Supporting Information

Mapping post-translational modifications of *de novo* purine biosynthetic enzymes: Implications for pathway regulation

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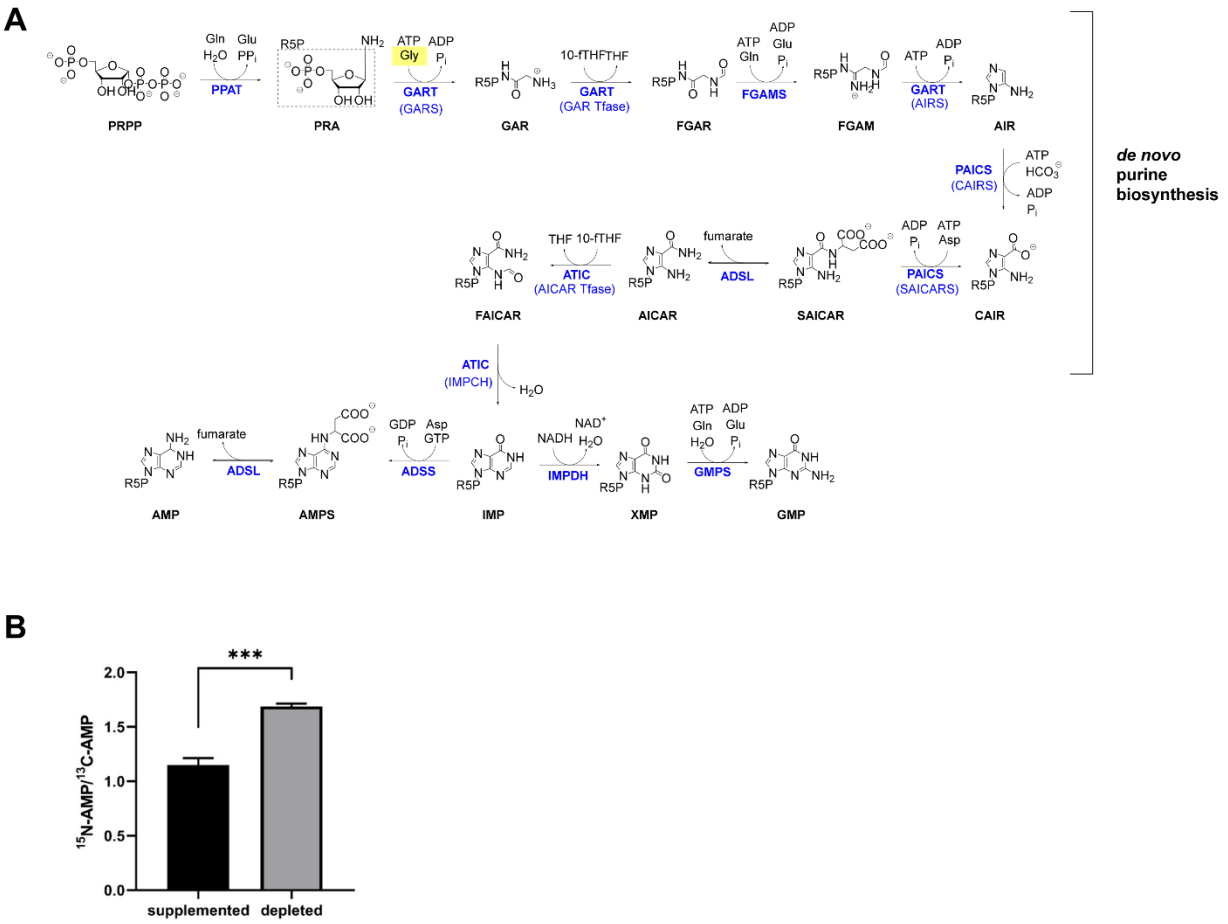
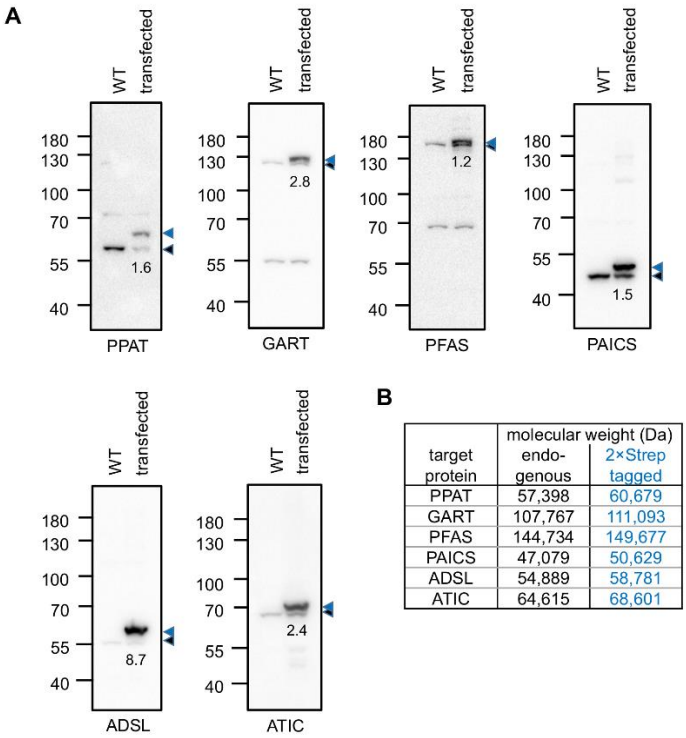


Figure S1. The *de novo* purine biosynthetic pathway is activated in 293T cells upon purine-depletion. (**A**) The *de novo* purine biosynthetic pathway converts phosphoribosyl pyrophosphate (PRPP) into inosine 5′ monophosphate (IMP) in 10 steps catalyzed by six human enzymes (blue). The second step of the pathway utilizes glycine (yellow highlight) for generation of glycinamide ribonucleotide (GAR) and is the site of ^{15}N-glycine incorporation for metabolic flux experiments. (**B**) ^{15}N-glycine incorporation into AMP in the presence (supplemented, black bar) or absence (depleted, gray bar) of purines. The ^{15}N-glycine pulse was added for 4 h, and the degree of incorporation (^{15}N-AMP/^{13}C-AMP) was determined by mass spectrometry. Data represent mean ± standard deviation, N = 4 independent experiments, *** p value = 0.0002 as determined by an unpaired t-test.



B

target protein	molecular weight (Da) endo-genous	2×Strep tagged
PPAT	57,398	60,679
GART	107,767	111,093
PFAS	144,734	149,677
PAICS	47,079	50,629
ADSL	54,889	58,781
ATIC	64,615	68,601

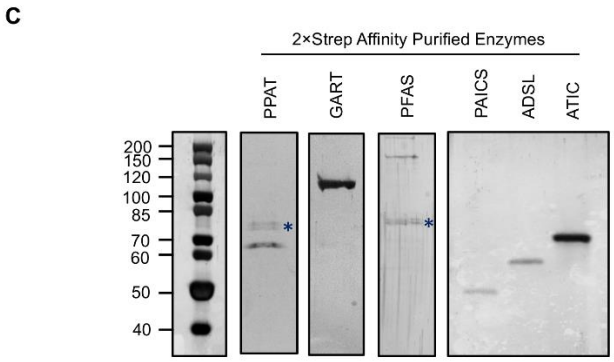


