

Table S1

Accessions	Leading Protein Name	Modified Sequence	Median Ratio M/L	Median Ratio H/L	Median Ratio H/M	Ratio M/L Biological Variability [%]	Ratio H/L Biological Variability [%]	Ratio H/M Biological Variability [%]	Significance counts M/L	Significance counts H/L	Significance counts H/M	Charge	m/z	Mass Error [ppm]	Localization Prob	Score	
P28223;F5GW68	5HT2A 5-hydroxytryptamine receptor 2A	IAS(ph)FSFIPQSS(ph)ISS(ph)EKIFQR	1.04	2.96	4.70	29.97	23.67	27.83	0	3	3	2	1256.552	0.30	0.80	211.06	
Q72392;B7WNP8;D6RHE5	TPC11 Trafficking protein particle complex subunit 11	IEITS(ph)VDAIAGNET(ph)GR	1.02	37.16	42.86	22.19	18.39	37.19	0	3	3	3	616.611	0.04	0.97	84.21	
Q9Y4A5;F222U4;HOY4W2	TRRAP Transformation/transcription domain-associated protein	QAMHS(ph)IQVIAQVT(ph)GK	9.87	171.15	20.38	70.05	45.66	117.29	2	2	2	2	885.904	0.77	1.00	88.10	
P29590;F8W9X2	PML Protein PML	S(ph)PVIGSEVFIPNSNHVAGAGEAEEER	0.42	0.26	0.62	9.05	34.68	32.86	2	2	2	3	911.755	0.15	1.00	84.68	
Q723C6	ATG9A Autophagy-related protein 9A	HPEPVPEEGS(ph)EDEIPPVQHKV	0.80	0.37	0.42	38.20	66.15	96.15	0	2	2	2	3	810.372	0.29	1.00	157.54
B3KTC7;P49959;F8W7U8	B3KTC7 MRE11 meiotic recombination 11 homolog A (S. cerevisiae)	GVDFES(ph)SEDDDDPFMNTSIRR	0.82	1.41	1.71	46.59	63.83	112.71	0	2	2	3	905.357	-0.13	0.89	243.72	
Q8N9T8;D3YTE0	KRI1 Protein KRI1 homolog	QIPAIIDGIMGPES(ph)PPAQEEAPVS(ph)PHKKPAPQK	0.59	0.63	0.58	57.53	60.42	280.88	2	1	2	4	930.940	-0.30	0.99	70.99	
Q5VY93;Q29274	Q5VY93 Rho/Rac guanine nucleotide exchange factor (GEF) 2	IQDSSDPDT(ph)GSEEE GSSRS(ph)PPHS(ph)PR	0.75	2.27	2.95	22.90	43.65	60.67	0	1	2	3	1003.051	-0.51	0.95	90.73	
Q43719;E9FPF2	HTSF1 HIV Tat-specific factor 1	VIDEEGS(ph)ERFDEDS(ph)DEKEEEDTYEK	0.81	0.81	0.62	7.49	10.02	10.43	0	1	2	3	1147.426	0.52	1.00	111.77	
Q14978	NOLC1 Nucleolar and coiled-body phosphoprotein 1	IQT(ph)PNT(ph)FPK	0.85	1.38	1.82	16.84	13.07	17.25	0	1	2	2	603.254	0.39	1.00	137.84	
Q96G66;E5RFB8	SRRC2 Scavenger receptor class F member 2	APS(ph)PPPPGSEAAP(s)ph)PSKR	0.55	0.22	0.48	38.07	74.61	54.58	0	1	2	3	630.611	-0.17	0.50	104.89	
E9PKC0;Q6IQ23;HOYDE2	E9PKC0 Pleckstrin homology domain containing, family A member 7	KVTS(ph)PIQS(ph)PTK	0.90	1.74	2.11	25.31	45.75	33.22	0	1	2	2	673.312	0.27	0.99	173.19	
Q96T58	MINT Msx2-interacting protein	IS(ph)PPVASGGIPHQS(ph)PPTK	0.43	0.35	0.59	24.15	75.39	167.91	0	1	2	2	965.447	-0.83	1.00	126.91	
C9JEE1;Q724V5;E9PGW4	C9JEE1 Uncharacterized protein	GSGGS(ph)S(ph)GDEIREDEPVKK	2.16	1.29	0.63	89.48	19.72	79.46	2	0	2	2	1061.422	-0.14	0.93	209.85	
