDEDK.S
gi|13435375|ref|N	1	2	0.034	563	61327	4.8	U	glucocorticoid modulatory element binding protein 1 isoform 2 [Homo sapiens]			
gi|13435377|ref|N	1	2	0.033	573	62591	4.8	U	glucocorticoid modulatory element binding protein 1 isoform 1 [Homo sapiens]			
	HsFLAG-Control_HeLa_NE	4.8468	0.4518	2312.77	2313.48	9210.3	1	1186.2	52.8	2	R.NQVEQGEEQFLYTLTDLER.Q
gi|4502111|ref|N	1	2	0.034	466	50316	6.6	U	annexin VII isoform 1 [Homo sapiens]			
gi|4809279|ref|N	1	2	0.033	488	52739	5.7	U	annexin VII isoform 2 [Homo sapiens]			
	HsFLAG-Control_HeLa_S1	4.8302	0.3691	1691.57	1691.84	7461.1	1	1381.7	63.3	2	K.GFGTDEQAIVDVVANR.S
gi|4885399|ref|N	2	2	0.033	1217	141541	7.2	U	chondroitin sulfate proteoglycan 6 (bamacan) [Homo sapiens]			
*	HsHeLa3_Ti_103.3598.359	2.7529	0.1778	2478.29	2475.75	7127.1	1	436.2	42.1	1	R.INNEIDQLMNQMQQIETQQR.K
*	HsFLAG-Control_HeLa_NE	2.6541	0.243	2065.15	2065.24	9065.9	6	341.6	34.2	1	R.ETEGGTVLTATTSELEAINK.R
gi|4507877|ref|N	2	2	0.033	1066	116722	6.1	U	vinculin isoform VCL [Homo sapiens]			
gi|7669550|ref|N	2	2	0.031	1134	123799	5.7	U	vinculin isoform meta-VCL [Homo sapiens]			
	HsFLAG-Control_HeLa_S1	3.9572	0.3489	2077.55	2077.43	10442.9	1	1665.5	38.8	1	K.AIPDLTAPVAAVQAAVSNLVR.V
	HsFLAG-Control_HeLa_S1	2.5982	0.0839	1487.33	1485.68	8169.3	1	758.1	61.5	1	R.VDQLTAQLADLAAR.G
gi|7706485|ref|N	2	2	0.033	704	80011	8	U	TNF receptor-associated protein 1 [Homo sapiens]			
*	HsFLAG-Control_293_Ti_2	2.8373	0.3129	1187.66	1185.33	7370.8	1	1265.4	88.9	1	R.YVAQAHDKPR.Y
*	Hs293FLP_TREX_Ti_104.2	3.6996	0.2951	1493.59	1493.75	4121.2	2	528.3	62.5	1	R.AQLLQPTLEINPR.H
gi|24307879|ref|N	1	5	0.033	638	71457	5.2	U	dynein, cytoplasmic, intermediate polypeptide 2 [Homo sapiens]			
*	HsFLAG-Control_HeLa_S1	4.6135	0.4851	1951.49	1951.96	8865	1	1434	60	5	K.SVSTPSEAGSQDSGDGAVGSR.T
gi|40538809|ref|N	1	2	0.033	510	55216	6.1	U	hypothetical protein LOC55571 [Homo sapiens]			
*	HsFLAG-Control_HeLa_NE	4.5896	0.395	1855.7	1856.08	6299.1	1	1163.5	68.8	2	K.SPLSSPQQTQLLGELEK.D
gi|7661892|ref|N	1	3	0.033	482	53028	7	U	REST corepressor 1 [Homo sapiens]			
*	HsFLAG-Control_HeLa_NE	4.3656	0.4021	1731.69	1731.95	5560.7	1	931.8	66.7	3	R.VGPQYQAVVPDFDPAK.L
gi|22749139|ref|N	1	2	0.033	427	48359	9.6	U	serum response factor binding protein 1 [Homo sapiens]			

*	HsHeLa3_Ti_105.1254.125	3.0223	0.3206	1429.91	1429.61	8633.5		1	1111	65.4	2	K.AVTIANSPSKPSEK.D
gi|4504511|ref|N	1	4	0.033	397	44868	7.1	U	DnaJ (Hsp40) homolog, subfamily A, member 1 [Homo sapiens]				
*	HsFLAG-Control_HeLa_S1	3.6068	0.2836	1393.95	1393.67	7198.1		2	954.6	70.8	4	R.TIVITSHPGQIVK.H
gi|12746590|ref|	2	2	0.032	985	106208	8	U	C-terminal binding protein 2 isoform 2 [Homo sapiens]				
gi|4557499|ref|N	2	2	0.072	445	48945	6.9	U	C-terminal binding protein 2 isoform 1 [Homo sapiens]				
	HsFLAG-MOCK_300mM_T	3.0572	0.0847	1057.75	1057.24	7465.3		1	1550.7	88.9	1	K.ALAQALKEGR.I
	HsFLAG-MOCK_300mM_T	2.7962	0.2491	2372.08	2370.67	7202.4		1	576.8	42.9	1	R.IRGAALDVHESEPFSFAQGPLK.D
SHUFFLED_gi|4	1	3	0.032	595	69690	6.5	U	FALSE POSITIVE				
*	HsHeLa_Control-MG_Ti_20	3.7332	0.1576	2374.72	2375.73	8702.9		1	1015.1	50	3	K.EQYGRVQNLFEFEKAFLKK.T
gi|7706254|ref|N	1	3	0.032	529	59578	8.9	U	nucleolar protein NOP5/NOP58 [Homo sapiens]				
*	HsGST-MOCK_Ti_302.523	5.3802	0.3903	1891.56	1890.2	8515.2		1	1732.9	65.6	3	K.VDTMIVQAISLLDDLDK.E
gi|24496789|ref|	2	4	0.031	1176	134411	7.2	U	leucyl-tRNA synthetase [Homo sapiens]				
*	HsFLAG-Control_HeLa_NE	2.863	0.2261	1924.78	1925.11	8825.5		4	421.4	43.3	2	R.SFITTDVNPYYDSFVR.W
*	HsFLAG-Control_HeLa_NE	3.0883	0.1357	1959.09	1958.13	4082.2		3	224.6	39.5	2	K.GTGVVTSVPSDSPDDIAALR.D
gi|32528306|ref|	2	4	0.031	1147	128183	9.4	U	replication factor C large subunit [Homo sapiens]				
*	HsFLAG-Control_HeLa_NE	4.0991	0.5082	1843.92	1842.06	6363		1	753.9	59.4	2	K.LTPTSVLDYFGTGSVQR.S
*	HsFLAG-Control_HeLa_NE	2.8116	0.1391	1936.09	1935.01	9446.6		6	547	41.2	2	K.ELSQNTDESGLNDEAIAK.Q
gi|51492636|ref|	2	2	0.031	1085	124025	8.6	U	PREDICTED: U2-associated SR140 protein [Homo sapiens]				
gi|88971174|ref|	2	2	0.031	1085	124025	8.6	U	PREDICTED: similar to U2-associated SR140 protein [Homo sapiens]				