Figure S2. Expression and purification of recombinant *de novo* purine biosynthetic enzymes. (**A**) 293T cells were transfected with plasmids encoding 2×Strep tagged enzymes for 48 h and the degree of transient expression of the 2×Strep tagged enzyme (blue marker) compared to endogenous (black marker) was determined by Western blot and corresponded roughly to the calculated molecular weights in (**B**). Fold change values were based on the band intensity of the 2×Strep tagged enzyme relative to the band intensity corresponding to the endogenous protein. These values are reported under the endogenous protein band in the transfected sample lane. Untransfected (wild-type, WT) 293T cell lysate was also analyzed to help identify the band corresponding to endogenous protein. For PPAT and PFAS, 40 µg of protein lysate was loaded in each lane; expression levels of all other proteins were determined with 30 µg of protein lysate. Rabbit polyclonal antibodies used included: PPAT (LifeSpan Biosciences, cat no: LS-C80815), GART (Bethyl Laboratories, cat no: A304-311A), PFAS (Bethyl Laboratories, cat no: A304-220A), PAICS (Bethyl Laboratories, cat no: A304-546A), ADSL (Bethyl Laboratories, cat no: A304-778A), and ATIC (Bethyl Laboratories, cat no: A304-271A). (**C**) Affinity purified 2×Strep enzymes from 293T cells with MagStrep “type3” XT beads was analyzed by SDS-PAGE and detected by silver staining. Eluted protein samples predominantly show the expression of the 2×Strep tagged enzyme and corresponds to the calculated molecular weight. Asterisks denote background protein from the affinity resin.

