

**Verrastro et al. Supplementary Tables for  
“The effect of HOCl-induced modifications on PTEN structure and function”**

**Supplementary Table 1.** Identification and quantification of PTEN oxidative modifications in the PTEN-GST intact band and aggregates following HOCl oxidizing treatment.

Peptide sequence <sup>a</sup>	Enzyme <sup>b</sup>	Mod <sup>c</sup>	Fraction detected <sup>d</sup>		HOCl:PTEN-GST molar ratios				
					15:1	30:1	60:1	150:1	300:1
TVEEPSNPEA SSSTSVTPDV SDNEPDH <b>Y</b> R	Trypsin	<b>Tyr377 CHLOR*</b>	Aggregates	FC	0	Infinity	Infinity	Infinity	Infinity
				p-value	>0.9999	>0.9999	0.6843	0.9908	<b>0.0417</b>
				%	0.00	0.00	0.00	0.01	0.29
FM <b>Y</b> FEFPQPL PVCGLDIK	Trypsin	<b>Tyr240 OX*</b>	Aggregates	FC	10.06	47.11	84.95	323.25	<b>1031.21</b>
				p-value	0.9997	0.3521	<b>0.0196</b>	<b>0.0001</b>	<b>0.0001</b>
				%	0.07	0.60	1.20	2.27	7.24
IYNL <b>C</b> AERHY DTAK	LysC	<b>Cys71 TRIOX*</b>	PTEN-GST band	FC	4.16	8.04	70.11	310.14	<b>405.21</b>
				p-value	> 0.9999	0.9998	0.5733	<b>0.0003</b>	<b>&lt;0.0001</b>
				%	0.12	0.24	2.08	9.20	12.02
FM <b>Y</b> FEFPQPL PVCGLDIKVEFF HK	LysC	<b>Tyr240 OX*</b>	PTEN-GST band	FC	4.20	5.67	28.18	197.52	<b>226.35</b>
				p-value	> 0.9999	0.9999	0.9868	<b>0.0252</b>	<b>0.0107</b>
				%	0.20	0.27	1.33	9.34	10.70
ADNDKE <b>Y</b> LVL TLTK	Trypsin	<b>Tyr315 CHLOR*</b>	PTEN-GST band	FC	1.22	4.82	25.45	88.76	<b>156.24</b>
				p-value	> 0.9999	0.9568	<b>0.0087</b>	<b>&lt; 0.0001</b>	<b>0.0001</b>
				%	0.07	0.27	1.44	5.03	8.85
			Aggregates	FC	0.92	0.86	0.80	3.66	3.56
				p-value	0.9999	0.9985	0.9801	<b>0.0131</b>	<b>0.0164</b>
				%	1.39	1.21	2.06	5.52	5.38
GRTGVMI <b>C</b> AY LLHRGK	LysC	<b>Cys136 TRIOX*</b>	PTEN-GST band	FC	0.91	1.22	11.59	<b>132.57</b>	131.08
				p-value	> 0.9999	> 0.9999	0.9958	<b>0.0039</b>	<b>0.0042</b>
				%	0.12	0.17	1.58	18.10	17.90
			Aggregates	FC	0.84	0.90	1.48	2.08	2.47
				p-value	0.9381	0.9874	0.2071	<b>0.0023</b>	<b>0.0002</b>
				%	23.61	25.04	41.39	58.32	69.00
TVEEPSNPEA SSSTSVTPDV SDNEPDH <b>Y</b> R	Trypsin	<b>Tyr377 DICHL*</b>	Aggregates	FC	6.31	9.78	15.99	41.92	<b>71.31</b>
				p-value	0.9916	0.6690	0.4131	<b>0.0305</b>	<b>0.0006</b>
				%	0.92	2.32	3.10	6.09	10.35
FM <b>Y</b> FEFPQPL PV <b>C</b> GLDIK	Trypsin	<b>Cys250 TRIOX*</b>	PTEN-GST band	FC	1.20	5.64	33.08	<b>51.84</b>	38.82
				p-value	> 0.9999	0.9899	<b>0.0449</b>	<b>0.0022</b>	<b>0.0176</b>
				%	1.60	7.52	44.11	69.12	51.76
			Aggregates	FC	1.77	2.26	3.66	13.20	16.48
				p-value	0.9674	0.2470	<b>0.0020</b>	<b>&lt; 0.0001</b>	<b>0.0001</b>
				%	5.34	11.02	22.54	39.74	49.61
YQEDGFDLDL TYIYPNIIA <b>M</b> GF PAER	Trypsin	<b>Met35 DIOX*</b>	PTEN-GST band	FC	1.05	1.07	1.98	14.78	20.67
				p-value	> 0.9999	> 0.9999	0.9982	<b>0.0059</b>	<b>0.0003</b>
				%	0.36	0.37	0.69	5.12	7.16
			Aggregates	FC	5.11	7.48	8.31	23.39	<b>42.33</b>
				p-value	0.7291	0.2585	0.1209	<b>0.0003</b>	<b>0.0001</b>
				%	1.13	1.84	2.24	5.18	9.37
<b>M</b> FHFVWNTFF IPGPEETSEK	LysC	<b>Met270 OX*</b>	PTEN-GST band	FC	0.27	0.61	1.92	<b>41.78</b>	27.76
				p-value	0.9999	> 0.9999	0.9999	<b>0.0021</b>	<b>0.0355</b>
				%	0.10	0.24	0.75	16.40	10.89
AQEALDF <b>Y</b> GE VRTRDK	LysC	<b>Tyr155 CHLOR*</b>	PTEN-GST band	FC	0.81	1.28	1.71	20.14	<b>24.67</b>
				p-value	> 0.9999	> 0.9999	0.9998	<b>0.0056</b>	<b>0.0011</b>
				%	0.02	0.02	0.03	0.39	0.47
			Aggregates	FC	0.64	0.84	1.65	3.21	2.28
				p-value	0.9864	0.9997	0.864	0.0546	0.3753
				%	0.59	0.76	1.50	2.92	2.08

