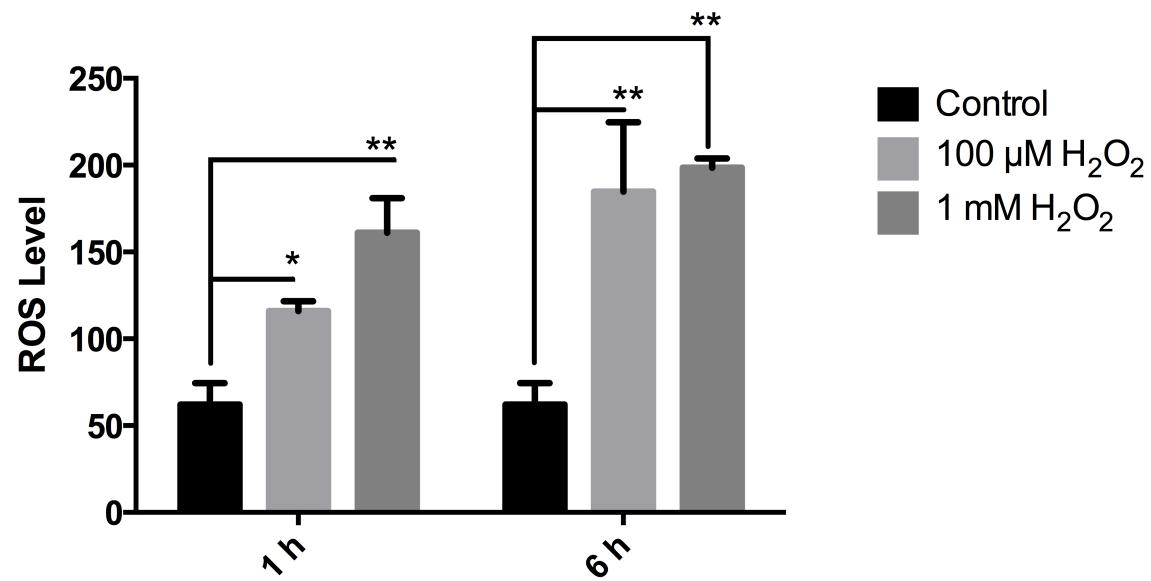
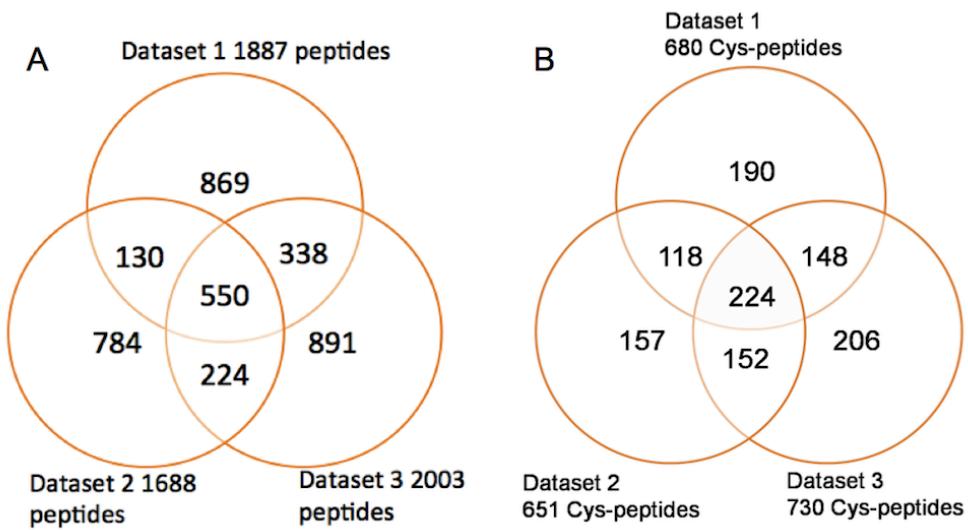


