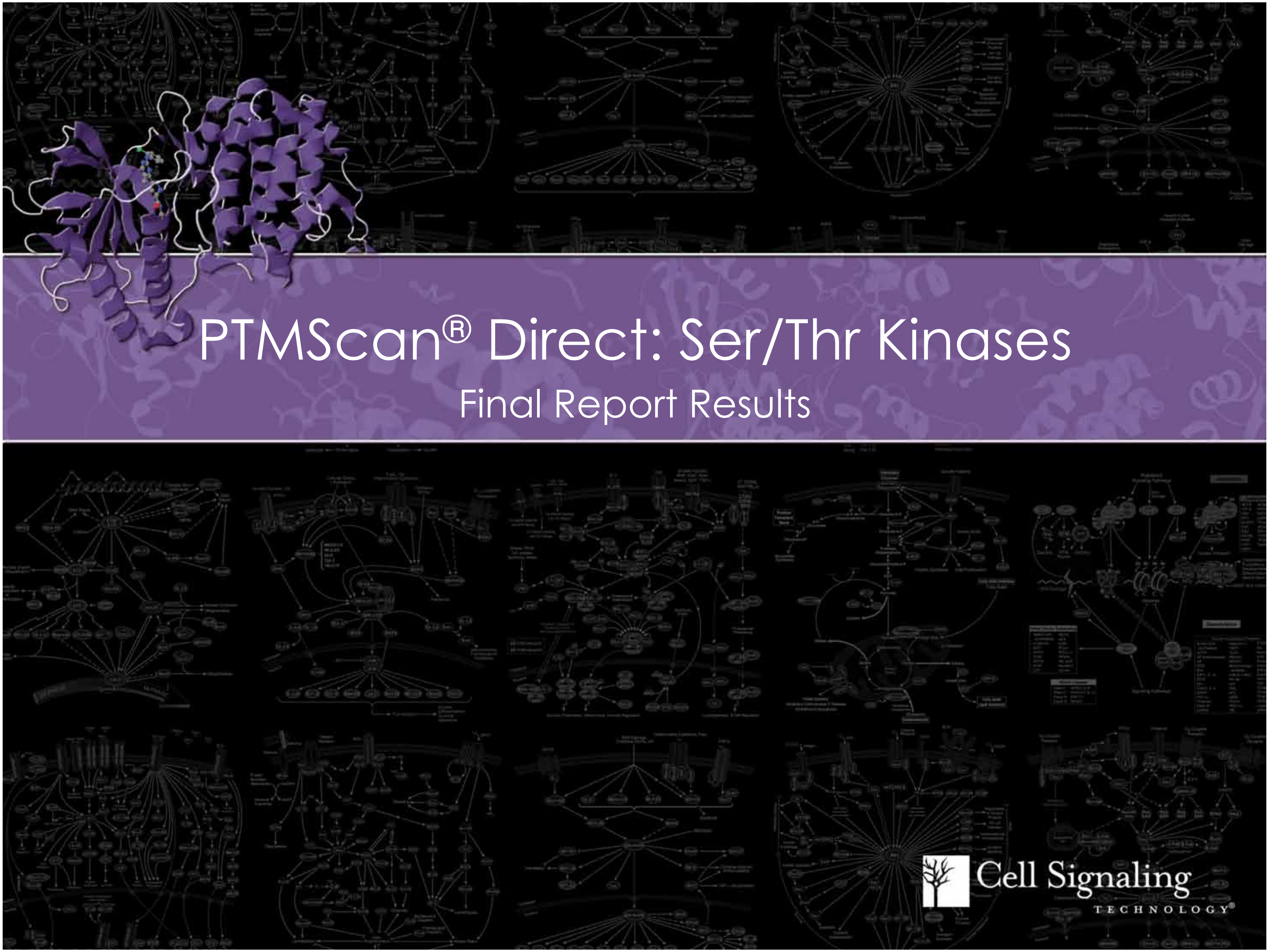
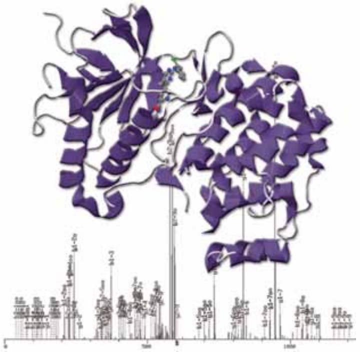


PTMScan® Direct: Ser/Thr Kinases

Final Report Results

Cell Signaling Technology®

Report Table of Contents



Significant Changes: HeLa Cells –/+ EGF

		Normalized Fold Change	Average Raw Intensity	
Protein Name	Site	EGF : Control	Control	EGF
Akt3	§472, 474	87.4	2,030	192,189
Akt3	473, 474	87.4	2,030	192,189
JNK2; JNK2 iso2; JNK2 iso3	§183, §185; §183, §185; §183, §185	8.1	4,851,520	42,785,466
JNK3; JNK3 iso2; JNK1; JNK1 iso2	§221, §223; §221, §223; §183, §185; §183, §185	7.6	3,582,605	29,401,470
GSK3A	§20	4.9	149,014	786,790
RSK2	§386	4.0	46,383	199,498
AMPKA1	§496	3.9	1,381,845	5,872,825
ERK1	§202, §204	3.6	76,024,108	299,779,023
p70S6K; p70S6K iso2	§447, §452; §424, §429	3.4	364,500	1,355,000
ERK5; ERK5 iso2	§218, §220; §219, §221	3.4	502,653	1,866,092
p70S6K; p70S6K iso2	§444, §447; §421, §424	3.4	12,474,667	45,809,266
GSK3A	§21	3.2	1,164,082	4,048,066
MEK1; MEK2	§218; §222	3.1	164,000	544,500
GSK3B; GSK3B iso2	§9; §9	2.9	890,792	2,758,587
MEK1; MEK2	§222; §226	2.8	1,150,040	3,542,525
MSK2; MSK2 iso2	§360; §360	2.7	40,527	119,674
MKK4	§257	2.7	3,001,038	8,639,953
ERK2	§185, §187	2.6	32,927,950	91,062,000
ERK2	§187, §190	2.6	32,927,950	91,062,000
MEK1; MEK2	§218, §222; §222, §226	2.5	48,996	131,359
OSR1; STLK3	§185; §233	-2.5	1,007,269	436,462
OSR1; STLK3	189; §237	-2.5	1,007,269	436,462
Chk1	307	-3.2	54,278	18,500
CDK2; CDK3	§14; §14	-3.7	1,021,685	296,307

Selected peptides that changed in abundance at least 2.5-fold with EGF treatment in HeLa cells. Green signifies fold change increases greater than 2.5, red signifies decreases. Red/Purple intensity denotes multiple identifications for 1 m/z due to ambiguous phosphorylation site localization. Blue intensity = peak area measurement. Blue = CST antibody available.

Significant Changes: HeLa Cells –/+ UV

		Fold Change	Average Raw Intensity	
Protein Name	Site	UV : Control	Control	UV
JNK3; JNK3 iso2; JNK1; JNK1 iso2	§221, §223; §221, §223; §183, §185; §183, §185	55.9	61,971	3,464,900
JNK3; JNK3 iso2; JNK1; JNK1 iso2	217, §223; 217, §223; 179, §185; 179, §185	53.4	35,000	1,870,000
JNK2; JNK2 iso2; JNK2 iso3	§183, §185; §183, §185; §183, §185	44.9	3,280,290	147,311,119
MKK4	§257, §261	28.4	4,835	137,191
MKK4	§257	24.6	2,701,006	66,311,558
MSK1	§376	23.3	6,697	156,288
MKK4	§261	11.6	4,131	47,885
JNK2; JNK2 iso2; JNK2 iso3	§183, 188; §183, 188; §183, 188	10.0	2,380	23,790
MKK3	212, §222	8.3	12,672	104,977
VRK1	§378	8.1	4,075	32,985
ZAK	§648, §649	7.9	614,387	4,874,404
MKK6; MKK6 iso2	§207, §211; §151, §155	7.9	648,974	5,102,919
MAPKAPK3	§313	7.7	404,399	3,093,923
ATM; LOC651610	§1981; 1859	7.6	1,148,442	8,724,508
MSK2; MSK2 iso2	§360; §360	7.6	10,138	76,800
dCK	§13	7.3	3,910	28,597
MAPKAPK2	§334	6.5	10,424,377	67,766,696
p70S6Kb	219	6.0	7,600	45,968
BRD2	256	5.6	243,509	1,352,156
p70S6K; p70S6K iso2	§441, §444, §447; §418, §421, §424	5.3	310,458	1,652,885
p70S6K; p70S6K iso2	§441, §444, §452; §418, §421, §429	5.3	310,458	1,652,885
p70S6K; p70S6K iso2	§441, §447, §452; §418, §424, §429	5.3	310,458	1,652,885
p70S6K; p70S6K iso2	§444, §447, §452; §421, §424, §429	5.3	310,458	1,652,885
p70S6K; p70S6K iso2	§444, §447; §421, §424	5.2	507,763	2,654,545

Selected peptides that increased in abundance at least 2.5-fold with UV treatment in HeLa cells. Green signifies fold change increases greater than 2.5. Red intensity denotes multiple identifications for 1 m/z due to ambiguous phosphorylation site localization. Blue intensity = peak area measurement. Blue = CST antibody available.

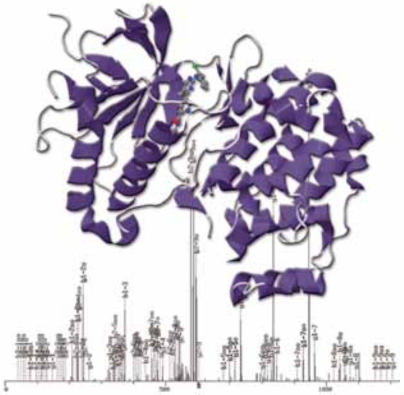
Summary of Results

HeLa cells with and without EGF treatment, H1650 cells with and without Phenformin treatment, and HeLa cells with and without UV treatment were subjected to PTMScan® analysis using the PTMScan® Direct Ser/Thr Kinases Reagent.

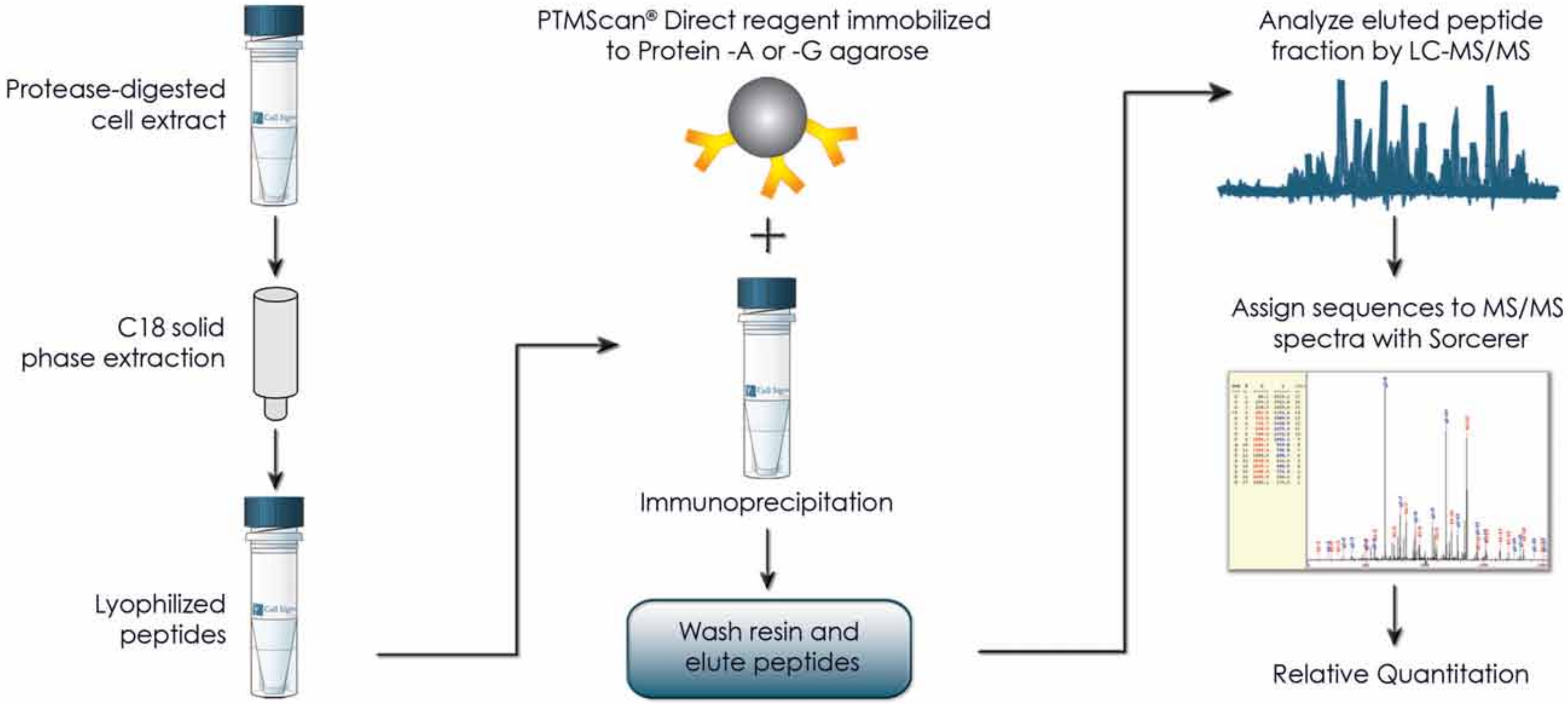
136 non-redundant peptides (400 redundant peptides) were identified in HeLa cells –/+ EGF.
26 of the 136 peptides changed in abundance at least 2.5-fold with EGF treatment.

181 non-redundant peptides (594 redundant peptides) were identified in H1650 cells –/+ Phenformin.
43 of the 181 peptides changed in abundance at least 2.5-fold with compound treatment.

186 non-redundant peptides (592 redundant peptides) were identified in HeLa cells –/+ UV.
52 of the 186 peptides changed in abundance at least 2.5-fold with UV treatment.



PTMScan® Direct Method



Protease-digested cell extract

C18 solid phase extraction

Lyophilized peptides

PTMScan® Direct reagent immobilized to Protein -A or -G agarose

+

Immunoprecipitation

Wash resin and elute peptides

Analyze eluted peptide fraction by LC-MS/MS

Assign sequences to MS/MS spectra with Sorcerer

Relative Quantitation

Method Summary

Phosphorylated peptide enrichment using the following antibodies: PTMScan® Direct: Ser/Thr Kinases Reagent

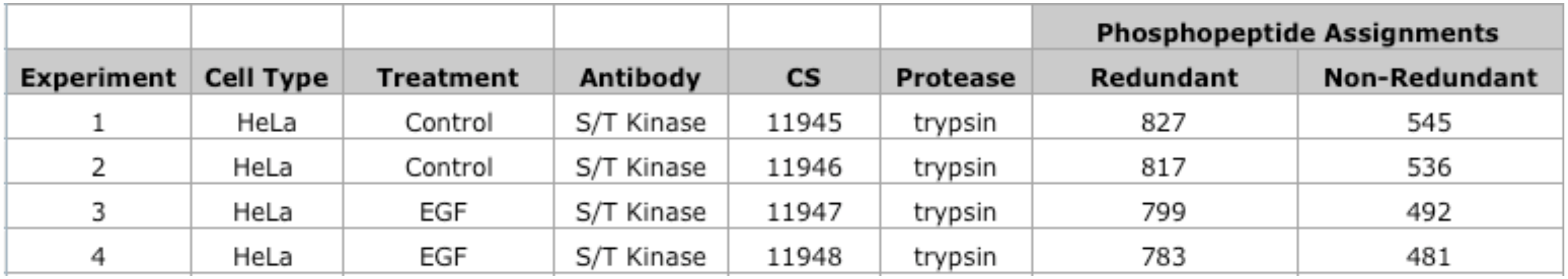
LC-MS/MS analysis (LTQ-Orbitrap-CID): Sorcerer search results

Label-free quantitation from phosphorylated peptide intensities (Tables 1 & 2).