AQEALDFYGE VR	Trypsin	Tyr155 CHLOR*	PTEN-GST band	FC	0.68	0.84	1.34	8.91	22.48
			Aggregates	p-value	0.9997	0.9999	0.9997	0.0035	< 0.0001
				%	0.32	0.39	0.62	4.14	10.45
				FC	0.91	0.77	0.57	1.52	3.42
				p-value	0.9885	0.2165	0.2214	0.1095	< 0.0001
				%	4.70	2.94	2.96	7.91	17.75
TGVMICAYLLH R	Trypsin	Cys136 DIOX*	PTEN-GST band	FC	2.68	3.71	12.40	15.39	3.63
				p-value	0.9952	0.9628	0.1075	0.0352	0.9672
				%	0.45	0.62	2.06	2.56	0.60
GRTGVMICAY LLHRGK	Lys C	Met134 OX*	PTEN-GST band	FC	1.25	1.13	2.58	14.14	12.15
				p-value	0.8655	0.8724	0.8247	0.0178	0.0065
				%	3.44	3.11	7.07	38.81	33.36
TGVMICAYLLH R	Trypsin	Cys136 TRIOX*	PTEN-GST band	FC	0.87	2.31	5.75	8.41	7.85
			Aggregates	p-value	0.9999	0.6478	0.0040	0.0001	0.0002
				%	9.22	24.41	60.64	88.72	82.82
				FC	1.00	1.01	1.04	1.11	1.12
				p-value	> 0.9999	0.5898	0.6901	0.0064	0.0048
				%	87.18	90.42	90.05	97.07	97.46
MFHFWVNTFF IPGPEETSEK	Trypsin	His272 OX*	Aggregates	FC	1.46	1.68	1.68	4.13	5.47
				p-value	0.8268	0.5526	0.6474	0.0002	< 0.0001
				%	5.50	6.33	6.05	15.58	20.65
TGVMICAYLLH R	Trypsin	Met134 OX*	PTEN-GST band	FC	0.91	1.64	4.01	5.05	4.89
			Aggregates	p-value	0.9998	0.7326	0.0013	0.0001	0.0002
				%	13.07	23.52	57.49	72.39	70.11
				FC	1.03	1.07	1.00	1.10	1.19
				p-value	0.9779	> 0.9999	0.5731	0.2360	0.0138
				%	65.55	63.97	68.18	70.35	75.81
MFHFWVNTFF IPGPEETSEK	Trypsin	Met270 OX*	PTEN-GST band	FC	1.13	1.08	1.47	4.78	4.86
			Aggregates	p-value	0.9985	0.9997	0.7986	< 0.0001	0.0001
				%	17.90	17.09	23.27	75.51	76.89
				FC	1.12	1.17	1.23	1.22	1.05
				p-value	0.3084	0.0172	0.0019	0.0227	0.8982
				%	58.51	64.31	68.59	63.78	55.06
MFHFWVNTFF IPGPEETSEK	Trypsin	Trp274 OX*	Aggregates	FC	1.16	1.20	1.04	2.63	4.86
				p-value	0.9926	0.9999	0.9997	0.0065	< 0.0001
				%	8.88	7.98	7.00	20.10	37.18
GRTGVMICAY LLHRGK	LysC	Cys136 DIOX*	PTEN-GST band	FC	0.00	0.01	0.12	3.49	3.35
				p-value	0.9952	0.9628	0.1075	0.0352	0.9672
				%	0.00	0.00	0.11	3.14	3.01
MMFETIPMFS GGTCNPQFVV CQLK	Trypsin	Met205 OX*	PTEN-GST band	FC	0.95	0.58	0.57	0.23	2.43
			Aggregates	p-value	> 0.9999	0.9985	0.9985	0.9799	0.8160
				%	0.03	0.02	0.02	0.01	0.09
				FC	2.02	2.64	2.72	3.41	3.22
				p-value	0.5278	0.1311	0.0493	0.0254	0.0398
				%	22.71	30.59	35.29	38.40	36.30
FMYFEFPQPL PVCGLDIK	Trypsin	Met239 OX*	PTEN-GST band	FC	1.09	1.26	1.80	3.18	3.34
			Aggregates	p-value	0.9968	0.8082	0.0483	< 0.0001	0.0001
				%	23.06	26.67	38.17	67.24	70.65
				FC	1.21	1.40	1.56	1.97	2.31
				p-value	0.6932	0.0457	0.0354	0.0010	< 0.0001
				%	35.0135	44.9442	45.7299	56.9346	66.5483
YQEDGFDLDL TYIYPNIIAMGF PAER		Met 35 OX*	PTEN-GST band	FC	1.05	0.99	1.34	1.80	1.74
				p-value	0.9942	0.9999	0.0950	0.0003	0.0006
				%	52.79	49.61	67.18	90.22	87.34