	HsFLAG-MOCK_300mM_T	4.5861	0.4144	1714.58	1713.8	8176.5		1	1004.5	56.7	1	R.GGVVNAAKEEHETDEK.R
	HsFLAG-Control_HeLa_NE	3.1208	0.3495	1905.33	1905.96	3590.4		1	332.5	50	1	K.SLDDDLDGVPLDATEDSK.K
gi|21614520|ref|	2	2	0.031	515	59258	6.7	U	glucose-6-phosphate dehydrogenase [Homo sapiens]				
*	HsHeLa_Control-MG_Ti_20	3.6974	0.227	1944.52	1944.12	6498.4		1	912.7	43.3	1	R.LQFHDVAGDIFHQQCK.R
*	HsHeLa_Control-MG_Ti_20	5.1362	0.4453	1946.11	1944.12	9374.3		1	1816.4	70	1	R.LQFHDVAGDIFHQQCK.R
gi|6005743|ref|N	1	4	0.031	479	53927	6.3	U	DEAD (Asp-Glu-Ala-As) box polypeptide 19 isoform 1 [Homo sapiens]				
gi|8922886|ref|N	1	4	0.031	478	53975	6.6	U	DDX19-like protein [Homo sapiens]				
gi|62632746|ref|	1	4	0.031	479	54137	6.3	U	DDX19-DDX19L protein [Homo sapiens]				
gi|62241024|ref|	1	4	0.033	448	50490	6.1	U	DEAD (Asp-Glu-Ala-As) box polypeptide 19 isoform 2 [Homo sapiens]				
	HsFLAG-Control_HeLa_NE	4.2978	0.1473	1731.2	1729.89	7963.7		1	1641.9	71.4	4	R.SNLVDNTNQVEVLQR.D
gi|5453593|ref|N	1	2	0.031	477	52824	6.4	U	adenylyl cyclase-associated protein 2 [Homo sapiens]				
*	HsFLAG-Control_HeLa_S1	4.1304	0.266	1591.38	1591.81	7551.2		1	1347.6	67.9	2	R.SALFAQLNQGEAITK.G
gi|23111032|ref|	1	2	0.031	457	51813	5.6	U	sorting nexin 1 isoform b [Homo sapiens]				
gi|23111036|ref|	1	2	0.03	474	53304	5	U	sorting nexin 1 isoform c [Homo sapiens]				
gi|23111034|ref|	1	2	0.027	522	59070	5.1	U	sorting nexin 1 isoform a [Homo sapiens]				
	HsFLAG-Control_HeLa_S1	3.3812	0.3231	1316.6	1316.54	7062.1		1	1483.1	76.9	2	R.AVGTQTLSGAGLLK.M
gi|4503729|ref|N	1	2	0.031	459	51805	5.4	U	FK506-binding protein 4 [Homo sapiens]				
*	Hs293FLP_TREX_Ti_101.0	3.9803	0.3717	1409.23	1409.41	9635.7		1	1450.8	69.2	2	K.SNTAGSQSQVETEA.-
gi|34482047|ref|	2	3	0.03	1082	119059	5.6	U	adaptor-related protein complex 3, beta 2 subunit [Homo sapiens]				
*	HsFLAG-Control_293_Ti_2	2.5036	0.2193	2260.68	2258.41	8848.9		9	344.1	36.8	1	K.ATGYQELPDWPEEAPDPSVR.N
*	HsFLAG-Control_MG_293_	3.6447	0.3769	1287.45	1286.43	8713.7		1	1346.3	75	2	R.PAGAAQLTVNSEK.M
gi|62244004|ref|	2	2	0.03	1016	115409	8.1	U	modulator of estrogen induced transcription isoform b [Homo sapiens]				
gi|63176611|ref|	2	2	0.029	1034	117149	7.9	U	modulator of estrogen induced transcription isoform a [Homo sapiens]				
	HsGST-MOCK_Ti_406.244	3.071	0.2376	1326.49	1326.55	9826.1		1	1394.7	72.7	1	K.SPGHMVILDQTK.G
	HsGST-MOCK_Ti_406.231	2.9943	0.2804	1812.32	1813	8321.9		2	663.2	47.1	1	R.AGAGMITQHSSNASPINR.I
gi|4557032|ref|N	1	2	0.03	334	36639	6.1	U	lactate dehydrogenase B [Homo sapiens]				
*	Hs293FLP_TREX_Ti_102.1	3.3728	0.1945	1177.5	1177.3	4569.1		2	810.8	77.8	2	K.SADTLWDIQK.D
gi|6382079|ref|N	5	12	0.029	3224	358173	6.2	U	RAN binding protein 2 [Homo sapiens]				
*	HsHeLa3_Ti_104.1407.140	3.0423	0.2962	1488.31	1487.67	4943.6		3	474.2	57.1	1	K.APGTNVAMASNQAVR.I
	HsFLAG-Control_HeLa_NE	3.202	0.4397	1825.13	1824.9	6354.4		1	517.7	47.1	8	K.QNQTTSAVSTPASSETSK.A

	HsFLAG-Control_HeLa_NE	3.3797	0.3548	2412.93	2411.41	6694		1	645.9	45.2	1	K.LNQSGTSVGTDEESDVTQEEER.D
*	HsFLAG-Control_HeLa_NE	2.9784	0.3318	2095.28	2096.3	4657.9		1	363.7	47.1	1	K.NLFASFPTEESSINYTFK.T
*	HsFLAG-Control_HeLa_NE	3.624	0.3457	2516.77	2517.53	10822.5		1	942.6	45	1	K.NRPDYVSEEEEDDEDFETAVK.K
gi|46430642|ref|N	2	2	0.029	1028	117949	9.4	U	myosin IC [Homo sapiens]				
	HsHeLa_Control-MG_Ti_10	2.615	0.2943	1602.47	1601.84	3648.7		4	280.6	50	1	R.LLQSNPVLEAFGNAK.T
*	HsHeLa_Control-MG_Ti_10	2.5777	0.1943	1554.7	1554.83	3260.5		1	346.9	60.7	1	K.GAPVGGHILSYLLEK.S
gi|10863889|ref|N	2	3	0.029	800	90255	6.1	U	squamous cell carcinoma antigen recognized by T cells 1 [Homo sapiens]				
*	HsFLAG-MOCK_300mM_T	3.828	0.2576	1426	1424.69	9218.6		1	1078.8	65	1	R.LRQLQQLQQLR.D
*	HsHeLa3_Ti_105.2394.239	4.203	0.2261	1273.73	1272.5	7661.4		1	1259.6	72.7	2	R.GLAAALLLCQNK.G
gi|5031579|ref|NI	1	3	0.029	692	76108	5.1	U	A-kinase anchor protein 8 [Homo sapiens]				
*	HsFLAG-Control_HeLa_NE	4.9624	0.5181	1970.24	1971.09	5755.3		1	1283.1	68.4	3	R.VAPAPAAADAEVEQTDAESK.D
gi|32526896|ref|N	1	2	0.029	659	73994	6.7	U	armadillo repeat containing 8 isoform 2 [Homo sapiens]				
gi|47458045|ref|N	1	2	0.049	385	42984	7.2	U	armadillo repeat containing 8 isoform 1 [Homo sapiens]				