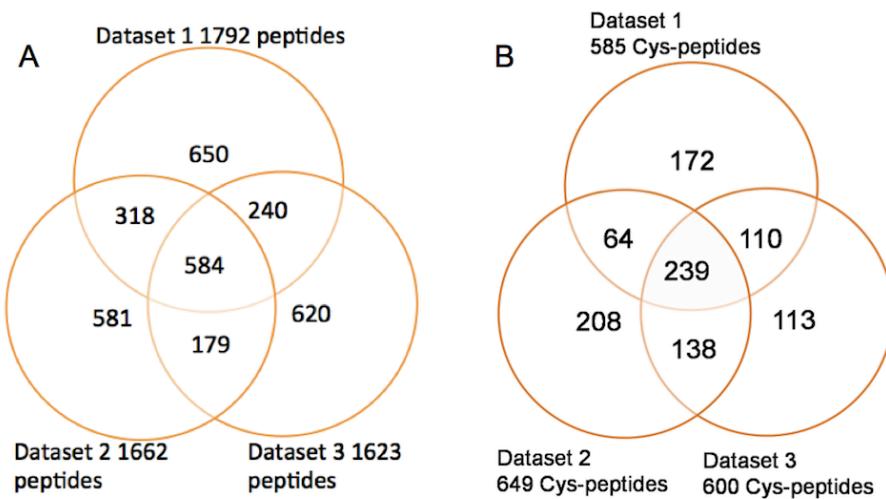
**Supplementary Figure 1.** Increased ROS production in THP-1 cells upon H<sub>2</sub>O<sub>2</sub> treatment for 1 h and 6 h.



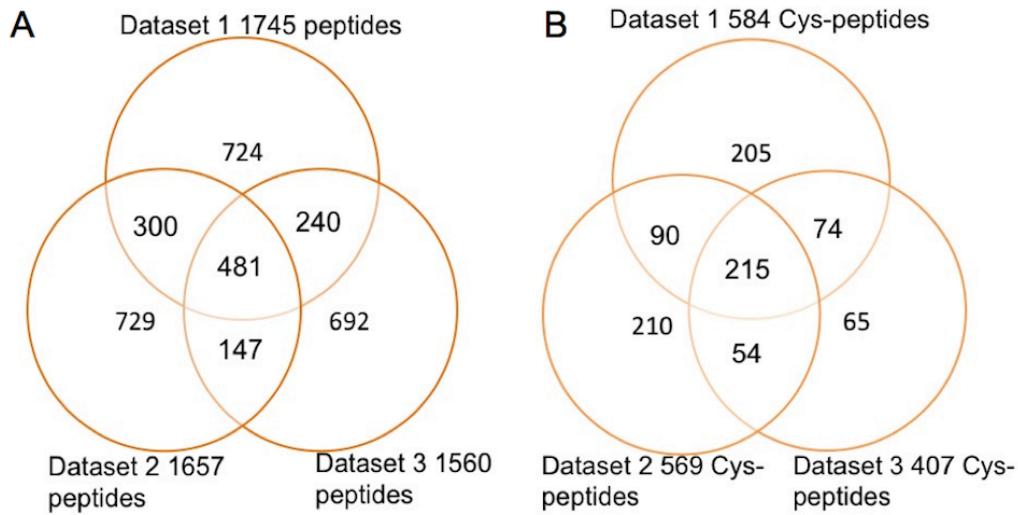
**Supplementary Figure 2.** The overlap of A. total peptides; B. Cys-containing peptides among three replicates in THP-1 cells with LPA-PR treatment for 6 h.



**Supplementary Figure 3.** The overlap of A. total peptides; B. Cys-containing peptides among three replicates in THP-1 cells with Thr-PR treatment for 6 h.



**Supplementary Figure 4.** The overlap of A. total peptides; B. Cys-containing peptides among three replicates in THP-1 cells with DPI 1h pretreatment following by LPA-PR 6 h treatment.



**Supplementary Table 1.** Enrichment Efficiency of the Modified Biotin switch assay on THP-1 cells with LPA-PR treatment for 6 h.