Qualitative Results Summary

Cells		Treatments		Curation Sets (CS)	Analysis
HeLa	▸	Control	▸	CS 11945, 11946	**LTQ-Orbitrap** **LC-MS/MS CID**
		EGF	▸	CS 11947, 11948	

2 samples, duplicate runs = 4 LC-MS/MS experiments



						Phosphopeptide Assignments	
Experiment	**Cell Type**	**Treatment**	**Antibody**	**CS**	**Protease**	**Redundant**	**Non-Redundant**
1	HeLa	Control	S/T Kinase	11945	trypsin	827	545
2	HeLa	Control	S/T Kinase	11946	trypsin	817	536
3	HeLa	EGF	S/T Kinase	11947	trypsin	799	492
4	HeLa	EGF	S/T Kinase	11948	trypsin	783	481

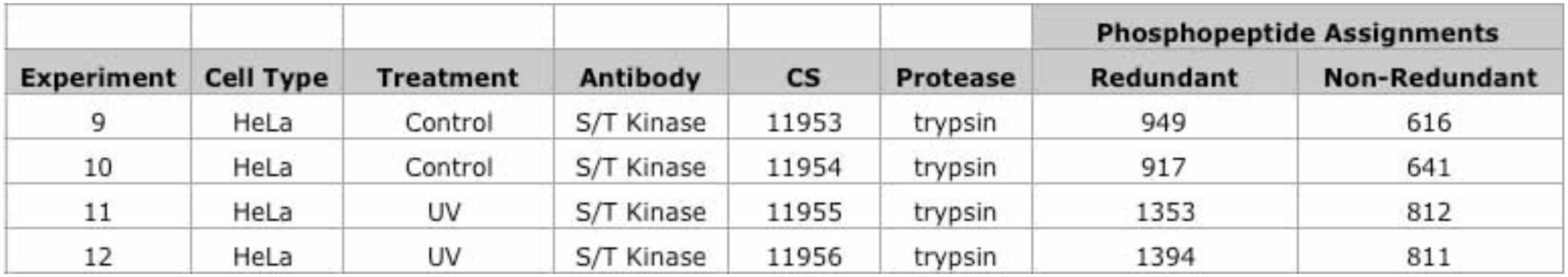
A total of **400** redundant peptide assignments (Table 1 Details Tab) to **136** non-redundant peptides (Table 1 Summary Tab) using the PTMScan® Direct: Ser/Thr Kinases Reagent.

A 5% default false positive rate was used to filter the SORCERER results.

Qualitative Results Summary

Cells	Treatments	Curation Sets (CS)	Analysis
HeLa ▸	Control ▸	CS 11953, 11954	**LTQ-Orbitrap** **LC-MS/MS CID**
	UV ▸	CS 11955, 11956	

2 samples, duplicate runs = 4 LC-MS/MS experiments



						Phosphopeptide Assignments	
Experiment	**Cell Type**	**Treatment**	**Antibody**	**CS**	**Protease**	**Redundant**	**Non-Redundant**
9	HeLa	Control	S/T Kinase	11953	trypsin	949	616
10	HeLa	Control	S/T Kinase	11954	trypsin	917	641
11	HeLa	UV	S/T Kinase	11955	trypsin	1353	812
12	HeLa	UV	S/T Kinase	11956	trypsin	1394	811

A total of **592** redundant peptide assignments (Table 3 Details Tab) to **186** non-redundant peptides (Table 3 Summary Tab) using the PTMScan® Direct: Ser/Thr Kinases Reagent.

A 5% default false positive rate was used to filter the SORCERER results.

Table Overview

Tables consist of 5 different sheets:

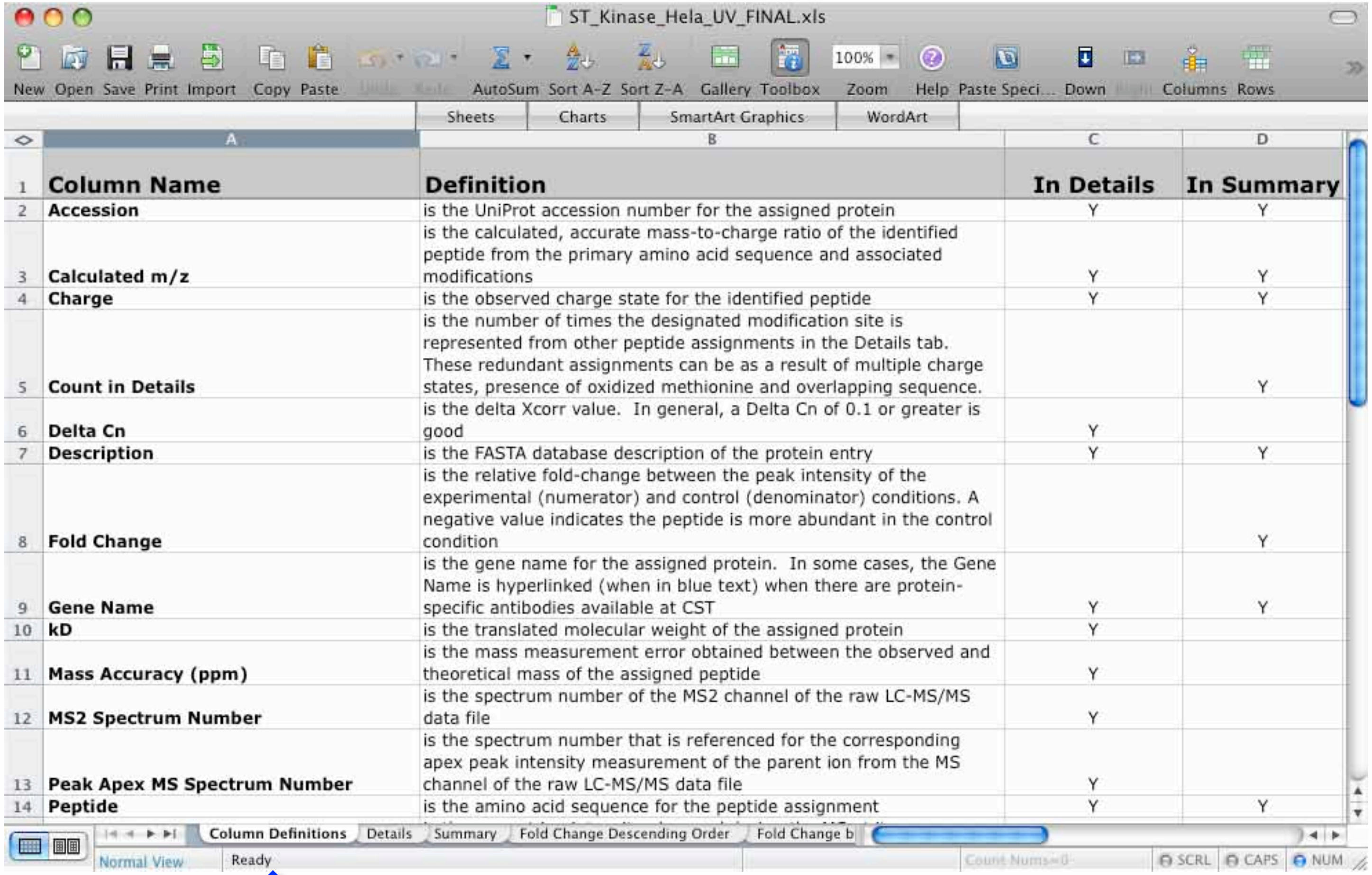
Column Definitions, Details (qualitative), Summary (quantitative), Fold Change Ascending Order, and Fold Change by Protein Type

Each sheet is accessed by clicking on the tabs located at the bottom of table window.

(More examples can be seen highlighted in **blue boxes** on the following slides).

Tables open to the Fold Change Descending Order Sheet.

Column Definitions Sheet

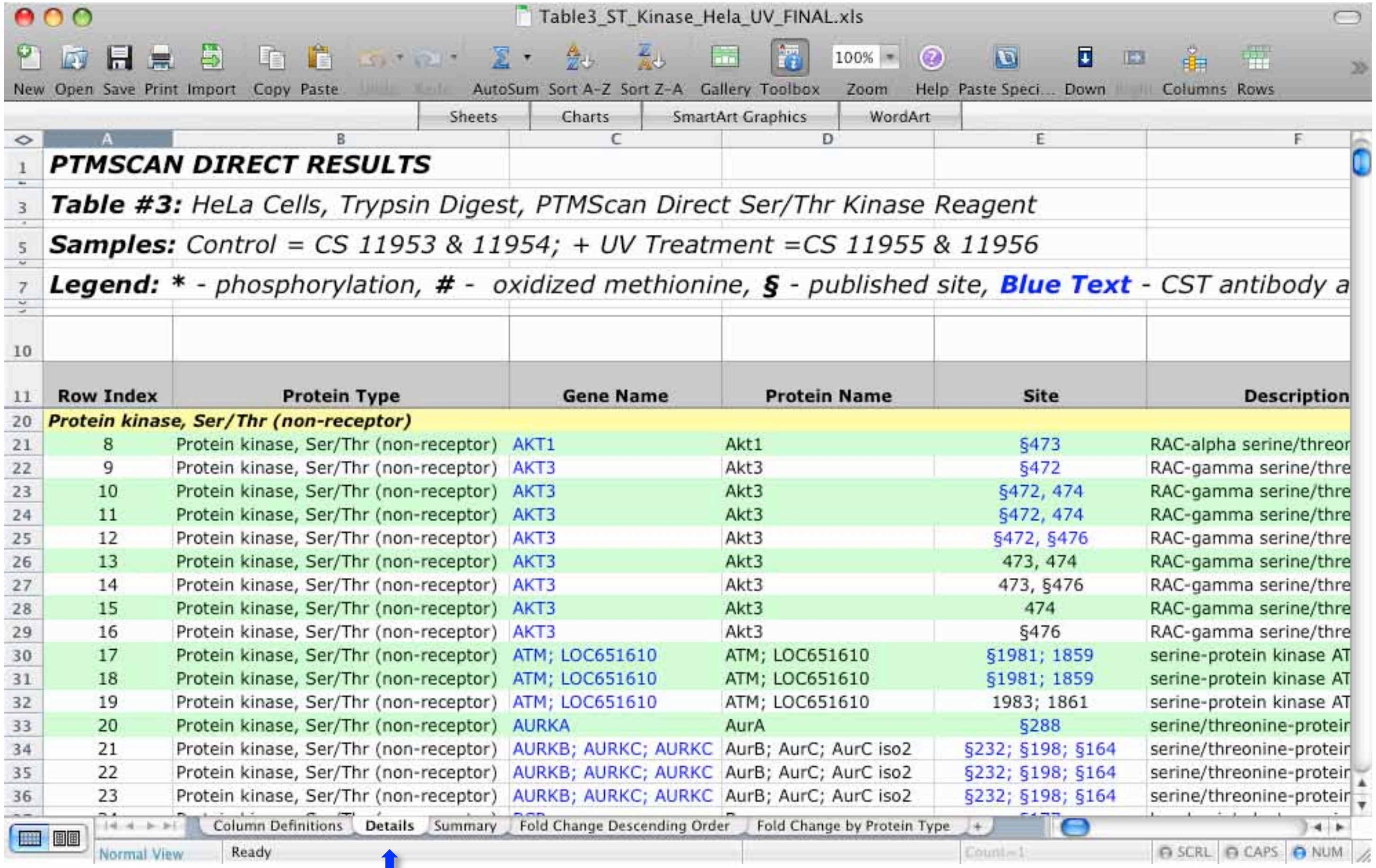


Column Name	Definition	In Details	In Summary
Accession	is the UniProt accession number for the assigned protein	Y	Y
Calculated m/z	is the calculated, accurate mass-to-charge ratio of the identified peptide from the primary amino acid sequence and associated modifications	Y	Y
Charge	is the observed charge state for the identified peptide	Y	Y
Count in Details	is the number of times the designated modification site is represented from other peptide assignments in the Details tab. These redundant assignments can be as a result of multiple charge states, presence of oxidized methionine and overlapping sequence.		Y
Delta Cn	is the delta Xcorr value. In general, a Delta Cn of 0.1 or greater is good	Y	
Description	is the FASTA database description of the protein entry	Y	Y
Fold Change	is the relative fold-change between the peak intensity of the experimental (numerator) and control (denominator) conditions. A negative value indicates the peptide is more abundant in the control condition		Y
Gene Name	is the gene name for the assigned protein. In some cases, the Gene Name is hyperlinked (when in blue text) when there are protein-specific antibodies available at CST	Y	Y
kD	is the translated molecular weight of the assigned protein	Y	
Mass Accuracy (ppm)	is the mass measurement error obtained between the observed and theoretical mass of the assigned peptide	Y	
MS2 Spectrum Number	is the spectrum number of the MS2 channel of the raw LC-MS/MS data file	Y	
Peak Apex MS Spectrum Number	is the spectrum number that is referenced for the corresponding apex peak intensity measurement of the parent ion from the MS channel of the raw LC-MS/MS data file	Y	
Peptide	is the amino acid sequence for the peptide assignment	Y	Y

Click tab to access sheets.

Column Definitions Sheets contain description of column headers in data tables.