gi|47458043|ref|N	1	2	0.049	385	42984	7.2	U	armadillo repeat containing 8 isoform 3 [Homo sapiens]				
	HsHeLa_Control-MG_Ti_20	4.2365	0.3212	2146.47	2146.4	7901.3		1	904.2	50	2	R.VEGAETLAYLIEPDVELQR.I
gi|4507521|ref|NI	1	2	0.029	623	67878	7.7	U	transketolase [Homo sapiens]				
*	Hs293FLP_TREX_Ti_102.1	3.3988	0.4378	1885.44	1886.07	5324.8		1	677.5	58.8	2	R.SVPTSTVFYPSDGVATEK.A
gi|38372909|ref|N	2	4	0.028	1761	191610	7.2	U	jumonji domain containing 1B [Homo sapiens]				
*	HsHeLa3_Ti_105.2940.294	4.6438	0.4816	2537.22	2536.8	5190.4		1	718.4	48	3	R.NSILASSGFGAPLPSSSQPLTFGSGR.S
*	HsHeLa3_Ti_106.2911.291	3.0143	0.3427	2457.21	2457.83	3426.3		1	215.7	34.8	1	K.LPQTPLDTGIPFPPVFSTSSAGVK.S
gi|62241042|ref|N	3	4	0.028	1512	170590	7.3	U	glutamyl-prolyl tRNA synthetase [Homo sapiens]				
*	HsFLAG-MOCK_300mM_T	2.6888	0.4012	1652.03	1651.86	8076.3		1	1046.9	64.3	1	K.TKVEATKNETSAPFK.E
*	HsGST-MOCK_Ti_105.131	2.9249	0.3085	1682.58	1682.84	10413.1		1	828.4	46.7	1	R.AIQGGTSHHLGQNFSK.M
*	HsFLAG-Control_293_Ti_2	2.7768	0.176	1204.24	1205.31	6877.6		1	1157.6	85	2	K.LTVAENEAETK.L
gi|40789229|ref|N	2	7	0.028	1147	125869	9.6	U	splicing factor, arginine/serine-rich 15 [Homo sapiens]				
	HsFLAG-Control_HeLa_NE	3.7821	0.31	1331.71	1331.6	7308		1	1695.9	86.4	3	K.VPGLYVIDSIVR.Q
*	HsFLAG-Control_HeLa_NE	4.4047	0.4053	2114.12	2114.31	3459.5		1	741.6	63.2	4	K.TVEPPISQVGNVDTASELEK.G
gi|5453998|ref|NI	2	4	0.028	1038	119516	4.8	U	importin 7 [Homo sapiens]				
*	HsFLAG-Control_HeLa_S1	4.2931	0.3006	1272.92	1273.56	5371.2		1	1330.9	86.4	1	K.AFAVGVQQVLLK.V
*	HsFLAG-Control_HeLa_S1	4.6454	0.4895	2056.03	2056.25	9392.5		1	1490.4	62.5	3	R.NPVWYQALTHGLNEEQR.K
gi|20127519|ref|N	1	3	0.028	747	85653	9.2	U	TPX2, microtubule-associated protein homolog [Homo sapiens]				
*	HsGST-MOCK_Ti_403.339	4.2251	0.4362	2191.44	2191.44	9316.2		1	716.5	42.5	3	K.SVAEGLSGSLVQEPFQLATEK.R
gi|29789006|ref|N	1	3	0.028	680	77861	6.7	U	pleckstrin homology domain containing, family C (with FERM domain) member 1 [Homo s				
*	HsFLAG-Control_HeLa_NE	3.5889	0.3483	2050.87	2051.34	4710.1		8	341.6	41.7	3	K.TSTILGDITSIPELADYIK.V
gi|20270212|ref|N	3	3	0.027	1729	181804	4.9	U	tankyrase 1-binding protein of 182 kDa [Homo sapiens]				
*	HsHeLa3_Ti_102.2223.222	2.7465	0.2523	1981.82	1982.08	10350.6		3	706.8	44.1	1	K.DTQSPSTCSEGLLGWSQK.D
*	HsHeLa3_Ti_105.2767.276	3.0572	0.0866	1344.76	1343.61	3013		3	558.4	75	1	K.VNLFPGLSPSALK.A
*	HsHeLa3_Ti_103.2408.241	2.6262	0.0906	1649.85	1648.77	4319.5		1	405.8	50	1	K.SSGSEGSSPNWLQALK.L
gi|39995084|ref|N	1	3	0.027	1042	118013	5.8	U	hypothetical protein LOC65123 [Homo sapiens]				
*	HsFLAG-Control_HeLa_NE	5.3724	0.3781	1953.49	1954.03	6505.7		1	2024.2	55.6	3	K.GAAAAAAASGAAGGGGGGAGAGAPGGGR.L
gi|38570097|ref|N	1	2	0.027	776	86436	5.9	U	hypothetical protein LOC54870 [Homo sapiens]				
gi|38570099|ref|N	1	2	0.027	776	86436	5.9	U	hypothetical protein LOC54870 [Homo sapiens]				
	HsHeLa3_Ti_105.3304.330	3.3088	0.2555	2490.69	2489.86	5401.3		1	378.9	42.5	2	R.VTPLGYVLPSHVTEEMLWECK.Q
gi|20357552|ref|N	1	3	0.027	550	61586	5.4	U	cortactin isoform a [Homo sapiens]				
gi|20357556|ref|N	1	3	0.029	513	57467	5.3	U	cortactin isoform b [Homo sapiens]				
	HsFLAG-MOCK_300mM_T	3.5724	0.3041	1686.04	1685.84	7278.8		1	855.9	57.1	3	K.TVQGSGHQEHINIHK.L
gi|4885105|ref|NI	1	2	0.027	559	61493	7.5	U	chromatin assembly factor 1 subunit B [Homo sapiens]				
*	HsHeLa3_Ti_103.1166.116	3.2412	0.2132	1540.65	1540.63	4898.8		1	787.1	67.9	2	R.TQDPSSPGTTPPQAR.Q
gi|23111038|ref|N	1	2	0.027	519	58471	5.1	U	sorting nexin 2 [Homo sapiens]				

*	HsFLAG-Control_HeLa_S1	3.7094	0.3369	1583.61	1583.87	7607.6		1	1535.6	76.9	2	K.YLHVGYIVPPAPEK.S
gi|89038196|ref|X	5	6	0.026	2855	315119	6.8	U	PREDICTED: MAX dimerization protein 5 isoform 1 [Homo sapiens]				
gi|89038895|ref|X	5	6	0.026	2855	315105	6.8	U	PREDICTED: similar to MAX-interacting protein isoform 6 [Homo sapiens]				
gi|89038893|ref|X	5	6	0.026	2855	315105	6.8	U	PREDICTED: similar to MAX-interacting protein isoform 5 [Homo sapiens]				
gi|89038198|ref|X	5	6	0.026	2855	315119	6.8	U	PREDICTED: MAX dimerization protein 5 isoform 2 [Homo sapiens]				
