Supporting Information

Expanded Cellular Amino Acid Pools Containing Phosphoserine, Phosphothreonine, and Phosphotyrosine

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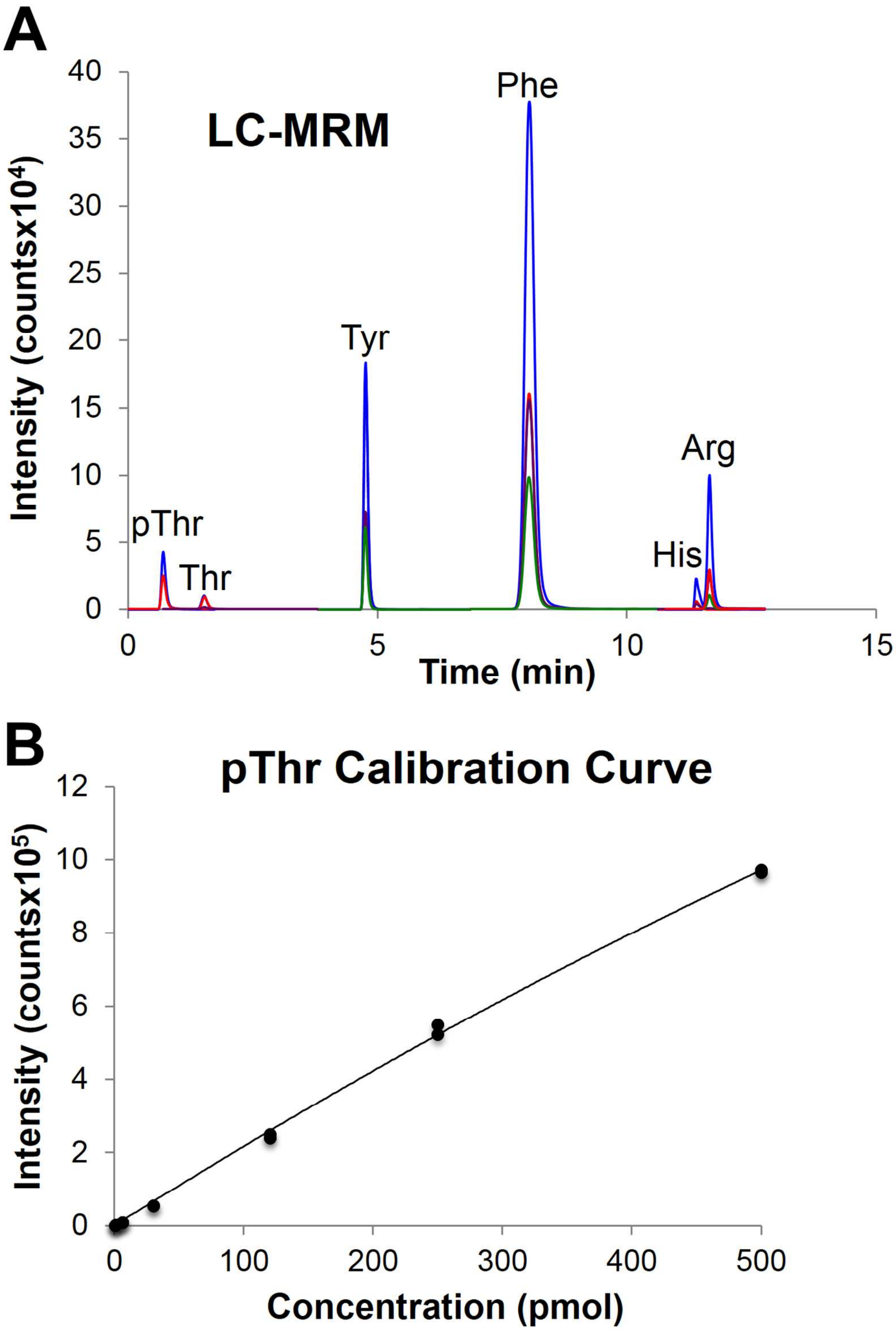
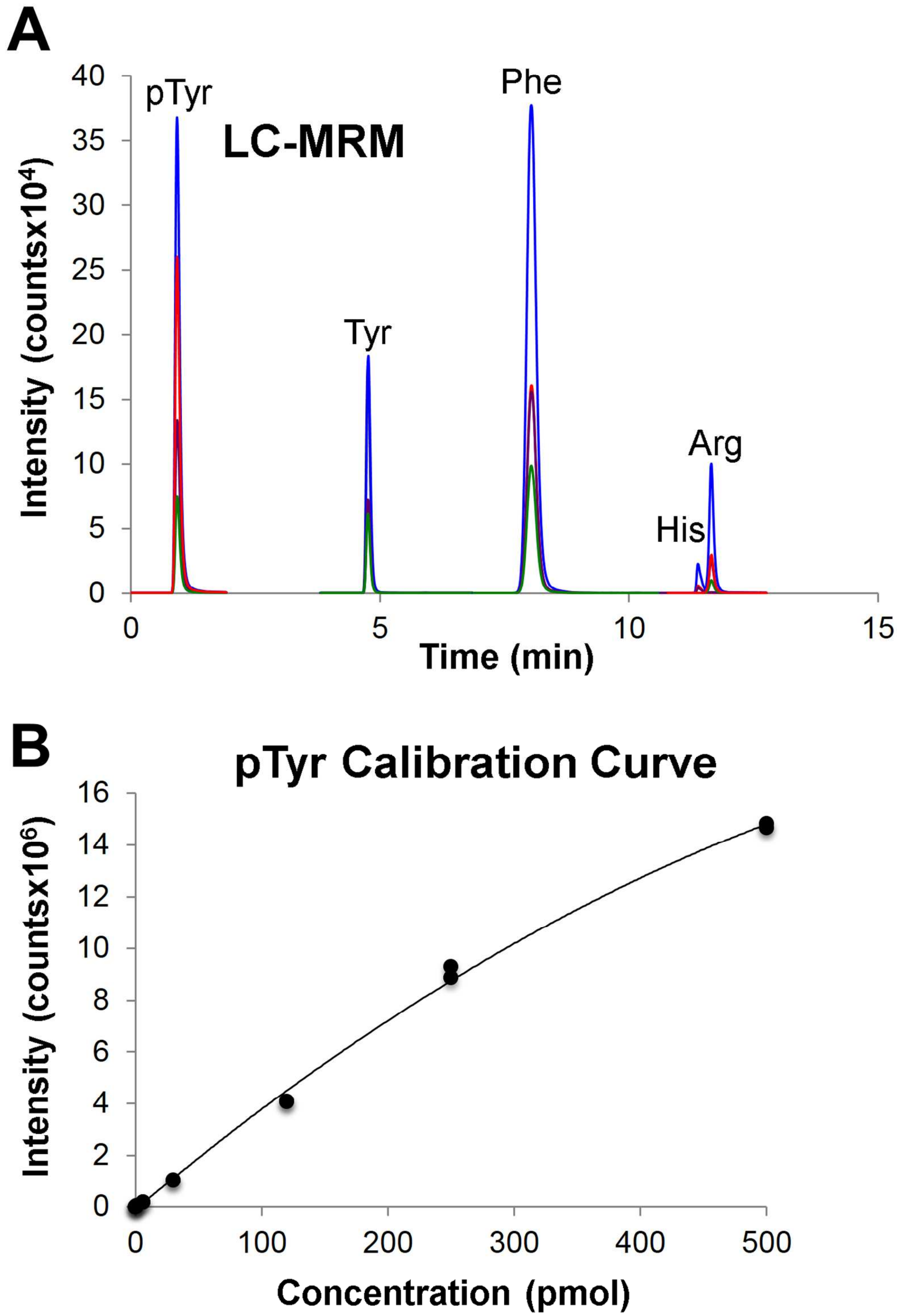
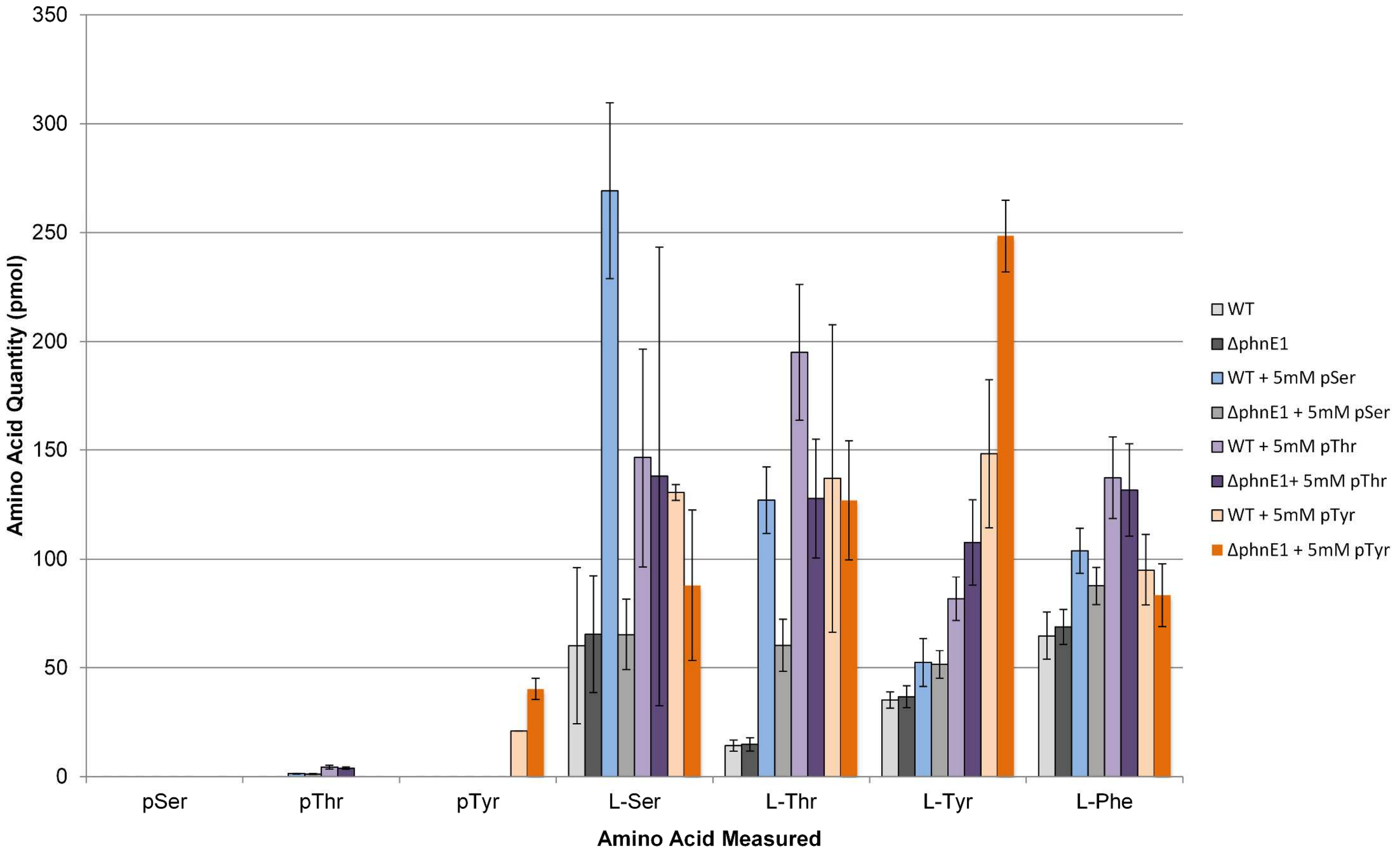