# of replicates	Total # of peptides	# of Cys-containing peptides
1	1887	680
2	1688	651
3	2003	730

**Supplementary Table 2.** The 120 Cys<sub>ox</sub> containing peptides in 6 h LPA-PR treatment with their H/L ratio.

UniProt ID	Sequence	H/L	SD
1433Z_HUMAN	YDDMAACMK	2.62	1.51
	DICNDVLSLLEK	1.44	0.00
ACTB_HUMAN	LCYVALDFEQEMATAASSSSLEK	2.02	0.47
	CDVDIR	2.67	1.10
ALDOA_HUMAN	ALANSLACQGK	1.39	0.17
ANXA6_HUMAN	CLIEILASR	1.53	0.27
ARP2_HUMAN	LCYVGYNIEQEQQK	2.79	0.64
	LPACVVDCGTGYTK	4.05	2.97
	YSYVCPDLVK	2.44	1.05
ARP3_HUMAN	LGYAGNTEPQFIIPSCIAIK	1.61	0.23
	HEQNIDCGGGYVK	1.57	0.23
	ALLVTASQCQQPAENK	2.36	1.06
CAP1_HUMAN	CVNTTLQIK	2.46	0.97
	NSLDCEIVSAK	1.69	0.42
	INSITVDNCK	1.57	0.19
	TDGCHAYLSK	1.53	0.16
	DYLLCDYNR	1.69	0.83
CAPZB_HUMAN	NLSLDLIDLVPSLCEDLLSSVDQPLK	2.11	0.17
CDC42_HUMAN	YVECSALTQK	2.54	0.69
CH60_HUMAN	AAVEEGIVLGGGCALLR	3.00	0.13
CLCB_HUMAN	VAQLCDFNPK	1.83	0.17
CLIC1_HUMAN	FLDGNELTADCNLLPK	2.50	1.23
	LHIVQVVCK	3.07	0.66
	IGNCPFSQR	2.72	0.60
COF1_HUMAN	AVLFCLSEDK	6.60	1.06
	HELQANCYEEVK	3.25	0.63
DDX17_HUMAN	STCIYGGAPK	2.19	0.28
DX39B_HUMAN	HFILDECQDK	1.95	0.47
EF2_HUMAN	STLTDSLVCK	4.15	2.17
	TFCQLILDPIFK	2.31	0.97
ENOA_HUMAN	SCNCLLLK	9.03	2.97
	VNQIGSVTESLQACK	4.18	2.25
ETFA_HUMAN	TIYAGNALCTVK	5.39	2.91
	LGGEVSCLVAGTK	12.91	1.18
G3P_HUMAN	IISNASCTTNCLAPLAK	1.41	0.03
GBB1_HUMAN	LFVSGACDASAK	2.45	0.50
GNAI2_HUMAN	IIHEDGYSEEECR	1.39	0.09
GNAI3_HUMAN	IIHEDGYSEDECK	1.36	0.05
GSTP1_HUMAN	ASCLYGQLPK	2.44	0.72
HNRPD_HUMAN	FGEVVDCTLK	3.35	1.67

UniProt ID	Sequence	H/L	SD
	GFCFITFK	2.39	0.40
HNRPQ_HUMAN	GFCFLEYEDHK	1.44	0.09
HS105_HUMAN	GCALQCAILSPAFK	2.93	1.33
HSP7C_HUMAN	CNEIINWLDK	2.47	0.65
	VCNPIITK	2.25	0.26
LDHA_HUMAN	VIGSGCNLDSAR	2.54	1.17
LEG1_HUMAN	IKCVAFD	3.49	1.61
	FNAHGDANTIVCNSK	1.43	0.12
MDHM_HUMAN	TIPLISQCTPK	1.70	0.62
MIF_HUMAN	LLCGLLAER	1.48	0.15
NDK8_HUMAN	GDFCIQVGR	5.21	0.72
NH2L1_HUMAN	PVIACSVTIK	2.17	0.88
PCBP1_HUMAN	LVVPATQCGSLIGK	2.21	1.03
PCBP2_HUMAN	LVVPASQCGSLIGK	1.54	0.53
	AITIAGIPQSIIECVK	1.51	0.04
PGK1_HUMAN	DCVGPEVEK	1.64	0.35
	GCITIIGGGDTATCCAK	1.71	0.13
PLSL_HUMAN	EGICAIGGTSEQSSVGTQHSYSEEEK	1.57	0.04
PP1G_HUMAN	IYGFYDECK	2.05	1.06
PPIA_HUMAN	KITIADCGQLE	1.93	0.70
	IIPGFMCQGGDFTR	1.97	0.59
PRDX6_HUMAN	DINAYNCEEPTEK	1.41	0.06
RAC2_HUMAN	AVLCPQPTR	2.18	1.00
	YLECSALTQR	3.27	0.82
RAN_HUMAN	VCENIPIVLCGNK	2.06	0.49
RINI_HUMAN	LDDCGLTEAR	2.98	0.62
RL12_HUMAN	EILGTAQSVGNCNVDGR	2.14	0.82
RL14_HUMAN	ALVDGPCTQVR	1.48	0.26
	CMQLTDFILK	1.44	0.05
RL18_HUMAN	GCGTVLLSGPR	2.29	0.70
RL18A_HUMAN	DLTTAGAVTQCYR	1.45	0.15
RL23_HUMAN	ISLGLPVGAVINCADNTGAK	1.96	0.68
RL24_HUMAN	VELCSFSGYK	2.32	0.80
RL28_HUMAN	NCSSFLIK	2.22	0.42
RL30_HUMAN	VCTLAIIDPGDSDIIR	1.62	0.60
RL32_HUMAN	SYCAEIAHNVSSK	2.94	0.97
RL34_HUMAN	SACGVCPGR	1.84	0.11
RL36L_HUMAN	LECVEPNCR	1.74	0.24
RL4_HUMAN	SGQQAFGNMCR	1.62	0.43
	FCIWTESAFR	1.49	0.04
RL5_HUMAN	DIICQIAYAR	1.70	0.28
RLF_HUMAN	SSEDEEMKASVCK	15.65	4.41
RS11_HUMAN	CPFTGNVSIR	1.51	0.12
RS12_HUMAN	KVVGSCVVVK	2.25	0.95
	LGEWVGLCK	2.31	0.82