Details Sheet



PTMSCAN DIRECT RESULTS

Table #3: *HeLa Cells, Trypsin Digest, PTMScan Direct Ser/Thr Kinase Reagent*

Samples: *Control = CS 11953 & 11954; + UV Treatment =CS 11955 & 11956*

Legend: ** - phosphorylation, # - oxidized methionine, § - published site,* ***Blue Text*** *- CST antibody a*

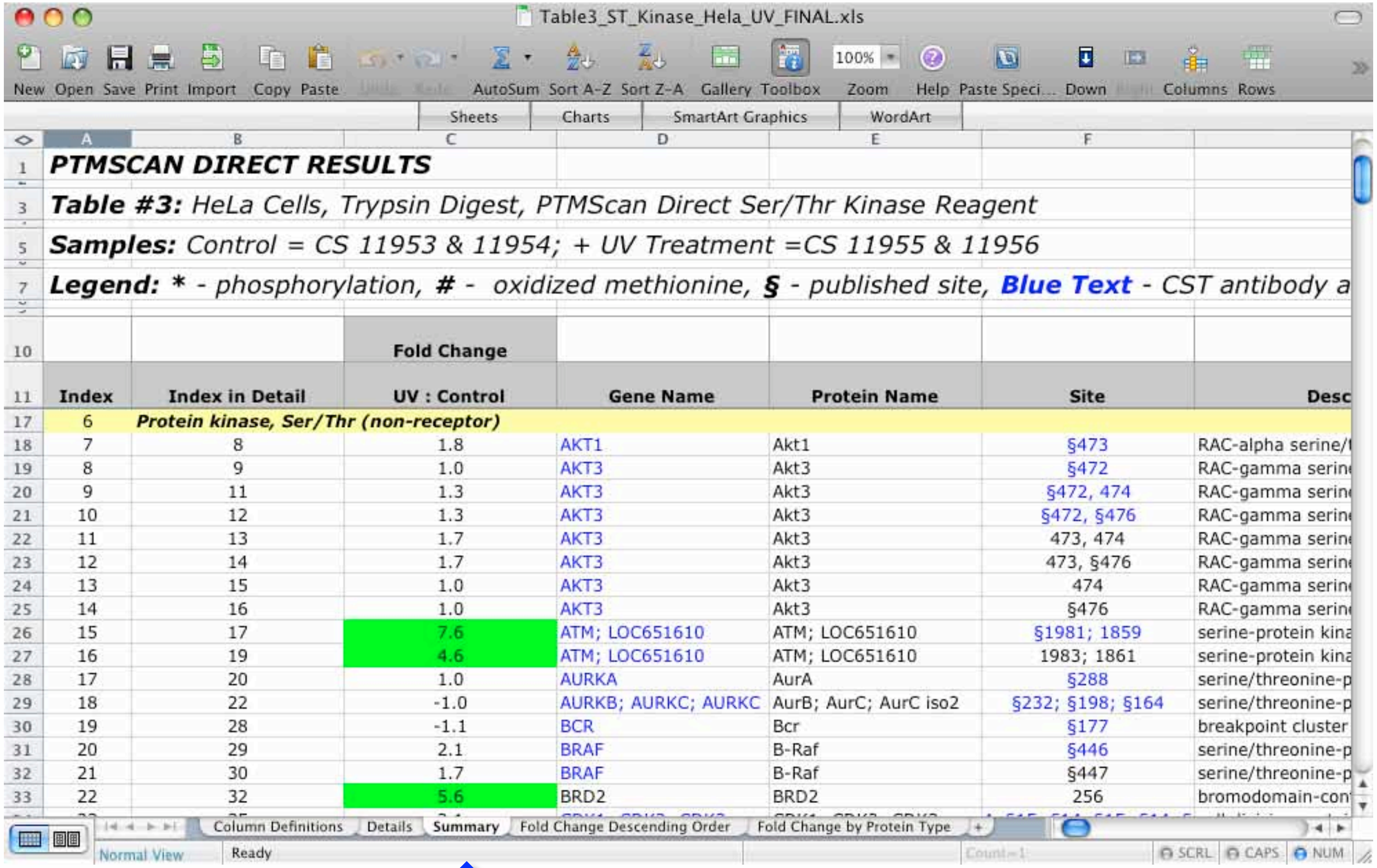
	Row Index	Protein Type	Gene Name	Protein Name	Site	Description
20	***Protein kinase, Ser/Thr (non-receptor)***					
21	8	Protein kinase, Ser/Thr (non-receptor)	AKT1	Akt1	§473	RAC-alpha serine/threor
22	9	Protein kinase, Ser/Thr (non-receptor)	AKT3	Akt3	§472	RAC-gamma serine/thre
23	10	Protein kinase, Ser/Thr (non-receptor)	AKT3	Akt3	§472, 474	RAC-gamma serine/thre
24	11	Protein kinase, Ser/Thr (non-receptor)	AKT3	Akt3	§472, 474	RAC-gamma serine/thre
25	12	Protein kinase, Ser/Thr (non-receptor)	AKT3	Akt3	§472, §476	RAC-gamma serine/thre
26	13	Protein kinase, Ser/Thr (non-receptor)	AKT3	Akt3	473, 474	RAC-gamma serine/thre
27	14	Protein kinase, Ser/Thr (non-receptor)	AKT3	Akt3	473, §476	RAC-gamma serine/thre
28	15	Protein kinase, Ser/Thr (non-receptor)	AKT3	Akt3	474	RAC-gamma serine/thre
29	16	Protein kinase, Ser/Thr (non-receptor)	AKT3	Akt3	§476	RAC-gamma serine/thre
30	17	Protein kinase, Ser/Thr (non-receptor)	ATM; LOC651610	ATM; LOC651610	§1981; 1859	serine-protein kinase AT
31	18	Protein kinase, Ser/Thr (non-receptor)	ATM; LOC651610	ATM; LOC651610	§1981; 1859	serine-protein kinase AT
32	19	Protein kinase, Ser/Thr (non-receptor)	ATM; LOC651610	ATM; LOC651610	1983; 1861	serine-protein kinase AT
33	20	Protein kinase, Ser/Thr (non-receptor)	AURKA	AurA	§288	serine/threonine-protein
34	21	Protein kinase, Ser/Thr (non-receptor)	AURKB; AURKC; AURKC	AurB; AurC; AurC iso2	§232; §198; §164	serine/threonine-protein
35	22	Protein kinase, Ser/Thr (non-receptor)	AURKB; AURKC; AURKC	AurB; AurC; AurC iso2	§232; §198; §164	serine/threonine-protein
36	23	Protein kinase, Ser/Thr (non-receptor)	AURKB; AURKC; AURKC	AurB; AurC; AurC iso2	§232; §198; §164	serine/threonine-protein

Click tab to access sheets.

Details Sheets (qualitative) contain a redundant list of all peptides identified in the study with their accompanying Sorcerer metrics. The Details Sheet includes all information from the Summary Sheet with additional data for each peptide.

Summary Sheet

Table Header contain information about the study and legend text.



PTMSCAN DIRECT RESULTS

Table #3: *HeLa Cells, Trypsin Digest, PTMScan Direct Ser/Thr Kinase Reagent*

Samples: *Control = CS 11953 & 11954; + UV Treatment =CS 11955 & 11956*

Legend: ** - phosphorylation, # - oxidized methionine, § - published site,* ***Blue Text*** *- CST antibody a*

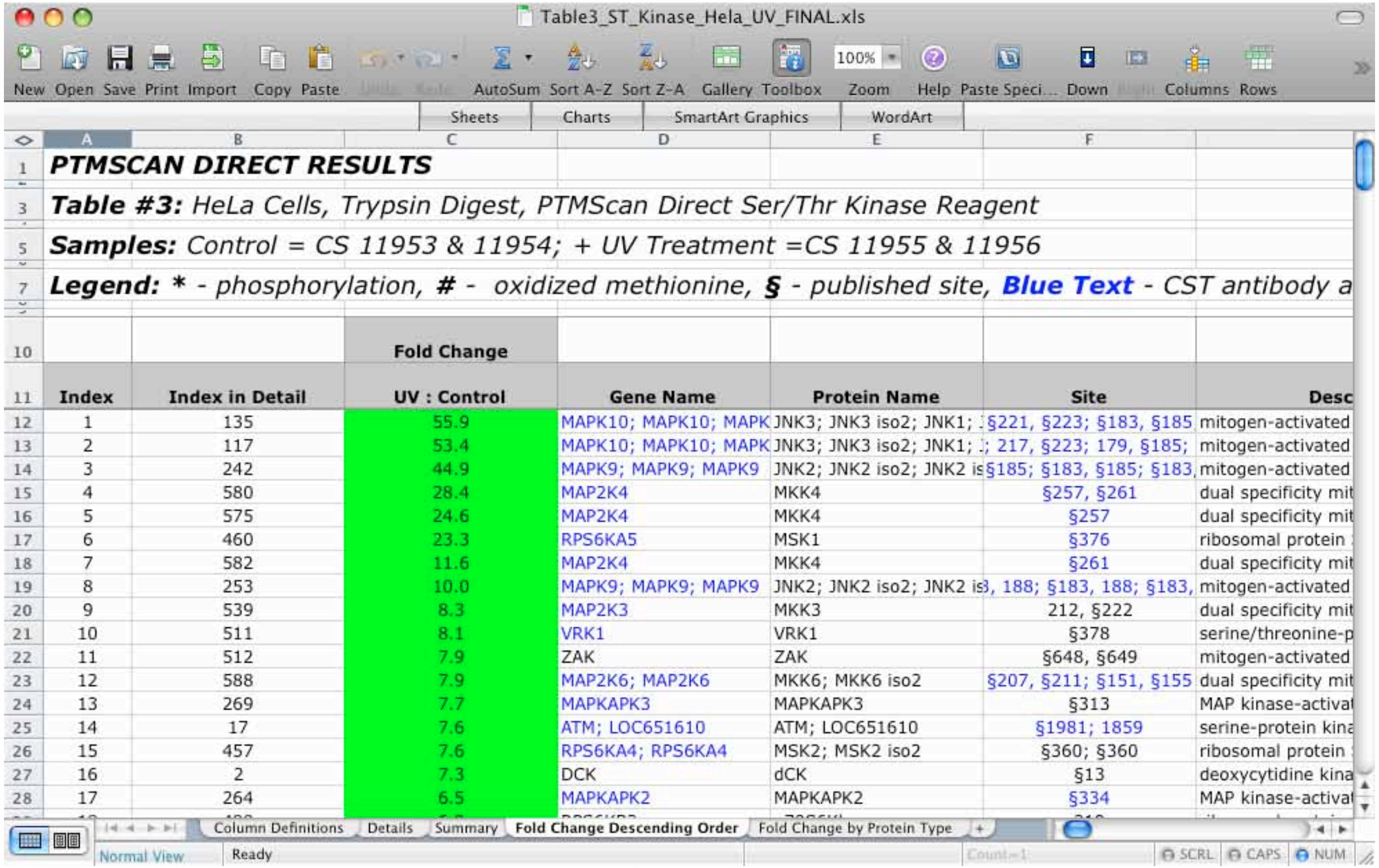
	Index	Index in Detail	Fold Change UV : Control	Gene Name	Protein Name	Site	Desc
17	6	***Protein kinase, Ser/Thr (non-receptor)***					
18	7	8	1.8	AKT1	Akt1	§473	RAC-alpha serine/t
19	8	9	1.0	AKT3	Akt3	§472	RAC-gamma serin
20	9	11	1.3	AKT3	Akt3	§472, 474	RAC-gamma serin
21	10	12	1.3	AKT3	Akt3	§472, §476	RAC-gamma serin
22	11	13	1.7	AKT3	Akt3	473, 474	RAC-gamma serin
23	12	14	1.7	AKT3	Akt3	473, §476	RAC-gamma serin
24	13	15	1.0	AKT3	Akt3	474	RAC-gamma serin
25	14	16	1.0	AKT3	Akt3	§476	RAC-gamma serin
26	15	17	7.6	ATM; LOC651610	ATM; LOC651610	§1981; 1859	serine-protein kina
27	16	19	4.6	ATM; LOC651610	ATM; LOC651610	1983; 1861	serine-protein kina
28	17	20	1.0	AURKA	AurA	§288	serine/threonine-p
29	18	22	-1.0	AURKB; AURKC; AURKC	AurB; AurC; AurC iso2	§232; §198; §164	serine/threonine-p
30	19	28	-1.1	BCR	Bcr	§177	breakpoint cluster
31	20	29	2.1	BRAF	B-Raf	§446	serine/threonine-p
32	21	30	1.7	BRAF	B-Raf	§447	serine/threonine-p
33	22	32	5.6	BRD2	BRD2	256	bromodomain-con

Click tab to access sheets.

Summary Sheets (quantitative) contain a non-redundant list of sites quantified in the study.

Fold Change Descending Order Sheet

Table Header contain information about the study and legend text.



PTMSCAN DIRECT RESULTS

***Table #3:** HeLa Cells, Trypsin Digest, PTMScan Direct Ser/Thr Kinase Reagent*

***Samples:** Control = CS 11953 & 11954; + UV Treatment =CS 11955 & 11956*

***Legend:** * - phosphorylation, # - oxidized methionine, § - published site, **Blue Text** - CST antibody a*

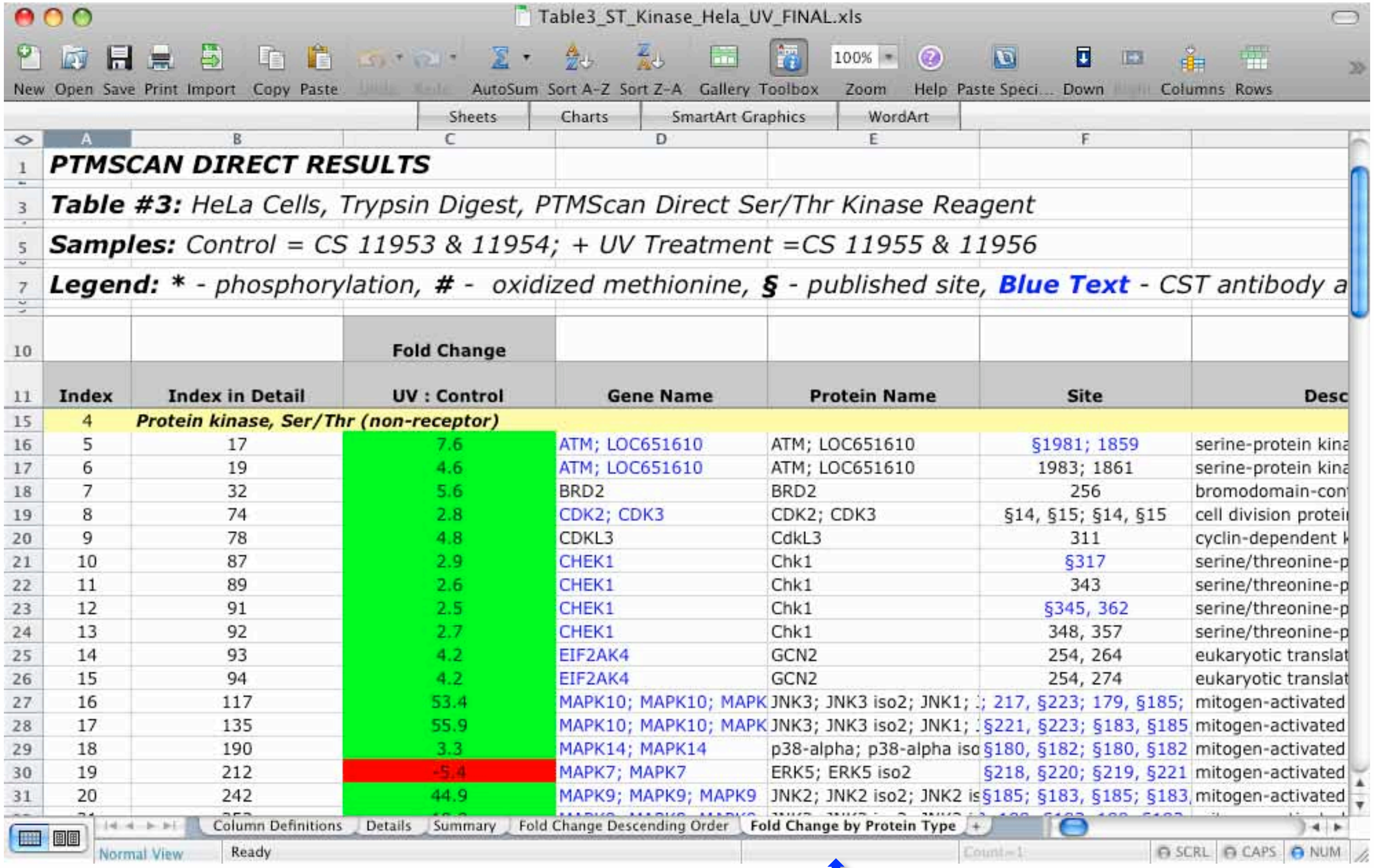
Index	Index in Detail	Fold Change UV : Control	Gene Name	Protein Name	Site	Desc
1	135	55.9	MAPK10; MAPK10; MAPK	JNK3; JNK3 iso2; JNK1;	§221, §223; §183, §185	mitogen-activated
2	117	53.4	MAPK10; MAPK10; MAPK	JNK3; JNK3 iso2; JNK1;	; 217, §223; 179, §185;	mitogen-activated
3	242	44.9	MAPK9; MAPK9; MAPK9	JNK2; JNK2 iso2; JNK2 is	§185; §183, §185; §183,	mitogen-activated
4	580	28.4	MAP2K4	MKK4	§257, §261	dual specificity mit
5	575	24.6	MAP2K4	MKK4	§257	dual specificity mit
6	460	23.3	RPS6KA5	MSK1	§376	ribosomal protein
7	582	11.6	MAP2K4	MKK4	§261	dual specificity mit
8	253	10.0	MAPK9; MAPK9; MAPK9	JNK2; JNK2 iso2; JNK2 is	3, 188; §183, 188; §183,	mitogen-activated
9	539	8.3	MAP2K3	MKK3	212, §222	dual specificity mit
10	511	8.1	VRK1	VRK1	§378	serine/threonine-p
11	512	7.9	ZAK	ZAK	§648, §649	mitogen-activated
12	588	7.9	MAP2K6; MAP2K6	MKK6; MKK6 iso2	§207, §211; §151, §155	dual specificity mit
13	269	7.7	MAPKAPK3	MAPKAPK3	§313	MAP kinase-activat
14	17	7.6	ATM; LOC651610	ATM; LOC651610	§1981; 1859	serine-protein kina
15	457	7.6	RPS6KA4; RPS6KA4	MSK2; MSK2 iso2	§360; §360	ribosomal protein
16	2	7.3	DCK	dCK	§13	deoxycytidine kina
17	264	6.5	MAPKAPK2	MAPKAPK2	§334	MAP kinase-activat

Click tab to access sheets.