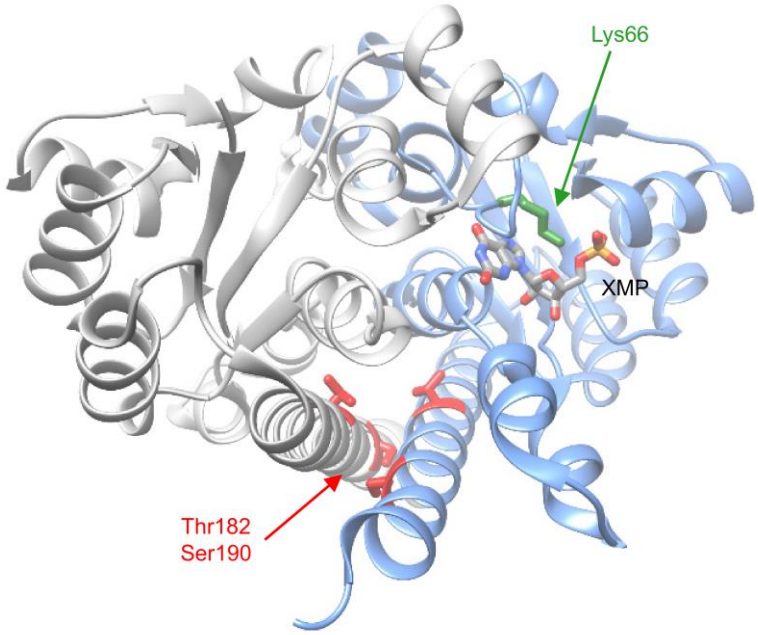


Figure S3. Structural model of human ATIC with identified sites of modification. The IMP cyclohydrolase domain of human ATIC showing the interface of two monomers (gray and light blue). At the interface are residues Thr182 and Ser190 (red), both shown to be phosphorylated. These phosphorylation events might impair proper dimer formation. Lys66 (green) was shown to be ubiquitinated, which could alter substrate (FAICAR, XMP) binding. PDB ID: 1PKX.

A

```
purD      --MKVLVIGNGGREHALAWKAAQSPLVETVFVAPGNAGTALEPALQNVAIGVTDIPALLD 58
GARS      MAARVLIIGSGGREHTLAWKLAQSHHVKQVLVAPGNAGTACSEKISNTAISISDHTALAQ 60
             :**:**.*****:**** ***  *: *:********* .  :.*.**.::*  ** :

purD      FAQNEKIDLTIVGPEAPLVKGVVDTFRAAGLKIFGPTAGAAQLEGSKAFTKDFLARHKIP 118
GARS      FCKEKKIEFVVVGPEAPLAAGIVGNLRSAGVQCFGPTAEAAQLESSKRFAKEFMDRHGIP 120
          *.:::**::.:*******. *:*..:*:**:: ***** *****.** *:*:*: ** **

purD      TAEYQNFTEVEPALAYLREKGA-PIVIKADGLAAGKGVIVAMTLEEAEAAVHDMLAGNAF 177
GARS      TAQWKAFTKPEEACSFILSADFPALVVKASGLAAGKGVIVAKSKEEACKAVQEIMQEKAF 180
          **::: **: * * ::: . .   :*:**.*********** : ***  **::::  :**

purD      GDAGHRIVIEEFLDGEEASFIVMVDGEHVLPMATSQDHKRVGDKDTGPNTGGMGAYSPAP 237
GARS      GAAGETIVIEELLDGEEVSCLCFTDGKTVAPMPPAQDHKRLLEGDGGPNTGGMGAYCPAP 240
          * **. *****:*****.* : :.**: * **  :*****: : * **********.***

purD      VVTDDVHQRTMERIIWPTVKGMAAEGNTYTGFLYAGLMIDKQGNPKVIEFNCRFGDPETQ 297
GARS      QVSNDLLLKIKDTVLQRTVDGMQQEGTPYTGILYAGIMLTKN-GPKVLEFNCRFGDPECQ 299
           *::*:  :  : ::  **.**  **. ***:****:*: *: .***:********** *

purD      PIMLRMKSDLVELCLAACESKLDEKTSEWDE-RASLGVVMAAGGYPGDYRTGDVIHGLPL 356
GARS      VILPLLKSDLYEVIQSTLDGLLCTSLPVWLENHTALTVVMASKGYPGDYTKGVEITGFPE 359
           *:  :**** *:  :: :. *  .   * * :::* ****: ****** .*  * *:*

purD      EEVAGGKVFHAGTKLADDEQVVTNGGRVLCVTALGHTVAEAQKRAYALMTDIHWDDCFCR 416
GARS      AQALGLEVFHAGTALKN-GKVVTHGGRVLAVTAIRENLISALEEAKKGLAAIKFEGAIYR 418
           :. * :****** * :  :***:*****.***: ..: .* :.*   :: *::::.: *

purD      KDIGWRAIEREQN     429
GARS      KDVGFRAIAFLQ-     430
          **:*:***   *
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B

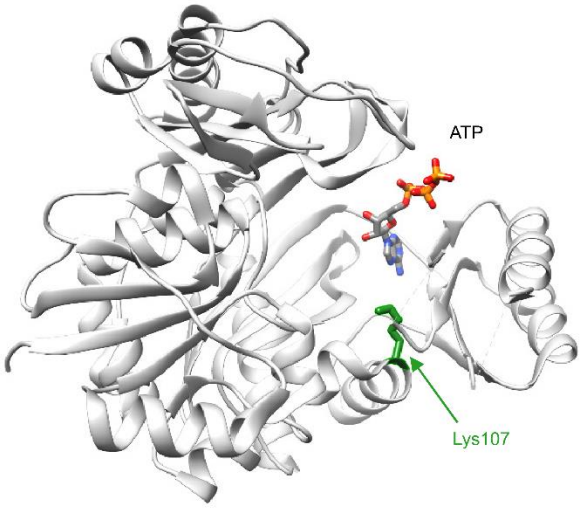