UniProt ID	Sequence	H/L	SD
	VVGCSVVVK	2.93	0.75
	LVEALCAEHQINLIK	1.69	0.20
RS15A_HUMAN	CGVISPR	1.70	0.57
RS17L_HUMAN	VCEEIAIIPSK	4.98	0.09
RS2_HUMAN	GCTATLGNFAK	2.43	0.67
RS21_HUMAN	TYAICGAIR	3.76	1.68
RS27L_HUMAN	LTEGCSFR	2.70	1.17
RS28_HUMAN	TGSQQCTQVR	4.25	2.10
RS3_HUMAN	GCEVVVSGK	12.41	1.59
	RACYGVLR	1.37	0.19
RS3A_HUMAN	ACQSIYPLHDVFVR	2.15	0.08
RS5_HUMAN	TIAECLADELINAAK	1.90	0.36
	VNQAIWLLCTGAR	1.98	0.32
	AQCPIVER	1.78	0.29
RS6_HUMAN	LNISFPATGCQK	2.50	1.20
RS8_HUMAN	LLACIASR	1.52	0.06
SER_A_HUMAN	VLISDSLDPCCRK	2.82	0.42
	NAGNCLSPAVIVGLLK	1.56	0.13
SMD2_HUMAN	HCNMVLENVK	1.72	0.49
TBA1B_HUMAN	SIQFVDWCPTGFK	1.63	0.30
	AVCMLSNTTAIAEAWAR	1.63	0.11
TBA1C_HUMAN	TIQFVDWCPTGFK	1.91	0.72
TBB3_HUMAN	NMMAACDPR	6.82	4.48
	EIVHIQAGQCGNQIGAK	1.91	0.82
TBB5_HUMAN	TAVCDIPPR	2.68	0.52
TCPA_HUMAN	VLCELADLQDK	1.57	0.59
TCPB_HUMAN	SLHDALCVLAQTVK	1.80	0.30
TCPG_HUMAN	TLIQNCGASTIR	2.73	0.23
TEBP_HUMAN	LTFSCLGGSDFNK	1.73	0.31
THIO_HUMAN	CMPTFQFFK	2.62	0.94
TPIS_HUMAN	IAVAAQNCYK	2.00	0.82
UB2L3_HUMAN	GQVCLPVISAENWKPATK	1.54	0.07
UBA1_HUMAN	YFLVGAGAIGCELLK	1.46	0.29
UBC12_HUMAN	LVICPDEGFYK	4.34	0.66
UBE2N_HUMAN	ICLDILK	1.60	0.17

**Supplementary Table 3.** Enrichment Efficiency of the Modified Biotin switch assay on THP-1 cells with Thr-PR treatment for 6 h.