Fold Change Descending Order Sheets contain a non-redundant list of sites quantified in the study organized by maximum fold change across samples.

Fold Change by Protein Type Sheet

Table Header contain information about the study and legend text.



1 ***PTMSCAN DIRECT RESULTS***

3 ***Table #3:*** *HeLa Cells, Trypsin Digest, PTMScan Direct Ser/Thr Kinase Reagent*

5 ***Samples:*** *Control = CS 11953 & 11954; + UV Treatment =CS 11955 & 11956*

7 ***Legend:*** ***** *- phosphorylation,* **#** *- oxidized methionine,* **§** *- published site,* ***Blue Text*** *- CST antibody a*

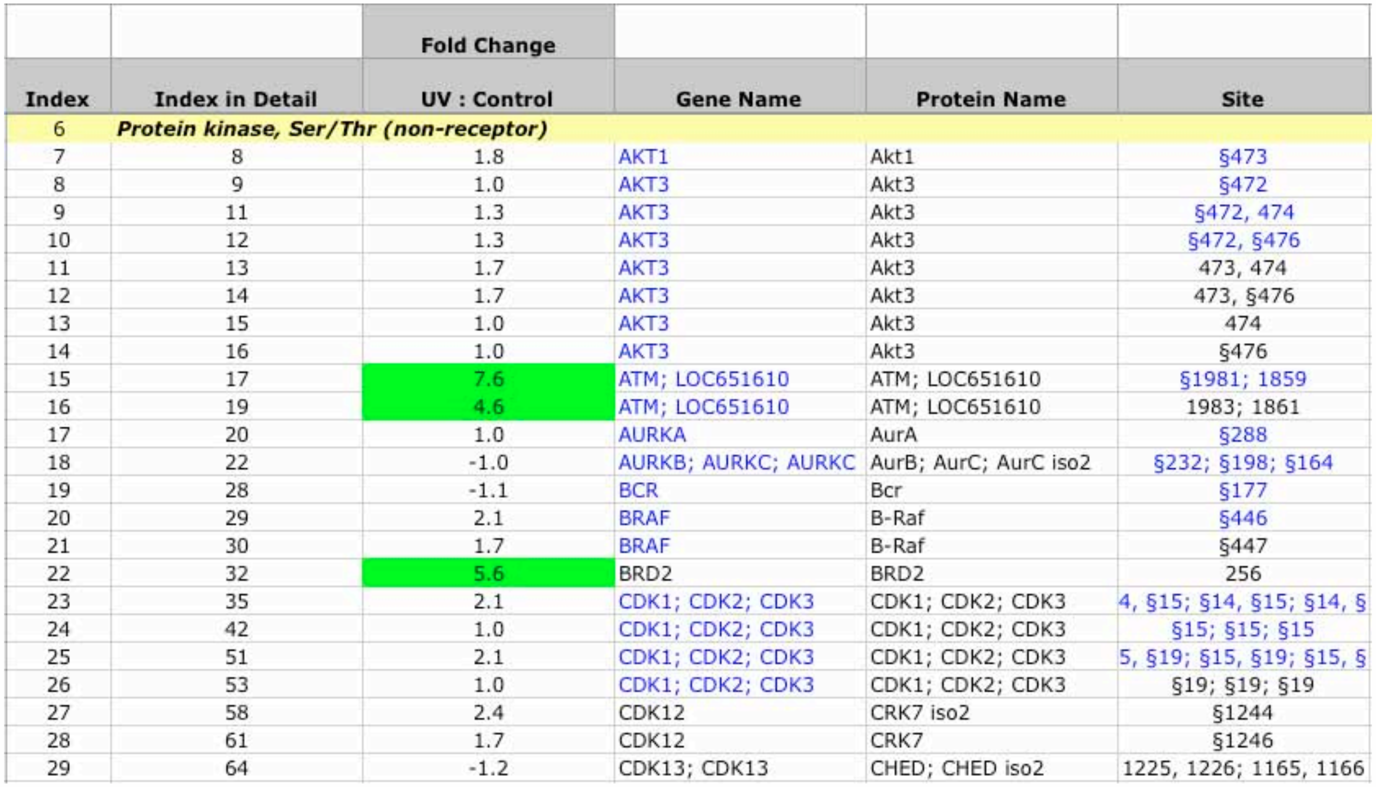
			Fold Change				
11	**Index**	**Index in Detail**	**UV : Control**	**Gene Name**	**Protein Name**	**Site**	**Desc**
15	4	***Protein kinase, Ser/Thr (non-receptor)***					
16	5	17	🟩 7.6	ATM; LOC651610	ATM; LOC651610	§1981; 1859	serine-protein kina
17	6	19	🟩 4.6	ATM; LOC651610	ATM; LOC651610	1983; 1861	serine-protein kina
18	7	32	🟩 5.6	BRD2	BRD2	256	bromodomain-con
19	8	74	🟩 2.8	CDK2; CDK3	CDK2; CDK3	§14, §15; §14, §15	cell division protei
20	9	78	🟩 4.8	CDKL3	CdkL3	311	cyclin-dependent k
21	10	87	🟩 2.9	CHEK1	Chk1	§317	serine/threonine-p
22	11	89	🟩 2.6	CHEK1	Chk1	343	serine/threonine-p
23	12	91	🟩 2.5	CHEK1	Chk1	§345, 362	serine/threonine-p
24	13	92	🟩 2.7	CHEK1	Chk1	348, 357	serine/threonine-p
25	14	93	🟩 4.2	EIF2AK4	GCN2	254, 264	eukaryotic translat
26	15	94	🟩 4.2	EIF2AK4	GCN2	254, 274	eukaryotic translat
27	16	117	🟩 53.4	MAPK10; MAPK10; MAPK	JNK3; JNK3 iso2; JNK1;	; 217, §223; 179, §185;	mitogen-activated
28	17	135	🟩 55.9	MAPK10; MAPK10; MAPK	JNK3; JNK3 iso2; JNK1;	§221, §223; §183, §185	mitogen-activated
29	18	190	🟩 3.3	MAPK14; MAPK14	p38-alpha; p38-alpha iso	§180, §182; §180, §182	mitogen-activated
30	19	212	🟥 -5.4	MAPK7; MAPK7	ERK5; ERK5 iso2	§218, §220; §219, §221	mitogen-activated
31	20	242	🟩 44.9	MAPK9; MAPK9; MAPK9	JNK2; JNK2 iso2; JNK2 is	§185; §183, §185; §183,	mitogen-activated

Click tab to access sheets.

Fold Change by Protein Type Sheets provide the overall quantitative results sorted by protein type containing only those sites that increase above 2.5-fold (**GREEN**) and those sites that decrease below 2.5-fold (**RED**).

Summary Sheet

Index
The table is indexed for easy re-sorting to original order.



		Fold Change			
Index	**Index in Detail**	**UV : Control**	**Gene Name**	**Protein Name**	**Site**
6	***Protein kinase, Ser/Thr (non-receptor)***				
7	8	1.8	AKT1	Akt1	§473
8	9	1.0	AKT3	Akt3	§472
9	11	1.3	AKT3	Akt3	§472, 474
10	12	1.3	AKT3	Akt3	§472, §476
11	13	1.7	AKT3	Akt3	473, 474
12	14	1.7	AKT3	Akt3	473, §476
13	15	1.0	AKT3	Akt3	474
14	16	1.0	AKT3	Akt3	§476
15	17	7.6	ATM; LOC651610	ATM; LOC651610	§1981; 1859
16	19	4.6	ATM; LOC651610	ATM; LOC651610	1983; 1861
17	20	1.0	AURKA	AurA	§288
18	22	-1.0	AURKB; AURKC; AURKC	AurB; AurC; AurC iso2	§232; §198; §164
19	28	-1.1	BCR	Bcr	§177
20	29	2.1	BRAF	B-Raf	§446
21	30	1.7	BRAF	B-Raf	§447
22	32	5.6	BRD2	BRD2	256
23	35	2.1	CDK1; CDK2; CDK3	CDK1; CDK2; CDK3	4, §15; §14, §15; §14, §
24	42	1.0	CDK1; CDK2; CDK3	CDK1; CDK2; CDK3	§15; §15; §15
25	51	2.1	CDK1; CDK2; CDK3	CDK1; CDK2; CDK3	5, §19; §15, §19; §15, §
26	53	1.0	CDK1; CDK2; CDK3	CDK1; CDK2; CDK3	§19; §19; §19
27	58	2.4	CDK12	CRK7 iso2	§1244
28	61	1.7	CDK12	CRK7	§1246
29	64	-1.2	CDK13; CDK13	CHED; CHED iso2	1225, 1226; 1165, 1166

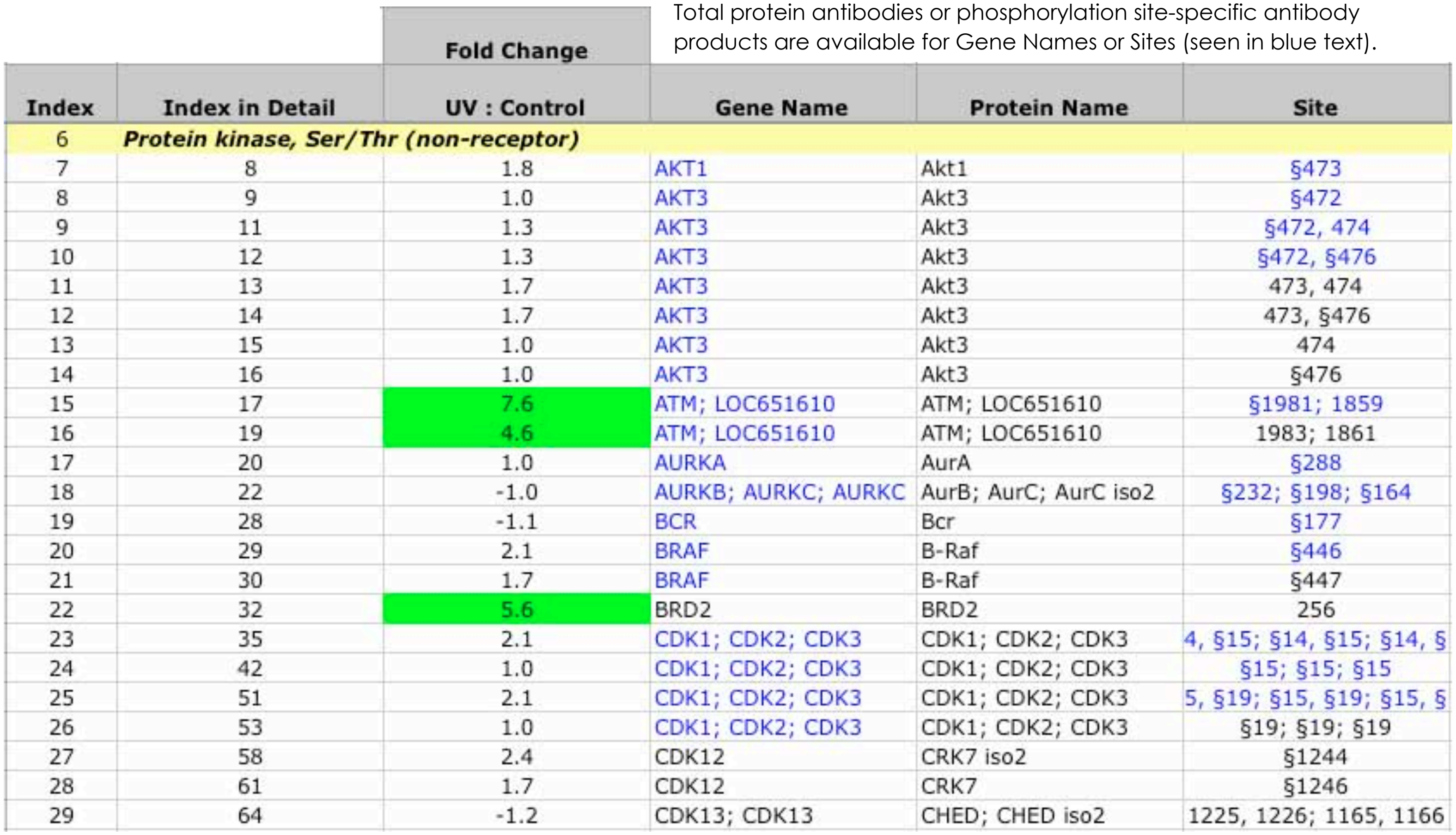
Index in Detail
Index numbers from the Details Sheet is included for easy lookup of peptides between tabs.

Fold Change Redundancy is eliminated from the Details Table to provide a summary of the quantitative results. Fold changes are expressed as the ratio of UV treated to Control peptide ion abundance in each cell line.

Green signifies sites that increase at least 2.5-fold. **Red** signifies sites that decrease at least 2.5-fold.

Summary Sheet

Total protein antibodies or phosphorylation site-specific antibody products are available for Gene Names or Sites (seen in blue text).



		Fold Change			
Index	**Index in Detail**	**UV : Control**	**Gene Name**	**Protein Name**	**Site**
6	***Protein kinase, Ser/Thr (non-receptor)***				
7	8	1.8	AKT1	Akt1	§473
8	9	1.0	AKT3	Akt3	§472
9	11	1.3	AKT3	Akt3	§472, 474
10	12	1.3	AKT3	Akt3	§472, §476
11	13	1.7	AKT3	Akt3	473, 474
12	14	1.7	AKT3	Akt3	473, §476
13	15	1.0	AKT3	Akt3	474
14	16	1.0	AKT3	Akt3	§476
15	17	🟩 7.6	ATM; LOC651610	ATM; LOC651610	§1981; 1859
16	19	🟩 4.6	ATM; LOC651610	ATM; LOC651610	1983; 1861
17	20	1.0	AURKA	AurA	§288
18	22	-1.0	AURKB; AURKC; AURKC	AurB; AurC; AurC iso2	§232; §198; §164
19	28	-1.1	BCR	Bcr	§177
20	29	2.1	BRAF	B-Raf	§446
21	30	1.7	BRAF	B-Raf	§447
22	32	🟩 5.6	BRD2	BRD2	256
23	35	2.1	CDK1; CDK2; CDK3	CDK1; CDK2; CDK3	4, §15; §14, §15; §14, §
24	42	1.0	CDK1; CDK2; CDK3	CDK1; CDK2; CDK3	§15; §15; §15
25	51	2.1	CDK1; CDK2; CDK3	CDK1; CDK2; CDK3	5, §19; §15, §19; §15, §
26	53	1.0	CDK1; CDK2; CDK3	CDK1; CDK2; CDK3	§19; §19; §19
27	58	2.4	CDK12	CRK7 iso2	§1244
28	61	1.7	CDK12	CRK7	§1246
29	64	-1.2	CDK13; CDK13	CHED; CHED iso2	1225, 1226; 1165, 1166

Novel sites of phosphorylation.