	HsFlag1P_Ti_102.2392.239	2.83	0.2464	1432.83	1433.66	6617.8		3	602.4	58.3	1	K.LNSVDPTMSIDLK.Y
	HsF-IP-293-MG_Ti_102.24	4.0219	0.3815	2396.96	2397.52	9038.1		1	1357	55	2	K.TCQENSDVFQQEQGISDLLGK.S
	HsF-IP-293-MG_Ti_103.19	2.838	0.2575	1288.42	1288.49	5452.6		1	804.6	72.7	1	R.ISNPSAFSIVPR.R
	HsFLAG-Control_HeLa_NE	2.8288	0.0956	1523.65	1523.64	9297.1		1	787.9	57.7	1	R.AFSEIQGLTDQADK.L
	Hs293FLP_TREX_Ti_104.2	2.581	0.2606	1388.51	1388.65	6845.5		2	625.2	58.3	1	R.VTLGPTQVFLANK.D
gi|21071056|ref|N	3	3	0.026	1647	184644	7.9	U	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin a4 [Homo sap				
*	HsHeLa3_Ti_105.2147.214	3.6155	0.3509	1667.59	1665.85	5578.5		1	1341.3	71.4	1	R.GLQSYYAVAHAVTER.V
	HsHeLa3_Ti_106.3032.303	3.5041	0.3648	1777.42	1776.14	5682.2		1	726.5	57.1	1	K.TIQTIALITYLMEHK.R
	HsHeLa3_Ti_106.2074.207	3.293	0.2414	1514.9	1512.75	7161.7		1	1568.5	75	1	K.LTQVLNTHYVAPR.R
gi|38201619|ref|N	2	2	0.026	1403	154804	5.2	U	eukaryotic translation initiation factor 4 gamma, 1 isoform 4 [Homo sapiens]				
gi|38201627|ref|N	2	2	0.024	1512	166588	5.2	U	eukaryotic translation initiation factor 4 gamma, 1 isoform 2 [Homo sapiens]				
gi|38201625|ref|N	2	2	0.025	1435	158516	5.2	U	eukaryotic translation initiation factor 4 gamma, 1 isoform 3 [Homo sapiens]				
gi|38201623|ref|N	2	2	0.023	1599	175460	5.3	U	eukaryotic translation initiation factor 4 gamma, 1 isoform 1 [Homo sapiens]				
gi|38201621|ref|N	2	2	0.023	1599	175460	5.3	U	eukaryotic translation initiation factor 4 gamma, 1 isoform 1 [Homo sapiens]				
	HsFLAG-Control_HeLa_NE	3.3975	0.3496	2066.15	2065.26	7227.3		1	440.4	41.7	1	R.LQGINCGPDFTPSFANLGR.T
	HsFLAG-Control_HeLa_S1	2.8669	0.1869	1770.56	1769.01	7602.8		1	750.9	53.1	1	R.GLPLVDDGGWNTVPISK.G
gi|31742532|ref|N	2	3	0.026	1248	138907	5.4	U	diaphanous 1 [Homo sapiens]				
*	HsFLAG-Control_HeLa_S1	4.3342	0.4179	2129.92	2129.24	7843.6		1	1085	58.8	2	R.VQLNVFDEQGEEDSYDLK.G
*	HsFLAG-Control_HeLa_S1	3.3304	0.3548	1521.9	1521.72	9287.6		1	1173.8	60.7	1	K.AGCAVTSLLASELTK.D
gi|13489083|ref|N	1	6	0.026	793	88952	4.6	U	SAPS domain family, member 3 [Homo sapiens]				
*	HsFLAG-Control_HeLa_S1	4.7711	0.4692	2388.81	2387.78	8482.9		1	1044.1	50	6	K.LYSFLLNDSPLNPLLASFFSK.V
gi|16753207|ref|N	1	3	0.026	624	65696	5.2	U	ubiquilin 2 [Homo sapiens]				
*	HsFLAG-Control_HeLa_S1	5.2369	0.411	1394.45	1394.53	8678.6		1	2406	80	3	R.GPAAAQGSAAAPAEPK.I
gi|4827050|ref|N	1	2	0.026	494	56069	5.3	U	ubiquitin specific protease 14 [Homo sapiens]				
*	HsFLAG-Control_MG_293_	4.1909	0.291	1372.93	1372.61	9773.5		1	1529.7	70.8	2	K.AQLFALTGVQPAR.Q
gi|30794368|ref|N	2	2	0.025	1582	181153	7	U	polybromo 1 isoform 2 [Homo sapiens]				
gi|41281917|ref|N	2	2	0.025	1582	182117	6.8	U	polybromo 1 isoform 4 [Homo sapiens]				
gi|30794372|ref|N	2	2	0.025	1602	183689	6.7	U	polybromo 1 isoform 1 [Homo sapiens]				
	HsHeLa3_Ti_105.3324.332	3.4492	0.3915	2426.7	2426.74	3652.4		1	423.9	47.5	1	R.LSNLPTVDPIAVCHELYNTIR.D
	HsGST-MOCK_Ti_302.372	2.6137	0.0802	2242.46	2242.52	3240.4		6	182.3	44.4	1	K.EVFLSNLEETCPMTCILGK.C
gi|30410720|ref|N	1	3	0.025	894	101982	6.6	U	Sec3 isoform 1 [Homo sapiens]				
gi|67944634|ref|N	1	3	0.025	894	101982	6.6	U	Sec3 isoform 1 [Homo sapiens]				
	HsHeLa3_Ti_106.4328.432	2.9349	0.3029	2415.1	2414.8	8980		1	551.9	38.1	3	K.VGILPFVAEFEEFAGLAESIFK.N
gi|30581135|ref|N	2	2	0.024	1233	143233	7.6	U	SMC1 structural maintenance of chromosomes 1-like 1 [Homo sapiens]				
*	HsFLAG-Control_HeLa_NE	2.9875	0.0829	1214.98	1215.35	10045.2		2	1210.8	77.8	1	K.LNEQQSVLQR.I
*	HsFLAG-Control_HeLa_NE	3.6269	0.3462	2176.76	2177.38	9999.4		1	916.6	47.2	1	K.VLTFDLTKYPDANPNPNEQ.-
gi|33356547|ref|N	1	2	0.024	904	101896	5.5	U	minichromosome maintenance protein 2 [Homo sapiens]				
*	HsHeLa3_Ti_102.3737.373	4.3791	0.3805	2540.7	2539.64	5875.5		1	877.4	50	2	R.ATEDGEEDEEMIESIENLEDLK.G
gi|11386151|ref|N	1	2	0.024	411	46369	8.6	U	TEA domain family member 1 [Homo sapiens]				
*	HsHeLa3_Ti_105.2283.228	3.17	0.2568	1122.93	1121.32	6558.1		2	889.8	77.8	2	K.GPQNAFFLVK.F
gi|77404397|ref|N	1	2	0.023	910	101997	7.2	U	staphylococcal nuclease domain containing 1 [Homo sapiens]				
