厚生労働科学研究費補助金

創薬バイオマーカー探索研究事業

重層的・定量的トキシコモディフィコーム解析を用いた安全性バイオマーカーの探索に関する研究

平成21年度　総括研究報告書

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平成 22 年(2010 年)4 月

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重層的・定量的トキシコモディフィコーム解析を用いた安全性バイオマーカーの探索に関する研究

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研究要旨

SILAC法を用いた定量的プロテオーム解析によるトキシコモディフィコーム解析システムを試行した。モデル物質として、ダイオキシン受容体リガンドかつ、サイクリン依存性キナーゼ阻害剤でもあるインディルビンを用いた。その結果、変動したリン酸化蛋白質を7個同定した。また本システムの律速段階である、LC-MS/MSによる蛋白質同定・定量解析処理作業の自動化を進め、処理効率を大幅に向上させた。さらに、パスウェイ解析、ジーンオントロジー解析、学習型蛋白質機能推定解析を行い、試験物質が作用する蛋白質、シグナル経路、細胞内部位、細胞内機能を推定するための情報処理基盤を整備した。アセチル化リジンプロテオーム解析については、抗体を用いて修飾ペプチドの濃縮を行ったが、大規模解析に十分な濃縮結果が得られなかったため、代わりにユビキチン化プロテオーム解析を新たに立ち上げた。

A. 研究目的

毒性物質・薬剤の標的因子、作用メカニズムの解明のため、2次元ゲルや、安定同位体標識技術を用いたショットガン式定量技術を用いたプロテオーム解析が幅広く取り入れられている。既存研究の多くは蛋白質の“量”の変化を検出することに主眼が置いてきたが、“量”の変化はトランスクリプトーム解析でも検出可能な場合が多い一方で、“質”の変化、例えば分子標的薬の受容体拮抗によるリン酸化阻害のような、標的因子の“質”（翻訳後修飾）を変化させる例はプロテオーム解析でのみ測定可能である。このような“質”の変化をプロテオームレベルで捉えて、毒性作用との関連を見いだすために、本研究ではシステイン酸化・ユビキチン化・リン酸化解析の3種類の蛋白質翻訳後修飾について、毒性物質の影響を定量する解析システムを構築し、毒性物質や薬剤によって変化する蛋白質の翻訳後修飾を同定し、システイン酸化・ユビキチン化・リン酸化の3枚の修飾変化マップを重ねた重層翻訳後修飾マップを作成し、安全性バイオマーカーや毒性シグナルネットワークを推定することを研究目的とする。本年度はトキシコモディフィコーム解析システムを試行することを目的として、具体的には以下の研究を遂行した。前年度までに確立した、安定同位体標識アミノ酸による培養細胞内蛋白質標識法（SILAC法：Stable Isotopic Labeling using Amino Acids in Cell Culture法）を用いたリン酸化プロテオーム、システイン酸化プロテオーム解析手法を用いて、ダイオキシン受容体リガンドかつ、サイクリン依存性キナーゼ阻害剤でもあるインディルビンがリン酸化、システイン酸化に与える影響を定量した。ま

たリジンアセチル化、ユビキチン化蛋白質の定量解析手法の検討、バイオインフォマティクス基盤整備も同時に行った。

B. 研究方法

リン酸化プロテオーム解析

[$^{12}C_6$]アルギニンと[$^{12}C_6$]リジンもしくは[$^{13}C_6$]-アルギニンと[$^{13}C_6$]-リジンで標識した SILAC-HepG2 細胞を用意した。一方にインディルビンを 1 μM、他方にコントロールとして DMSO をそれぞれ 10 分間曝露し、曝露後、等量混合した。変動したリン酸化ペプチド・蛋白質を検出するために、酸化チタンビーズ、チロシンリン酸化抗体による濃縮法を併用した。

○酸化チタンビーズを用いたリン酸化ペプチド濃縮

上述の SILAC-HepG2 細胞を等量混合し、細胞溶解し、細胞質画分を調製した。細胞質画分を定法に従いリシルエンドペプチダーゼ C とトリプシンで消化した後、ペプチドを C18 カートリッジを用いて固相抽出した。続いて酸化チタンビーズ（GL Science）にリン酸化ペプチドを選択的に結合させた。なお選択性を高めるエンハンサーとして 25%酪酸を用いた。その後、5%アンモニアと 0.5%ピペリジンでリン酸化ペプチドを溶出し、C18 Stagetip で脱塩濃縮して LC-MS/MS に供した。LC-MS/MS の設定、データ解析方法は以下の通りである。C18 Stagetip から溶出させたペプチドを 0.5%酢酸、5%アセトニトリルに溶解させて LC (Hitachi nano LC)-MS/MS (Waters QTof ultima) で分析した。カラムは ReproSil-Pur C_{18}-AQ 3 μm resin (Dr. Maisch GmbH)を長さ 10 cm 内径 50 μm のヒューズドシリカチューブにパックしたものを使用し、移動相は A: 2%アセトニトリル、0.5%酢酸、B: 98%アセトニトリル、0.5%酢酸によるリニアグラジエント（流速 200 nl/min、測定時間 85 分）であった。MS 及び MS/MS 測定は MS1 秒、第 1MS/MS～第 3MS/MS 各 2 秒の合計 7 秒の自動測定（Data dependent analysis）で行い、*m/Z* 300-750、750-900、900-1100、1100-1600 の 4 分割したレンジで MS 測定した。データ処理は解析ソフト Mascot Server と Mascot Distiller を用いて行い、デコイデータベースによる検索で偽陽性確率が 5%以内となるように同定基準を定めた。