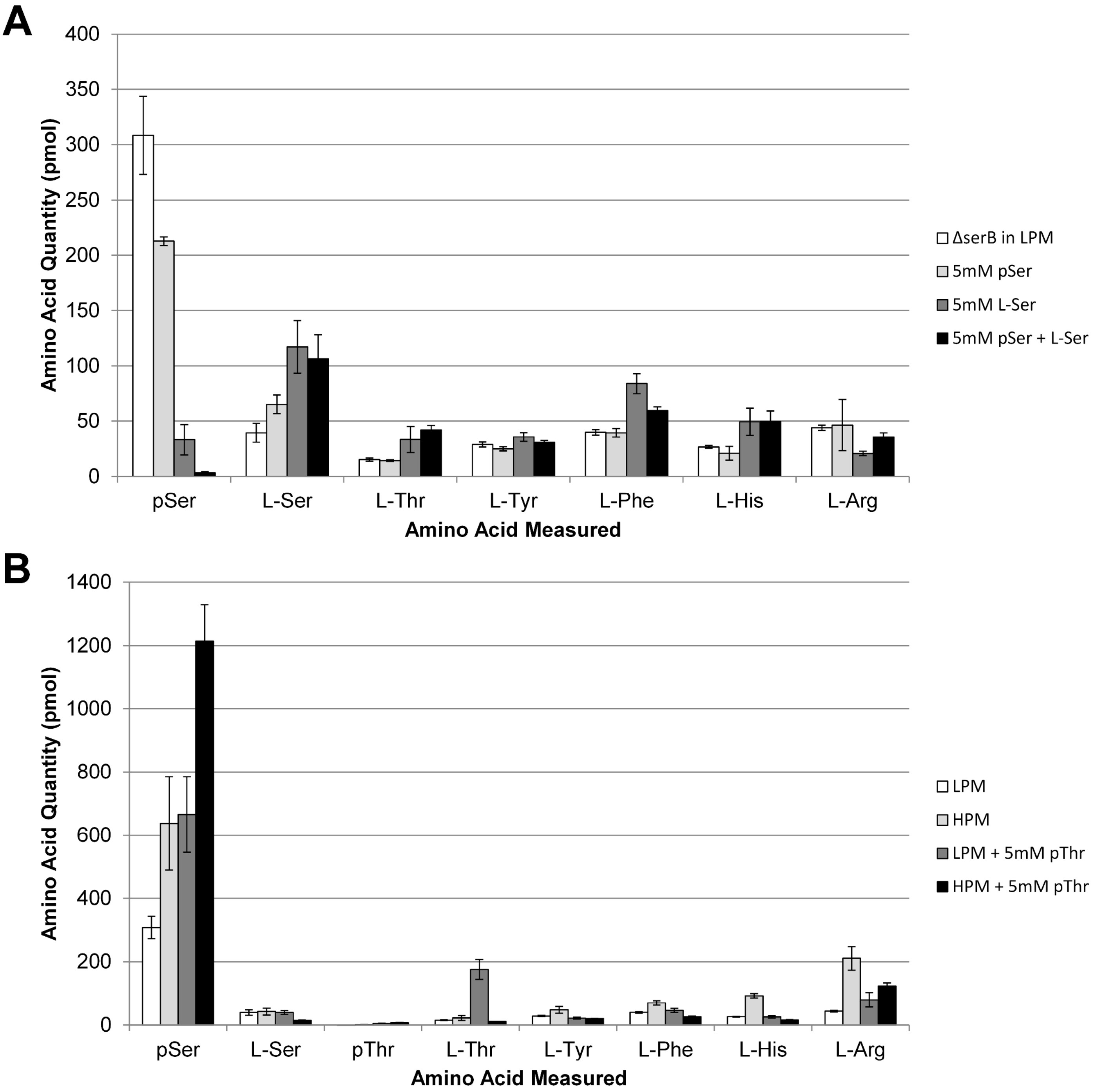
Supplemental Figure 1. LC-MS/MS analysis of pThr.
A) A typical chromatogram of an LC-MS/MS run is shown. Unique MRM transitions are plotted for the amino acids indicated above the individual peaks. **B)** A representative calibration curve for pThr is shown. The fitted calibration function for this curve was $y = -1.596345x^2 + 3797.168958x - 862.935161$ and the maximum % residual was 8.7.