E7EUC7;C9JKD6;Q16851;C9JNZ1;C9JVG3;C9KOU9;C9JWG0;C9JLW1;C9JTZ5;C9JVV7;F223H1;F8WC70;F223P4;C9J3M0	E7EUC7 UDP-glucose pyrophosphorylase 2	(ac)S(ph)QDGASQFQIEVR	0.98	1.41	1.52	38.66	35.60	71.31	1	0	2	2	793.846	0.30	1.00	180.84	
Q0IRZ9;E9PG79	FCHO2 FCH domain only protein 2	VSGNIT(ph)JSPAIS(ph)RHSPVQM(ox)NRR	1.82	0.86	0.63	2.93	30.48	14.74	1	0	2	3	851.740	0.51	0.50	128.06	
Q96JM3	CHAP1 Chromosome alignment-maintaining phosphoprotein 1	RPAPAVS(ph)PGSWKPGPPGS(ph)PR	0.76	0.35	0.76	47.30	64.46	66.33	1	3	1	3	720.005	0.04	1.00	115.39	
P28223;F5GW68	5HT2A 5-hydroxytryptamine receptor 2A	S(ph)IHREPSYTYGR	2.03	0.51	0.74	104.66	139.03	76.41	3	2	1	3	480.552	-0.17	0.98	85.55	
Q9H5H4;C9JH27;Y7	ZN768 Zinc finger protein 768	SPGIVPPS(ph)PEFAPR	0.69	0.53	0.79	9.20	8.99	6.61	1	2	1	2	765.871	0.05	1.00	162.37	
B5MC40;Q86YP4;C9JUK9;C9JHD7;C9JGN4;C9JIM3	B5MC40 GATA zinc finger domain containing 2A	RPPS(ph)PDIVIS(ph)DNEQPS(ph)SPR	0.57	0.51	0.84	17.90	44.12	38.33	1	2	1	2	3	810.676	-0.12	1.00	201.12
Q9UQ35;F5GWZ7	SRRM2 Serine/arginine repetitive matrix protein 2	VKAOT(ph)PPGSPSGSKS(ph)PCPOEK	1.03	0.98	1.34	35.53	26.13	14.57	1	2	1	3	814.037	0.07	1.00	181.87	
Q9NYZ3	GTSE1 G2 and 5 phase-expressed protein 1	IVDVS(ph)PDRSGS(ph)PPSRVQAINFSPESDSTFSK	0.59	0.74	1.61	9.45	24.94	67.19	0	2	1	3	1202.545	0.19	0.80	94.20	
DOUFD1;C9J502;DOUFD3;P55327;ESRKB4;D3YTI0;ESRKS3;F5H0B0	DOUFD1 Prostate leucine zipper variant 1	NSPTFKS(ph)FEKVENIK	1.31	2.08	1.87	16.05	32.69	65.98	0	2	1	3	659.650	-0.01	0.97	73.21	
P07948;ESR137	LYN Tyrosine-protein kinase LYN	GKDSIS(ph)DDGVDIK	1.20	1.98	2.00	26.23	44.67	39.50	0	2	1	2	714.816	-0.18	1.00	208.15	
Q5SYE7	NHSL1 NHS-like protein 1	NHSL(ph)PS(ph)PPVPTGGAAPSASP	0.55	0.24	0.43	24.34	59.42	68.63	0	2	1	3	724.996	0.00	1.00	123.60	
Q9UN36;B4DE86;G3V3N4;HOYIT9;G3V578;HOYJ57	NDRG2 Protein NDRG2	TAS(ph)ITSAAS(ph)VDGNNR	1.29	1.55	1.09	23.54	21.26	47.33	0	2	1	2	755.303	-0.07	0.99	233.49	
P06400;F5HG61	RB Retinoblastoma-associated protein	IPGGNIVIS(ph)PIKS(ph)PKYSEGIPTTK	0.91	0.37	0.79	28.62	21.16	42.27	0	1	3	3	977.495	0.50	0.99	169.64	
Q43683;F5GXIS;E9PC26;F5GZ80	BUB1 Mitotic checkpoint serine/threonine-protein kinase BUB1	DGKFS(ph)PIQEKs(ph)PK	1.04	0.58	0.49	145.58	90.19	21.98	2	1	2	2	810.857	1.44	1.00	114.27	
B057P1;HOY5T9;HOY6K2;P25440;F8VXF8;Q658Y7;BOV073;HOY602;BOV072;E9PIQ3;HOYDJ7	B057P1 Bromodomain containing 2	KADTTTPTTAAIAPGSPAS(ph)PPGSIIEPK	0.45	0.70	0.93	36.11	33.23	40.17	2	1	1	3	928.135	-0.01	0.72	142.79	