Figure S4. Structural model of GART with identified ubiquitination site (Lys107). (**A**) Structural alignment of *E.coli* PurD homolog to human GAR synthetase (GARS). The yellow highlighted lysine residue corresponds to Lys107 (human) and Lys105 (*E.coli*), a noted ubiquitination site in the lid region of ATP grasp family proteins. (**B**) Human GARS domain showing the proximity of Lys107 (green, site of identified ubiquitination) to the ATP binding site. PDB ID: 2QK4.

Table S1. 2×Strep-tagged protein construct sequences. The amino acid sequence (prepared by ExPASy ProtParam tool) is colored such that the blue amino acids correspond to the amino acid sequence of the target protein, gray and underlined for the spacer region between the target protein and 2×Strep tag (orange).

target protein	amino acid sequence of 2×Strep tagged construct
PPAT	MELEELGIRE ECGVFGCIAS GEWPTQLDVP HVITLGLVGL QHRGQESAGI VTSDGSSVPT FKSHKGMGLV NHVFTEDNLK KLYVSNLGIG HTRYATTGKC ELENCQPFVV ETLHGKIAVA HNGELVNAAR LRKKLLRHGI GLSTSSDSEM ITQLLAYTPP QEQDDTPDWV ARIKNLMKEA PTAYSLLIMH RDVIYAVRDP YGNRPLCIGR LIPVSDINDK EKKTSETEGW VVSSESCSFL SIGARYYREV LPGEIVEISR HNVQTLDIIS RSEGNPVAFC IFEYVYFARP DSMFEDQMVY TVRYRCGQQL AIEAPVDADL VSTVPESATP AALAYAGKCG LPYVEVLCKN RYVGRTFIQP NMRLRQLGVA KKFGVLSDNF KGKRIVLVDD SIVRGNTISP IIKLLKESGA KEVHIRVASP PIKYPCFMGI NIPTKEELIA NKPEFDHLAE YLGANSVVYL SVEGLVSSVQ EGIKFKKQKE KKHDIMIQEN GNGLECFEKS GHCTACLTGK YPVELEWVPG SAWSHPQFEK GGGSGGGSGG SAWSHPQFEK
GART	MAARVLIIGS GGREHTLAWK LAQSHHVKQV LVAPGNAGTA CSEKISNTAI SISDHTALAQ FCKEKKIEFV VVGPEAPLAA GIVGNLRSAG VQCFGPTAEA AQLESSKRFA KEFMDRHGIP TAQWKAFTKP EEACSFILSA DFPALVVKAS GLAAGKGVIV AKSKEEACKA VQEIMQEKAF GAAGETIVIE ELLDGEEVSC LCFTDGKTVA PMPPAQDHKR LLEGDGGPNT GGMGAYCPAP QVSNDLLLKI KDTVLQRTVD GMQQEGTPYT GILYAGIMLT KNGPKVLEFN CRFGDPECQV

	ILPLLKSDLY EVIQSTLDGL LCTSLPVWLE NHTALTVVMA SKGYPGDYTK GVEITGFPEA 370 380 390 400 410 420 QALGLEVFHA GTALKNGKVV THGGRVLAVT AIRENLISAL EEAKKGLAAI KFEGAIYRKD 430 440 450 460 470 480 VGFRAIAFLQ QPRSLTYKES GVDIAAGNML VKKIQPLAKA TSRSGCKVDL GGFAGLFDLK 490 500 510 520 530 540 AAGFKDPLLA SGTDGVGTKL KIAQLCNKHD TIGQDLVAMC VNDILAQGAE PLFFLDYFSC 550 560 570 580 590 600 GKLDLSVTEA VVAGIAKACG KAGCALLGGE TAEMPDMYPP GEYDLAGFAV GAMERDQKLP 610 620 630 640 650 660 HLERITEGDV VVGIASSGLH SNGFSLVRKI VAKSSLQYSS PAPDGCGDQT LGDLLLTPTR 670 680 