Supplemental Figure 2. LC-MS/MS analysis of pTyr.
A) A typical chromatogram of an LC-MS/MS run is shown. Unique MRM transitions are plotted for the amino acids indicated above the individual peaks. **B)** A representative calibration curve for pTyr is shown. The fitted calibration function for this curve was $y = -17.446301x^2 + 34286.990110x - 2974.004316$ and the maximum % residual was 4.4.



Supplemental Figure 3. Quantitation of intracellular amino acids in a Δ*pnhE1 E. coli* strain.
Measured amino acid quantities of select amino acids in K12 BW25113 WT vs. Δ*phnE1 E. coli* grown in LPM media (light grey vs. dark grey), in LPM media with 5mM pSer (light blue vs. grey), in LPM with 5mM pThr (light violet vs. dark violet), and LPM media with 5mM pTyr (light orange vs. dark orange). Error bars were calculated using the 95% confidence interval, n=5.



Supplemental Figure 4. Dynamic levels of pSer in the cell extracts.
A) Measured amino acid quantities of select amino acids in K12 BW25113 Δ*serB E. coli* grown in LPM media without (white) or with 5mM pSer (light grey), L-Ser (grey), and pSer/L-Ser (black). **B)** Measured amino acid quantities of select amino acids in K12 BW25113 Δ*serB E. coli* grown in LPM media (white), HPM media (light grey), in LPM media with 5mM pThr (grey), and HPM media with 5mM pThr (black). Error bars were calculated using the 95% confidence interval, n=5.

Supplementary Table 1. Optimized Transitions for the Determination of Amino Acids by LC-MS/MS

Amino Acid	Retention Time (min)	Precursor Ion MS^1	Product Ion MS^2	Collision Energy (V)
pSer	0.68	186.02	87.9*	8
pSer	0.68	186.02	70.0	16
pThr	0.74	200.03	102.1*	4
pThr	0.74	200.03	56.0	20
pTyr	0.92	262.05	216.0*	4
pTyr	0.92	262.05	118.1	20
pTyr	0.92	262.05	117.1	48
pTyr	0.92	262.05	91.0	44
L-Ser	1.30	106.05	60.0*	4
L-Ser	1.30	106.05	42.0	20
L-Ser	1.30	106.05	30.1	20
L-Thr	1.70	120.07	74.0*	4
L-Thr	1.70	120.07	56.2	12
L-Thr	1.70	120.07	29.2	28
L-Tyr	4.80	182.08	136.1	8
L-Tyr	4.80	182.08	91.0*	28
L-Tyr	4.80	182.08	76.9	40
L-Tyr	4.80	182.08	51.0	68
L-Phe	8.10	166.09	120.0*	8
L-Phe	8.10	166.09	103.0	28
L-Phe	8.10	166.09	76.9	48
L-Phe	8.10	166.09	51.0	60
L-His	11.43	156.08	110.1*	13
L-His	11.43	156.08	82.9	25
L-His	11.43	156.08	56.1	37
L-Lys	11.43	147.12	130.3*	8
L-Lys	11.43	147.12	84.3	0
L-Lys	11.43	147.12	56.1	28
L-Arg	11.77	175.12	130.1	12
L-Arg	11.77	175.12	116.1	12
L-Arg	11.77	175.12	70.0*	24
L-Arg	11.77	175.12	60.0	12

*Primary transition used for quantitation.

Supplementary Table 2. Upper and Lower Limits of Detection for Measured Amino Acids

	Lower Limit of Detection (pmol)	Upper Calibration Limit (pmol)
pSer	0.5	500
pThr	1	500
pTyr	0.5	500
L-Ser	3	500
L-Thr	2	500
L-Tyr	0.5	500
L-Phe	0.5	500
L-Lys	5	500
L-His	3	500
L-Arg	1	500

Supplementary Table 3. Table of Bacterial Strains.

Strain	Name	Reference
E. coli K12 BW25113	WT (K12)	(*1*)
E. coli K12 Keio Collection JW4351	Δ*serB* (K12 Δ*serB*)	(*1*)
E. coli BL-21 Δ*serB*	Δ*serB* (BL-21 Δ*serB*)	(*2*)
E. coli Keio Collection (JW4064)	Δ*phnE1*	(*1*)
rEc7.ΔprfA.ΔtolC.bla:T7.ΔserB	EcAR7	(*3*)

Supplementary Table 4. Final Dynamic MRM Method

Method Name	120801_dMRM_final5.m
Method Description	This is 20 pmol/ul of amino acids in solvent A with 3 ul injection volume. This is dMRM with large windows for Y and Thr

Device List

µHiP ALS
NanoPump
CapPump
MS QQQ

MS QQQ Mass Spectrometer

Ion Source	AJS ESI	**Tune File**	atunes.TUNE.XML
Stop Mode	No Limit/As Pump	**Stop Time (min)**	1
Time Filter	On	**Time Filter Width (min)**	0.07

Time Segments

Index	**Start Time (min)**	**Scan Type**	**Ion Mode**	**Div Valve**	**Delta EMV**	**Store**	**Cycle Time (ms)**	**Triggered ?**	**MRM Repeats**
1	0.04	DynamicMRM	ESI+Agilent Jet	To MS	350	Yes	800	No	0