# of replicates	Total # of peptides	# of Cys-containing peptides
1	1792	585
2	1662	649
3	1623	600

**Supplementary Table 4.** The 105 Cys<sub>ox</sub> containing peptides in 6 h Thr-PR treatment with their H/L ratio

UniProt ID	Sequence	H/L	SD
1433Z_HUMAN	YDDMAACMK	2.54	0.81
	DICNDVLSLEK	1.70	0.40
ACTB_HUMAN	LCYVALDFEQEMATAASSSSLEK	2.00	0.31
	CDVDIR	2.70	0.82
ALDOA_HUMAN	ALANSLACQGK	1.41	0.06
ARP2_HUMAN	LCYVGYNIEQEQQK	1.53	0.07
ARP3_HUMAN	KDYEEIGPSICR	2.43	1.56
	YSYVCPDLVK	1.67	0.11
	LPACVVDCGTGYTK	1.38	0.07
CALR_HUMAN	HEQNIDCGGGYVK	2.18	0.86
	ALLVTASQCQQPAENK	2.79	1.30
CAP1_HUMAN	NSLDCEIVSAK	1.65	0.28
	CVNTTLQIK	1.69	0.49
	INSITVDNCK	1.79	0.29
	TDGCHAYLSK	1.64	0.30
	NLSLDLIDLVPSLCEDLLSSVDQPLK	1.74	0.04
CAPZB_HUMAN	DYLLCDYNR	1.58	0.00
CATA_HUMAN	LCENIAGHLK	3.35	2.05
CDC42_HUMAN	YVECSALTQK	4.30	2.31
CH60_HUMAN	AAVEEGIVLGGGCALLR	1.36	0.03
CLCB_HUMAN	VAQLCDFNPK	1.56	0.22
CLIC1_HUMAN	LHIVQVVCK	6.86	3.45
	LHIVQVVCKK	9.87	3.04
	FLDGNELTLADCNLLPK	2.68	0.99
	IGNCPFSQR	1.54	0.03
CNBP_HUMAN	CGETGHVAINC SK	2.14	0.90
COF1_HUMAN	AVLFCLSEDK	2.77	0.88
	AVLFCLSEDKK	2.85	0.93
	HELQANCYEEVK	1.37	0.07
DDX5_HUMAN	LIDFLECGK	1.69	0.07
ECHM_HUMAN	ICPVETLVEEAIQCAEK	18.14	13.90
EF2_HUMAN	TFCQLILDPIFK	1.64	0.48
	STLTDSLVCK	1.48	0.19
ENOA_HUMAN	SCNCLLK	1.95	0.23
	SGETEDTFIADLVVGLCTGQIK	2.44	0.33
	VNQIGSVTESLQACK	2.22	0.91
ETFA_HUMAN	LGGEVSCVLVAGTK	6.16	3.91
	TIYAGNALCTVK	10.55	0.94
GBB1_HUMAN	LFVSGACDASAK	1.72	0.40
GPV_HUMAN	LRGTLCAVLGLLR	7.61	6.53
GPX1_HUMAN	LITWSPVCR	1.39	0.05
GSTP1_HUMAN	ASCLYGQLPK	1.78	0.13
HNRPD_HUMAN	FGEVVDCTLK	1.83	0.63

UniProt ID	Sequence	H/L	SD
	GFCFITFK	2.25	0.88
HNRPK_HUMAN	GSDFDCELR	1.41	0.03
HNRPQ_HUMAN	GFCFLEYEDHK	1.75	0.55
HSP74_HUMAN	GCALQCAILSPAFK	2.58	0.79
HSP7C_HUMAN	VCNPIITK	1.54	0.33
	CNEIINWLDK	1.39	0.09
IDH3A_HUMAN	IEAACFATIK	4.53	0.91
ITB2_HUMAN	YISCAECLK	1.89	0.58
LDHA_HUMAN	VIGSGCNLDSAR	16.67	0.78
LEG1_HUMAN	FNAHGDANTIVCNSK	1.37	0.04
	DSNNLCLHFNPRL	1.49	0.00
	IKCVAFD	1.75	0.44
MDHC_HUMAN	VIVVGNPANTNCLTASK	1.38	0.06
MDHM_HUMAN	TIIPLISQCTPK	1.43	0.06
MIF_HUMAN	LLCGLLAER	1.49	0.08
NDKA_HUMAN	GDFCIQVGR	1.88	0.29
NTAL_HUMAN	FSKPPEDDDANSYENVLICK	4.94	0.91
PCBP2_HUMAN	AITIAGIPQSIIECVK	2.48	0.01
PGK1_HUMAN	DVLFLKDCVGPEVEK	1.74	0.13
	GCITIIGGGDTATCCAK	1.70	0.41
PLSL_HUMAN	EGICAIGGTSEQSSVGTQHSYSEEK	1.80	0.34
PPIA_HUMAN	KITIADCGQLE	1.89	0.95
PRDX6_HUMAN	DINAYNCEEPTEK	1.33	0.13
PTN6_HUMAN	AYGPYSVTNCGEHDTTEYK	2.20	0.65
RAC2_HUMAN	CVVVGDGAVGK	6.07	0.51
	YLECSALTQR	1.35	0.05
RAN_HUMAN	VCENIPIVLCGNK	1.46	0.08
RHOA_HUMAN	IGAFGYMECSAK	3.29	0.37
	LVIVGDGACGK	2.00	0.46
RINI_HUMAN	LDDCGLTEAR	1.88	0.23
	SNELGDVGVHCVLQGLQTPSCK	1.81	0.32
RL10A_HUMAN	FSVCVLGDQQHCDEAK	6.79	3.42
RL14_HUMAN	CMQLTDFILK	3.27	0.81
RL23_HUMAN	ISLGLPVGAVINCADNTGAK	1.85	0.17
ROA3_HUMAN	WGTLTDCVVMR	1.86	0.11
RS12_HUMAN	KVVGSCSVVVK	1.43	0.08
	LVEALCAEHQINLIK	1.67	0.11
	LGEWVGLCK	1.33	0.18
RS27L_HUMAN	LTEGCSFR	2.03	0.25
RS3A_HUMAN	ACQSIYPLHDVFVR	3.46	0.88
RS5_HUMAN	TIAECLADELINAAK	1.72	0.36
RSSA_HUMAN	YVDIAIPCNNK	3.50	0.25
SERA_HUMAN	NAGNCLSPAIVGLLK	1.91	0.46
	VLISDSDLPCCRK	1.84	0.18
SMD2_HUMAN	HCNMVLENVK	1.89	0.44
SRSF9_HUMAN	EAGDV CYADVQK	2.77	0.60
SYWC_HUMAN	GIFGFTDSDCIGK	11.29	7.50
TALDO_HUMAN	LAGCDFLTISP K	1.80	0.07
TBA1B_HUMAN	SIQFVDWCPTGFK	1.49	0.13