	Trypsin		Aggregates	FC	0.92	0.99	1.06	1.11	1.24
				p-value	0.9433	0.9819	0.9998	0.8455	0.2735
				%	62.35	72.23	66.89	75.57	84.18
IYNLC <b>A</b> ER	Trypsin	<b>Cys71</b> <b>TRIOX</b>	PTEN-GST band	FC	1.20	2.62	3.58	4.20	3.42
				p-value	0.9998	0.7290	0.3467	0.1874	0.4026
				%	10.43	22.85	31.23	36.62	29.79
			Aggregates	FC	0.88	0.79	0.74	2.33	2.53
				p-value	0.9998	0.9971	0.9725	0.3804	0.2653
				%	3.72	3.14	2.37	9.84	10.70
TGV <b>M</b> ICAYLLH R	Trypsin	Met134 DIOX	PTEN-GST band	FC	0.85	2.59	1.20	0.38	1.01
				p-value	0.9997	0.1617	0.9985	0.8523	>
				%	13.07	23.52	57.49	72.39	0.9999
GRTGV <b>M</b> ICAY LLHRGK	LysC	Met134 DIOX	Aggregates	FC	1.01	0.75	1.02	2.42	2.30
				p-value	> 0.9999	0.9811	> 0.9999	0.0576	0.0866
				%	1.97	1.47	1.99	4.73	4.50
<b>M</b> MFETIPMFS GGTCNPQFVV CQLK	Trypsin	Met198 OX	PTEN-GST band	FC	0.96	1.32	1.27	1.09	1.36
				p-value	0.9999	0.8843	0.9388	0.9997	0.8426
				%	0.35	0.48	0.46	0.40	0.49
			Aggregates	FC	1.53	1.82	1.70	2.00	1.93
				p-value	0.5635	0.3338	0.2112	0.1034	0.1328
				%	38.16	42.23	45.30	49.67	48.18
<b>M</b> MFETIPMFS GGTCNPQFVV CQLK	Trypsin	Met199 OX	PTEN-GST band	FC	0.96	1.32	1.26	1.09	1.42
				p-value	0.9999	0.8920	0.9484	0.9989	0.7536
				%	0.35	0.48	0.46	0.40	0.52
			Aggregates	FC	1.57	1.93	1.63	1.86	1.92
				p-value	0.5032	0.6319	0.1596	0.5086	0.4257
				%	30.82	31.98	33.18	36.44	37.67
MMFETIP <b>M</b> FS GGTCNPQFVV CQLK	Trypsin	Pro204 OX	PTEN-GST band	FC	1.13	1.39	1.37	0.53	0.70
				p-value	0.9910	0.6105	0.6534	0.4490	0.7928
				%	33.36	41.09	40.49	15.50	20.54
			Aggregates	FC	0.94	0.87	0.97	0.88	0.97
				p-value	0.9965	0.9998	0.9631	0.9543	0.9997
				%	29.24	30.40	34.63	27.57	30.16
MMFETIP <b>M</b> FS GGTCNPQFVV CQLK	Trypsin	Met205 DIOX	PTEN-GST band	FC	1.10	0.63	0.37	0.39	0.85
				p-value	0.9998	0.9644	0.7835	0.8006	0.9996
				%	0.09	0.05	0.03	0.03	0.07
VKI <b>Y</b> SSNSGPT R	Trypsin	Tyr225 CHLOR	Aggregates	FC	0.99	0.96	1.14	1.35	1.40
				p-value	> 0.9999	0.8106	0.5871	0.1363	0.0780
				%	67.54	77.73	81.32	91.78	95.16
MFHFWVNTFF <b>I</b> PGEETSEK	Trypsin	Pro281 OX	PTEN-GST band	FC	0.37	0.77	0.65	0.00	0.00
				p-value	0.8137	0.9960	0.9770	0.4673	0.4673
				%	0.12	0.25	0.21	0.00	0.00
<b>Y</b> SDTTDSDE NEPDEDQHT QITK	Trypsin	<b>Tyr379</b> <b>CHLOR</b>	Aggregates	FC	7.37	12.40	14.83	170.06	459.86
				p-value	> 0.9999	0.9999	0.9107	0.8143	0.0944
				%	0.26	0.53	4.80	6.03	16.31
GRTGV <b>M</b> ICAY LLHRGK	LysC	<b>Met134</b> <b>DIOX</b>	Aggregates	FC	1.01	0.75	1.02	2.42	2.30
				p-value	> 0.9999	0.9811	> 0.9999	0.0576	0.0866
				%	1.97	1.47	1.99	4.73	4.50

a Peptide sequence obtained from the Mascot database search of LC-MS runs aligned on Progenesis Q1, carrying the modified residue (in red).

b Enzyme used for the digestion of

c Gel Fraction corresponding to the LC-MS run where the peptide was detected

d Modification type and position within the protein amino acid sequence

F.C = fold change relative to untreated control; p-value was returned by one-way ANOVA with Dunnett's multiple comparison test for each modification detected following relative quantification. % = average percentage abundance of the modification;

**Bold** indicates more than 2.5-maximum fold change in abundance of the modification in at least one HOCl to PTEN-GST molar ratio used; \* indicates modification with a statistically significant increase in abundance, and the significant p-values are highlighted in **bold red**. Infinity indicates FC values obtained when the abundance of the modification in the untreated control was 0.