○チロシンリン酸化抗体による濃縮

上述の SILAC-HepG2 細胞を等量混合し、チロシンリン酸化抗体ビーズ（4G10、ミリポア）を用いて、チロシンリン酸化蛋白質を濃縮した。濃縮した蛋白質を 1 次元電気泳動で分離し、ゲル内消化法を用いてペプチドに断片化し、C18 Stagetip で脱塩濃縮して LC-MS/MS に供した。LC-MS/MS の設定、データ解析方法は上述の手法に以下の変更点を加えて行った。MS 及び MS/MS 測定は MS1 秒、第 1MS/MS～第 5MS/MS 各 1 秒の合計 1 秒の自動測定（Data Dependent Analysis）で行い、*m/Z* 300-1600 のレンジで MS 測定した。

システイン酸化プロテオーム解析

上述の SILAC-HepG2 細胞の一方にインディルビンを 1 μM、他方にコントロールとして DMSO を 8 時間曝露し、曝露後、等量混合し、細胞質画分を調製した。ヨード酢酸で分画中の蛋白質の還元型システイン(-SH)をブロックし、次に還元剤（DTT）で酸化型システインを還元し、Biotin-HPDP タグで標識した。その後、トリプシン消化、ストレプトアビジンビーズによる標識ペプチドの精製を行い、タグの付いたペプチドを脱塩濃縮してナノ LC-MS/MS でペプチドの同定・定量を行った。LC-MS/MS の設定、データ解析方法はチロシンリン酸化抗体による濃縮時と同じ手法を用いた。

アセチル化リジンプロテオーム解析

A549 細胞にヒストン脱アセチル化酵素(HDAC)阻害剤である、tricostatin A 0.3 μM (TSA; class I/II HDAC inhibitor) と sirtinol 50 μM (class III HDAC inhibitor)を 24 時間曝露後、細胞溶解し、細胞質画分を調製した。

また上記細胞質画分の他に、標準蛋白質としてアセチル化シトクロム C を用意し、それぞれをリ

シルエンドペプチダーゼ C とトリプシンで消化し、消化ペプチドを固相抽出した後、4 種類の抗アセチルリジン抗体（Immunochem Pharmaceuticals, Santacruz Biotech, Upstate, Cell Signaling Technology 社製）を用いて疫沈降法によりリジンアセチル化ペプチドを濃縮した。濃縮したアセチル化ペプチドを 0.05% トリフルオロ酢酸で溶出し、C18 Stagetip で脱塩濃縮して LC-MS/MS に供した。LC-MS/MS の設定、データ解析方法はチロシンリン酸化抗体による濃縮時と同じ手法を用いた。

ユビキチン化プロテオーム解析

上述の SILAC-HepG2 細胞の一方にプロテアソーム阻害剤 MG132 を 10 μM、他方にコントロールとして DMSO を 4 時間曝露し、曝露後、等量混合しユビキチン抗体を用いて、ユビキチン化蛋白質を濃縮した。濃縮した蛋白質を 1 次元電気泳動で分離し、ゲル内消化法を用いてペプチドに断片化し、C18 Stagetip で脱塩濃縮して LC-MS/MS に供した。LC-MS/MS の設定、データ解析方法はチロシンリン酸化抗体による濃縮時と同じ手法を用いた。

（倫理面への配慮）

本研究ではサンプルとして培養細胞を用いるため、人権・動物愛護に関する問題には抵触しません。

C. 研究結果

リン酸化プロテオーム解析

酸化チタンビーズを用いた濃縮法では、702 個の蛋白質、794 個のリン酸化ペプチド、961 個のリン酸化サイトを同定した（表 1）。そのうち 1.33 倍以上に増減が見られた蛋白質は ADP-ribosylation factor GTPase-activating protein 2 (0.65 倍)、Tight junction protein ZO-2 (1.36 倍)、FAM134C(1.42 倍)の 3 個であった。

チロシンリン酸化抗体による濃縮法では、236 個の蛋白質を同定した。そのうち 1.33 倍以上に増減が見られた蛋白質は Non-receptor tyrosine-protein kinase TYK2 (1.67 倍)、GTF21(1.50 倍)、40S ribosomal protein S10 (1.40 倍)、β actin(0.53 倍) の 4 個であった（表 2）。上記蛋白質のリン酸化はこれまでダイオキシン受容体シグナルの対象としては知られていないものである。

システイン酸化プロテオーム解析

DTT によって可逆的に酸化されるシステインを含むペプチドを 115 個、蛋白質を 107 個同定した。表 3 に示すようにこのなかで 1.33 倍以上に増減するペプチド、蛋白質は検出されなかった。