*	HsFLAG-Control_HeLa_S1	3.9857	0.3531	2306.72	2307.56	5193.5		1	660.9	52.5	2	R.NLPGLVQEGEPFSEEATLFTK.E
gi|89030074|ref|X	1	2	0.023	828	89468	5.5	U	PREDICTED: inositol polyphosphate-5-phosphatase E isoform 3 [Homo sapiens]				
gi|89030711|ref|X	1	2	0.015	1261	137715	5.9	U	PREDICTED: similar to Protein KIAA0310 isoform 40 [Homo sapiens]				

gi|89030709|ref|X	1	2	0.022	852	92244	6	U	PREDICTED: similar to Protein KIAA0310 isoform 39 [Homo sapiens]				
gi|89030707|ref|X	1	2	0.022	879	94595	5.8	U	PREDICTED: similar to Protein KIAA0310 isoform 38 [Homo sapiens]				
gi|89030705|ref|X	1	2	0.021	899	96861	6	U	PREDICTED: similar to Protein KIAA0310 isoform 37 [Homo sapiens]				
gi|89030703|ref|X	1	2	0.023	832	89978	5.8	U	PREDICTED: similar to Protein KIAA0310 isoform 36 [Homo sapiens]				
gi|89030701|ref|X	1	2	0.023	810	87048	5.5	U	PREDICTED: similar to Protein KIAA0310 isoform 35 [Homo sapiens]				
gi|89030697|ref|X	1	2	0.045	426	44371	5.6	U	PREDICTED: similar to Protein KIAA0310 isoform 33 [Homo sapiens]				
gi|89030685|ref|X	1	2	0.022	879	94595	5.8	U	PREDICTED: similar to Protein KIAA0310 isoform 27 [Homo sapiens]				
gi|89030683|ref|X	1	2	0.023	828	89468	5.5	U	PREDICTED: similar to Protein KIAA0310 isoform 26 [Homo sapiens]				
gi|89030675|ref|X	1	2	0.015	1281	139980	6	U	PREDICTED: similar to Protein KIAA0310 isoform 21 [Homo sapiens]				
gi|89030110|ref|X	1	2	0.015	1281	139980	6	U	PREDICTED: inositol polyphosphate-5-phosphatase E isoform 1 [Homo sapiens]				
gi|89030108|ref|X	1	2	0.015	1261	137715	5.9	U	PREDICTED: inositol polyphosphate-5-phosphatase E isoform 20 [Homo sapiens]				
gi|89030106|ref|X	1	2	0.022	852	92244	6	U	PREDICTED: inositol polyphosphate-5-phosphatase E isoform 19 [Homo sapiens]				
gi|89030104|ref|X	1	2	0.022	879	94595	5.8	U	PREDICTED: inositol polyphosphate-5-phosphatase E isoform 18 [Homo sapiens]				
gi|89030102|ref|X	1	2	0.021	899	96861	6	U	PREDICTED: inositol polyphosphate-5-phosphatase E isoform 17 [Homo sapiens]				
gi|89030100|ref|X	1	2	0.023	832	89978	5.8	U	PREDICTED: inositol polyphosphate-5-phosphatase E isoform 16 [Homo sapiens]				
gi|89030098|ref|X	1	2	0.023	810	87048	5.5	U	PREDICTED: inositol polyphosphate-5-phosphatase E isoform 15 [Homo sapiens]				
gi|89030094|ref|X	1	2	0.045	426	44371	5.6	U	PREDICTED: inositol polyphosphate-5-phosphatase E isoform 13 [Homo sapiens]				
gi|89030082|ref|X	1	2	0.022	879	94595	5.8	U	PREDICTED: inositol polyphosphate-5-phosphatase E isoform 7 [Homo sapiens]				
	HsFLAG-Control_HeLa_S1	3.3396	0.3824	1903.74	1902.2	5768.8		1	490	50	2	R.LLPSAPQTLPDGPLASPAR.V
gi|39777601|ref|N	1	2	0.023	693	76731	6	U	transglutaminase 3 precursor [Homo sapiens]				
*	HsFLAG-Control_Hela_Ti_1	4.7449	0.3552	1662.52	1662.85	7210.5		1	1883.3	76.7	2	R.SQGVFQCGPASVIGVR.E
gi|89037519|ref|X	3	4	0.022	2779	295336	5.2	U	PREDICTED: AHNAK nucleoprotein 2 isoform 1 [Homo sapiens]				
gi|89037828|ref|X	3	4	0.076	793	85128	4.8	U	PREDICTED: AHNAK nucleoprotein 2 isoform 3 [Homo sapiens]				
gi|89037826|ref|X	3	4	0.022	2779	295336	5.2	U	PREDICTED: similar to AHNAK nucleoprotein isoform 1 isoform 2 [Homo sapiens]				
	HsHeLa3_Ti_103.3208.320	2.9323	0.2802	2010.81	2012.23	7795.1		1	1095.4	55.9	2	R.FSFPAPSSEDDVFIPTVR.E
	HsHeLa3_Ti_103.2834.283	4.0361	0.2818	2370.98	2370.71	5514.4		3	574.7	45.7	1	K.AGAGVPGEQPVDLNLPLEAPPISK.V
	HsHeLa3_Ti_104.1551.155	3.489	0.2265	1964.54	1963.2	5645.2		1	534	50	1	R.SAPIQTQPEARPEAELPK.K
gi|62122917|ref|N	3	5	0.022	2391	248072	8.3	U	filaggrin 2 [Homo sapiens]				
*	HsFLAG-Control_Hela_Ti_1	3.4944	0.3349	1270.39	1270.51	5182.7		1	1080.6	85	2	R.SVVTVIDVFYK.Y
*	HsFLAG-Control_Hela_Ti_1	5.3008	0.3371	3210.52	3209.18	9854.1		1	1346.1	29.2	2	K.GGQGHGCVSGGQPSGCGQPESNPCSQSYSQR.G
*	HsFLAG-Control_293_Ti_1	2.6922	0.2451	1273.22	1273.31	7588.5		1	766.2	65	1	R.ASHFQSHSSER.Q
gi|19913408|ref|N	2	3	0.022	1621	182661	8.1	U	DNA topoisomerase II, beta isozyme [Homo sapiens]				
	HsFLAG-Control_HeLa_NE	4.0224	0.2394	1462.63	1462.64	7531.2		1	2080	87.5	1	K.IFDEILVNAADNK.Q
*	HsGST-MOCK_Ti_403.485	5.5362	0.4339	2488.22	2488.75	8800.7		1	1602.2	57.1	2	K.VYVPALIFGQLLTSSNYDDDEK.K
gi|17017991|ref|N	1	3	0.022	847	96576	8.2	U	FtsJ homolog 3 [Homo sapiens]				