The data was obtained from the analysis of PTEN-GST intact band and protein aggregates features present in three independent HOCl oxidation experiments.

Ranking of modifications with \* is based on maximum FC, highlighted in **bold blue**. Ranking of other modification is based on their position within PTEN structure.

**Supplementary Table 2. Surface accessibility of PTEN residues**

AA <sup>a</sup>	AA position <sup>b</sup>	RSA <sup>c</sup>	ASA <sup>d</sup>	Z-Score	Class assignment
M	1	0.625	125.143	-2.026	Exposed
T	2	0.425	58.892	-0.289	Exposed
A	3	0.495	54.582	-0.833	Exposed
I	4	0.307	56.832	0.949	Exposed
I	5	0.162	30.062	-0.631	Buried
K	6	0.274	56.465	0.904	Buried
E	7	0.421	73.619	0.447	Exposed
I	8	0.103	19.073	0.663	Buried
V	9	0.098	15.124	-0.324	Buried
S	10	0.416	48.708	-0.458	Exposed
R	11	0.494	113.24	0.467	Exposed
N	12	0.345	50.523	0.018	Exposed
K	13	0.441	90.631	-0.405	Exposed

AA <sup>a</sup>	AA position <sup>b</sup>	Total	Apolar	Backbone	Sidechain	Ratio (%)	Class assignment
R	14	223.13	109.05	27.57	195.57	100	e
R	15	105.18	39.11	7.18	98	50.1	e
Y	16	102.3	64.06	4.34	97.96	50.7	e
Q	17	71.89	8.43	17.93	53.96	37.6	i
E	18	31.36	10.42	9.65	21.71	15.4	b
D	19	100.54	37.05	30.35	70.19	62.1	e
G	20	68.42	35.77	68.42	0	78.5	e
F	21	83.85	69.03	29.11	54.74	30.4	i
D	22	96.71	29.6	14.88	81.83	72.4	e
L	23	13.41	13.41	1.75	11.66	8	b
D	24	32.49	11.81	0.24	32.25	28.5	i
L	25	0.49	0.1	0.39	0.1	0.1	b
T	26	3.44	3.44	2.02	1.42	1.3	b
Y	27	39.59	38.2	1.08	38.51	19.9	b
I	28	6.52	0	6.52	0	0	b
Y	29	36.99	36.21	5.36	31.63	16.4	b
P	30	114.09	109.51	11.45	102.64	97.6	e
N	31	41.62	9.54	0.25	41.38	36.2	i
I	32	5.99	5.99	0	5.99	4.1	b
I	33	0	0	0	0	0	b
A	34	0	0	0	0	0	b
M	35	0	0	0	0	0	b
G	36	2.05	2.05	2.05	0	2.4	b
F	37	7.1	5.07	2.05	5.05	2.8	b
P	38	0	0	0	0	0	b
A	39	1.04	0.74	0.36	0.69	1.1	b
E	40	93.03	29	26.3	66.72	47.3	i

R	41	190.84	87.36	10.07	180.77	92.5	e
L	42	79.45	75.1	4.35	75.1	51.4	e
E	43	123.71	46.35	13.95	109.77	77.7	e
G	44	66.83	47.58	66.83	0	76.6	e
V	45	91.43	83.93	14.75	76.68	62.7	e
Y	46	29.42	24.85	5.07	24.36	12.6	b
R	47	180.11	74.06	15.84	164.27	84	e
N	48	5.78	3.21	3.16	2.63	2.3	b
N	49	59.73	5.01	0.63	59.1	51.7	e
I	50	4.56	4.56	0	4.56	3.1	b
D	51	64.65	14.92	1.62	63.03	55.8	e
D	52	45.27	3.52	0	45.27	40.1	i
V	53	0	0	0	0	0	b
V	54	23.14	23.14	0	23.14	18.9	b
R	55	131.63	69.96	6.77	124.86	63.9	e
F	56	0	0	0	0	0	b
L	57	0	0	0	0	0	b
D	58	45.25	27.53	5.98	39.27	34.8	i
S	59	80.59	52.74	41.11	39.48	51	e
K	60	97.55	63.22	29.79	67.76	41.2	i
H	61	24.44	18.04	6.48	17.97	11.6	b
K	62	149.21	108.18	5.16	144.04	87.6	e
N	63	92.69	35.83	9.85	82.83	72.5	e
H	64	61.27	42.64	0.07	61.2	39.6	i
Y	65	1.72	0.14	1.58	0.14	0.1	b
K	66	22.24	2.34	0	22.24	13.5	b
I	67	0	0	0	0	0	b
Y	68	0	0	0	0	0	b
N	69	0.49	0	0.02	0.46	0.4	b
L	70	0	0	0	0	0	b
C	71	5.06	0	3.39	1.66	1.6	b
A	72	40.75	16.66	26.28	14.47	22.3	i
E	73	80.91	45.69	30.71	50.2	35.6	i
R	74	130.96	56.78	6.42	124.54	63.7	e
H	75	76.3	55.17	19.37	56.93	36.8	i
Y	76	6.69	5.9	6.69	0	0	b
D	77	113.28	34.01	9.09	104.2	92.2	e
T	78	48.42	9.98	8.76	39.66	37.3	i
A	79	84.99	66.63	34.64	50.35	77.6	e
K	80	101.7	78.35	14.97	86.73	52.7	e
F	81	4.85	0	4.85	0	0	b
N	82	90.64	30.88	15.63	75.01	65.6	e
C	83	39.95	22.13	36.7	3.24	3.2	b
R	84	149.84	75.13	7.8	142.04	72.7	e
V	85	8.02	3.41	4.62	3.4	2.8	b
A	86	9.48	9.48	1.63	7.85	12.1	b
Q	87	94.74	16.57	21.95	72.79	50.7	e
Y	88	30.29	18.54	0.61	29.67	15.4	b
P	89	67.22	54.69	12.53	54.69	52	e