§ Published sites

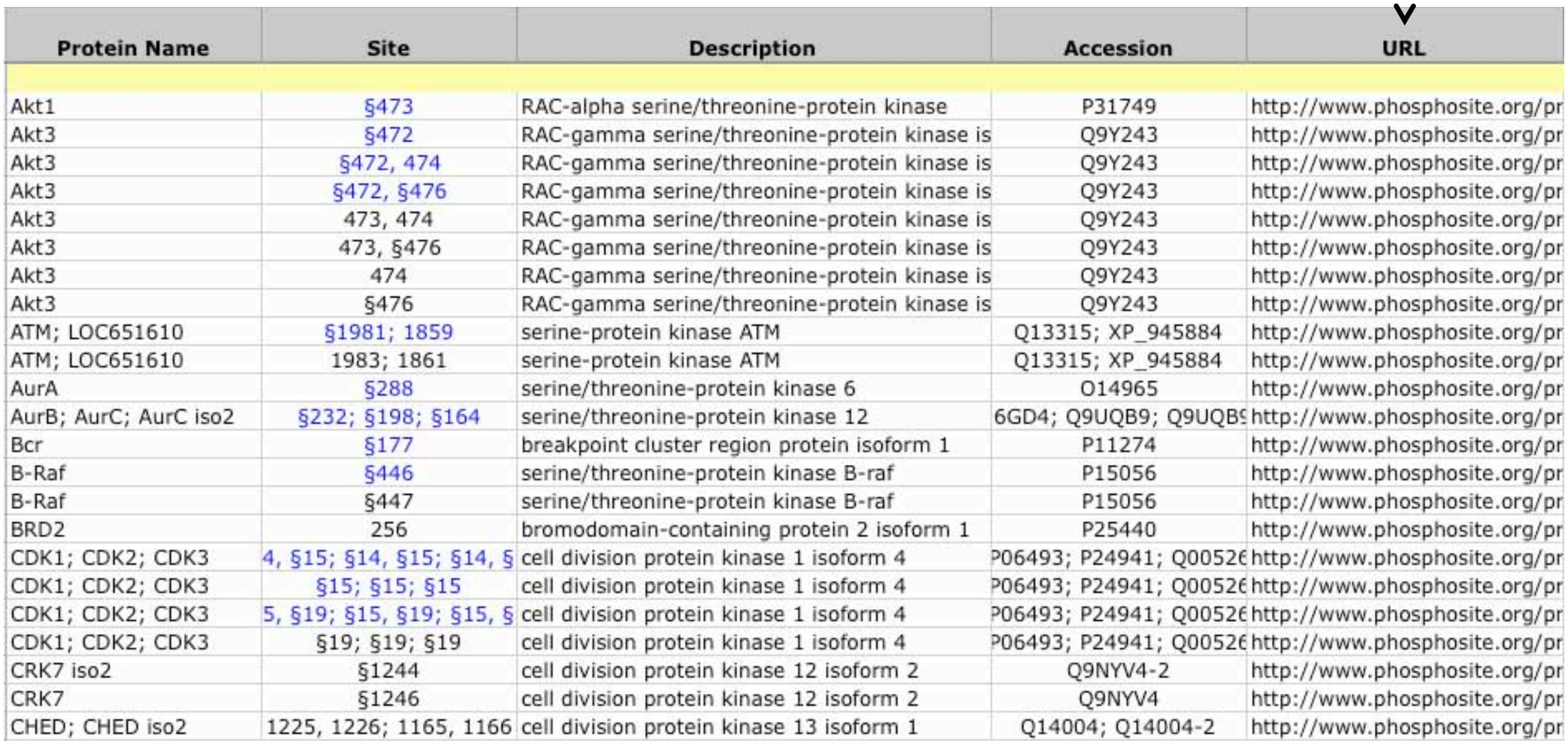
Hypertext links to product pages (blue text).

Summary Sheets contain Gene Name, Protein Name, and phosphorylation Site for each identified peptide.

Summary Sheet

URL

Links to PhosphoSitePlus® pages are given for each protein.



Protein Name	Site	Description	Accession	URL
Akt1	§473	RAC-alpha serine/threonine-protein kinase	P31749	http://www.phosphosite.org/pr
Akt3	§472	RAC-gamma serine/threonine-protein kinase is	Q9Y243	http://www.phosphosite.org/pr
Akt3	§472, 474	RAC-gamma serine/threonine-protein kinase is	Q9Y243	http://www.phosphosite.org/pr
Akt3	§472, §476	RAC-gamma serine/threonine-protein kinase is	Q9Y243	http://www.phosphosite.org/pr
Akt3	473, 474	RAC-gamma serine/threonine-protein kinase is	Q9Y243	http://www.phosphosite.org/pr
Akt3	473, §476	RAC-gamma serine/threonine-protein kinase is	Q9Y243	http://www.phosphosite.org/pr
Akt3	474	RAC-gamma serine/threonine-protein kinase is	Q9Y243	http://www.phosphosite.org/pr
Akt3	§476	RAC-gamma serine/threonine-protein kinase is	Q9Y243	http://www.phosphosite.org/pr
ATM; LOC651610	§1981; 1859	serine-protein kinase ATM	Q13315; XP_945884	http://www.phosphosite.org/pr
ATM; LOC651610	1983; 1861	serine-protein kinase ATM	Q13315; XP_945884	http://www.phosphosite.org/pr
AurA	§288	serine/threonine-protein kinase 6	O14965	http://www.phosphosite.org/pr
AurB; AurC; AurC iso2	§232; §198; §164	serine/threonine-protein kinase 12	6GD4; Q9UQB9; Q9UQB	http://www.phosphosite.org/pr
Bcr	§177	breakpoint cluster region protein isoform 1	P11274	http://www.phosphosite.org/pr
B-Raf	§446	serine/threonine-protein kinase B-raf	P15056	http://www.phosphosite.org/pr
B-Raf	§447	serine/threonine-protein kinase B-raf	P15056	http://www.phosphosite.org/pr
BRD2	256	bromodomain-containing protein 2 isoform 1	P25440	http://www.phosphosite.org/pr
CDK1; CDK2; CDK3	4, §15; §14, §15; §14, §	cell division protein kinase 1 isoform 4	P06493; P24941; Q0052	http://www.phosphosite.org/pr
CDK1; CDK2; CDK3	§15; §15; §15	cell division protein kinase 1 isoform 4	P06493; P24941; Q0052	http://www.phosphosite.org/pr
CDK1; CDK2; CDK3	5, §19; §15, §19; §15, §	cell division protein kinase 1 isoform 4	P06493; P24941; Q0052	http://www.phosphosite.org/pr
CDK1; CDK2; CDK3	§19; §19; §19	cell division protein kinase 1 isoform 4	P06493; P24941; Q0052	http://www.phosphosite.org/pr
CRK7 iso2	§1244	cell division protein kinase 12 isoform 2	Q9NYV4-2	http://www.phosphosite.org/pr
CRK7	§1246	cell division protein kinase 12 isoform 2	Q9NYV4	http://www.phosphosite.org/pr
CHED; CHED iso2	1225, 1226; 1165, 1166	cell division protein kinase 13 isoform 1	Q14004; Q14004-2	http://www.phosphosite.org/pr

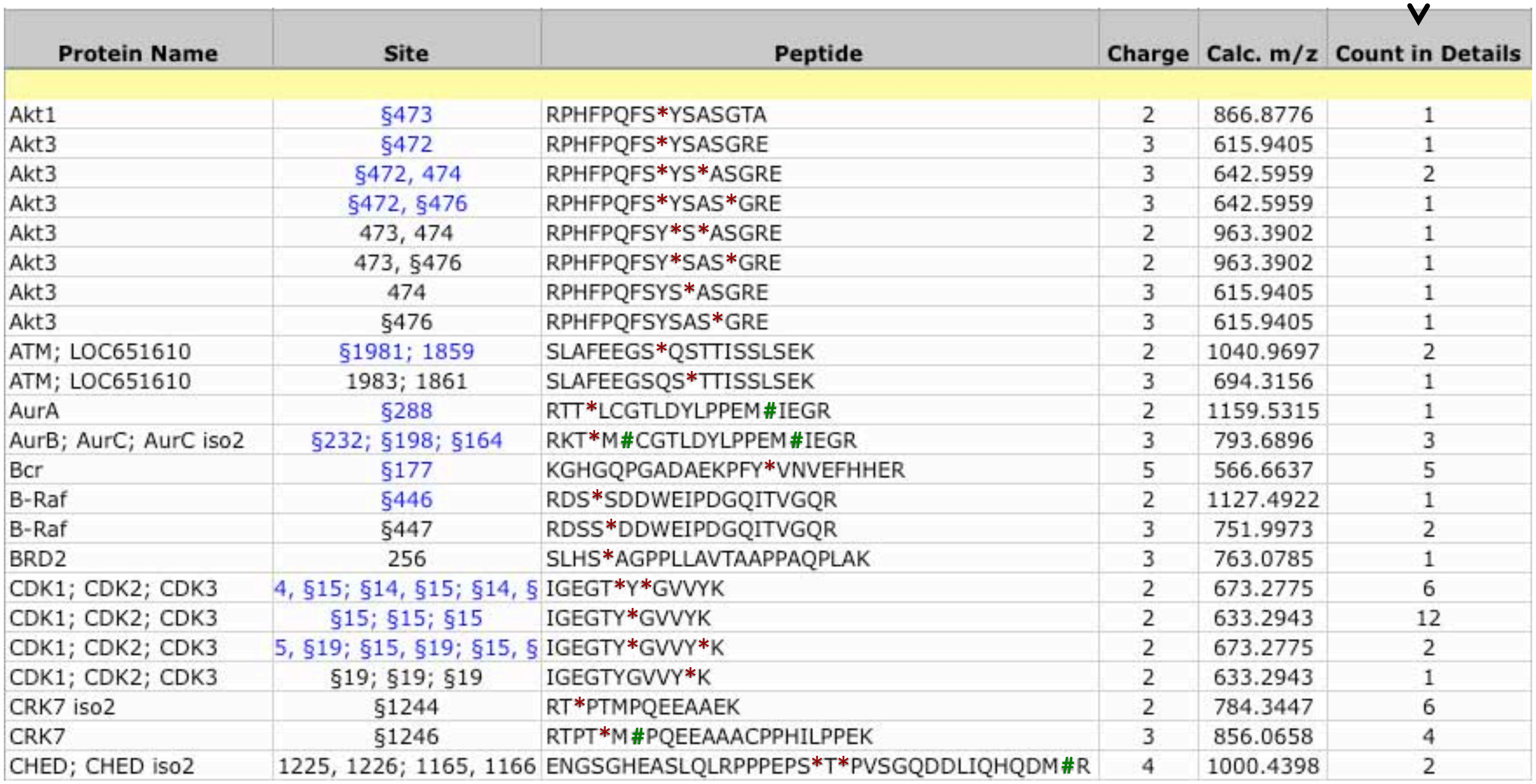
Multiple isoforms for a single peptide are separated by semicolon.

Summary Sheets include protein/peptide/site information (Description, Accession).

Summary Sheet

Count in Details

The Summary Sheet includes the Count in Details: number of peptides in the Details Tab for each site.



Protein Name	Site	Peptide	Charge	Calc. m/z	Count in Details
Akt1	§473	RPHFPQFS*YSASGTA	2	866.8776	1
Akt3	§472	RPHFPQFS*YSASGRE	3	615.9405	1
Akt3	§472, 474	RPHFPQFS*YS*ASGRE	3	642.5959	2
Akt3	§472, §476	RPHFPQFS*YSAS*GRE	3	642.5959	1
Akt3	473, 474	RPHFPQFSY*S*ASGRE	2	963.3902	1
Akt3	473, §476	RPHFPQFSY*SAS*GRE	2	963.3902	1
Akt3	474	RPHFPQFSYS*ASGRE	3	615.9405	1
Akt3	§476	RPHFPQFSYSAS*GRE	3	615.9405	1
ATM; LOC651610	§1981; 1859	SLAFEEGS*QSTTISSLSEK	2	1040.9697	2
ATM; LOC651610	1983; 1861	SLAFEEGSQS*TTISSLSEK	3	694.3156	1
AurA	§288	RTT*LCGTLDYLPPEM#IEGR	2	1159.5315	1
AurB; AurC; AurC iso2	§232; §198; §164	RKT*M#CGTLDYLPPEM#IEGR	3	793.6896	3
Bcr	§177	KGHGQPGADAEKPFY*VNVEFHHER	5	566.6637	5
B-Raf	§446	RDS*SDDWEIPDGQITVGQR	2	1127.4922	1
B-Raf	§447	RDSS*DDWEIPDGQITVGQR	3	751.9973	2
BRD2	256	SLHS*AGPPLLAVTAAPPAQPLAK	3	763.0785	1
CDK1; CDK2; CDK3	4, §15; §14, §15; §14, §	IGEGT*Y*GVVYK	2	673.2775	6
CDK1; CDK2; CDK3	§15; §15; §15	IGEGTY*GVVYK	2	633.2943	12
CDK1; CDK2; CDK3	5, §19; §15, §19; §15, §	IGEGTY*GVVY*K	2	673.2775	2
CDK1; CDK2; CDK3	§19; §19; §19	IGEGTYGVVY*K	2	633.2943	1
CRK7 iso2	§1244	RT*PTMPQEEAAEK	2	784.3447	6
CRK7	§1246	RTPT*M#PQEEAAACPPHILPPEK	3	856.0658	4
CHED; CHED iso2	1225, 1226; 1165, 1166	ENGSGHEASLQLRPPPEPS*T*PVSGQDDLIQHQDM#R	4	1000.4398	2

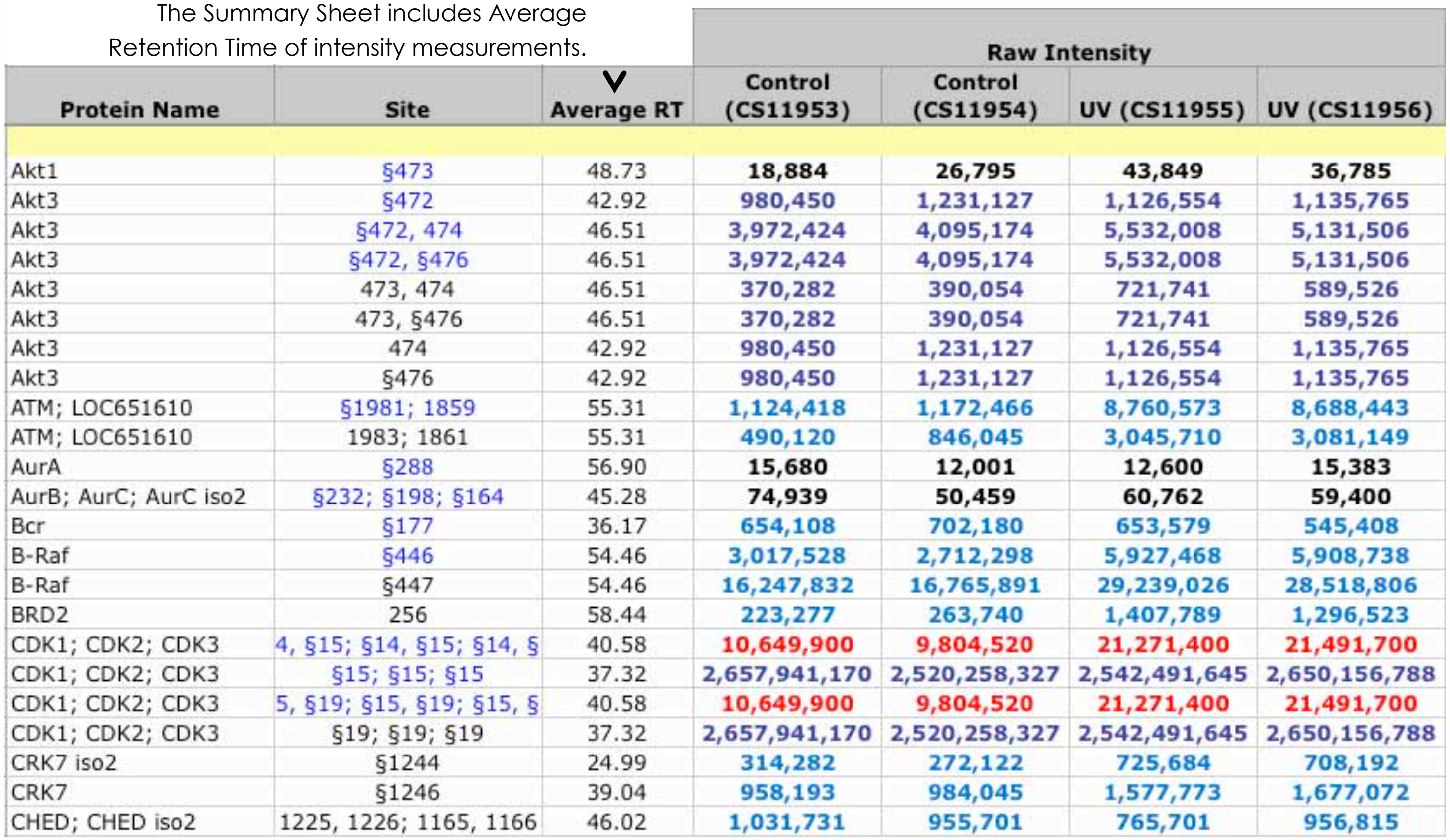
* Phosphorylation # Oxidized methionine

Summary Sheets includes protein/peptide/site information (Peptide, Charge, Calc. m/z, Count in Details).