P13796;Q5TBN3;Q5TBN5	PLS1 Plastin-2	GS(ph)VSDEEMM(ox)EIR	1.33	0.68	0.58	52.47	18.82	55.07	2	0	1	2	739.781	-0.04	0.93	153.63	
Q9NTJ3;E9PD53;C9JRH3;E7ET04;C9JUE4;C9JYK2;C9JWFO;F8WC87	SMC4 Structural maintenance of chromosomes protein 4	RREGPPPPS(ph)PDGAS(ph)SDAEPEPPSPGR	0.16	1.20	0.66	60.69	11.35	35.65	2	0	1	3	944.394	-0.12	1.00	142.40	
P22314;E7ERL1;B4DDE4;Q5JRR6	UBA1 Ubiquitin-like modifier-activating enzyme 1	IHVSI(ph)DQEIQSANASVSDRSIEIEK	1.40	1.80	1.16	24.84	9.22	16.63	0	3	0	3	921.766	0.65	1.00	119.48	
Q43823;B7Z8L8	AKAP8 A-kinase anchor protein 8	S(ph)GDDEFKGEDEICDSGR	0.65	0.43	0.66	86.13	121.89	31.60	2	2	0	2	1005.375	0.19	1.00	176.49	
D6RGX4	D6RGX4 Uncharacterized protein	GSAIAS(ph)IS(ph)PIR	0.08	0.10	1.36	29.21	57.44	26.93	2	2	0	2	616.278	0.14	1.00	74.99	
Q07955	SRSF1 Serine/arginine-rich splicing factor 1	SRGS(ph)PRYS(ph)PR	0.55	0.55	0.93	125.07	121.91	17.80	2	2	0	2	661.774	0.03	0.81	64.22	
Q9UQ35;F5GWZ7	SRRM2 Serine/arginine repetitive matrix protein 2	S(ph)TRPPASQSR	1.14	1.36	1.03	8.32	15.01	4.17	1	2	0	3	450.877	0.30	0.33	103.14	
Q5JWU6;Q5U0E0;Q43399;B4DPJ6	Q5JWU6 Tumor protein D52-like 2	NSATFKS(ph)FDR	2.00	1.96	1.16	20.33	9.46	20.28	1	2	0	2	691.293	0.25	1.00	189.24	
Q14654	IRS4 Insulin receptor substrate 4	VPRPREDIS(ph)DNDDDDTHVR	0.88	0.62	0.80	62.80	49.14	22.12	1	2	0	3	777.000	-0.98	1.00	98.17	
Q6VY07;B4DF77	PACS1 Phosphofurin acidic cluster sorting protein 1	TNSS(ph)DSERS(ph)PDIGHSTQIPR	0.66	1.25	1.04	58.37	65.69	9.43	1	2	0	3	781.992	-0.41	0.84	134.32	
Q9UQ35	SRRM2 Serine/arginine repetitive matrix protein 2	HGGSPQIATTPISEPVPVNPSEAS(ph)PTR	0.75	0.61	0.91	64.39	60.45	44.07	1	2	0	3	978.133	-0.30	0.81	250.18	
Q13523;F5H2U2	PRP4B Serine/threonine-protein kinase PRP4 homolog	KS(ph)S(ph)PTIR	1.23	1.73	1.35	29.57	28.23	20.32	0	2	0	2	538.749	-0.25	0.50	101.38	
Q86U06;E7EU28	RBM23 Probable RNA-binding protein 23	EKS(ph)PVREVDNISPEER	0.56	0.34	0.65	11.31	29.98	17.48	0	2	0	3	687.660	-0.36	0.98	56.53	
P46821	MAP1B Microtubule-associated protein 1B	TTKS(ph)PSDSGYSYETIGK	1.43	1.81	1.26	18.65	32.62	15.50	0	2	0	2	950.914	0.50	0.99	244.32	
Q15121;B1AKZ5	PEA15 Astrocytic phosphoprotein PEA-15	YKDIIRQPS(ph)EEIEIK	1.47	1.64	1.25	17.47	19.14	17.09	0	2	0	2	970.990	0.01	1.00	76.07	
Q96B36	AKT51 Proline-rich AKT1 substrate 1	AATAARPPAPPAPQPPS(ph)PTPS(ph)PPRPTIAR	0.40	0.48	1.12	64.50	67.26	16.59	3	1	0	3	1042.188	0.76	0.98	146.76	
Q9B7C0	DIDO1 Death-inducer obliterator 1	YPCISADAAVSTT(ph)PPGS(ph)PPPPPIPEPVVK	0.51	0.61	1.33	27.65	15.99	43.02	2	1	0	3	1103.857	0.06	0.78	133.58	