F	90	14.04	14.04	5.68	8.35	4.6	b
E	91	74.36	34.38	0.29	74.06	52.5	e
D	92	54.59	24.33	8.96	45.63	40.4	i
H	93	114.36	90	3.99	110.37	71.4	e
N	94	23.66	2.24	0.71	22.95	20.1	i
P	95	8.23	1.27	6.97	1.27	1.2	b
P	96	1.63	0.99	1.63	0	0	b
Q	97	97.29	22.52	2.2	95.09	66.2	e
L	98	4.54	3.5	1.04	3.5	2.4	b
E	99	105.29	34.87	8.27	97.02	68.7	e
L	100	41.59	41.57	3.01	38.58	26.4	i
I	101	0.31	0.31	0	0.31	0.2	b
K	102	96.77	73.04	0.03	96.73	58.8	e
P	103	62.95	60.57	4.2	58.75	55.8	e
F	104	0	0	0	0	0	b
C	105	0	0	0	0	0	b
E	106	76.23	30.42	4.36	71.87	50.9	e
D	107	32.68	16.81	10.04	22.64	20	i
L	108	0	0	0	0	0	b
D	109	41.6	0.35	0.13	41.47	36.7	i
Q	110	93.42	34.86	2.28	91.14	63.4	e
W	111	24.48	24.48	0	24.48	10.9	b
L	112	18.33	7.22	11.12	7.22	4.9	b
S	113	70.47	51.28	29.25	41.22	53.3	e
E	114	108.9	61.82	22.8	86.1	61	e
D	115	62.26	25.98	38.04	24.22	21.4	i
D	116	93.7	18.6	33.31	60.39	53.4	e
N	117	25.01	2.72	2.72	22.29	19.5	b
H	118	68.86	55.41	0	68.86	44.5	i
V	119	6.42	6.42	0	6.42	5.2	b
A	120	0	0	0	0	0	b
A	121	0.01	0.01	0	0.01	0	b
I	122	0	0	0	0	0	b
H	123	0	0	0	0	0	b
C	124	4.86	0	0	4.86	4.8	b
K	125	39.52	17.97	2.61	36.9	22.4	i
A	126	46.97	40.96	8.24	38.73	59.7	e
G	127	1.19	0	1.19	0	1.4	b
K	128	87.8	83.55	0.27	87.53	53.2	e
G	129	10.09	8.85	10.09	0	11.6	b
R	130	7.19	3.11	0.56	6.63	3.4	b
T	131	0	0	0	0	0	b
G	132	0	0	0	0	0	b
V	133	0	0	0	0	0	b
M	134	0	0	0	0	0	b
I	135	0	0	0	0	0	b
C	136	0	0	0	0	0	b
A	137	0	0	0	0	0	b
Y	138	6.39	2.45	0	6.39	3.3	b