*	HsFLAG-MOCK_300mM_T	5.0419	0.4236	2391.17	2390.52	6633.8		1	815	52.8	3	R.YTFNEDEGELPEWFVQEEK.Q
gi|27735067|ref|N	2	2	0.022	679	75357	6.8	U	hypothetical protein LOC126353 [Homo sapiens]				
*	HsHeLa3_Ti_103.1130.113	2.1708	0.232	1340.58	1341.46	6354.9		1	420.3	50	1	R.GTPAGTTPGASQAPK.A
*	HsHeLa3_Ti_103.1122.112	2.6618	0.162	1341.67	1341.46	4851.9		1	547.2	60.7	1	R.GTPAGTTPGASQAPK.A
gi|38569466|ref|N	1	2	0.022	552	59690	9	U	ROD1 regulator of differentiation 1 [Homo sapiens]				
*	HsFLAG-Control_HeLa_NE	3.3078	0.308	1493.37	1492.63	5318.3		1	994.4	81.8	2	R.SQPVYIQYSNHR.E
gi|4758032|ref|N	1	2	0.021	906	102487	5.3	U	coatomer protein complex, subunit beta 2 (beta prime) [Homo sapiens]				
*	HsFLAG-Control_HeLa_NE	3.9681	0.3865	2065.29	2066.27	7294		1	1208.7	61.1	2	K.AAESLADPTEYENLFPGLK.E
gi|11559929|ref|N	1	2	0.021	874	97718	5.5	U	coatomer protein complex, subunit gamma 1 [Homo sapiens]				
*	HsFLAG-Control_HeLa_S1	4.111	0.4025	2007.94	2008.19	6651.8		1	802.8	52.9	2	K.SSPEPVALTESETEYVIR.C
gi|21040314|ref|N	3	4	0.02	2303	250386	5.6	U	SON DNA-binding protein isoform B [Homo sapiens]				
gi|38146099|ref|N	3	4	0.019	2386	259619	5.7	U	SON DNA-binding protein isoform G [Homo sapiens]				
gi|21040326|ref|N	3	4	0.019	2426	263827	5.6	U	SON DNA-binding protein isoform F [Homo sapiens]				
gi|21040322|ref|N	3	4	0.019	2325	252251	5.4	U	SON DNA-binding protein isoform C [Homo sapiens]				

gi|21040320|ref|N	3	4	0.021	2140	232307	6	U	SON DNA-binding protein isoform A [Homo sapiens]			
gi|21040318|ref|N	3	4	0.021	2108	228179	5.4	U	SON DNA-binding protein isoform E [Homo sapiens]			
	HsFlag1P_Ti_104.3127.312	2.9349	0.2942	1857.76	1858.23	3753.3	4	347.3	47.1	1	K.ILDSFAAAPVPTTTLVLK.S
	Hs293FLP_TREX_Ti_102.2	3.305	0.2497	1375.8	1373.55	8153.9	3	1040.9	66.7	2	K.ESDQTLAALLSPK.E
	Hs293FLP_TREX_Ti_102.1	3.8843	0.4	1355.36	1355.53	6844.9	1	1572.4	76.9	1	R.AGIEGPLLASDVGR.D
gi|44890062|ref|N	1	2	0.02	1045	114989	9.2	U	hypothetical protein LOC91748 [Homo sapiens]			
*	HsHeLa3_Ti_106.2698.269	3.7305	0.2732	2288.05	2287.67	5035.2	1	811.5	52.5	2	K.ALLQDSAPQPALPQVQIPFPR.R
gi|24308033|ref|N	1	3	0.02	1015	110064	4.7	U	formin binding protein 4 [Homo sapiens]			
*	HsHeLa3_Ti_102.1229.122	5.1196	0.4672	2050.85	2050.02	6622.1	1	1294.2	57.9	3	K.TGTDSNSTESSETSTGSLCK.E
gi|7662018|ref|N	2	3	0.019	2039	229479	7	U	PHD finger protein 3 [Homo sapiens]			
*	HsGST-MOCK_Ti_403.430	3.1959	0.164	2147.51	2146.45	6655.7	1	504.8	44.4	1	K.SFSLDEPPLFIPDNIATIR.R
*	HsFLAG-MOCK_300mM_T	4.2153	0.4816	2019.71	2019.27	4124.5	1	769	57.9	2	K.GVLNVHPAASASKPSADQIR.Q
gi|33946327|ref|N	2	3	0.019	2090	213618	7.5	U	nucleoporin 214kDa [Homo sapiens]			
*	HsFLAG-Control_HeLa_S1	2.8455	0.2698	1672.32	1672.79	4415.6	4	343.4	50	1	K.SPGSTPTTPTSSQAPQK.L
*	HsFLAG-Control_HeLa_NE	4.5084	0.4278	2251.59	2252.57	4890.2	1	573.7	47.6	2	K.LGELLFPSSLAGETLGSFSGLR.V
gi|34577122|ref|N	1	2	0.019	969	105427	5.4	U	nuclear factor kappa-B, subunit 1 [Homo sapiens]			
*	HsHeLa3_Ti_105.1458.145	3.896	0.3991	1833.89	1832.93	6156.6	1	935.8	61.8	2	R.YVCEGPSHGGLPGASSEK.N
gi|4503337|ref|N	1	3	0.019	514	57674	9.4	U	dyskerin [Homo sapiens]			
*	HsHeLa3_Ti_103.1255.125	2.1134	0.1929	983.56	984.14	5223.6	1	590.8	72.2	3	K.APQVVAEAAK.T
gi|41406064|ref|N	2	6	0.018	1976	228997	5.5	U	myosin, heavy polypeptide 10, non-muscle [Homo sapiens]			
	HsFLAG-Control_Hela_Ti_1	4.7548	0.4555	1962.12	1963.06	8836.7	1	1809.5	68.8	5	R.TQLEELEDELQATEDAK.L
*	HsFLAG-Control_293_Ti_2	2.9209	0.113	2046.93	2046.24	9660.3	1	569.5	44.1	1	K.SLEAEILQLQEELASSER.A
gi|15987121|ref|N	1	2	0.018	1297	143732	8.8	U	hypothetical protein LOC23223 [Homo sapiens]			
*	HsHeLa3_Ti_105.3934.393	2.8352	0.4091	2472.53	2472.85	9264.8	1	496.4	36.4	2	K.NFLPILFNLYGGQPVAAGDTPAPR.R
gi|13491166|ref|N	2	2	0.018	1186	126473	6.8	U	pumilio 1 isoform 2 [Homo sapiens]			
gi|66932909|ref|N	2	2	0.018	1188	126685	6.8	U	pumilio 1 isoform 1 [Homo sapiens]			
gi|13491168|ref|N	2	2	0.02	1064	114003	7.1	U	pumilio homolog 2 [Homo sapiens]			
	HsHeLa3_Ti_103.1278.127	2.1616	0.1994	1077.51	1078.21	3903.8	5	405	60	1	R.YISAAPGAEAK.Y
	HsHeLa3_Ti_102.1585.158	2.9948	0.26	1227.54	1228.35	7696.7	1	846.4	77.8	1	K.DQYANYVVQK.M