Summary Sheet

Average Retention Time

The Summary Sheet includes Average Retention Time of intensity measurements.



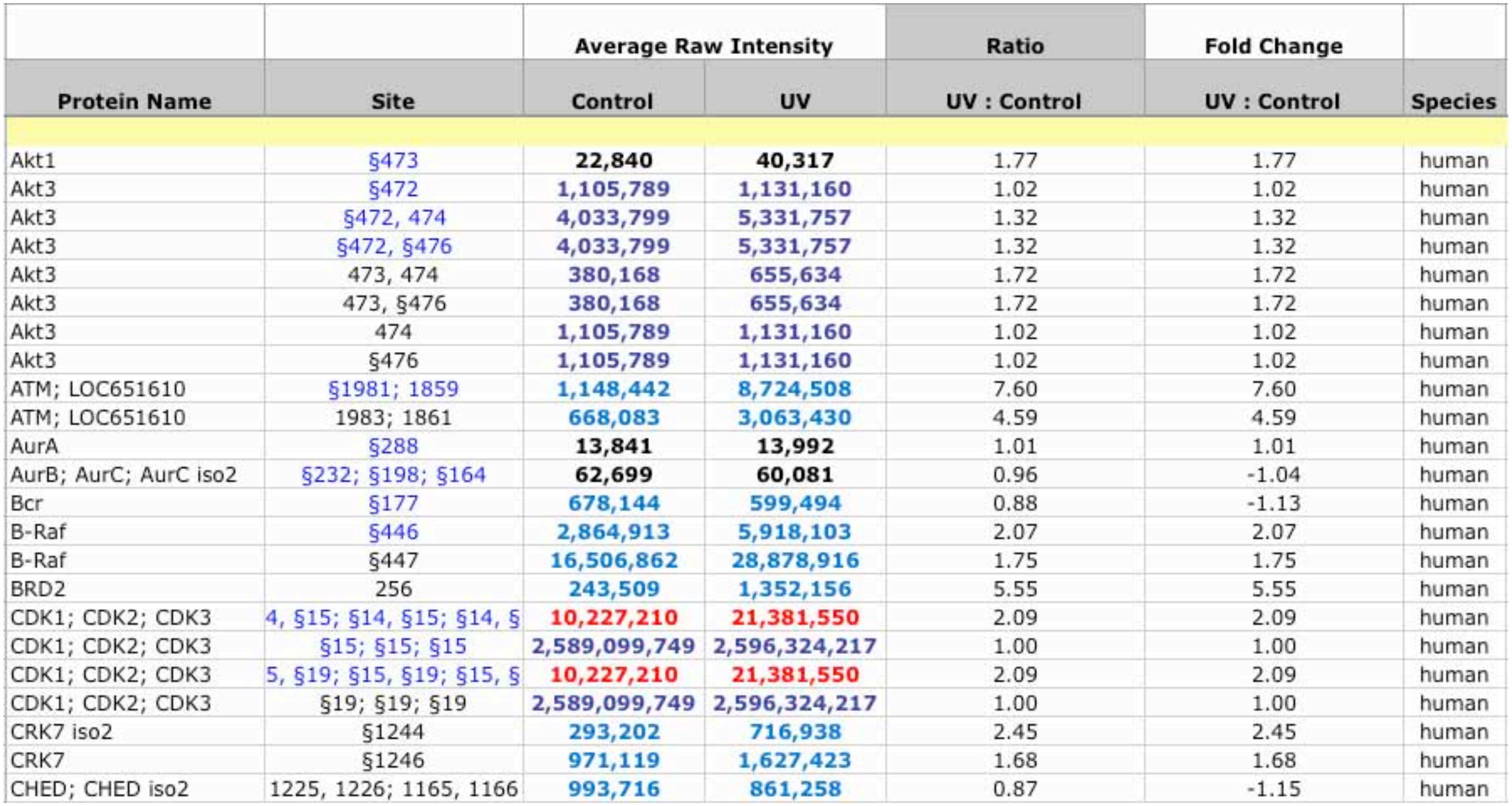
Protein Name	Site	Average RT	Raw Intensity Control (CS11953)	Control (CS11954)	UV (CS11955)	UV (CS11956)
Akt1	§473	48.73	18,884	26,795	43,849	36,785
Akt3	§472	42.92	980,450	1,231,127	1,126,554	1,135,765
Akt3	§472, 474	46.51	3,972,424	4,095,174	5,532,008	5,131,506
Akt3	§472, §476	46.51	3,972,424	4,095,174	5,532,008	5,131,506
Akt3	473, 474	46.51	370,282	390,054	721,741	589,526
Akt3	473, §476	46.51	370,282	390,054	721,741	589,526
Akt3	474	42.92	980,450	1,231,127	1,126,554	1,135,765
Akt3	§476	42.92	980,450	1,231,127	1,126,554	1,135,765
ATM; LOC651610	§1981; 1859	55.31	1,124,418	1,172,466	8,760,573	8,688,443
ATM; LOC651610	1983; 1861	55.31	490,120	846,045	3,045,710	3,081,149
AurA	§288	56.90	15,680	12,001	12,600	15,383
AurB; AurC; AurC iso2	§232; §198; §164	45.28	74,939	50,459	60,762	59,400
Bcr	§177	36.17	654,108	702,180	653,579	545,408
B-Raf	§446	54.46	3,017,528	2,712,298	5,927,468	5,908,738
B-Raf	§447	54.46	16,247,832	16,765,891	29,239,026	28,518,806
BRD2	256	58.44	223,277	263,740	1,407,789	1,296,523
CDK1; CDK2; CDK3	4, §15; §14, §15; §14, §	40.58	10,649,900	9,804,520	21,271,400	21,491,700
CDK1; CDK2; CDK3	§15; §15; §15	37.32	2,657,941,170	2,520,258,327	2,542,491,645	2,650,156,788
CDK1; CDK2; CDK3	5, §19; §15, §19; §15, §	40.58	10,649,900	9,804,520	21,271,400	21,491,700
CDK1; CDK2; CDK3	§19; §19; §19	37.32	2,657,941,170	2,520,258,327	2,542,491,645	2,650,156,788
CRK7 iso2	§1244	24.99	314,282	272,122	725,684	708,192
CRK7	§1246	39.04	958,193	984,045	1,577,773	1,677,072
CHED; CHED iso2	1225, 1226; 1165, 1166	46.02	1,031,731	955,701	765,701	956,815

Raw Intensity

Also included is the raw peak heights (Raw Intensity).

Bold values = intensities manually reviewed. **Red values** = multiple identifications for 1 m/z measurement due to ambiguous phosphorylation site localization. **Blue values** = peak area measurement. **Purple values** = Peak area and multiple identifications.

Summary Sheet



		Average Raw Intensity		Ratio	Fold Change	
Protein Name	**Site**	**Control**	**UV**	**UV : Control**	**UV : Control**	**Species**
Akt1	§473	22,840	40,317	1.77	1.77	human
Akt3	§472	1,105,789	1,131,160	1.02	1.02	human
Akt3	§472, 474	4,033,799	5,331,757	1.32	1.32	human
Akt3	§472, §476	4,033,799	5,331,757	1.32	1.32	human
Akt3	473, 474	380,168	655,634	1.72	1.72	human
Akt3	473, §476	380,168	655,634	1.72	1.72	human
Akt3	474	1,105,789	1,131,160	1.02	1.02	human
Akt3	§476	1,105,789	1,131,160	1.02	1.02	human
ATM; LOC651610	§1981; 1859	1,148,442	8,724,508	7.60	7.60	human
ATM; LOC651610	1983; 1861	668,083	3,063,430	4.59	4.59	human
AurA	§288	13,841	13,992	1.01	1.01	human
AurB; AurC; AurC iso2	§232; §198; §164	62,699	60,081	0.96	-1.04	human
Bcr	§177	678,144	599,494	0.88	-1.13	human
B-Raf	§446	2,864,913	5,918,103	2.07	2.07	human
B-Raf	§447	16,506,862	28,878,916	1.75	1.75	human
BRD2	256	243,509	1,352,156	5.55	5.55	human
CDK1; CDK2; CDK3	4, §15; §14, §15; §14, §	10,227,210	21,381,550	2.09	2.09	human
CDK1; CDK2; CDK3	§15; §15; §15	2,589,099,749	2,596,324,217	1.00	1.00	human
CDK1; CDK2; CDK3	5, §19; §15, §19; §15, §	10,227,210	21,381,550	2.09	2.09	human
CDK1; CDK2; CDK3	§19; §19; §19	2,589,099,749	2,596,324,217	1.00	1.00	human
CRK7 iso2	§1244	293,202	716,938	2.45	2.45	human
CRK7	§1246	971,119	1,627,423	1.68	1.68	human
CHED; CHED iso2	1225, 1226; 1165, 1166	993,716	861,258	0.87	-1.15	human

Summary Sheets include Average Raw Intensity, Ratio, Fold Change, and species of samples profiled. When necessary, ratios are normalized based on the median Log2 Ratio (not shown).

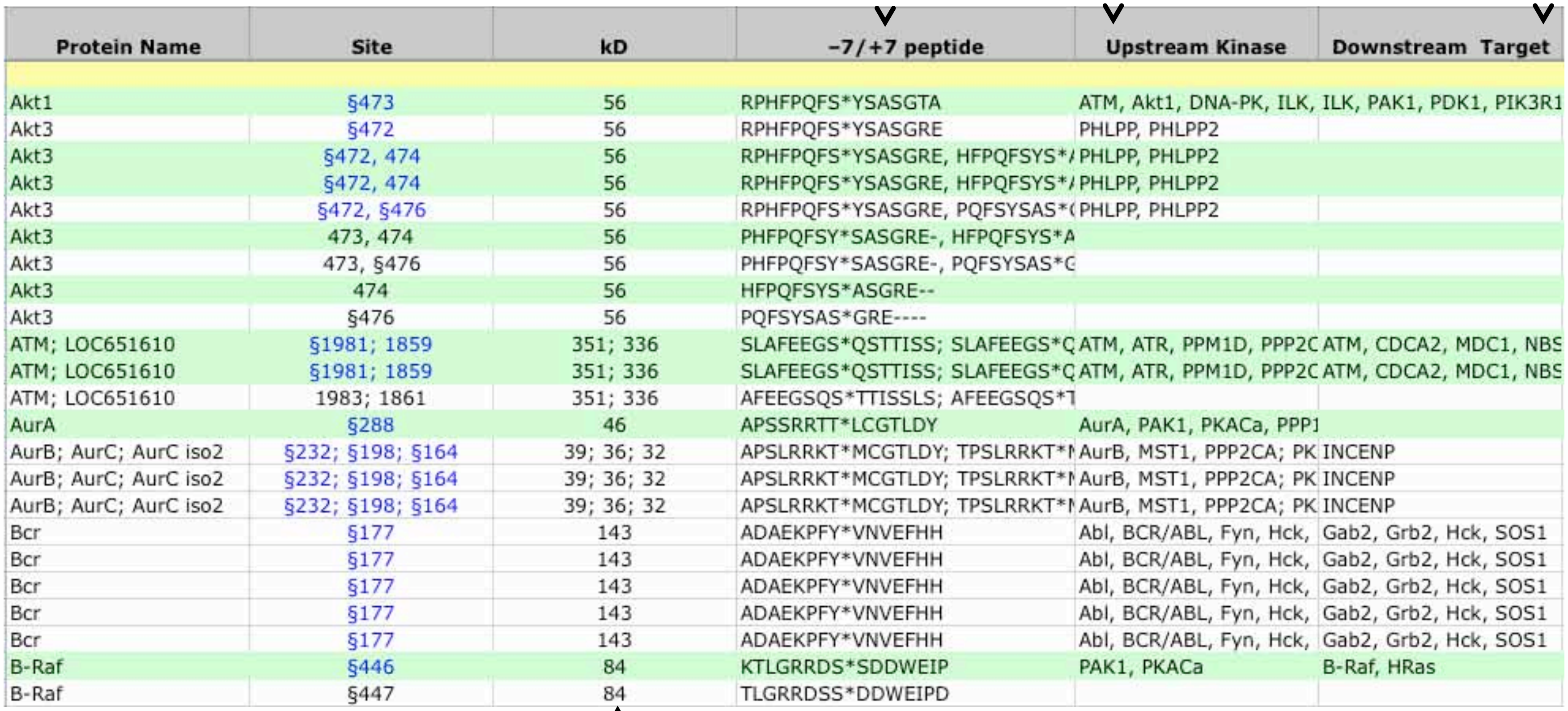
Details Sheet

7 Amino Acids

Peptide sequence 7 amino acids to each side of the modified residue also included.

Upstream/Downstream

Includes any known upstream effectors and downstream substrates.