L	139	1.95	1.95	0	1.95	1.3	b
L	140	10.76	1.63	9.16	1.6	1.1	b
H	141	48.45	23.73	18.54	29.9	19.3	b
R	142	146.16	39.7	19	127.16	65	e
G	143	42.16	22.98	42.16	0	48.3	i
K	144	117.6	65.86	19.52	98.08	59.6	e
F	145	37.9	37.78	1.95	35.95	20	b
L	146	136.85	129.59	9.16	127.68	87.3	e
K	147	126.69	90.14	2.03	124.66	75.8	e
A	148	3	2.12	0.88	2.12	3.3	b
Q	149	100.77	22.34	0.15	100.62	70	e
E	150	67.68	36.32	9.44	58.24	41.2	i
A	151	0	0	0	0	0	b
L	152	4.47	0.39	4.08	0.39	0.3	b
D	153	70.53	26.32	7.95	62.58	55.4	e
F	154	57.22	57.22	3.13	54.08	30	i
Y	155	0	0	0	0	0	b
G	156	2.47	2.47	2.47	0	2.8	b
E	157	77.34	15.54	0.89	76.45	54.1	e
V	158	28.45	28.45	0.98	27.46	22.5	i
R	159	10.17	5.49	0.26	9.91	5.1	b
T	160	12.67	12.42	0.25	12.42	11.7	b
R	161	139.76	62.73	28.98	110.77	56.7	e
D	162	73.48	38.8	15.77	57.71	51.1	e
K	163	145.82	88.33	21	124.82	75.9	e
K	164	113.69	74.64	0.85	112.83	68.6	e
G	165	3.34	1.07	3.34	0	3.8	b
V	166	3.44	0.18	3.26	0.18	0.1	b
T	167	37.46	25.66	8.36	29.1	27.4	i
I	168	30.2	30.2	0.32	29.88	20.3	i
P	169	11.56	10.55	1.63	9.93	9.4	b
S	170	0.09	0.09	0	0.09	0.1	b
Q	171	0.57	0	0	0.57	0.4	b
R	172	60.97	32.48	0	60.97	31.2	i
R	173	30.38	21.53	6.45	23.93	12.2	b
Y	174	0.07	0.07	0	0.07	0	b
V	175	0	0	0	0	0	b
Y	176	94.9	84.79	2.61	92.29	47.8	i
Y	177	20.92	18.76	0.51	20.41	10.6	b
Y	178	3.86	2.91	0	3.86	2	b
S	179	5.63	3.11	1.16	4.48	5.8	b
Y	180	98.71	64.47	1.15	97.56	50.5	e
L	181	9.01	8.7	0.31	8.7	6	b
L	182	54.31	51.04	6.95	47.36	32.4	i
K	183	125.09	95.21	27.32	97.77	59.4	e
N	184	60.66	13.56	21.21	39.45	34.5	i
H	185	161.65	119.85	29.09	132.57	85.7	e



L	186	77.61	68.27	13.53	64.08	43.8	i
D	187	108.01	34.38	10.3	97.71	86.5	e
Y	188	34.36	15.26	16.25	18.1	9.4	b
R	189	170.47	75.89	1.14	169.33	86.6	e
P	190	95.65	78.22	17.43	78.22	74.4	e
V	191	42.89	42.89	3.7	39.19	32	i
A	192	47.41	42.12	5.29	42.12	64.9	e
L	193	0.31	0.04	0.27	0.04	0	b
L	194	53.88	53.88	0	53.88	36.9	i
F	195	0.14	0.14	0	0.14	0.1	b
H	196	43.72	28.36	5.24	38.48	24.9	i
K	197	31.65	8.29	0	31.65	19.2	b
M	198	0	0	0	0	0	b
M	199	18.13	18.13	0	18.13	11.5	b
F	200	0	0	0	0	0	b
E	201	41.55	7.94	1.09	40.46	28.7	i
T	202	31.35	30.8	0.01	31.34	29.5	i
I	203	21.94	15.83	6.28	15.66	10.6	b
P	204	0.12	0.12	0.12	0	0	b
M	205	63.81	58.97	5.15	58.66	37.1	i
F	206	38.11	14.14	28.34	9.77	5.4	b
S	207	42.26	18.31	15.74	26.52	34.3	i
G	208	85.78	57.06	85.78	0	98.4	e
G	209	46.34	33.65	46.34	0	53.1	e
T	210	54.49	34.95	0	54.49	51.3	e
C	211	7.6	0.82	7.6	0	0	b
N	212	65.84	6.51	0.97	64.88	56.8	e
P	213	0.19	0.07	0.12	0.07	0.1	b
Q	214	9.5	1.03	0.37	9.13	6.4	b
F	215	5.56	5.56	0	5.56	3.1	b
V	216	29.15	28.47	0.67	28.47	23.3	i
V	217	0	0	0	0	0	b
C	218	24.08	1.52	0	24.08	23.5	i
Q	219	43.93	3.08	0.27	43.66	30.4	i
L	220	84.89	82.82	4.89	80.01	54.7	e
K	221	176.37	110.59	33.3	143.07	87	e
V	222	98.18	98.18	3.69	94.49	77.3	e
K	223	149.85	91.3	14.21	135.64	82.5	e
I	224	60.44	38.19	30.15	30.3	20.6	i
Y	225	54.73	40.95	7.04	47.68	24.7	i
S	226	72.4	33.67	19.86	52.54	67.9	e
S	227	15.64	8.81	8.83	6.81	8.8	b
N	228	119.12	58.93	17.07	102.06	89.3	e
S	229	52.02	34.19	13.83	38.19	49.3	i
G	230	22.46	16.76	22.46	0	25.8	i
P	231	35.5	17.43	18.09	17.41	16.6	b
T	232	78.82	51.97	39.9	38.92	36.6	i
R	233	105.48	73.5	7.64	97.84	50	e
R	234	114.6	52.15	24.05	90.55	46.3	i