gi|55749531|ref|N	2	2	0.018	895	100228	5.7	U	splicing factor 3B subunit 2 [Homo sapiens]			
*	HsFLAG-Control_293_Ti_2	2.7773	0.1685	1185.77	1185.37	8316.9	2	621.2	66.7	1	K.RAAVLLEQER.Q
*	HsFLAG-MOCK_300mM_T	3.0579	0.1567	1885.18	1883.16	4225.5	3	331.7	50	1	K.RAAVLLEQERQQEIAK.M
gi|11345460|ref|N	1	2	0.018	669	74266	8.5	U	hypothetical protein LOC60558 [Homo sapiens]			
*	HsHeLa_Control-MG_Ti_10	3.3073	0.3117	1325.02	1324.48	7321.3	1	1136.9	77.3	2	R.NFSIVAHVDHGK.S
gi|18105007|ref|N	1	6	0.017	2225	242981	6.5	U	carbamoylphosphate synthetase 2/aspartate transcarbamylase/dihydroorotase [Homo sap			
*	Hs293FLP_Ti_306.3340.33	5.6471	0.3719	3705.76	3704.18	4141.9	1	517.2	24.3	6	R.AAFALGGLGSGFASNREELSALVAPAFAHTSQVLVDK.S
gi|22748937|ref|N	1	2	0.017	1204	136311	5.8	U	exportin 5 [Homo sapiens]			
*	HsFLAG-Control_HeLa_S1	3.8566	0.369	2151.77	2152.54	4046.4	1	665.5	57.9	2	K.SAILGLPQPLLELNDSPVFK.T
gi|8922388|ref|N	1	2	0.017	759	85766	9.2	U	RNA binding motif protein 28 [Homo sapiens]			
*	Hs293FLP_TREX_Ti_105.2	3.131	0.1631	1470.2	1469.72	4508.4	9	518.8	66.7	2	R.LINNNPEIFGPLK.R
gi|61676188|ref|N	3	3	0.016	4374	481896	5.2	U	HECT, UBA and WWE domain containing 1 [Homo sapiens]			
*	HsFLAG-Control_HeLa_S1	2.8547	0.2959	1819.73	1818.21	3982	2	284.5	53.1	1	K.TTPLKPSPLPVIPDTIK.E
*	HsFLAG-Control_HeLa_S1	3.0817	0.265	2237.76	2238.59	11593.3	1	729.5	40.5	1	R.LLGPSAAADILQLSSSLPLQSR.G
*	HsFLAG-Control_HeLa_S1	3.7483	0.2754	3546.42	3544.99	7505	1	618.4	24.2	1	R.ESQLAHIKDEPPPLSPAPLTPATPSSLDPFFSR.E
gi|24430149|ref|N	1	3	0.016	1391	155199	6.2	U	nucleoporin 155kDa isoform 1 [Homo sapiens]			
gi|4758844|ref|N	1	3	0.017	1332	149016	6.3	U	nucleoporin 155kDa isoform 2 [Homo sapiens]			
	HsGST-MOCK_Ti_403.559	2.922	0.1288	2486.44	2487.82	4070.9	5	222.2	35.7	3	R.EITAIESSVPCQLLESVLQELK.G
SHUFFLED_gi|2	1	3	0.016	492	53132	9.4	U	FALSE POSITIVE			

SHUFFLED_gi|5	1	3	0.016	492	53132	9.4	U		FALSE POSITIVE			
	HsFLAG-Control_HeLa_S1	2.1823	0.1214	897.58	898.137	4242.6		5	493.1	71.4	3	K.PLTAVRLK.A
gi|19718731|ref|N	2	3	0.015	1362	152218	9.2	U		bromodomain-containing protein 4 isoform long [Homo sapiens]			
	HsFLAG-MOCK_300mM_T	4.0791	0.2595	1507.85	1506.79	6798.6		1	1130.5	70.8	2	R.VVHIIQSREPSLK.N
*	HsFLAG-MOCK_300mM_T	1.843	0.0826	836.9	836.025	4520.4		2	260.3	75	1	K.IHSPIIR.S
gi|4502945|ref|N	3	6	0.015	1464	138912	5.9	U		alpha 1 type I collagen preproprotein [Homo sapiens]			
*	HsHeLa_Control-MG_Ti_10	3.9882	0.4608	1963.04	1963.12	5233.8		1	686.8	52.4	2	K.SGDRGETGPAGPAGPVGPVGAR.G
*	HsHeLa_Control-MG_Ti_10	3.5906	0.1136	1963.62	1963.12	6931		2	1235.7	40.5	2	K.SGDRGETGPAGPAGPVGPVGAR.G
*	HsHeLa_Control-MG_Ti_10	3.331	0.4249	1548.09	1547.71	5772.6		1	704.3	55.9	2	R.GETGPAGPAGPVGPVGAR.G
gi|51702222|ref|N	1	2	0.015	685	75599	9.8	U		hypothetical protein LOC144108 [Homo sapiens]			
*	HsHeLa_Control-MG_Ti_20	3.0213	0.1809	1238.62	1238.48	8290.1		2	1113.9	77.8	2	R.IELKHDKKAR.A
gi|38679960|ref|N	2	3	0.014	2383	269997	6.5	U		acetyl-Coenzyme A carboxylase alpha isoform 1 [Homo sapiens]			
gi|38679977|ref|N	2	3	0.014	2346	265551	6.4	U		acetyl-Coenzyme A carboxylase alpha isoform 2 [Homo sapiens]			
gi|38679967|ref|N	2	3	0.014	2346	265551	6.4	U		acetyl-Coenzyme A carboxylase alpha isoform 2 [Homo sapiens]			
	HsFLAG-Control_HeLa_S1	4.6342	0.3931	2198.41	2196.37	8595.4		1	1313	57.9	2	R.FIIGSVSEDNSEDEISNLVK.L
	HsFLAG-Control_HeLa_S1	2.9831	0.2579	1594.17	1592.84	7283.9		1	483.8	50	1	R.IGSFGPQEDLLFLR.A
gi|41281521|ref|N	1	3	0.014	1401	157168	6.6	U		chromosome condensation-related SMC-associated protein 1 [Homo sapiens]			
*	HsFLAG-Control_HeLa_NE	3.4254	0.3825	2108.3	2109.26	8005.3		1	576	47.2	3	R.YQPLASTASDNDFVTPEPR.R
gi|39930353|ref|N	1	2	0.013	1042	117761	6.7	U		superkiller viralicidic activity 2-like 2 [Homo sapiens]			
*	HsFLAG-Control_HeLa_NE	3.6928	0.415	1568.77	1569.67	7400.2		1	962.5	61.5	2	R.DVDFEGTDEPIFGK.K
gi|60097902|ref|N	4	14	0.012	4061	435180	9.2	U		filaggrin [Homo sapiens]			
*	HsFLAG-Control_Hela_Ti_1	3.2487	0.2209	960.32	959.991	5197.6		2	920.8	100	1	K.RHESSSEK.K
*	HsFLAG-Control_Hela_Ti_1	3.4631	0.3323	1553.22	1553.63	9694.2		1	1196.9	66.7	2	K.GYSPTHREEEYGK.N