アセチル化リジンプロテオーム解析

アセチル化リジン抗体を用いて、アセチル化リジンを含むペプチドもしくは蛋白質を濃縮し、同定するという本研究の戦略の鍵はアセチル化リジン抗体の性能にある。そこで、アセチル化シトクロム C もしくはヒストン脱アセチル化酵素 (HDAC)阻害剤を曝露させた A549 細胞溶解液を用いて、抗体の性能を評価した。まずそれぞれのサンプルを消化して生成したペプチドを 4 種の抗体を用いて免疫沈降法で濃縮し、LC-MS/MS で同定を試みた。その結果、アセチル化シトクロム C を用いた場合、アセチル化リジンを含むペプチドは検出されなかった。また A549 細胞溶解液を用いて、濃縮効率を検討した結果、最も結果が良かった immuno chem parma 社の抗体を用いた場合でも同定されたペプチドのおよそ 1%がアセチル化ペプチドであった。

ユビキチン化プロテオーム解析

ユビキチン抗体を用いた免疫沈降法で濃縮したユビキチン化蛋白質を 1 次元電気泳動で分離し、ゲル内消化法を用いてペプチドに断片化し LC-MS/MS で同定、定量を行った結果、699 個の蛋白質が同定された。そのうち 0.75 倍以下に減少する蛋白質を 185 個、1.33 倍以上に増加する蛋白

質は 66 個同定した。この中には、HSP90 のように、同定された分画によって、ratio が異なる蛋白質も見られた。

データ解析

Mascot Server システムを導入し、LC-MS/MS による蛋白質同定・定量解析処理作業の自動化を進め、処理効率を大幅に向上させた。さらに、パスウェイ解析、ジーンオントロジー解析、学習型蛋白質機能推定解析を行い、試験物質が作用する蛋白質、シグナル経路、細胞内部位、細胞内機能を推定するための情報処理基盤を整備した。

D. 考察

SILAC 法は実験の初期段階で曝露群と非曝露群を混合し、その後の操作過程による影響を受けないため、極めて優れた定量精度を持つ。前年度は 1.5 倍以上の差異を検出可能であることを確認したが、今年度は、曝露群と対照群の細胞を入れ替えるスワップ実験をすることによって、1.33 倍以上の差異を検出可能であることを確かめた。蛋白質の翻訳後修飾サイトの同定は、通常の非修飾ペプチド配列の同定と比較して、擬陽性確率が高まるが、SILAC 法を用いた場合、同一配列の「軽い」ペプチドと「重い」ペプチドが偶然同一配列のペプチドに誤同定される確率は極めて低く、また MS/MS スペクトルを比較することで、y イオン、b イオンシリーズの判別がつくため（y イオンシリーズのみがリジンもしくはアルジニンを含むため、質量差を有する）、擬陽性確率を減らすことができる。この SILAC 法のメリットは特にリン酸化プロテオーム解析にて、ペプチド同定が正しいかどうか、MS/MS スペクトルをマニュアルでチェックする際に大きく貢献した。この利点は iTRAQ 法では得られないものであり、SILAC 法の大きなメリットである。

リン酸化プロテオーム解析については、インディルビンを曝露して 10 分後という短期間の non genomic な影響を、リン酸化ペプチドを濃縮する手法とチロシンリン酸化蛋白質を濃縮する方法を併用して調査した。その結果、それぞれの手法で 3 個、4 個、計 7 個の蛋白質のリン酸化が変動することを確認した。それぞれの手法で同定された蛋白質は大部分が重複していないため、リン酸化蛋白の同定数を増やすために有効であった。リン酸化ペプチドを濃縮する手法では、リン酸化サイトを直接同定・定量することが出来る反面、そのペプチドがうまくフラグメント化しなかったり、イオン化効率が低いなどの理由で同定できなかった場合も多かった。一方で蛋白質を濃縮する方法では、1 次元のゲルによって、細かく分離することができ、分子量情報も得られるが、リン酸化サイトまで同定できることはまれであった。

アセチル化リジンプロテオーム解析においては、免疫沈降で効率よくアセチル化ペプチドを濃縮することができないことが問題点である。同じ ICP 社の抗体を使用した研究がマン博士のグループから発表されたが、彼らの場合も 3%程度しか濃縮されなかったので、おそらく抗体価が不足していることが推測される。マンらは大量の抗体を使用することで大規模な解析を行っているが、本研究においては、そのような解析は費用面で困難である。そこで新たに、重要な翻訳後修飾の一つであるユビキチン化プロテオーム解析を実施することに変更した。

ユビキチン化プロテオーム解析では、抗体を用いて、ユビキチン化蛋白質を濃縮する手法を採用した。解析手法の確立を目的として、プロテアソーム阻害剤 MG132 の有無による、蛋白質の定量を行ったところ、699 個の蛋白質が同定された。そのうち 0.75 倍以下に減少する蛋白質を 185 個、1.33 倍以上に増加する蛋白質は 66 個同定できた。今年度、解析手法を確立したので、次年度以降、本手法もトキシコモディフィコーム解析システムに取り入れて、解析を進める予定である。

E. 結論

トキシコモディフィコーム解析システムを試行し、運用できることを確認した。同時にシステムの定量精度・感度・効率性を向上させた。また本研究の基盤技術となる、リン酸化、システイン酸化に加えてユビキチン化蛋白質を定量する手法を新たに確立した。

F. 健康危険情報

なし

G. 研究発表

1. 論文発表

なし

2. 学会発表

Jun Adachi, Keishi Kihara and Tomonari Matsuda, Oxidative modificomics analysis of cysteine thiols. 10th International Conference on Environmental Mutagens, Florence, Italy August 2009.