Time Segment 1 **Scan Segments**

Cpd Name	**ISTD ?**	**Prec Ion**	**MS1 Res**	**Prod Ion**	**MS2 Res**	**Frag (V)**	**CE (V)**	**Cell Acc (V)**	**Ret Time**	**Ret Window**	**Polarity**
F	No	166.09	Wide / Unit (6490)	120	Wide / Unit (6490)	380	8	5	8.1	2.46	Positive
F	No	166.09	Wide / Unit (6490)	103	Wide / Unit (6490)	380	28	5	8.1	2.46	Positive
F	No	166.09	Wide / Unit (6490)	76.9	Wide / Unit (6490)	380	48	5	8.1	2.46	Positive
F	No	166.09	Wide / Unit (6490)	51	Wide / Unit (6490)	380	60	5	8.1	2.46	Positive
H	No	156.08	Wide / Unit (6490)	110.1	Wide / Unit (6490)	380	13	5	11.43	1.62	Positive
H	No	156.08	Wide / Unit (6490)	82.9	Wide / Unit (6490)	380	25	5	11.43	1.62	Positive
H	No	156.08	Wide / Unit (6490)	56.1	Wide / Unit (6490)	380	37	5	11.43	1.62	Positive
K	No	147.12	Wide / Unit (6490)	130.3	Wide / Unit (6490)	380	8	5	11.43	1.4	Positive
K	No	147.12	Wide / Unit (6490)	84.3	Wide / Unit (6490)	380	0	5	11.43	1.4	Positive
K	No	147.12	Wide / Unit (6490)	56.1	Wide / Unit (6490)	380	28	5	11.43	1.4	Positive
L-Serine	No	106.05	Wide / Unit (6490)	60	Wide / Unit (6490)	380	4	5	1.3	2	Positive
L-Serine	No	106.05	Wide / Unit (6490)	42	Wide / Unit (6490)	380	20	5	1.3	2	Positive
L-Serine	No	106.05	Wide / Unit (6490)	30.1	Wide / Unit (6490)	380	20	5	1.3	2	Positive
L-Threonine	No	120.07	Wide / Unit (6490)	74	Wide / Unit (6490)	380	4	5	1.7	2	Positive
L-Threonine	No	120.07	Wide / Unit (6490)	56.2	Wide / Unit (6490)	380	12	5	1.7	2	Positive
L-Threonine	No	120.07	Wide / Unit (6490)	29.2	Wide / Unit (6490)	380	28	5	1.7	2	Positive
L-Tyrosine	No	182.08	Wide / Unit (6490)	136.1	Wide / Unit (6490)	380	8	5	4.8	2	Positive
L-Tyrosine	No	182.08	Wide / Unit (6490)	91	Wide / Unit (6490)	380	28	5	4.8	2	Positive
L-Tyrosine	No	182.08	Wide / Unit (6490)	76.9	Wide / Unit (6490)	380	40	5	4.8	2	Positive
L-Tyrosine	No	182.08	Wide / Unit (6490)	51	Wide / Unit (6490)	380	68	5	4.8	2	Positive
pSer	No	186.02	Wide / Unit (6490)	87.9	Wide / Unit (6490)	380	8	5	0.68	2.5	Positive
pSer	No	186.02	Wide / Unit (6490)	70	Wide / Unit (6490)	380	16	5	0.68	2.5	Positive
pThr	No	200.03	Wide / Unit (6490)	102.1	Wide / Unit (6490)	380	4	5	0.74	2	Positive
pThr	No	200.03	Wide / Unit (6490)	56	Wide / Unit (6490)	380	20	5	0.74	2	Positive
pTyr	No	262.05	Wide / Unit (6490)	216	Wide / Unit (6490)	380	4	5	0.92	2	Positive
pTyr	No	262.05	Wide / Unit (6490)	118.1	Wide / Unit (6490)	380	20	5	0.92	2	Positive
pTyr	No	262.05	Wide / Unit (6490)	117.1	Wide / Unit (6490)	380	48	5	0.92	2	Positive
pTyr	No	262.05	Wide / Unit (6490)	91	Wide / Unit (6490)	380	44	5	0.92	2	Positive
R	No	175.12	Wide / Unit (6490)	130.1	Wide / Unit (6490)	380	12	5	11.77	2	Positive
R	No	175.12	Wide / Unit (6490)	116.1	Wide / Unit (6490)	380	12	5	11.77	2	Positive
R	No	175.12	Wide / Unit (6490)	70	Wide / Unit (6490)	380	24	5	11.77	2	Positive
R	No	175.12	Wide / Unit (6490)	60	Wide / Unit (6490)	380	12	5	11.77	2	Positive

Supplementary Table 4 (continued). Final Dynamic MRM Method

Source Parameters

Parameter	Value (+)	Value (-)
Gas Temp (°C)	350	350
Gas Flow (l/min)	11	11
Nebulizer (psi)	23	23
SheathGasHeater	150	150
SheathGasFlow	12	12
Capillary (V)	2500	3000
VCharging	500	1500