690 700 710 720 IYSHSLLPVL RSGHVKAFAH ITGGGLLENI PRVLPEKLGV DLDAQTWRIP RVFSWLQQEG 730 740 750 760 770 780 HLSEEEMART FNCGVGAVLV VSKEQTEQIL RDIQQHKEEA WVIGSVVARA EGSPRVKVKN 790 800 810 820 830 840 LIESMQINGS VLKNGSLTNH FSFEKKKARV AVLISGTGSN LQALIDSTRE PNSSAQIDIV 850 860 870 880 890 900 ISNKAAVAGL DKAERAGIPT RVINHKLYKN RVEFDSAIDL VLEEFSIDIV CLAGFMRILS 910 920 930 940 950 960 GPFVQKWNGK MLNIHPSLLP SFKGSNAHEQ ALETGVTVTG CTVHFVAEDV DAGQIILQEA 970 980 990 1000 1010 1020 VPVKRGDTVA TLSERVKLAE HKIFPAALQL VASGTVQLGE NGKICWVKEE LEGSAWSHPQ 1030 1040 FEKGGGSGGG SGGSAWSHPQ FEK
PFAS	10 20 30 40 50 60 MSPVLHFYVR PSGHEGAAPG HTRRKLQGKL PELQGVETEL CYNVNWTAEA LPSAEETKKL 70 80 90 100 110 120 MWLFGCPLLL DDVARESWLL PGSNDLLLEV GPRLNFSTPT STNIVSVCRA TGLGPVDRVE 130 140 150 160 170 180 TTRRYRLSFA HPPSAEVEAI ALATLHDRMT EQHFPHPIQS FSPESMPEPL NGPINILGEG 190 200 210 220 230 240 RLALEKANQE LGLALDSWDL DFYTKRFQEL QRNPSTVEAF DLAQSNSEHS RHWFFKGQLH 250 260 270 280 290 300 VDGQKLVHSL FESIMSTQES SNPNNVLKFC DNSSAIQGKE VRFLRPEDPT RPSRFQQQQG 310 320 330 340 350 360 LRHVVFTAET HNFPTGVCPF SGATTGTGGR IRDVQCTGRG AHVVAGTAGY CFGNLHIPGY 370 380 390 400 410 420 NLPWEDPSFQ YPGNFARPLE VAIEASNGAS DYGNKFGEPV LAGFARSLGL QLPDGQRREW 430 440 450 460 470 480 IKPIMFSGGI GSMEADHISK EAPEPGMEVV KVGGPVYRIG VGGGAASSVQ VQGDNTSDLD 490 500 510 520 530 540 FGAVQRGDPE MEQKMNRVIR ACVEAPKGNP ICSLHDQGAG GNGNVLKELS DPAGAIIYTS

	550 560 570 580 590 600 RFQLGDPTLN ALEIWGAEYQ ESNALLLRSP NRDFLTHVSA RERCPACFVG TITGDRRIVL 610 620 630 640 650 660 VDDRECPVRR NGQGDAPPTP LPTPVDLELE WVLGKMPRKE FFLQRKPPML QPLALPPGLS 670 680 690 700 710 720 VHQALERVLR LPAVASKRYL TNKVDRSVGG LVAQQQCVGP LQTPLADVAV VALSHEELIG 730 740 750 760 770 780 AATALGEQPV KSLLDPKVAA RLAVAEALTN LVFALVTDLR DVKCSGNWMW AAKLPGEGAA 790 800 810 820 830 840 LADACEAMVA VMAALGVAVD GGKDSLSMAA RVGTETVRAP GSLVISAYAV CPDITATVTP 850 860 870 880 890 900 DLKHPEGRGH LLYVALSPGQ HRLGGTALAQ CFSQLGEHPP DLDLPENLVR AFSITQGLLK 910 920 930 940 950 960 DRLLCSGHDV SDGGLVTCLL EMAFAGNCGL QVDVPVPRVD VLSVLFAEEP GLVLEVQEPD 970 980 990 1000 1010 1020 LAQVLKRYRD AGLHCLELGH TGEAGPHAMV RVSVNGAVVL EEPVGELRAL WEETSFQLDR 1030 1040 1050 1060 1070 1080 LQAEPRCVAE EERGLRERMG PSYCLPPTFP KASVPREPGG PSPRVAILRE EGSNGDREMA 1090 1100 1110 1120 1130 1140 DAFHLAGFEV WDVTMQDLCS GAIGLDTFRG VAFVGGFSYA DVLGSAKGWA