UniProt ID	Sequence	H/L	SD
	AVCMLSNTTAIAEAWAR	1.55	0.11
TBA1C_HUMAN	TIQFVDWCPTGFK	1.73	0.22
TBB3_HUMAN	EIVHIQAGQCGNQIGAK	1.45	0.09
	NMMAACDPR	1.49	0.14
TBB5_HUMAN	TAVCDIPPR	2.17	0.51
TCPB_HUMAN	SLHDALCVLAQTVK	1.64	0.41
TCPG_HUMAN	TLIQNCGASTIR	1.31	0.07
TEBP_HUMAN	LTFSCLLGGSDNFK	2.54	0.31
THIO_HUMAN	CMPTFQFFK	2.42	0.40
TPIS_HUMAN	IAVAAQNCYK	1.95	0.58
UBC12_HUMAN	LVICPDEGFYK	1.88	0.59
VDAC1_HUMAN	YQIDPDACFSAK	3.27	1.58

**Supplementary Table 5.** Cys<sub>ox</sub> containing peptides overlap between LPA-PR and Thr-PR with their H/L ratio.

UniProt ID	Sequence	LPA-PR	Thr-PR
		H/L±SD	H/L±SD
1433Z_HUMAN	DICNDVLSLLEK	1.44±0	1.7±0.4
	YDDMAACMK	2.62±1.5	2.54±0.8
ACTB_HUMAN	CDVDIR	2.67±1.1	2.7±0.82
	LCYVALDFEQEMATAASSSSL	2.02±0.4	2±0.31
ALDOA_HUMA	ALANSLACQGK	1.39±0.1	1.41±0.0
ARP2_HUMAN	LCYVGYNIEQEQQK	2.79±0.6	1.53±0.0
ARP3_HUMAN	LPACVVDCGTGYTK	4.05±2.9	1.38±0.0
	YSYVCPDLVK	2.44±1.0	1.67±0.1
CALR_HUMAN	HEQNIDCGGGYVK	1.57±0.2	2.18±0.8
CAP1_HUMAN	ALLVTASQCQQPAENK	2.36±1.0	2.79±1.3
	CVNTTLQIK	2.46±0.9	1.69±0.4
	INSITVDNCK	1.57±0.1	1.79±0.2
	NSLDCEIVSAK	1.69±0.4	1.65±0.2
	TDGCHAYLSK	1.53±0.1	1.64±0.3
CAPZB_HUMAN	DYLLCDYNR	1.69±0.8	1.58±0
	NLSLDLIDLVPSLCEDLLSSVDQ	2.11±0.1	1.74±0.0
CDC42_HUMAN	YVECSALTQK	2.54±0.6	4.3±2.31
CH60_HUMAN	AAVEEGIVLGGGCALLR	3±0.13	1.36±0.0
CLCB_HUMAN	VAQLCDFNPK	1.83±0.1	1.56±0.2
CLIC1_HUMAN	FLDGNELTADCNLLPK	2.5±1.23	2.68±0.9
	IGNCPFSQR	2.72±0.6	1.54±0.0
	LHIVQVVCK	3.07±0.6	6.86±3.4
COF1_HUMAN	AVLFCLSEDK	6.6±1.06	2.77±0.8
	HELQANCYEEVK	3.25±0.6	1.37±0.0
EF2_HUMAN	STLTDSLVCK	4.15±2.1	1.48±0.1
	TFCQLILDPIFK	2.31±0.9	1.64±0.4
ENOA_HUMAN	SCNCLLLK	9.03±2.9	1.95±0.2
	VNQIGSVTESLQACK	4.18±2.2	2.22±0.9
ETFA_HUMAN	LGGEVSCLVAGTK	12.91±1.	6.16±3.9
	TIYAGNALCTVK	5.39±2.9	10.55±0.
GBB1_HUMAN	LFVSGACDASAK	2.45±0.5	1.72±0.4
GSTP1_HUMAN	ASCLYGQLPK	2.44±0.7	1.78±0.1
HNRPD_HUMAN	FGEVVDCTLK	3.35±1.6	1.83±0.6
	GFCFITFK	2.39±0.4	2.25±0.8
HNRPQ_HUMAN	GFCFLEYEDHK	1.44±0.0	1.75±0.5
HSP74_HUMAN	GCALQCAILSPAFK	2.93±1.3	2.58±0.7
HSP7C_HUMAN	CNEIINWLDK	2.47±0.6	1.39±0.0
	VCNPIITK	2.25±0.2	1.54±0.3