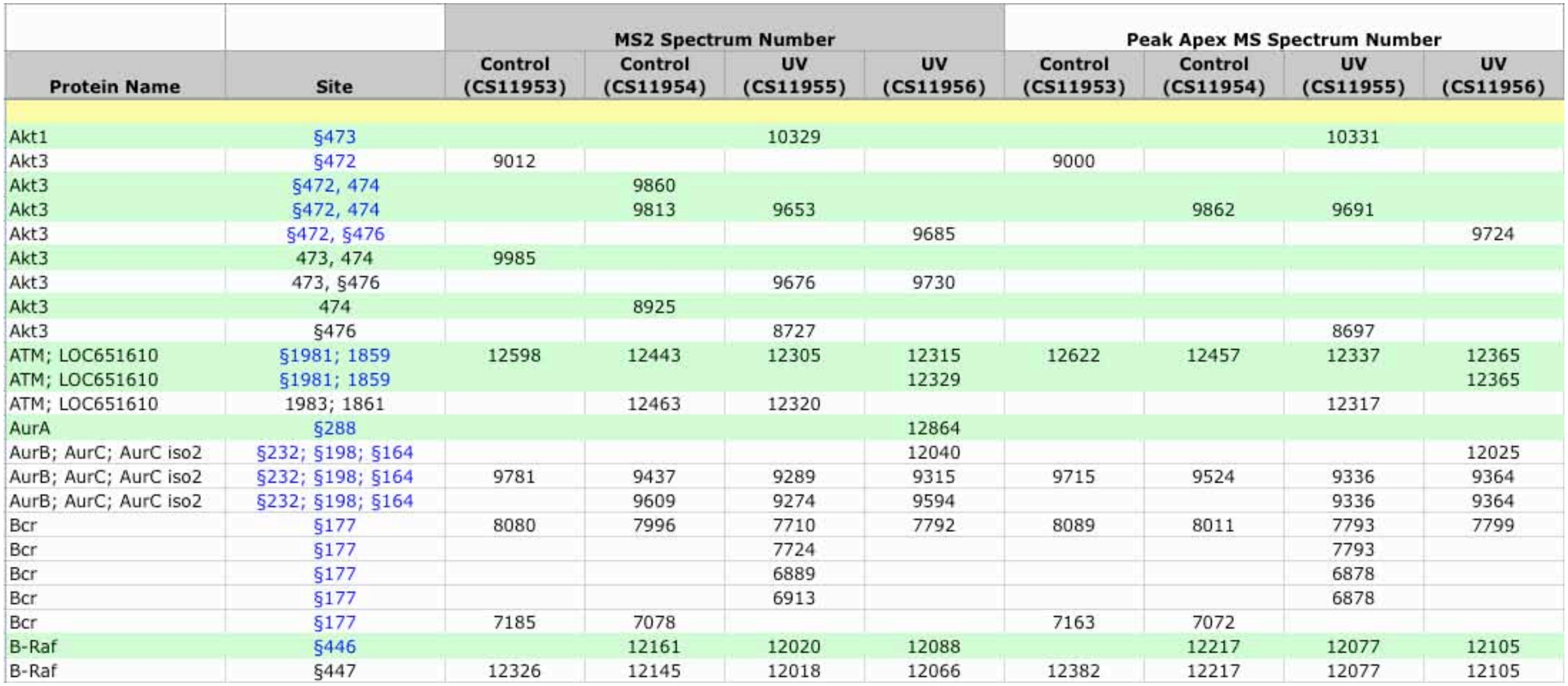
Protein Name	Site	kD	-7/+7 peptide	Upstream Kinase	Downstream Target
Akt1	§473	56	RPHFPQFS*YSASGTA	ATM, Akt1, DNA-PK, ILK,	ILK, PAK1, PDK1, PIK3R1
Akt3	§472	56	RPHFPQFS*YSASGRE	PHLPP, PHLPP2	
Akt3	§472, 474	56	RPHFPQFS*YSASGRE, HFPQFSYS*	PHLPP, PHLPP2	
Akt3	§472, 474	56	RPHFPQFS*YSASGRE, HFPQFSYS*	PHLPP, PHLPP2	
Akt3	§472, §476	56	RPHFPQFS*YSASGRE, PQFSYSAS*	PHLPP, PHLPP2	
Akt3	473, 474	56	PHFPQFSY*SASGRE-, HFPQFSYS*A		
Akt3	473, §476	56	PHFPQFSY*SASGRE-, PQFSYSAS*		
Akt3	474	56	HFPQFSYS*ASGRE--		
Akt3	§476	56	PQFSYSAS*GRE----		
ATM; LOC651610	§1981; 1859	351; 336	SLAFEEGS*QSTTISS; SLAFEEGS*Q	ATM, ATR, PPM1D, PPP2C	ATM, CDCA2, MDC1, NBS
ATM; LOC651610	§1981; 1859	351; 336	SLAFEEGS*QSTTISS; SLAFEEGS*Q	ATM, ATR, PPM1D, PPP2C	ATM, CDCA2, MDC1, NBS
ATM; LOC651610	1983; 1861	351; 336	AFEEGSQS*TTISSLS; AFEEGSQS*T		
AurA	§288	46	APSSRRTT*LCGTLDY	AurA, PAK1, PKACa, PPP1	
AurB; AurC; AurC iso2	§232; §198; §164	39; 36; 32	APSLRRKT*MCGTLDY; TPSLRRKT*	AurB, MST1, PPP2CA; PK	INCENP
AurB; AurC; AurC iso2	§232; §198; §164	39; 36; 32	APSLRRKT*MCGTLDY; TPSLRRKT*	AurB, MST1, PPP2CA; PK	INCENP
AurB; AurC; AurC iso2	§232; §198; §164	39; 36; 32	APSLRRKT*MCGTLDY; TPSLRRKT*	AurB, MST1, PPP2CA; PK	INCENP
Bcr	§177	143	ADAEKPFY*VNVEFHH	Abl, BCR/ABL, Fyn, Hck,	Gab2, Grb2, Hck, SOS1
Bcr	§177	143	ADAEKPFY*VNVEFHH	Abl, BCR/ABL, Fyn, Hck,	Gab2, Grb2, Hck, SOS1
Bcr	§177	143	ADAEKPFY*VNVEFHH	Abl, BCR/ABL, Fyn, Hck,	Gab2, Grb2, Hck, SOS1
Bcr	§177	143	ADAEKPFY*VNVEFHH	Abl, BCR/ABL, Fyn, Hck,	Gab2, Grb2, Hck, SOS1
Bcr	§177	143	ADAEKPFY*VNVEFHH	Abl, BCR/ABL, Fyn, Hck,	Gab2, Grb2, Hck, SOS1
B-Raf	§446	84	KTLGRRDS*SDDWEIP	PAK1, PKACa	B-Raf, HRas
B-Raf	§447	84	TLGRRDSS*DDWEIPD		

kD Included is the molecular weight of the protein from which the peptide is derived.

Details Sheet

Spectrum Numbers

The Details Sheet includes the MS/MS (or MS2)
and MS scan numbers for each peptide assignment.



		MS2 Spectrum Number				Peak Apex MS Spectrum Number			
Protein Name	**Site**	**Control (CS11953)**	**Control (CS11954)**	**UV (CS11955)**	**UV (CS11956)**	**Control (CS11953)**	**Control (CS11954)**	**UV (CS11955)**	**UV (CS11956)**
Akt1	§473			10329				10331	
Akt3	§472	9012				9000			
Akt3	§472, 474		9860						
Akt3	§472, 474		9813	9653			9862	9691	
Akt3	§472, §476				9685				9724
Akt3	473, 474	9985							
Akt3	473, §476			9676	9730				
Akt3	474		8925						
Akt3	§476			8727				8697	
ATM; LOC651610	§1981; 1859	12598	12443	12305	12315	12622	12457	12337	12365
ATM; LOC651610	§1981; 1859				12329				12365
ATM; LOC651610	1983; 1861		12463	12320				12317	
AurA	§288				12864				
AurB; AurC; AurC iso2	§232; §198; §164				12040				12025
AurB; AurC; AurC iso2	§232; §198; §164	9781	9437	9289	9315	9715	9524	9336	9364
AurB; AurC; AurC iso2	§232; §198; §164		9609	9274	9594			9336	9364
Bcr	§177	8080	7996	7710	7792	8089	8011	7793	7799
Bcr	§177			7724				7793	
Bcr	§177			6889				6878	
Bcr	§177			6913				6878	
Bcr	§177	7185	7078			7163	7072		
B-Raf	§446		12161	12020	12088		12217	12077	12105
B-Raf	§447	12326	12145	12018	12066	12382	12217	12077	12105

Experimental details that are mainly used as a reference to raw data.

Details Sheet

Retention Time

The Details Sheet includes the Retention Time.

Xcorr Values

Xcorr values (or Sorcerer cross-correlation value) for each peptide assignment.

		Retention Time				Xcorr			
Protein Name	Site	Control (CS11953)	Control (CS11954)	UV (CS11955)	UV (CS11956)	Control (CS11953)	Control (CS11954)	UV (CS11955)	UV (CS11956)
Akt1	§473	48.75	48.84	48.68	48.65			2.945	
Akt3	§472					2.723			
Akt3	§472, 474						1.759		
Akt3	§472, 474	46.51	46.50	46.49	46.55		2.241	2.610	
Akt3	§472, §476								2.475
Akt3	473, 474					2.096			
Akt3	473, §476	46.51	46.50	46.49	46.55			2.416	1.920
Akt3	474	42.88	43.01	42.90	42.87		2.342		
Akt3	§476							2.386	
ATM; LOC651610	§1981; 1859	55.34	55.22	55.30	55.36	4.470	4.043	4.954	5.206
ATM; LOC651610	§1981; 1859								3.095
ATM; LOC651610	1983; 1861	55.34	55.22	55.30	55.36		2.225	3.010	
AurA	§288	56.85	56.88	56.96	56.91				2.245
AurB; AurC; AurC iso2	§232; §198; §164	54.40	54.29	54.11	54.25				2.628
AurB; AurC; AurC iso2	§232; §198; §164	45.49	45.21	45.17	45.23	3.103	3.262	3.560	3.557
AurB; AurC; AurC iso2	§232; §198; §164	45.49	45.21	45.17	45.23		2.510	2.646	3.342
Bcr	§177	39.59	39.71	39.70	39.53	3.655	3.574	3.450	2.871
Bcr	§177	39.59	39.71	39.70	39.53			2.399	
Bcr	§177	36.20	36.25	36.32	35.97			3.908	
Bcr	§177	36.20	36.25	36.32	35.97			2.968	
Bcr	§177	36.13	36.25	36.40	35.91	3.236	3.101		
B-Raf	§446	54.52	54.43	54.42	54.48		4.489	4.548	4.499
B-Raf	§447	54.52	54.43	54.42	54.48	3.522	2.970	4.075	3.575

Experimental details that are used as a reference and measure of confidence to the peptide assignment.

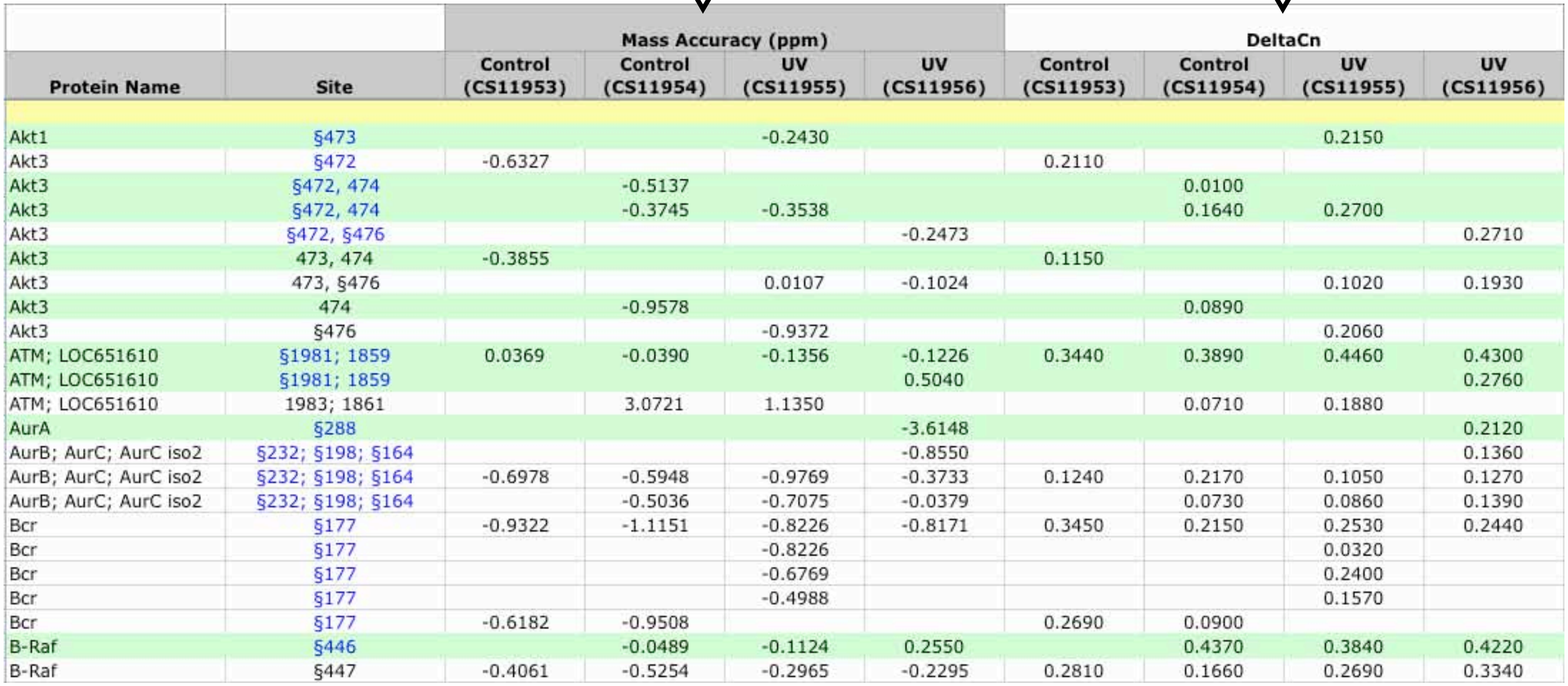
Details Sheet

Mass Accuracy

Details Sheet includes the measured peptide mass accuracy.

DeltaCN

The Details Sheet also includes the DeltaCN value for each peptide assignment.

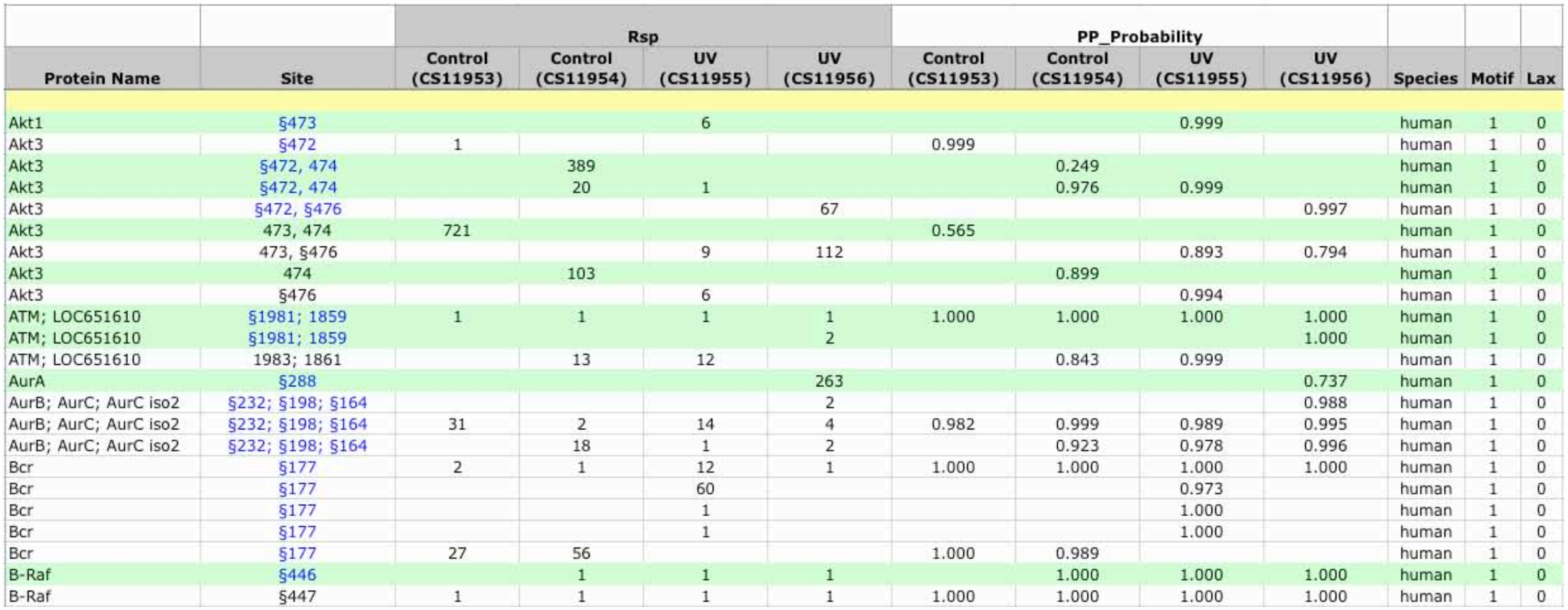


		Mass Accuracy (ppm)				DeltaCn			
Protein Name	**Site**	**Control (CS11953)**	**Control (CS11954)**	**UV (CS11955)**	**UV (CS11956)**	**Control (CS11953)**	**Control (CS11954)**	**UV (CS11955)**	**UV (CS11956)**
Akt1	§473			-0.2430				0.2150	
Akt3	§472	-0.6327				0.2110			
Akt3	§472, 474		-0.5137				0.0100		
Akt3	§472, 474		-0.3745	-0.3538			0.1640	0.2700	
Akt3	§472, §476				-0.2473				0.2710
Akt3	473, 474	-0.3855				0.1150			
Akt3	473, §476			0.0107	-0.1024			0.1020	0.1930
Akt3	474		-0.9578				0.0890		
Akt3	§476			-0.9372				0.2060	
ATM; LOC651610	§1981; 1859	0.0369	-0.0390	-0.1356	-0.1226	0.3440	0.3890	0.4460	0.4300
ATM; LOC651610	§1981; 1859				0.5040				0.2760
ATM; LOC651610	1983; 1861		3.0721	1.1350			0.0710	0.1880	
AurA	§288				-3.6148				0.2120
AurB; AurC; AurC iso2	§232; §198; §164				-0.8550				0.1360
AurB; AurC; AurC iso2	§232; §198; §164	-0.6978	-0.5948	-0.9769	-0.3733	0.1240	0.2170	0.1050	0.1270
AurB; AurC; AurC iso2	§232; §198; §164		-0.5036	-0.7075	-0.0379		0.0730	0.0860	0.1390
Bcr	§177	-0.9322	-1.1151	-0.8226	-0.8171	0.3450	0.2150	0.2530	0.2440
Bcr	§177			-0.8226				0.0320	
Bcr	§177			-0.6769				0.2400	
Bcr	§177			-0.4988				0.1570	
Bcr	§177	-0.6182	-0.9508			0.2690	0.0900		
B-Raf	§446		-0.0489	-0.1124	0.2550		0.4370	0.3840	0.4220
B-Raf	§447	-0.4061	-0.5254	-0.2965	-0.2295	0.2810	0.1660	0.2690	0.3340