Chromatograms

Chrom Type	Label	Offset	Y-Range
MRM	MRM	10	10000

Instrument Curves

Capillary Pump

Name	CapPump	**Model**	G1376A
Ordinal #	1	**Options**	SSV_FS1_FCC
Stop Time (min)	30	**Post Time (min)**	Off
Mode	Normal Flow	**Flow (µl/min)**	200
Pressure Min (bar)	0	**Pressure Max (bar)**	400
Fast Reconditioning	Off	**Max Flow Gradient (ml/min)**	100
Primary Flow (µl/min)	500	**Column Flow Ready**	N/A
Calibrated As	Uncalibrated(H2O-H2O)		
Solvent A	99.5 % Water, 0.5 % ACN, 0.1 % FA, 0.1 % PFOA		
Solvent Ratio A	100		
Compress. A (*10-6/bar)	100		
Solvent B	90 % ACN 0.1 FA, 0.1 % PFOA		
Solvent Ratio B	0		
Compress. B (*10-6/bar)	115		
Stroke B (µl)	Auto		
Stroke A (µl)	Auto		
Contact 1	Off		
Contact 2	Off		
Contact 3	Off		
Contact 4	Off		

Pump Time Table

Time	Flow	Pressure	SolvRatioB
0	200	400	0
2	200	400	0
3	200	400	30
15	200	400	62
15.5	300	400	100
21.5	350	400	100
22.5	200	400	0

Signals Selected

Description
Pressure
Solvent% B

Supplementary Table 4 (continued). Final Dynamic MRM Method

Micro Wellplate Sampler

Name	µHiP ALS	**Model**	G1377A
Ordinal #	1	**Options**	THM
Stop Time (min)	No Limit	**Post Time (min)**	Off
Injection Type	Needle Wash	**Injection Volume (µl)**	3
Overlap Time (min)	Disable Overlapped	**Draw Position (mm)**	1
Vial/Well bottom sensing	Yes	**Draw Speed (µl/min)**	20
Eject Speed (µl/min)	100	**Flush Out Factor**	5
Automatic Delay Volume Reduction	No	**Equilibration Time (sec)**	0
Wash Vessel	N/A	**Wash Location**	FlushPort
Wash Time	10	**Wash Cycles**	N/A
Contact 1	Off		
Contact 2	Off		
Contact 3	Off		
Contact 4	Off		

Nano Pump		**Model**	G2226A
Name	NanoPump	**Options**	SSV_FS3_FCC
Ordinal #	1		

Stop Time (min)	No Limit	**Post Time (min)**	Off
Mode	Normal Flow	**Flow (µl/min)**	3
Pressure Min (bar)	0	**Pressure Max (bar)**	400
Fast Reconditioning	Off	**Max Flow Gradient (ml/m**	100
Primary Flow (µl/min)	500	**Column Flow Ready**	N/A
Calibrated As	Uncalibrated(H2O-H2O)		
Solvent A		**Solvent B**	
Solvent Ratio A	100	**Solvent Ratio B**	0
Compress. A (*10-6/bar)	100	**Compress. B (*10-6/bar)**	115
Stroke A (µl)	Auto		
Contact 1	Off		
Contact 2	Off		
Contact 3	Off		
Contact 4	Off		