E	235	79.99	45.32	9.1	70.89	50.2	e
D	236	99.17	43.85	9.63	89.54	79.2	e
K	237	127.61	87	0.71	126.89	77.1	e
F	238	59.52	59.52	0	59.52	33	i
M	239	4.7	4.7	0	4.7	3	b
Y	240	22.78	8.63	0	22.78	11.8	b
F	241	2.78	2.68	0.41	2.37	1.3	b
E	242	66.83	18.59	8.05	58.78	41.6	i
F	243	12.82	1.18	11.81	1.01	0.6	b
P	244	98.74	78.59	34.67	64.07	60.9	e
Q	245	128.06	68.32	4.61	123.45	85.9	e
P	246	62.79	55.68	7.42	55.37	52.6	e
L	247	13.06	13.06	2.38	10.69	7.3	b
P	248	95.59	92.37	3.23	92.36	87.8	e
V	249	2.76	1.98	2.76	0	0	b
C	250	42.32	18.24	7.29	35.03	34.2	i
G	251	13.53	13.53	13.53	0	15.5	b
D	252	10.06	1.15	1.5	8.56	7.6	b
I	253	3.43	3.43	0	3.43	2.3	b
K	254	43.04	9.36	0.02	43.03	26.2	i
V	255	0.36	0.36	0	0.36	0.3	b
E	256	27.29	2.09	0	27.29	19.3	b
F	257	0.03	0	0.03	0	0	b
F	258	21.21	21.21	0	21.21	11.8	b
H	259	0.47	0.47	0	0.47	0.3	b
K	260	66.99	47.95	3.55	63.44	38.6	i
Q	261	44.34	14.74	6.61	37.73	26.3	i
N	262	92.57	43.07	15.02	77.55	67.8	e
K	263	195.49	141.34	36.12	159.38	96.9	e
M	264	111.29	99	21.23	90.07	56.9	e
L	265	190.76	171.01	27.66	163.11	100	e
K	266	134.4	94.91	14.2	120.2	73.1	e
K	267	78.71	25.7	14.03	64.69	39.3	i
D	268	60.14	18.07	5.85	54.29	48	i
K	269	97.57	84.55	4	93.57	56.9	e
M	270	0.62	0	0.62	0	0	b
F	271	0.6	0.48	0.6	0	0	b
H	272	31.53	18.71	0	31.53	20.4	i
F	273	0.79	0.79	0	0.79	0.4	b
W	274	25.58	24.98	0	25.58	11.4	b
V	275	2.74	2.74	0	2.74	2.2	b
N	276	0.43	0	0	0.43	0.4	b
T	277	0.19	0.19	0	0.19	0.2	b
F	278	32.44	24.88	7.55	24.88	13.8	b
F	279	29.9	12.19	20.48	9.42	5.2	b
I	280	18.35	1.08	17.35	1	0.7	b
P	281	82.58	54.28	54.76	27.82	26.4	i
G	282	247.54	161.65	67.66	179.88	100	e
P	283	146.54	44.25	40.34	106.19	75.2	e

E	284	59.77	21.64	15.01	44.76	23.2	i
E	285	33.8	33.8	10.43	23.38	16	b
T	286	69.58	41.97	27.62	41.95	34.3	i
S	287	43.54	43.54	1.9	41.64	28.5	i
E	288	59.02	20.1	14.3	44.71	42.1	i
K	289	8.46	8.46	0	8.46	5.8	b
V	290	48.32	44.23	0	48.32	45.5	i
E	291	15.32	14.57	0.02	15.3	9.3	b
N	292	103.91	28.56	9.41	94.5	82.7	e
G	293	49.68	5.6	2.07	47.61	42.1	i
S	294	0	0	0	0	0	b
L	295	10.16	1.69	8.03	2.13	1.9	b
C	296	98.62	75.72	5.24	93.38	56.8	e
D	297	1.25	1.25	1.25	0	0	b
Q	298	13.14	4.49	1.88	11.26	9.9	b
E	299	116.76	67.96	17.26	99.5	60.5	e
I	300	18.34	14.86	9.11	9.23	8.2	b
D	301	146.01	109.15	20.17	125.83	76.5	e
S	302	77.13	65.55	27.15	49.99	77	e
I	303	59.06	13.63	11.78	47.28	41.4	i
C	304	168.36	64.7	13.78	154.58	79.1	e
S	305	107.27	66.86	0	107.27	55.6	e
I	306	2.83	2.83	0.37	2.45	1.4	b
E	307	29.93	28.64	0.47	29.46	38.1	i
R	308	74.31	74.31	4.09	70.22	66.8	e
A	309	103.17	25.6	15.38	87.79	76.8	e

AA <sup>a</sup>	AA position <sup>b</sup>	RSA <sup>c</sup>	ASA <sup>d</sup>	Z-Score	Class assignment <sup>e</sup>
D	310	0.424	61.026	-1.278	Exposed
N	311	0.44	64.401	-2.283	Exposed
D	312	0.369	53.216	-2.157	Exposed
K	313	0.277	56.897	-1.363	Buried
E	314	0.316	55.258	-1.470	Exposed
Y	315	0.177	37.932	0.048	Buried
L	316	0.092	16.809	-0.174	Buried
V	317	0.097	14.863	0.417	Buried
L	318	0.041	7.58	-0.148	Buried
T	319	0.273	37.851	0.733	Exposed
L	320	0.031	5.694	0.612	Buried
T	321	0.403	55.868	0.548	Exposed
K	322	0.227	46.714	0.052	Buried
N	323	0.517	75.689	-0.953	Exposed
D	324	0.391	56.386	-0.797	Exposed
L	325	0.098	17.999	-0.515	Buried
D	326	0.193	27.811	-0.911	Buried
K	327	0.62	127.616	-0.058	Exposed
A	328	0.316	34.867	-1.196	Exposed
N	329	0.274	40.172	-0.312	Buried