H. 知的財産権の出願・登録状況

特になし

表１　リン酸化プロテオーム解析結果

(TiO2 ビーズによる濃縮法を使用)

Fraction	z	Sequence	L/H	Std.Err.	Modifications
E1 03 2	3	AAAAGLGHPASPGGSEDGPPGSEEEDAAR	0.99833	0.03342	(11) Phospho (ST);(15) Phospho (ST)
E1 03 1	3	AAAAGLGHPASPGGSEDGPPGSEEEDAAR	0.91667	0.03674	(11) Phospho (ST);(22) Phospho (ST)
E1 03 2	3	AAAAGLGHPASPGGSEDGPPGSEEEDAAR	0.98083	0.02573	(11) Phospho (ST);(22) Phospho (ST)
E1 03	3	AALGLQDSDDEDAAVDIDEQIESMFNSK	0.93516	0.02928	(8) Phospho (ST)
E1 03 1	3	AALGLQDSDDEDAAVDIDEQIESMFNSK	1.13333	0.00869	(8) Phospho (ST)
E1 03 2	3	AALGLQDSDDEDAAVDIDEQIESMFNSK	1.14417	0.01679	(8) Phospho (ST)
E2 03 2	3	AALGLQDSDDEDAAVDIDEQIESMFNSK	1.18083	0.01193	(8) Phospho (ST)
E1 03 1	3	AALGLQDSDDEDAAVDIDEQIESMFNSK	1.0775	0.03497	(8) Phospho (ST);(24) Oxidation (M)
E1 03 2	3	AALGLQDSDDEDAAVDIDEQIESMFNSK	1.0875	0.0423	(8) Phospho (ST);(24) Oxidation (M)
E2 01 2	3	AASLNYLNQPSAAPLQVSR	0.89833	0.01815	(3) Phospho (ST)
E2 03 2	2	AASLNYLNQPSAAPLQVSR	0.93	0.01547	(3) Phospho (ST)
E2 03	2	AASLNYLNQPSAAPLQVSR	1.06383	0.02739	(3) Phospho (ST)
E2 01 1	3	AASLNYLNQPSAAPLQVSR	0.92833	0.01586	(3) Phospho (ST);(9) Deamidated (NQ)
E2 03 2	2	AASPPASASDLIEQQQK	0.82467	0.04506	(3) Phospho (ST)
E1 03 2	2	AASPPASASDLIEQQQK	0.91833	0.02762	(3) Phospho (ST)
E1 03 1	2	AASPPASASDLIEQQQK	0.94167	0.02071	(3) Phospho (ST)
E1 03	2	AASPPASASDLIEQQQK	1.06308	0.04678	(3) Phospho (ST)
E1 02 2	3	AASSDQLRDNSPPPAFKPEPPK	1.36167	0.04048	(3) Phospho (ST);(11) Phospho (ST)
E1 02 1	3	AASSDQLRDNSPPPAFKPEPPK	1.3875	0.03507	(4) Phospho (ST);(11) Phospho (ST)
E1 03 2	3	ADAPDAGAQSDSELPSYHQNDVSLDR	1.04	0.01166	(10) Phospho (ST)
E1 03 1	3	ADAPDAGAQSDSELPSYHQNDVSLDR	1.0575	0.02245	(10) Phospho (ST)
E2 01 1	2	ADLINNLGTIAK	1.00417	0.0998	
E1 02 1	2	ADSGEGDFLAEGGGVR	0.74383	0.03353	(3) Phospho (ST)
E1 02 2	2	ADSGEGDFLAEGGGVR	0.7615	0.0454	(3) Phospho (ST)
E2 02 1	2	ADSGEGDFLAEGGGVR	0.78067	0.02702	(3) Phospho (ST)
E2 02 2	2	ADSGEGDFLAEGGGVR	0.79383	0.02895	(3) Phospho (ST)
E1 02	2	ADSGEGDFLAEGGGVR	1.15385	0.01364	(3) Phospho (ST)
E1 03 1	4	ADVLEAHEAEAEEPEAGKSEAEDDEDEVDDLP SSR	1.18333	0.038	(19) Phospho (ST)
E1 03 2	4	ADVLEAHEAEAEEPEAGKSEAEDDEDEVDDLP SSR	1.18667	0.03172	(19) Phospho (ST)
E2 02 2	2	AEEDEILNRSPR	0.78583	0.0308	(10) Phospho (ST)
E2 01 1	3	AEEDEILNRSPR	0.80992	0.01522	(10) Phospho (ST)
E2 02 1	2	AEEDEILNRSPR	0.81342	0.03699	(10) Phospho (ST)
E2 01 2	3	AEEDEILNRSPR	0.81583	0.02661	(10) Phospho (ST)
E1 01 1	3	AEEDEILNRSPR	0.84583	0.01911	(10) Phospho (ST)
E1 01 3	3	AEEDEILNRSPR	0.87833	0.01175	(10) Phospho (ST)
E1 02	2	AEEDEILNRSPR	1.28866	0.01487	(10) Phospho (ST)
E2 01 1	3	AEEDEILNRSPR	0.82317	0.0611	(8) Deamidated (NQ);(10) Phospho (ST)
E1 01 3	2	AFLAELEQNSPK	0.79758	0.00953	(10) Phospho (ST)
E1 01 3	2	AFLAELEQNSPK	0.79758	0.00953	(10) Phospho (ST)