Experimental details that are used as a reference and measure of confidence to the peptide assignment.

Details Sheet

Include the Rsp value and the Peptide Prophet Probability for each peptide assignment.



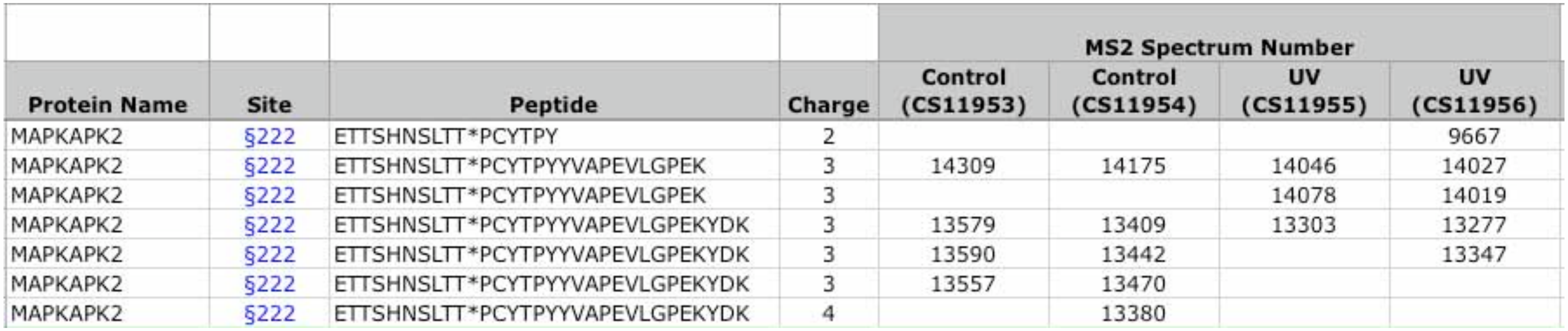
		Rsp				PP_Probability						
Protein Name	**Site**	**Control (CS11953)**	**Control (CS11954)**	**UV (CS11955)**	**UV (CS11956)**	**Control (CS11953)**	**Control (CS11954)**	**UV (CS11955)**	**UV (CS11956)**	**Species**	**Motif**	**Lax**
Akt1	§473			6				0.999		human	1	0
Akt3	§472	1				0.999				human	1	0
Akt3	§472, 474		389				0.249			human	1	0
Akt3	§472, 474		20	1			0.976	0.999		human	1	0
Akt3	§472, §476				67				0.997	human	1	0
Akt3	473, 474	721				0.565				human	1	0
Akt3	473, §476			9	112			0.893	0.794	human	1	0
Akt3	474		103				0.899			human	1	0
Akt3	§476			6				0.994		human	1	0
ATM; LOC651610	§1981; 1859	1	1	1	1	1.000	1.000	1.000	1.000	human	1	0
ATM; LOC651610	§1981; 1859				2				1.000	human	1	0
ATM; LOC651610	1983; 1861		13	12			0.843	0.999		human	1	0
AurA	§288				263				0.737	human	1	0
AurB; AurC; AurC iso2	§232; §198; §164				2				0.988	human	1	0
AurB; AurC; AurC iso2	§232; §198; §164	31	2	14	4	0.982	0.999	0.989	0.995	human	1	0
AurB; AurC; AurC iso2	§232; §198; §164		18	1	2		0.923	0.978	0.996	human	1	0
Bcr	§177	2	1	12	1	1.000	1.000	1.000	1.000	human	1	0
Bcr	§177			60				0.973		human	1	0
Bcr	§177			1				1.000		human	1	0
Bcr	§177			1				1.000		human	1	0
Bcr	§177	27	56			1.000	0.989			human	1	0
B-Raf	§446		1	1	1		1.000	1.000	1.000	human	1	0
B-Raf	§447	1	1	1	1	1.000	1.000	1.000	1.000	human	1	0

Includes whether the preptide is motif or lax.

Experimental details that are used as a reference and measure of confidence to the peptide assignment.

Qualitative Table

MS2 Spectrum Number
The site, T222, is assigned 17 times in all curation sets (count number of MS2 entries).

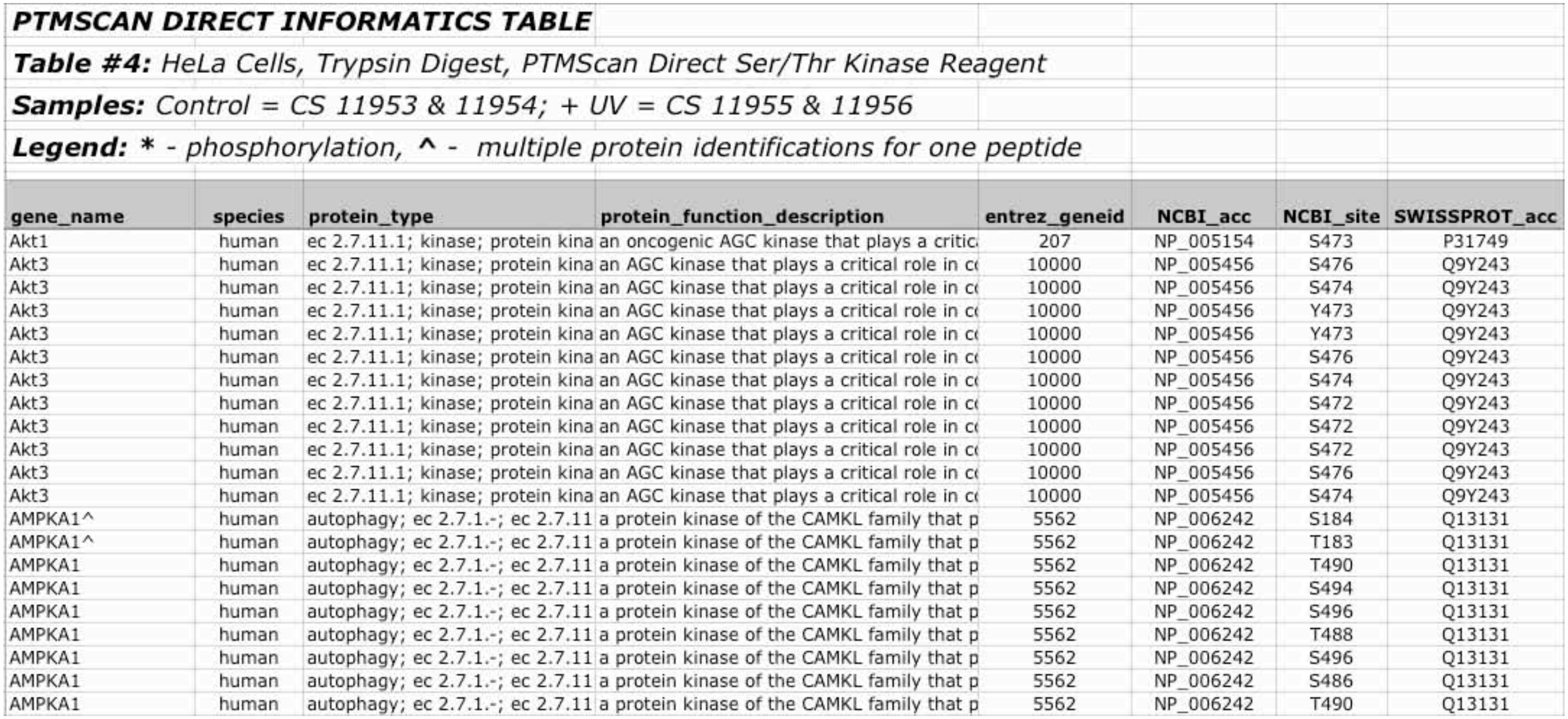


				MS2 Spectrum Number			
Protein Name	Site	Peptide	Charge	Control (CS11953)	Control (CS11954)	UV (CS11955)	UV (CS11956)
MAPKAPK2	§222	ETTSHNSLTT*PCYTPY	2				9667
MAPKAPK2	§222	ETTSHNSLTT*PCYTPYYVAPEVLGPEK	3	14309	14175	14046	14027
MAPKAPK2	§222	ETTSHNSLTT*PCYTPYYVAPEVLGPEK	3			14078	14019
MAPKAPK2	§222	ETTSHNSLTT*PCYTPYYVAPEVLGPEKYDK	3	13579	13409	13303	13277
MAPKAPK2	§222	ETTSHNSLTT*PCYTPYYVAPEVLGPEKYDK	3	13590	13442		13347
MAPKAPK2	§222	ETTSHNSLTT*PCYTPYYVAPEVLGPEKYDK	3	13557	13470		
MAPKAPK2	§222	ETTSHNSLTT*PCYTPYYVAPEVLGPEKYDK	4		13380		

Peptide
The site is represented in 3 overlapping sequences (incomplete digestion).

Charge
The phosphorylated peptide assignments are seen in multiple charge states.

Informatics Table



PTMSCAN DIRECT INFORMATICS TABLE

Table #4: *HeLa Cells, Trypsin Digest, PTMScan Direct Ser/Thr Kinase Reagent*

Samples: *Control = CS 11953 & 11954; + UV = CS 11955 & 11956*

Legend: ** - phosphorylation, ^ - multiple protein identifications for one peptide*

gene_name	species	protein_type	protein_function_description	entrez_geneid	NCBI_acc	NCBI_site	SWISSPROT_acc
Akt1	human	ec 2.7.11.1; kinase; protein kina	an oncogenic AGC kinase that plays a critic	207	NP_005154	S473	P31749
Akt3	human	ec 2.7.11.1; kinase; protein kina	an AGC kinase that plays a critical role in c	10000	NP_005456	S476	Q9Y243
Akt3	human	ec 2.7.11.1; kinase; protein kina	an AGC kinase that plays a critical role in c	10000	NP_005456	S474	Q9Y243
Akt3	human	ec 2.7.11.1; kinase; protein kina	an AGC kinase that plays a critical role in c	10000	NP_005456	Y473	Q9Y243
Akt3	human	ec 2.7.11.1; kinase; protein kina	an AGC kinase that plays a critical role in c	10000	NP_005456	Y473	Q9Y243
Akt3	human	ec 2.7.11.1; kinase; protein kina	an AGC kinase that plays a critical role in c	10000	NP_005456	S476	Q9Y243
Akt3	human	ec 2.7.11.1; kinase; protein kina	an AGC kinase that plays a critical role in c	10000	NP_005456	S474	Q9Y243
Akt3	human	ec 2.7.11.1; kinase; protein kina	an AGC kinase that plays a critical role in c	10000	NP_005456	S472	Q9Y243
Akt3	human	ec 2.7.11.1; kinase; protein kina	an AGC kinase that plays a critical role in c	10000	NP_005456	S472	Q9Y243
Akt3	human	ec 2.7.11.1; kinase; protein kina	an AGC kinase that plays a critical role in c	10000	NP_005456	S472	Q9Y243
Akt3	human	ec 2.7.11.1; kinase; protein kina	an AGC kinase that plays a critical role in c	10000	NP_005456	S476	Q9Y243
Akt3	human	ec 2.7.11.1; kinase; protein kina	an AGC kinase that plays a critical role in c	10000	NP_005456	S474	Q9Y243
AMPKA1^	human	autophagy; ec 2.7.1.-; ec 2.7.11	a protein kinase of the CAMKL family that p	5562	NP_006242	S184	Q13131
AMPKA1^	human	autophagy; ec 2.7.1.-; ec 2.7.11	a protein kinase of the CAMKL family that p	5562	NP_006242	T183	Q13131
AMPKA1	human	autophagy; ec 2.7.1.-; ec 2.7.11	a protein kinase of the CAMKL family that p	5562	NP_006242	T490	Q13131
AMPKA1	human	autophagy; ec 2.7.1.-; ec 2.7.11	a protein kinase of the CAMKL family that p	5562	NP_006242	S494	Q13131
AMPKA1	human	autophagy; ec 2.7.1.-; ec 2.7.11	a protein kinase of the CAMKL family that p	5562	NP_006242	S496	Q13131
AMPKA1	human	autophagy; ec 2.7.1.-; ec 2.7.11	a protein kinase of the CAMKL family that p	5562	NP_006242	T488	Q13131
AMPKA1	human	autophagy; ec 2.7.1.-; ec 2.7.11	a protein kinase of the CAMKL family that p	5562	NP_006242	S496	Q13131
AMPKA1	human	autophagy; ec 2.7.1.-; ec 2.7.11	a protein kinase of the CAMKL family that p	5562	NP_006242	S486	Q13131
AMPKA1	human	autophagy; ec 2.7.1.-; ec 2.7.11	a protein kinase of the CAMKL family that p	5562	NP_006242	T490	Q13131

The **Informatics Table** contains specific information for each identified peptide: Gene ontology protein type, accession numbers, site designation, PubMed references, ScanSite, Upstream and downstream genes. The Informatics Table also includes statistical data within the context of this study, peptide count in each curation set and in cell type.

Summary of Available Services

Service Offerings from Cell Signaling Technology

PTMScan® Discovery Services - a discovery-mode proteomics technology for identifying and quantifying post-translational modifications.

KinomeView™ Services - a western blotting service using Phospho-Motif Antibodies to provide a kinome-wide view of cellular phosphorylation.

PTMScan® Motif Antibody Kits and Proteomics System - product lines that enable the use of PTMScan Technology on your own.

AQUA™ Peptide Synthesis - custom synthesized, isotope-labeled AQUA peptides for validating and quantifying protein markers and post-translational modifications.

PTMScan® Direct Services - a targeted-mode proteomics screening technology with defined assay endpoints.