UniProt ID	Sequence	LPA-PR	Thr-PR
		H/L±SD	H/L±SD
LDHA_HUMAN	VIGSGCNLDSAR	2.54±1.1	16.67±0.
LEG1_HUMAN	FNAHGDANTIVCNSK	1.43±0.1	1.37±0.0
	IKCVAFD	3.49±1.6	1.75±0.4
MDHM_HUMAN	TIIPLISQCTPK	1.7±0.62	1.43±0.0
MIF_HUMAN	LLCGLLAER	1.48±0.1	1.49±0.0
NDKA_HUMAN	GDFCIQVGR	5.21±0.7	1.88±0.2
PCBP2_HUMAN	AITIAGIPQSIIECVK	1.51±0.0	2.48±0.0
PGK1_HUMAN	GCITIIGGGDTATCCAK	1.71±0.1	1.7±0.41
PLSL_HUMAN	EGICAIGGTSEQSSVGTQHSYS	1.57±0.0	1.8±0.34
PPIA_HUMAN	KITIADCGQLE	1.93±0.7	1.89±0.9
PRDX6_HUMAN	DINA YNCEEPTEK	1.41±0.0	1.33±0.1
RAC2_HUMAN	YLECSALTQR	3.27±0.8	1.35±0.0
RAN_HUMAN	VCENIPIVLCGNK	2.06±0.4	1.46±0.0
RINI_HUMAN	LDDCGLTEAR	2.98±0.6	1.88±0.2
RL14_HUMAN	CMQLTDFILK	1.44±0.0	3.27±0.8
RL23_HUMAN	ISLGLPVGAVINCADNTGAK	1.96±0.6	1.85±0.1
RS12_HUMAN	KVVGCSCVVVK	2.25±0.9	1.43±0.0
	LGEWVGLCK	2.31±0.8	1.33±0.1
	LVEALCAEHQINLIK	1.69±0.2	1.67±0.1
RS27L_HUMAN	LTEGCSFR	2.7±1.17	2.03±0.2
RS3A_HUMAN	ACQSIYPLHDVFVR	2.15±0.0	3.46±0.8
RS5_HUMAN	TIAECLADELINAAK	1.9±0.36	1.72±0.3
SERA_HUMAN	NAGNCLSPA VIVGLLK	1.56±0.1	1.91±0.4
	VLISDSLDPCCRK	2.82±0.4	1.84±0.1
SMD2_HUMAN	HCNMVLENVK	1.72±0.4	1.89±0.4
TBA1B_HUMAN	AVCMLSNTTAIAEAWAR	1.63±0.1	1.55±0.1
	SIQFVDWCPTGFK	1.63±0.3	1.49±0.1
TBA1C_HUMAN	TIQFVDWCPTGFK	1.91±0.7	1.73±0.2
TBB3_HUMAN	EIVHIQAGQCGQNQIGAK	1.91±0.8	1.45±0.0
	NMMAACDPR	6.82±4.4	1.49±0.1
TBB5_HUMAN	TAVCDIPPR	2.68±0.5	2.17±0.5
TCPB_HUMAN	SLHDALCVLAQTVK	1.8±0.3	1.64±0.4
TCPG_HUMAN	TLIQNCGASTIR	2.73±0.2	1.31±0.0
TEBP_HUMAN	LTFSCLGGSNDNFK	1.73±0.3	2.54±0.3
THIO_HUMAN	CMPTFQFFK	2.62±0.9	2.42±0.4
TPIS_HUMAN	IAVAAQNCYK	2±0.82	1.95±0.5
UBC12_HUMAN	LVICPDEGFYK	4.34±0.6	1.88±0.5

**Supplementary Table 6.** Enrichment Efficiency of the Modified Biotin switch assay on THP-1 cells with DPI 1 h pretreatment following by LPA-PR 6 h treatment.