AAVTFHPRAG 1150 1160 1170 1180 1190 1200 AELRRFRKRP DTFSLGVCNG CQLLALLGWV GGDPNEDAAE MGPDSQPARP GLLLRHNLSG 1210 1220 1230 1240 1250 1260 RYESRWASVR VGPGPALMLR GMEGAVLPVW SAHGEGYVAF SSPELQAQIE ARGLAPLHWA 1270 1280 1290 1300 1310 1320 DDDGNPTEQY PLNPNGSPGG VAGICSCDGR HLAVMPHPER AVRPWQWAWR PPPFDTLTTS 1330 1340 1350 1360 1370 1380 PWLQLFINAR NWTLEGSCRI LQSTVPRARD PPVATGSAWS HPQFEKGGGS GGGSGGSAWS HPQFEK
PAICS	10 20 30 40 50 60 MATAEVLNIG KKLYEGKTKE VYELLDSPGK VLLQSKDQIT AGNAARKNHL EGKAAISNKI 70 80 90 100 110 120 TSCIFQLLQE AGIKTAFTRK CGETAFIAPQ CEMIPIEWVC RRIATGSFLK RNPGVKEGYK 130 140 150 160 170 180 FYPPKVELFF KDDANNDPQW SEEQLIAAKF CFAGLLIGQT EVDIMSHATQ AIFEILEKSW 190 200 210 220 230 240 LPQNCTLVDM KIEFGVDVTT KEIVLADVID NDSWRLWPSG DRSQQKDKQS YRDLKEVTPE 250 260 270 280 290 300 GLQMVKKNFE WVAERVELLL KSESQCRVVV LMGSTSDLGH CEKIKKACGN FGIPCELRVT 310 320 330 340 350 360 SAHKGPDETL RIKAEYEGDG IPTVFVAVAG RSNGLGPVMS GNTAYPVISC PPLTPDWGVQ

	370 380 390 400 410 420 DVWSSLRLPS GLGCSTVLSP EGSAQFAAQI FGLSNHLVWS KLRASILNTW ISLKQADKKI 430 440 450 460 RECNLPPVAT GSAWSHPQFE KGGGSGGGSG GSAWSHPQFE K
ADSL	10 20 30 40 50 60 MAAGGDHGSP DSYRSPLASR YASPEMCFVF SDRYKFRTWR QLWLWLAEAE QTLGLPITDE 70 80 90 100 110 120 QIQEMKSNLE NIDFKMAAEE EKRLRHDVMA HVHTFGHCCP KAAGIIHLGA TSCYVGDNTD 130 140 150 160 170 180 LIILRNALDL LLPKLARVIS RLADFAKERA SLPTLGFTHF QPAQLTTVGK RCCLWIQDLC 190 200 210 220 230 240 MDLQNLKRVR DDLRFRGVKG TTGTQASFLQ LFEGDDHKVE QLDKMVTEKA GFKRAFIITG 250 260 270 280 290 300 QTYTRKVDIE VLSVLASLGA SVHKICTDIR LLANLKEMEE PFEKQQIGSS AMPYKRNPMR 310 320 330 340 350 360 SERCCSLARH LMTLVMDPLQ TASVQWFERT LDDSANRRIC LAEAFLTADT ILNTLQNISE 370 380 390 400 410 420 GLVVYPKVIE RRIRQELPFM ATENIIMAMV KAGGSRQDCH EKIRVLSQQA ASVVKQEGGD 430 440 450 460 470 480 NDLIERIQVD AYFSPIHSQL DHLLDPSSFT GRASQQVQRF LEEEVYPLLK PYESVMKVKA 490 500 510 520 ELCLARDPPV ATGSAWSHPQ FEKGGGSGGG SGGSAWSHPQ FEK
ATIC	10 20 30 40 50 60 MASAWSHPQF EKGGGSGGGS GGSAWSHPQF EKSGRIRSVM APGQLALFSV SDKTGLVEFA 70 80 90 100 110 120 RNLTALGLNL VASGGTAKAL RDAGLAVRDV SELTGFPEML GGRVKTLHPA VHAGILARNI 130 140 150 160 170 180 PEDNADMARL DFNLIRVVAC NLYPFVKTVA SPGVTVEEAV EQIDIGGVTL LRAAAKNHAR 190 200 210 220 230 240 VTVVCEPEDY VVVSTEMQSS ESKDTSLETR RQLALKAFTH TAQYDEAISD YFRKQYSKGV 250 260 270 280 290 300 SQMPLRYGMN PHQTPAQLYT