Supplementary Table 5. Table of Amino Acid Measurements

Figure	Strain (media)	pSer	Error	pThr	Error	pTyr	Error	Ser	Error	Thr	Error	Tyr	Error	Phe	Error	Lys	Error	His	Error	Arg	Error
Fig. 2A	K-12 LPM	LOQ	*nd*	LOQ	*nd*	LOQ	*nd*	60.2	36.0	14.1	2.6	35.2	3.7	64.8	10.8	114.3	34.1	40.0	6.4	37.6	12.5
Fig. 2A	K-12 LB	LOQ	*nd*	7.6	1.1	LOQ	*nd*	12.8	4.9	6.6	0.8	149.8	12.6	292.5	23.0	315.4	29.7	93.4	13.8	162.8	16.8
Fig. 2B	K-12 LPM	LOQ	*nd*	LOQ	0.0	LOQ	*nd*	60.2	36.0	14.1	2.6	35.2	3.7	64.8	10.8	114.3	34.1	40.0	6.4	37.6	12.5
Fig. 2B	K-12 LPM 5mM pSer	LOQ	*nd*	1.3	0.1	LOQ	*nd*	269.2	40.3	127.0	15.3	52.5	11.1	103.8	10.2	329.7	44.8	107.7	11.9	68.3	17.2
Fig. 2B	K-12 LPM 5mM pThr	LOQ	*nd*	4.3	0.9	LOQ	*nd*	146.5	50.1	195.1	31.2	81.8	9.9	137.2	18.8	462.9	39.1	117.1	17.3	47.1	8.1
Fig. 2B	K-12 LPM 5mM pTyr	LOQ	*nd*	LOQ	*nd*	20.8	3.6	130.5	70.7	137.0	34.0	148.2	16.2	95.0	16.4	360.3	33.5	97.0	10.6	42.5	10.7
Fig. 2B	K-12 LB	LOQ	*nd*	7.6	1.1	LOQ	*nd*	12.8	4.9	6.6	0.8	149.8	12.6	292.5	23.0	315.4	29.7	93.4	13.8	162.8	16.8
Fig. 2B	K-12 LB 5mM pSer	2.5	1.3	8.1	3.4	LOQ	*nd*	10.1	3.2	7.4	1.5	125.3	43.0	230.6	20.3	121.1	32.5	70.2	6.0	61.1	19.3
Fig. 2B	K-12 LB 5mM pThr	LOQ	*nd*	11.4	1.2	LOQ	*nd*	14.1	6.4	8.1	2.5	131.5	76.8	240.8	48.3	172.1	38.3	80.1	21.1	86.8	23.6
Fig. 2B	K-12 LB 5mM pTyr	LOQ	*nd*	6.3	2.1	LOQ	*nd*	8.4	3.4	5.5	1.6	1016.7	471.5	181.7	47.9	152.5	35.3	90.3	20.7	86.3	28.2
Fig. 3A	K-12 LPM	LOQ	*nd*	LOQ	*nd*	LOQ	*nd*	60.2	36.0	14.1	2.6	35.2	3.7	64.8	10.8	114.3	34.1	40.0	6.4	37.6	12.5
Fig. 3A	K-12 LB	LOQ	*nd*	7.6	1.1	LOQ	*nd*	12.8	4.9	6.6	0.8	149.8	12.6	292.5	23.0	315.4	29.7	93.4	13.8	162.8	16.8
Fig. 3A	K-12 ΔserB LPM	308.3	35.3	LOQ	*nd*	LOQ	*nd*	39.3	8.6	15.1	1.4	28.7	2.2	39.9	2.5	115.0	7.6	26.5	1.3	44.0	2.4
Fig. 3A	K-12 ΔserB LB	7.6	0.8	5.8	1.0	LOQ	*nd*	9.4	2.7	3.9	0.9	87.1	19.4	190.6	24.8	248.9	24.7	58.1	6.4	143.0	26.8
Fig. 3B	K-12 ΔserB LPM	308.3	35.3	LOQ	*nd*	LOQ	*nd*	39.3	8.6	15.1	1.4	28.7	2.2	39.9	2.5	115.0	7.6	26.5	1.3	44.0	2.4
Fig. 3B	K-12 ΔserB LPM 5mM pSer	212.7	3.9	LOQ	*nd*	LOQ	*nd*	65.1	8.3	14.3	0.7	24.7	1.9	39.3	3.9	124.6	37.3	20.8	6.2	46.3	23.3
Fig. 3B	K-12 ΔserB LPM 5mM pThr	665.8	119.2	5.4	0.7	LOQ	*nd*	39.7	5.9	175.7	31.4	22.0	3.2	46.2	6.7	165.7	29.3	25.6	3.7	80.3	22.9
Fig. 3B	K-12 ΔserB LPM 5mM pTyr	462.5	53.4	LOQ	*nd*	82.6	8.9	21.5	4.1	16.3	1.7	41.9	5.5	25.6	4.5	109.4	21.5	15.6	1.9	57.7	20.7
Fig. 3B	K-12 ΔserB LB	7.6	0.8	5.8	1.0	LOQ	*nd*	9.4	2.7	3.9	0.9	87.1	19.4	190.6	24.8	248.9	24.7	58.1	6.4	143.0	26.8
Fig. 3B	K-12 ΔserB LB 5mM pSer	12.2	1.5	7.2	1.5	LOQ	*nd*	11.9	4.3	5.1	0.9	70.2	4.4	161.2	11.1	130.5	18.6	63.9	7.3	59.3	5.9
Fig. 3B	K-12 ΔserB LB 5mM pThr	9.2	1.1	10.8	1.0	LOQ	*nd*	10.1	3.1	6.0	0.5	86.8	18.9	186.3	9.3	152.2	21.8	71.3	7.3	66.4	12.9
Fig. 3B	K-12 ΔserB LB 5mM pTyr	7.8	1.8	8.3	2.4	LOQ	*nd*	13.5	4.8	6.2	1.4	910.8	177.3	185.8	35.0	138.4	22.2	88.4	16.6	68.4	5.0
Fig. 4A	K-12 WT LPM	LOQ	*nd*	LOQ	*nd*	LOQ	*nd*	60.2	36.0	14.1	2.6	35.2	3.7	64.8	10.8	114.3	34.1	40.0	6.4	37.6	12.5
Fig. 4A	K-12 WT LB	LOQ	*nd*	7.6	1.1	LOQ	*nd*	12.8	4.9	6.6	0.8	149.8	12.6	292.5	23.0	315.4	29.7	93.4	13.8	162.8	16.8
Fig. 4A	K-12 ΔserB LPM	308.3	35.3	LOQ	*nd*	LOQ	*nd*	39.3	8.6	15.1	1.4	28.7	2.2	39.9	2.5	115.0	7.6	26.5	1.3	44.0	2.4