E2 02 1	2	AFLSPPTLLEGPLR	0.70183	0.01764	(4) Phospho (ST)
E2 02 2	2	AFLSPPTLLEGPLR	0.70892	0.01458	(4) Phospho (ST)
E1 01 3	2	AFSDPFVEAEK	1.1625	0.09088	(3) Phospho (ST)
E1 04 1	2	AFVEDSEDEDGAGEGGSSLLQK	0.90583	0.0113	(6) Phospho (ST)
E1 02	2	AGDLLEDSPKRPK	0.87873	0.08724	(8) Phospho (ST)
E1 02 2	2	AGDLLEDSPKRPK	0.9125	0.02004	(8) Phospho (ST)
E2 01 2	3	AGDLLEDSPKRPK	0.92833	0.01845	(8) Phospho (ST)
E1 01 1	3	AGDLLEDSPKRPK	0.995	0.01169	(8) Phospho (ST)
E1 01 3	3	AGDLLEDSPKRPK	0.99583	0.01653	(8) Phospho (ST)
E1 03 1	3	AGEPNSPDAEEANSPDVTAGCDPAGVHPPR	1.36583	0.01427	(6) Phospho (ST);(14) Phospho (ST)
E1 03 2	3	AGEQQLSEPEDMEMEAGDTDDPPR	1.3425	0.0693	(7) Phospho (ST)
E1 02 2	2	AGLESGAEPGDGDSDTTK	1.12167	0.0581	(17) Phospho (ST)
E1 02 2	2	AGSISTLDSLDFAR	0.94833	0.02145	(3) Phospho (ST)
E1 02 1	2	AGSISTLDSLDFAR	0.99833	0.01181	(3) Phospho (ST)
E1 02	2	AGSISTLDSLDFAR	1.02389	0.00936	(3) Phospho (ST)
E2 02 2	2	AGSISTLDSLDFAR	1.08583	0.07353	(3) Phospho (ST)
E2 01 1	3	AHLTVGQAAAGGSGNLLTER	0.76642	0.03915	(13) Phospho (ST)
E2 01 2	3	AHLTVGQAAAGGSGNLLTQR	0.71092	0.06265	(13) Phospho (ST);(19) Deamidated (NQ)
E2 02 1	3	AIGGILTASHNPGGPNGDFGIK	1.0025	0.00743	(10) Phospho (ST);(17) Deamidated (NQ)
E2 02 2	3	AIGGILTASHNPGGPNGDFGIK	1.03667	0.01091	(10) Phospho (ST);(17) Deamidated (NQ)
E2 01 1	2	AISSDMFFGR	0.64442	0.03024	(3) Phospho (ST)
E2 01 2	2	AISSDMFFGR	0.665	0.02012	(3) Phospho (ST)
E1 01	2	AISSDMFFGR	0.70588	0.06284	(3) Phospho (ST)
E2 01 1	2	AITSLLGGGSPK	1.0775	0.0434	(10) Phospho (ST)
E1 03 2	3	ALAEEASEEELPSDVDLNDPYFAEEVK	1.115	0.01433	(7) Phospho (ST);(13) Phospho (ST)
E2 04	2	ALDISLSSGEEDEGDEEDSTAGTTK	1.17555	0.03403	(7) Phospho (ST);(8) Phospho (ST)
E2 01 1	4	ALELPLAASSIPRPRTPSPESHR	1.09833	0.03906	(16) Phospho (ST);(18) Phospho (ST)
E2 01 2	4	ALELPLAASSIPRPRTPSPESHR	1.15667	0.04759	(16) Phospho (ST);(18) Phospho (ST)
E1 04 1	3	ALENGDADEPSFSDPEDFVDDVSEEELLGDVL K	1.12083	0.02617	(11) Phospho (ST);(13) Phospho (ST);(23) Phospho (ST)
E1 04 3	3	ALENGDADEPSFSDPEDFVDDVSEEELLGDVL K	1.14417	0.00584	(13) Phospho (ST)
E2 04 2	3	ALENGDADEPSFSDPEDFVDDVSEEELLGDVL K	1.17083	0.02716	(4) Deamidated (NQ);(11) Phospho (ST);(13) Phospho (ST)
E1 04 3	3	ALENGDADEPSFSDPEDFVDDVSEEELLGDVL K	1.2475	0.01376	(4) Deamidated (NQ);(11) Phospho (ST);(13) Phospho (ST)
E1 04 3	3	ALENGDADEPSFSDPEDFVDDVSEEELLGDVL K	1.18917	0.0283	(4) Deamidated (NQ);(11) Phospho (ST);(13) Phospho (ST);(23) Phospho (ST)
E2 01 1	3	ALESPERPFLAILGGAK	0.98083	0.01899	(4) Phospho (ST)
E2 01 2	3	ALESPERPFLAILGGAK	1.01417	0.02175	(4) Phospho (ST)
E2 03 1	2	ALSSGGSITSPPLSPALPK	0.98917	0.01711	(10) Phospho (ST)
E1 04	2	ALSSLHGDDQDSEDEVLTIPEVK	0.7371	0.04772	(12) Phospho (ST)
E1 02	3	ALSSLHGDDQDSEDEVLTIPEVK	0.88705	0.00913	(12) Phospho (ST)
E1 04 1	2	ALSSLHGDDQDSEDEVLTIPEVK	0.9525	0.01752	(12) Phospho (ST)