LQPKLPITVL NGAPGFINLC DALNAWQLVK ELKEALGIPA 310 320 330 340 350 360 AASFKHVSPA GAAVGIPLSE DEAKVCMVYD LYKTLTPISA AYARARGADR MSSFGDFVAL 370 380 390 400 410 420 SDVCDVPTAK IISREVSDGI IAPGYEEEAL TILSKKKNGN YCVLQMDQSY KPDENEVRTL 430 440 450 460 470 480 FGLHLSQKRN NGVVDKSLFS NVVTKNKDLP ESALRDLIVA TIAVKYTQSN SVCYAKNGQV 490 500 510 520 530 540 IGIGAGQQSR IHCTRLAGDK ANYWWLRHHP QVLSMKFKTG VKRAEISNAI DQYVTGTIGE 550 560 570 580 590 600 DEDLIKWKAL FEEVPELLTE AEKKEWVEKL TEVSISSDAF FPFRDNVDRA KRSGVAYIAA 610 620 630 PSGSAADKVV IEACDELGII LAHTNLRLFH H

Table S5. Comparison of phosphorylated residues between selected studies.

target protein	res. no.	this study	Olsen, J. *et al.* 2010[†]	Mertins, P. *et al.* 2013[‡]
PPAT	259	X		
	356		X	
	397	X		
GART	46		X	
	48		X	
	51		X	
	53		X	
	121		X	
	128	X		
	390		X	
	398	X		
	440	X		
	491	X		
	498	X		
	546		X	
	548		X	
	714			X
	730		X	
	796			X
	802			X
	900		X	
	973	X		
PFAS	83	X		
	128	X		
	215	X		X
	216	X		
	261	X		
	290	X		
	530		X	
	538		X	
	539		X	
	569		X	X
	576	X		
	619	X	X	
	623	X	X	
	826	X		
	857	X		
	873	X		
	893	X		
	1062	X	X	
PAICS	18	X		
	27	X		X
	35	X		
	53		X	
	62			X
	107			X

target protein	res. no.	this study	Olsen, J. *et al.* 2010[†]	Mertins, P. *et al.* 2013[‡]
PAICS (cont'd)	238	X		X
	274			X
	276			X
	300	X		
	323	X		
	409	X		
	412	X		
ADSL	9		X	X
	12		X	
	15		X	X
	21	X		
	114	X		
	239		X	
	242		X	
	243		X	
	244		X	
	253		X	
	257		X	
	261		X	
	407	X		
	412	X		
	434	X		
ATIC	25		X	
	34		X	
	37		X	
	52	X		
	55	X		
	67	X		
	143		X	
	155		X	
	156		X	
	160		X	
	161		X	
	163		X	
	180	X		
	182	X		
	190	X		
	215	X		
	264	X		
	269	X		
	322	X		
	346	X		
	387	X		
	413	X		
	422	X		

† Olsen, J. V.; Vermeulen, M.; Santamaria, A.; Kumar, C.; Miller, M. L.; Jensen, L. J.; Gnad, F.; Cox, J.; Jensen, T. S.; Nigg, E. A.; Brunak, S.; Mann, M., Quantitative phosphoproteomics reveals widespread full phosphorylation site occupancy during mitosis. *Sci Signal* **2010,** *3* (104), ra3.

‡ only included data from 'high' proteome analysis coverage from Mertins, P.; Qiao, J. W.; Patel, J.; Udeshi, N. D.; Clauser, K. R.; Mani, D. R.; Burgess, M. W.; Gillette, M. A.; Jaffe, J. D.; Carr, S. A., Integrated proteomic analysis of post-translational modifications by serial enrichment. *Nat Methods* **2013,** *10* (7), 634-7.