Q8N707;Q14247;Q96H99;B4E358;HOYCD9;HOYEV2	Q8N707 CTTN protein	GPVSGTEPEPVYS(ph)MGAADYR	0.41	0.60	1.41	10.37	16.37	17.25	2	1	0	2	1117.969	-0.08	1.00	288.92	
P18887;F5H8D7	XRCC1 DNA repair protein XRCC1	TKPTQAAGPSS(ph)PQKPTT(ph)PEETK	0.51	0.51	1.06	45.47	40.53	7.33	2	1	0	3	813.400	0.29	0.95	136.43	
Q9H2G4	TSYL2 Testis-specific Y-encoded-like protein 2	RS(ph)SSES(ph)PQRDPVPPPPPPPIIR	0.35	0.44	1.03	10.20	6.30	12.70	2	1	0	3	893.101	0.01	0.87	172.37	
P50502;Q3KNR6;F6VDH7;Q8IZP2;F5H3M7	F10A1 Hsc70-interacting protein	KVEEDIKADEPS(ph)S(ph)EES(ph)DEIDK	0.80	0.95	0.80	47.46	62.43	31.58	2	1	0	3	915.695	-0.40	1.00	194.75	
Q96JM3	CHAP1 Chromosome alignment-maintaining phosphoprotein 1	SSVSPSSWKS(ph)PPAS(ph)PESWK	0.41	0.80	1.11	9.96	7.79	15.76	2	0	0	2	1139.477	0.73	0.82	115.33	
P31350;HOY855	RIR2 Ribonucleoside-diphosphate reductase subunit M2	VPIAIPDTPQQQIS(ph)PKIGSIVDKENTPPAISGR	0.54	0.80	1.74	26.09	23.59	41.04	2	0	0	3	1292.029	0.06	1.00	258.14	
E9PCT1;Q8YB3;A9Z1X7	E9PCT1 Serine/arginine repetitive matrix 1	RS(ph)PS(ph)ASPPRR	1.40	1.07	1.06	54.75	17.56	34.64	2	0	0	3	461.881	0.61	0.56	149.41	
Q60841	IF2P Eukaryotic translation initiation factor 5B	VEVMY(ph)S(ph)GSDDDDDFKNPKPK	1.36	1.16	1.04	40.24	44.70	21.52	2	0	0	4	591.485	-0.51	0.84	268.65	
Q9UQ35;F5GWZ7	SRRM2 Serine/arginine repetitive matrix protein 2	S(ph)RS(ph)GSS(ph)QEIWDKVPASPOER	1.44	1.05	0.67	14.13	26.51	42.90	2	0	0	3	795.656	0.10	0.87	241.38	
P45985;B4DH44	MP2K4 Dual specificity mitogen-activated protein kinase kinase 4	IKIS(ph)PEQHWDFEAEDIKDIEIGR	1.82	1.07	0.72	17.19	10.34	25.43	2	0	0	3	959.799	-0.06	1.00	136.43	

Table S1. List of phosphorylated peptides significantly regulated by DOI and/or lisuride.

For each phosphorylation site, the leading protein accession number from the human complete proteome set database (<http://www.uniprot.org>), the protein name, the sequence of the peptide carrying the phosphorylation site(s), normalized SILAC ratios M/L (lisuride/vehicle), H/L (DOI/vehicle) and H/M (DOI/lisuride), ratio variability (%), the number of biological replicates where those ratios have been found significantly different from 1 according to the calculation of the B significance, the charge state, the mass over charge of the detected phosphopeptide, the deviation (in ppm) of the measured mass over charge, the probability of phosphorylation site assignment and the peptide Andromeda score for identification are indicated.