E1 02 1	3	ALSSLHGDDQDSEDEVLTIPEVK	0.96583	0.01854	(12) Phospho (ST)
E2 02 2	3	ALSSLHGDDQDSEDEVLTIPEVK	1.005	0.01793	(12) Phospho (ST)
E1 04 3	2	ALSSLHGDDQDSEDEVLTIPEVK	1.0225	0.04422	(12) Phospho (ST)
E1 02 2	3	ALSSLHGDDQDSEDEVLTIPEVK	1.04333	0.02281	(12) Phospho (ST)
E2 04 2	2	ALSSLHGDDQDSEDEVLTIPEVK	1.04583	0.02367	(12) Phospho (ST)
E1 02 2	3	ALVEFESNPEETREPGSPPSVQR	1.29333	0.01119	(12) Phospho (ST)
E1 02	3	ALVEFESNPEETREPGSPPSVQR	0.86957	0.02859	(17) Phospho (ST)
E2 02 2	3	ALVEFESNPEETREPGSPPSVQR	1.1775	0.02508	(17) Phospho (ST)
E1 02 2	3	ALVEFESNPEETREPGSPPSVQR	1.29333	0.01119	(17) Phospho (ST)
E1 03	2	ALVVPEPEPDSDSNQER	0.98039	0.02571	(13) Phospho (ST)
E1 03 1	2	ALVVPEPEPDSDSNQER	1.02667	0.01765	(13) Phospho (ST)
E1 03 2	2	ALVVPEPEPDSDSNQER	1.05417	0.01482	(13) Phospho (ST)
E1 03 2	3	AMDNHSDSEEELAAFCPQLDDSTVAR	0.9375	0.01332	(6) Phospho (ST);(8) Phospho (ST)
E1 01 3	3	AMLDQLMGTSRDGDTTR	1.13	0.04246	(10) Phospho (ST)
E2 03 1	2	ANSFVGTAQYVSPELLTEK	1.09	0.01722	(3) Phospho (ST)
E2 03 2	2	ANSFVGTAQYVSPELLTEK	1.1225	0.01731	(3) Phospho (ST)
E1 01 3	3	APSDSSLGTPSDGRPELR	1.20667	0.05792	(3) Phospho (ST)
E1 04 1	3	APVSSTESVIQSNTPTPPPSQPLNETAEEESR	1.32583	0.05209	(12) Phospho (ST)
E1 04 1	3	APVSSTESVIQSNTPTPPPSQPLNETAEEESR	1.19917	0.01227	(12) Phospho (ST);(14) Phospho (ST)
E1 04	3	APVSSTESVIQSNTPTPPPSQPLNETAEEESR	0.69832	0.02439	(14) Phospho (ST);(16) Phospho (ST)
E2 04 1	3	APVSSTESVIQSNTPTPPPSQPLNETAEEESR	1.11083	0.02396	(14) Phospho (ST);(16) Phospho (ST)
E1 04 3	3	APVSSTESVIQSNTPTPPPSQPLNETAEEESR	1.18833	0.01628	(14) Phospho (ST);(16) Phospho (ST)
E1 04 1	3	APVSSTESVIQSNTPTPPPSQPLNETAEEESR	1.19917	0.01227	(14) Phospho (ST);(16) Phospho (ST)
E2 04 1	3	APVSSTESVIQSNTPTPPPSQPLNETAEEESR	1.32583	0.05543	(16) Phospho (ST)
E1 01 3	3	AQGEPVAGHESPKIPYEK	0.96417	0.09786	(11) Phospho (ST)
E1 01 3	2	AQSPGAVEEILDR	0.84333	0.02497	(3) Phospho (ST)
E1 01 1	2	AQSPGAVEEILDR	0.89333	0.03407	(3) Phospho (ST)
E2 01 1	3	ARSPSVAAMASPQLCR	1.00333	0.01592	(3) Phospho (ST)
E2 01 2	3	ARSPSVAAMASPQLCR	1.08917	0.04337	(3) Phospho (ST);(9) Oxidation (M)
E2 01 1	3	ARSPSVAAMASPQLCR	1.17333	0.05875	(5) Phospho (ST)
E1 01 1	3	ARSVDALDDLTPPSTAESGSR	0.92583	0.03876	(3) Phospho (ST)
E2 01 2	2	ASAVSELSPR	0.92583	0.05781	(8) Phospho (ST)
E1 01	2	ASAVSELSPR	0.95541	0.00917	(8) Phospho (ST)
E2 01 1	2	ASAVSELSPR	0.9575	0.06759	(8) Phospho (ST)
E1 01 3	2	ASAVSELSPR	0.97	0.01484	(8) Phospho (ST)
E1 01 1	2	ASAVSELSPR	0.97583	0.01672	(8) Phospho (ST)
E1 01 1	3	ASLGSLEGEAEAEASSPK	0.78217	0.04043	(5) Phospho (ST)
E1 01 3	3	ASLGSLEGEAEAEASSPK	0.81325	0.0211	(5) Phospho (ST)
E1 03	2	ASLGSLEGEAEAEASSPK	1.67879	0.01194	(5) Phospho (ST)
E1 01 1	3	ASLGSLEGEAEAEASSPKGK	0.93667	0.09279	(16) Phospho (ST)
E1 02	3	ASPAPGSGHPEGPGAHLDMNSLDR	0.82418	0.09034	(2) Phospho (ST)