# of Replicates	Total # of peptide	# of Cys-containing peptides
1	1745	584
2	1657	569
3	1560	407

**Supplementary Table 7.** The 43 Cys<sub>ox</sub> containing peptides in DPI pre-treatment following by 6 h LPA-PR treatment with their H/L ratio.

UniProt ID	Sequence	H/L	SD
1433Z_HUMAN	DICNDVLSLLEK	1.79	0.06
5HT1E_HUMAN	LIRCREHT	5.25	0.45
APT_HUMAN	GFLFGPSLAQELGLGCVLIR	1.37	0.04
C1TC_HUMAN	STTTIGLVQALGAHYQNVFACVR	2.17	0.84
CAP1_HUMAN	INSITVDNCKK	28.15	15.85
	GKINSITVDNCK	1.42	0.07
CHCH2_HUMAN	LCEGFNEVLK	1.80	0.35
ENOA_HUMAN	FGANAILGVSLAVCK	2.70	0.05
	SGETEDTFIADLVVGLCTGQIK	2.31	0.03
HNRPK_HUMAN	GSDFDCEL R	1.62	0.13
LEG1_HUMAN	SFVLNLGKDSNNLCLHFNP R	1.75	0.20
MDHC_HUMAN	VIVVGNPANTNCLTASK	1.49	0.13
MDHM_HUMAN	TIIPLISQCTPK	2.89	0.12
	GCDVVVIPAGVPR	1.51	0.12
ERP44_HUMAN	TPADCPVIAIDSFR	1.74	0.47
ABRAL_HUMAN	CANLFEALVGTLK	1.80	0.39
CL042_HUMAN	MSTVICMKQR	1.86	0.25
COR1A_HUMAN	ADQCYEDV R	1.42	0.03
DOCK2_HUMAN	TTQRNVEVIMCVCAEDGK	1.55	0.02
DX39B_HUMAN	HFILDEC DK	1.54	0.09
PRR9_HUMAN	VQEKCSSPGKG	1.57	0.09
PUR6_HUMAN	ITSCIFQLLQEAGIK	2.10	0.03
RINI_HUMAN	WAELLPLLQQCQVVR	1.51	0.14
RTCA_HUMAN	VSTALSCLLGLPLRVQK	2.04	0.57
SYAC_HUMAN	NVGCLQEALQLATSFAQLR	2.02	0.03
TBA1B_HUMAN	SIQFVDWCPTGFK	1.46	0.13
TOIP1_HUMAN	YCDHENAAFK	1.43	0.23
ZN579_HUMAN	APLPCPTCGR	2.65	0.01
TPIS_HUMAN	IIYGGSVTGATCK	1.64	0.29
	VAHALAEGLGVIACIGEK	1.93	0.13
CUL7_HUMAN	CQQGGIDTRIR	1.36	0.04
FBN2_HUMAN	SFCYRSYNGTTCENELPFNVTK	1.74	0.47
KAD2_HUMAN	NLETPLCK	1.96	0.68
	LVSDEMVVELIEKNLETPLCK	1.93	0.13
LDHA_HUMAN	GLYGIKDDVFLSVPCLGQNGISDLVK	1.75	0.20
NLRC4_HUMAN	LQIKRCAGVAGSLSLVLSTCK	1.58	0.21
PARK7_HUMAN	GLIAAICAGPTALLAHEIGFGSK	1.46	0.13
PROF1_HUMAN	CYEMASHLR	1.35	0.21
RTCA_HUMAN	VSTALSCLLGLPLRVQK	1.52	0.15
TDRD6_HUMAN	MCSTPGMPAPGASLALR	1.51	0.14
TF3C1_HUMAN	CTMVEAFDR	2.61	3.49
Z804B_HUMAN	YSPQSCLSR	1.59	0.49
ZBT38_HUMAN	CKYPAEELDCAVGK	1.81	0.49