	HsFLAG-Control_293_Ti_1	3.2934	0.3912	1659.87	1660.66	8671.9		1	1266.6	60	9	R.SGHSGSHHSHTTSQGR.S
	HsFLAG-Control_293_Ti_1	2.6776	0.2348	1362.36	1361.42	6307.3		8	561.5	59.1	2	R.HHEASTHADISR.H
SHUFFLED_gi|1	1	3	0.012	689	78439	9	U		FALSE POSITIVE			
*	HsFLAG-Control_HeLa_S1	2.0385	0.1586	790.44	790.935	3448.1		9	284.2	71.4	3	K.SGLVSVTK.V
gi|41322908|ref|N	3	5	0.01	4525	513712	5.8	U		plectin 1 isoform 3 [Homo sapiens]			
gi|47607492|ref|N	3	5	0.01	4574	518478	5.7	U		plectin 1 isoform 1 [Homo sapiens]			
gi|41322923|ref|N	3	5	0.01	4547	516204	5.8	U		plectin 1 isoform 11 [Homo sapiens]			
gi|41322919|ref|N	3	5	0.01	4547	516282	5.8	U		plectin 1 isoform 8 [Homo sapiens]			
gi|41322916|ref|N	3	5	0.01	4684	531796	6	U		plectin 1 isoform 6 [Homo sapiens]			
gi|41322914|ref|N	3	5	0.01	4551	516484	5.8	U		plectin 1 isoform 10 [Homo sapiens]			
gi|41322912|ref|N	3	5	0.01	4533	514780	5.7	U		plectin 1 isoform 2 [Homo sapiens]			
gi|41322910|ref|N	3	5	0.01	4515	512609	5.8	U		plectin 1 isoform 7 [Homo sapiens]			
	HsFLAG-Control_HeLa_S1	3.9036	0.4077	1710.38	1709.85	5691.6		1	1033.7	71.4	2	R.LLDPEDVDVPQPDEK.S
	HsFLAG-Control_HeLa_S1	3.0473	0.2497	1810.78	1809.97	9841.6		1	899.3	56.7	1	K.VQSGSESVIQEYVDLR.T
	HsHeLa3_Ti_104.2633.263	4.343	0.3226	1570.69	1567.83	4953.4		1	1289.7	73.3	2	R.APVPASELLASGVLSR.A
gi|42716275|ref|N	1	2	0.01	2376	266937	7.1	U		CCR4-NOT transcription complex, subunit 1 isoform a [Homo sapiens]			
*	HsHeLa3_Ti_104.3264.326	3.494	0.3986	2473.8	2473.85	4261.4		1	339.7	45.5	2	R.NVPGFLPTNDLSQPTGFLAQPMK.Q
gi|48762934|ref|N	1	5	0.01	1366	129314	9	U		alpha 2 type I collagen [Homo sapiens]			
*	HsHeLa_Control-MG_Ti_10	3.2127	0.4349	1225.77	1224.32	7852.7		1	1239.2	69.2	5	R.GPAGPSGPAGKDGR.T
gi|19923287|ref|N	2	2	0.009	3703	404474	6.2	U		AT-binding transcription factor 1 [Homo sapiens]			
*	HsHeLa3_Ti_103.1202.120	2.6648	0.196	1612.51	1612.74	4282.4		1	480.4	57.1	1	K.LAEAPSAQPNQTQEK.Q
*	HsHeLa3_Ti_103.2984.298	3.0803	0.3312	1987.54	1988.27	8452.1		1	849.2	52.9	1	R.TPTMLECEVLGNDIGLPK.R
gi|4504795|ref|N	1	2	0.009	2671	304115	6.5	U		inositol 1,4,5-triphosphate receptor, type 3 [Homo sapiens]			
*	HsFLAG-Control_293_Ti_1	3.8378	0.3713	2527.53	2527.72	7401.3		1	786.9	45.7	2	R.GDLPDPIGTGLDPDWSAIAATQCR.L
gi|50897852|ref|N	1	2	0.009	1843	212619	6	U		Hook-related protein 1 [Homo sapiens]			
*	Hs283FLP_Ti_105.1619.16	3.7866	0.3672	2011.97	2011.2	8037.7		1	845	56.2	2	K.ILEQENEHLNQTVSSLR.Q

gi|32483416|ref|N	4	8	0.009	1020	111838	6.1	U		neurofilament, heavy polypeptide 200kDa [Homo sapiens]			
	HsFLAG-Control_HeLa_S1	3.2971	0.1073	1133.86	1134.24	6961.9		1	1357.9	93.8	3	R.KLLEGEECR.I
	HsFLAG-Control_HeLa_S1	1.9146	0.087	1005.53	1006.07	5228.8		2	405.5	71.4	1	K.LLEGEECR.I
	HsFLAG-Control_HeLa_S1	2.9661	0.1081	1006.13	1006.07	3435.3		2	655.9	92.9	2	K.LLEGEECR.I
	HsHeLa_Control_Ti_102.11	2.6647	0.1446	1007.08	1006.07	2807		2	532.2	85.7	2	K.LLEGEECR.I
gi|57634534|ref|N	1	2	0.007	2012	227918	6.2	U		nucleoporin 205kDa [Homo sapiens]			
*	HsFLAG-Control_293_Ti_1	3.7099	0.3266	1503.38	1503.61	8374.8		1	1461.6	67.9	2	K.ASTEGVAIQGQQGTR.L
gi|27436959|ref|N	2	2	0.005	4167	460996	6.3	U		ALMS1 [Homo sapiens]			
*	Hs283FLP_Ti_104.1233.12	2.459	0.2712	1212.69	1212.35	5962.9		2	502.9	60	1	K.SHISNINVEAK.F
*	Hs283FLP_Ti_103.1527.15	2.2116	0.1868	979.65	980.106	4015.9		4	349.8	75	1	K.TPLSAFSEK.L
gi|88953266|ref|X	1	5	0.005	1732	186906	7.6	U		PREDICTED: hypothetical protein LOC200424 [Homo sapiens]			
gi|88955191|ref|X	1	5	0.005	1720	185841	7.5	U		PREDICTED: similar to CXXC finger 6 [Homo sapiens]			
	Hs293FLP-MG_Ti_104.133	2.6619	0.2687	1009.72	1010.18	4367.8		1	442.3	75	5	R.ELHATTPLK.K
gi|28466991|ref|N	2	2	0.005	1649	182466	7	U		tau tubulin kinase 2 [Homo sapiens]			
	HsFLAG-Control_HeLa_S1	2.7801	0.1854	1153.56	1154.32	6137.9		6	488.1	75	1	R.EYQELMNVK.L
	HsFLAG-Control_HeLa_NE	2.5173	0.1064	1154.14	1154.32	7891.6		3	773.6	75	1	R.EYQELMNVK.L
gi|54112403|ref|N	1	3	0.004	2997	335928	6.3	U		chromodomain helicase DNA binding protein 7 [Homo sapiens]			
*	HsHeLa3_Ti_105.2067.206	3.4392	0.3053	1483.76	1481.69	5607.5		2	674.9	62.5	3	K.NADVLFSSFQKPK.Q

	Proteins	eptide ID	Copies
Redundant	1374	7075	34834
Nonredundant	814	6985	33209