E1 02 2	3	ASPAPGSGHPEGPGAHLDMNSLDR	1.0525	0.03524	(2) Phospho (ST)
E1 02 1	3	ASPAPGSGHPEGPGAHLDMNSLDR	1.10583	0.02414	(2) Phospho (ST)
E1 02	2	ASPSPQPSSQPLQIHR	0.83241	0.02575	(4) Phospho (ST)
E1 03	2	ASPSPQPSSQPLQIHR	0.84602	0.02747	(4) Phospho (ST)
E2 01 2	3	ASPSPQPSSQPLQIHR	1.02333	0.0208	(4) Phospho (ST)
E1 02 1	2	ASPSPQPSSQPLQIHR	1.06833	0.01994	(4) Phospho (ST)
E1 03 2	2	ASPSPQPSSQPLQIHR	1.07333	0.02387	(4) Phospho (ST)
E1 02 2	2	ASPSPQPSSQPLQIHR	1.10917	0.01758	(4) Phospho (ST)
E2 01 1	2	ASSFADMMGILK	0.80383	0.01152	(3) Phospho (ST)
E2 01 2	2	ASSFADMMGILK	0.83667	0.01698	(3) Phospho (ST)
E2 01 1	2	ASSFADMMGILK	0.654	0.06255	(3) Phospho (ST);(8) Oxidation (M)
E2 01 1	2	ASSLEDLVLK	0.88	0.01559	(3) Phospho (ST)
E1 01 1	2	ASSLEDLVLK	0.89333	0.01688	(3) Phospho (ST)
E2 01	2	ASSLEDLVLK	1.24688	0.01797	(3) Phospho (ST)
E1 01	2	ASSLEDLVLK	1.3089	0.01214	(3) Phospho (ST)
E1 01 3	2	ASSLNVLNVGGK	0.91417	0.05207	(3) Phospho (ST)
E2 01 1	2	ASSLNVLNVGGK	0.92667	0.02604	(3) Phospho (ST)
E1 01 1	2	ASSLNVLNVGGK	0.97583	0.06544	(3) Phospho (ST)
E1 01 1	3	ASSPPDRIDIFGR	0.94917	0.01423	(3) Phospho (ST)
E1 01 3	3	ASSPPDRIDIFGR	0.95583	0.01875	(3) Phospho (ST)
E2 01 1	3	ASSPPDRIDIFGR	0.96	0.01774	(3) Phospho (ST)
E2 01 2	3	ASSPPDRIDIFGR	0.98667	0.01936	(3) Phospho (ST)
E1 03 1	2	ATDEDMQSLASLMSMK	0.99583	0.02129	(8) Phospho (ST);(11) Phospho (ST)
E1 02 1	3	ATTPPNQGRPDSPVYANLQELK	0.93833	0.04678	(3) Phospho (ST);(12) Phospho (ST)
E1 03 1	2	AVDSSSEEIEVEVPVVDR	0.96583	0.06579	(5) Phospho (ST);(6) Phospho (ST)
E1 01	3	AVDSSSEEIEVEVPVVDRR	0.19802	0.1863	(4) Phospho (ST)
E1 01 3	3	AVDSSSEEIEVEVPVVDRR	1.0925	0.08991	(4) Phospho (ST)
E2 02	3	AVDSSSEEIEVEVPVVDRR	0.82554	0.02737	(4) Phospho (ST);(5) Phospho (ST)
E1 04	2	AVDSSSEEIEVEVPVVDRR	0.85911	0.03366	(4) Phospho (ST);(5) Phospho (ST)
E2 02 2	3	AVDSSSEEIEVEVPVVDRR	1.05083	0.00995	(4) Phospho (ST);(5) Phospho (ST)
E2 02 1	3	AVDSSSEEIEVEVPVVDRR	1.06167	0.01146	(4) Phospho (ST);(5) Phospho (ST)
E1 04 3	2	AVDSSSEEIEVEVPVVDRR	1.06417	0.05259	(4) Phospho (ST);(5) Phospho (ST)
E1 02 2	3	AVDSSSEEIEVEVPVVDRR	1.19667	0.02794	(4) Phospho (ST);(5) Phospho (ST)
E1 02	3	AVDSSSEEIEVEVPVVDRR	1.29088	0.07837	(4) Phospho (ST);(5) Phospho (ST)
E1 02 1	3	AVDSSSEEIEVEVPVVDRR	1.2975	0.03193	(4) Phospho (ST);(5) Phospho (ST);(6) Phospho (ST)
E1 02 2	3	AVDSSSEEIEVEVPVVDRR	1.31	0.04134	(4) Phospho (ST);(5) Phospho (ST);(6) Phospho (ST)
E2 02 1	3	AVDSSSEEIEVEVPVVDRR	1.335	0.01866	(4) Phospho (ST);(5) Phospho (ST);(6) Phospho (ST)
E2 02 2	3	AVDSSSEEIEVEVPVVDRR	1.37917	0.02852	(4) Phospho (ST);(5) Phospho (ST);(6) Phospho (ST)
E2 04 2	2	AVDSSSEEIEVEVPVVDRR	1.445	0.02838	(4) Phospho (ST);(5) Phospho (ST);(6) Phospho (ST)
E2 04	2	AVDSSSEEIEVEVPVVDRR	0.77121	0.01602	(4) Phospho (ST);(6) Phospho (ST)