Table S6. Comparison of ubiquitinated residues between selected studies.

target protein	res. no.	this study	Kim, W. *et al.* 2011†	Mertins, P. *et al.* 2013‡
PPAT	62		X	X
	80		X	
	99			X
	349			X
	381		X	X
	403		X	X
	411		X	X
GART	28			X
	66		X	
	107	X	X	X
	111		X	X
	156		X	
	219		X	
	251		X	X
	281		X	
	285			X
	350		X	
	375		X	
	378	X	X	
	404		X	
	411		X	
	438		X	
	459			X
	467			X
	485		X	X
	557			X
	598			X
	697		X	X
	852			X
PFAS	205		X	
	422		X	X
	451		X	
	494		X	X
	507			X
	527			X
	646			X
	683		X	X
	737		X	
	843			X
	900		X	
PAICS	11	X	X	X
	19			X
	30			X
	36			X
	45		X	
	53			X
	56		X	
	62		X	

target protein	res. no.	this study	Kim, W. *et al.* 2011†	Mertins, P. *et al.* 2013‡
PAICS (cont'd)	79		X	
	80			X
	100		X	
	110			X
	116			X
	136		X	
	142		X	
	157		X	
	235			X
	247			X
	261		X	
	272		X	
	273		X	
	286			X
	304			X
	330		X	
	339		X	
	414			X
	440		X	
ADSL	75		X	X
	134	X		X
	170	X		X
	218			X
	243		X	
	264	X		
	276			X
	290		X	
	298		X	
	391	X		
	415			X
	429		X	
	479			X
ATIC	39	X		
	66	X	X	X
	177			X
	199			X
	254			X
	266			X
	331	X		
	356		X	
	397		X	X
	406		X	
	437			X
	461	X		X
	477	X		
	507		X	
	524		X	X

† Kim, W.; Bennett, E. J.; Huttlin, E. L.; Guo, A.; Li, J.; Possemato, A.; Sowa, M. E.; Rad, R.; Rush, J.; Comb, M. J.; Harper, J. W.; Gygi, S. P., Systematic and quantitative assessment of the ubiquitin-modified proteome. *Mol Cell* **2011,** *44* (2), 325-40.

‡ only included data from 'high' proteome analysis coverage from Mertins, P.; Qiao, J. W.; Patel, J.; Udeshi, N. D.; Clauser, K. R.; Mani, D. R.; Burgess, M. W.; Gillette, M. A.; Jaffe, J. D.; Carr, S. A., Integrated proteomic analysis of post-translational modifications by serial enrichment. *Nat Methods* **2013,** *10* (7), 634-7.

Table S7. Comparison of acetylated residues between selected studies.

target protein	res. no.	this study	Choudhary, C. *et al.* 2009†	Mertins, P. *et al.* 2013‡
PPAT	65	X		
	81	X	X	X
	99			X
	349	X		
	371	X		
	372	X		X
GART	28			X
	107	X		
	251	X		
	350		X	
	378	X		
	438	X		
	452	X		
	459	X		
	499	X		
	852	X		X
	906	X		
PAICS	11	X		
	19	X		
	30	X		X
	36	X		
	53	X		
	59	X		
	79		X	
	80	X		
	110			X
	246	X		X
	247	X		X
	261			X
	273		X	
	283	X		X
	285			X
PAICS (cont'd)	286	X		
	304	X		
	309		X	
	311		X	
	313	X		
ADSL	82			X
	134	X		
	147	X	X	
	170	X		
	187	X		
	199	X		
	264	X		
	295	X	X	X
	391	X		
	402	X		
	415	X		
ATIC	66	X		
	164	X		
	199	X	X	
	285	X		
	294	X		
	331	X		
	356		X	X
	357		X	
	372	X		
	389	X		
	397	X		
	408	X		
	437	X		
	461	X		
	477	X		

† Choudhary, C.; Kumar, C.; Gnad, F.; Nielsen, M. L.; Rehman, M.; Walther, T. C.; Olsen, J. V.; Mann, M., Lysine acetylation targets protein complexes and co-regulates major cellular functions. *Science* **2009,** *325* (5942), 834-40.

‡ only included data from 'high' proteome analysis coverage from Mertins, P.; Qiao, J. W.; Patel, J.; Udeshi, N. D.; Clauser, K. R.; Mani, D. R.; Burgess, M. W.; Gillette, M. A.; Jaffe, J. D.; Carr, S. A., Integrated proteomic analysis of post-translational modifications by serial enrichment. *Nat Methods* **2013,** *10* (7), 634-7.