Fig. 4A	K-12 ΔserB LB	7.6	0.8	5.8	1.0	LOQ	*nd*	9.4	2.7	3.9	0.9	87.1	19.4	190.6	24.8	248.9	24.7	58.1	6.4	143.0	26.8
Fig. 4A	K-12 ΔserB LPM	308.3	35.3	LOQ	*nd*	LOQ	*nd*	39.3	8.6	15.1	1.4	28.7	2.2	39.9	2.5	115.0	7.6	26.5	1.3	44.0	2.4
Fig. 4A	K-12 ΔserB LPM 5mM pSer	212.7	3.9	LOQ	*nd*	LOQ	*nd*	65.1	8.3	14.3	0.7	24.7	1.9	39.3	3.9	124.6	37.3	20.8	6.2	46.3	23.3
Fig. 4A	K-12 ΔserB LPM 5mM Ser	33.0	13.8	LOQ	*nd*	LOQ	*nd*	117.2	23.8	33.2	11.9	35.5	4.1	83.9	9.2	170.5	43.2	49.4	12.3	20.6	1.9
Fig. 4A	K-12 ΔserB LPM 5mM Ser&pSer	3.4	0.8	LOQ	*nd*	LOQ	*nd*	106.4	21.5	42.0	4.2	30.5	1.8	59.5	3.4	216.1	25.9	49.7	9.3	35.4	3.9
Fig. 4A	K-12 ΔserB LPM	308.3	35.3	LOQ	*nd*	LOQ	*nd*	39.3	8.6	15.1	1.4	28.7	2.2	39.9	2.5	115.0	7.6	26.5	1.3	44.0	2.4
Fig. 4A	K-12 ΔserB HPM	637.6	147.5	0.9	0.4	LOQ	*nd*	42.6	10.7	22.2	7.6	48.0	10.6	70.3	7.1	529.0	78.6	93.0	6.8	210.7	37.1
Fig. 4A	K-12 ΔserB LPM 5mM pThr	665.8	119.2	5.4	0.7	LOQ	*nd*	39.7	5.9	175.7	31.4	22.0	3.2	46.2	6.7	165.7	29.3	25.6	3.7	80.3	22.9
Fig. 4A	K-12 ΔserB HPM 5mM pThr	1213.6	115.9	6.9	0.9	LOQ	*nd*	14.6	1.0	11.1	1.1	20.4	1.0	26.0	2.2	125.3	3.3	16.0	1.4	123.9	9.7
	BL-21 ΔserB LB	11.6	1.4	3.0	0.6	LOQ	*nd*	10.4	2.7	8.0	0.7	108.7	3.3	236.4	29.8	497.8	48.3	94.2	14.1	14.7	3.7
	BL-21 ΔserB LB 5mM pSer	16.8	1.6	7.1	0.9	LOQ	*nd*	10.2	4.7	8.5	1.1	67.9	3.4	177.7	17.7	380.3	13.9	92.8	5.3	5.8	0.5
	BL-21 ΔserB LB 5mM pThr	16.8	2.5	7.0	1.9	LOQ	*nd*	8.9	1.5	9.1	1.2	83.1	23.8	184.4	10.8	443.5	65.5	114.3	14.1	5.8	0.9
	BL-21 ΔserB LB 5mM pTyr	15.2	2.2	4.6	1.9	4.3	2.2	7.7	1.1	8.5	0.7	246.2	17.3	169.8	15.0	398.5	19.9	98.6	6.6	7.0	1.8
	BL-21 ΔserB LPM	25.4	5.1	LOQ	*nd*	LOQ	*nd*	23.8	2.8	11.4	1.8	66.8	6.2	162.7	19.1	240.2	13.6	29.1	5.0	23.3	5.5
	BL-21 ΔserB LPM 5mM pSer	2.5	0.2	LOQ	*nd*	LOQ	*nd*	114.7	19.5	10.9	1.2	95.4	10.3	220.6	25.1	396.1	59.8	28.6	4.1	42.0	9.6
	BL-21 ΔserB LPM 5mM pThr	24.2	4.9	2.6	0.3	LOQ	*nd*	22.5	5.9	10.5	2.5	79.5	10.0	192.7	18.7	396.6	76.6	27.1	6.5	48.6	22.8
	BL-21 ΔserB LPM 5mM pTyr	24.5	3.4	LOQ	*nd*	30.5	6.67	22.9	4.4	12.6	1.7	199.3	20.4	120.5	18.5	433.5	46.0	32.1	4.7	22.4	2.2
	K-12 ΔserB LB	7.6	0.8	5.8	1.0	LOQ	0	9.4	2.7	3.9	0.9	87.1	19.4	190.6	24.8	248.9	24.7	58.1	6.4	143.0	26.8
	K-12 ΔserB LB 5mM pSer	12.2	1.47	7.2	1.5	LOQ	0	11.9	4.3	5.1	0.9	70.2	4.4	161.2	11.1	130.5	18.6	63.9	7.3	59.3	5.9
	K-12 ΔserB LB 5mM pThr	9.2	1.1	10.8	1.0	LOQ	*nd*	10.1	3.1	6.0	0.5	86.8	18.9	186.3	9.3	152.2	21.8	71.3	7.3	66.4	12.9
	K-12 ΔserB LB 5mM pTyr	7.8	1.8	8.3	2.4	LOQ	*nd*	13.5	4.8	6.2	1.4	910.8	177.3	185.8	35.0	138.4	22.2	88.4	16.6	68.4	5.0
	K-12 ΔserB LPM	308.3	35.3	LOQ	0	LOQ	0	39.3	8.6	15.1	1.4	28.7	2.2	39.9	2.5	115.0	7.6	26.5	1.3	44.0	2.4
	K-12 ΔserB LPM 5mM pSer	212.7	3.9	LOQ	*nd*	LOQ	*nd*	65.1	8.3	14.3	0.7	24.7	1.9	39.3	3.9	124.6	37.3	20.8	6.2	46.3	23.3
	K-12 ΔserB LPM 5mM pThr	665.8	119.2	5.4	0.7	LOQ	*nd*	39.7	5.9	175.7	31.4	22.0	3.2	46.2	6.7	165.7	29.3	25.6	3.7	80.3	22.9
	K-12 ΔserB LPM 5mM pTyr	462.5	53.4	LOQ	*nd*	82.6	8.9	21.5	4.1	16.3	1.7	41.9	5.5	25.6	4.5	109.4	21.5	15.6	1.9	57.7	20.7

Errors were calculated using the 95% confidence interval, n=5; LOQ=below limit of quantitation; *nd*=no data

Supplementary References

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