K	330	0.555	114.122	-0.170	Exposed
D	331	0.508	73.26	-0.896	Exposed
K	332	0.59	121.363	0.184	Exposed
A	333	0.546	60.202	0.237	Exposed
N	334	0.309	45.238	0.043	Exposed
R	335	0.682	156.178	0.613	Exposed
Y	336	0.332	71.034	0.663	Exposed
F	337	0.061	12.323	0.919	Buried
S	338	0.319	37.363	0.887	Exposed
P	339	0.758	107.503	-0.106	Exposed
N	340	0.63	92.217	0.415	Exposed
F	341	0.043	8.59	-0.172	Buried
K	342	0.427	87.875	1.712	Exposed
V	343	0.052	7.962	0.22	Buried
K	344	0.192	39.556	0.917	Buried
L	345	0.066	12.14	0.321	Buried
Y	346	0.16	34.256	0.832	Buried
F	347	0.043	8.65	-0.603	Buried
T	348	0.333	46.187	0.269	Exposed
K	349	0.555	114.225	0.06	Exposed
T	350	0.209	29.058	0.074	Buried
V	351	0.433	66.475	-0.384	Exposed
E	352	0.563	98.286	-0.035	Exposed
E	353	0.622	108.646	0.17	Exposed
P	354	0.262	37.22	-0.597	Exposed
S	355	0.67	78.524	0.089	Exposed
N	356	0.578	84.605	-0.571	Exposed
P	357	0.491	69.687	-1.625	Exposed
E	358	0.708	123.757	-0.558	Exposed
A	359	0.272	29.93	-0.330	Buried
S	360	0.536	62.772	-0.547	Exposed
S	361	0.62	72.711	-1.781	Exposed
S	362	0.462	54.1	-0.984	Exposed
T	363	0.543	75.342	-0.723	Exposed
S	364	0.615	72.031	-0.832	Exposed
V	365	0.276	42.452	-0.380	Exposed
T	366	0.484	67.089	-0.052	Exposed
P	367	0.405	57.498	-1.305	Exposed
D	368	0.566	81.546	-1.095	Exposed
V	369	0.324	49.799	-0.405	Exposed
S	370	0.37	43.329	-0.989	Exposed
D	371	0.625	90.077	-1.035	Exposed
N	372	0.623	91.163	-1.923	Exposed
E	373	0.534	93.22	-0.386	Exposed
P	374	0.287	40.754	-1.197	Buried
D	375	0.54	77.785	-1.074	Exposed
H	376	0.345	62.701	-0.945	Exposed
Y	377	0.325	69.41	-1.253	Exposed
R	378	0.612	140.217	-0.378	Exposed

Y	379	0.419	89.626	-1.669	Exposed
S	380	0.434	50.877	-1.696	Exposed
D	381	0.652	93.939	-1.746	Exposed
T	382	0.386	53.483	-0.547	Exposed
T	383	0.484	67.145	-2.135	Exposed
D	384	0.651	93.751	-1.375	Exposed
S	385	0.577	67.624	-1.643	Exposed
D	386	0.411	59.153	-0.394	Exposed
P	387	0.446	63.231	-0.994	Exposed
E	388	0.595	103.859	-0.758	Exposed
N	389	0.644	94.34	-0.928	Exposed
E	390	0.422	73.776	-0.732	Exposed
P	391	0.604	85.651	-1.141	Exposed
F	392	0.368	73.898	-1.544	Exposed
D	393	0.403	58.043	-0.967	Exposed
E	394	0.475	82.948	-2.052	Exposed
D	395	0.472	68.087	-1.271	Exposed
Q	396	0.289	51.633	-0.103	Buried
H	397	0.241	43.82	0.088	Buried
T	398	0.166	23.094	-0.150	Buried
Q	399	0.452	80.799	0.882	Exposed
I	400	0.129	23.958	-0.236	Buried
T	401	0.479	66.465	0.851	Exposed
K	402	0.562	115.645	0.516	Exposed
V	403	0.68	104.455	-0.634	Exposed

a AA=Amino acid. Residues 1-13 and the C-terminal tail (residue 352 onwards) are disordered in the crystal structure so for this region NetsurfP (ver. 1.1) (<http://www.cbs.dtu.dk/services/NetSurfP>) was used to predict solvent accessibility of PTEN residues using the PTEN FASTA sequence obtained from Uniprot [36]. Class assignment was predicted using a threshold of 50 exposed accessible surface area, based on the Absolute Solvent Accessibility<sub>max</sub> of a given amino acid. For Residues 14-351, class assignment was predicted using GETAREA with a probe diameter of 1.4Å (equivalent to water) and the 1d5r.pdb 3D-data file from the PDB database. The higher the ratio the more solvent accessible the residue. Ratios <20 are considered buried and >50 exposed. Intermediate values show some solvent accessibility.

b Amino acid position

c RSA= Relative Surface Accessibility

d ASA= Absolute Solvent Accessibility