E1 02 2	3	AVPIAVADEGESESEDDDLKPR	0.78992	0.1581	(12) Phospho (ST);(14) Phospho (ST)
E2 02 2	3	AVQLMQQVASNGATLPSALSASK	0.67283	0.1365	(11) Deamidated (NQ);(22) Phospho (ST)
E1 01 3	3	AVTPVPTKTEEVSNLK	0.94917	0.0294	(3) Phospho (ST)
E1 01 1	3	AVTPVPTKTEEVSNLK	0.96167	0.03605	(3) Phospho (ST)
E2 01 1	3	AVTPVPTKTEEVSNLK	1.02417	0.04874	(3) Phospho (ST)
E2 02 2	2	AYTPVVVTLWYR	0.96833	0.03065	(3) Phospho (ST)
E2 02 1	2	AYTPVVVTLWYR	1.03417	0.02561	(3) Phospho (ST)
E2 04 2	3	CGSGPVHISGQHLVAVEEDAESEDEEEEDVK	1.03583	0.0421	(11) Deamidated (NQ);(22) Phospho (ST)
E2 02 2	4	CGSGPVHISGQHLVAVEEDAESEDEEEEDVK	1.075	0.03728	(11) Deamidated (NQ);(22) Phospho (ST)
E1 04	3	CGSGPVHISGQHLVAVEEDAESEDEEEEDVK	0.78125	0.02497	(22) Phospho (ST)
E2 04	3	CGSGPVHISGQHLVAVEEDAESEDEEEEDVK	0.80819	0.03154	(22) Phospho (ST)
E1 02	4	CGSGPVHISGQHLVAVEEDAESEDEEEEDVK	0.98684	0.00877	(22) Phospho (ST)
E2 02 2	4	CGSGPVHISGQHLVAVEEDAESEDEEEEDVK	1.07167	0.03672	(22) Phospho (ST)
E1 02 2	4	CGSGPVHISGQHLVAVEEDAESEDEEEEDVK	1.08083	0.00816	(22) Phospho (ST)
E1 02 1	4	CGSGPVHISGQHLVAVEEDAESEDEEEEDVK	1.09917	0.00733	(22) Phospho (ST)
E2 04 1	3	CGSGPVHISGQHLVAVEEDAESEDEEEEDVK	1.15	0.06462	(22) Phospho (ST)
E1 02 1	2	CTELNQAWSSLGK	0.82525	0.05058	(10) Phospho (ST)
E2 01	2	DAGTIAGLNVMR	1.41777	0.02642	
E1 01	3	DAPEEEDHVLVLR	1.50618	0.02234	
E1 01 1	3	DAQRLSPIPEEVPK	0.28817	0.07323	(6) Phospho (ST)
E1 03 1	2	DATNVGDEGGFAPNILENK	1.005	0.02528	
E1 01	3	DELHIVEAEAMNYEGSPIK	1.0989	0.04302	(16) Phospho (ST)
E1 02 2	2	DELQRQLDSMLAK	1.0675	0.01783	(4) Deamidated (NQ);(9) Phospho (ST)
E1 01 3	2	DFTPVCTTELGR	0.845	0.08129	
E2 01 1	3	DGLNQTTIPVSPPSTTKPSR	1.26333	0.06114	(11) Phospho (ST)
E2 01 2	3	DGLNQTTIPVSPPSTTKPSR	1.35583	0.06577	(11) Phospho (ST)
E1 01 3	2	DGSFGEGLTMK	0.596	0.0248	(3) Phospho (ST)
E1 02 1	3	DGSGDSHPDFPEDADIDLKDVDK	1.29667	0.08184	(3) Phospho (ST);(6) Phospho (ST)
E1 01 1	2	DIDISSPEFK	0.95333	0.01859	(6) Phospho (ST)
E1 02	2	DIIRQPSEEEIIK	0.7768	0.01906	(7) Phospho (ST)
E1 01 1	3	DIIRQPSEEEIIK	0.87583	0.01166	(7) Phospho (ST)
E1 01	3	DIIRQPSEEEIIK	0.89499	0.01273	(7) Phospho (ST)
E1 02 1	2	DIIRQPSEEEIIK	0.97333	0.253	(7) Phospho (ST)
E2 01 1	4	DKQSPSQANGCSDHRPIDILEMLSR	0.97333	0.05069	(4) Phospho (ST);(9) Deamidated (NQ)
E1 03	2	DKSPVREPIDNLTPEER	0.79787	0.02534	(3) Phospho (ST)
E1 01	3	DKSPVREPIDNLTPEER	0.98039	0.03023	(3) Phospho (ST)
E1 01 3	3	DKSPVREPIDNLTPEER	1.04917	0.02645	(3) Phospho (ST)
E1 01 1	3	DKSPVREPIDNLTPEER	1.055	0.02847	(3) Phospho (ST)
E2 01 1	3	DKSPVREPIDNLTPEER	1.11583	0.02418	(3) Phospho (ST)
E2 01 2	3	DKSPVREPIDNLTPEER	1.12083	0.02358	(3) Phospho (ST)
E1 03 1	2	DKSPVREPIDNLTPEER	1.3875	0.05739	(3) Phospho (ST)
E1 03 2	2	DKSPVREPIDNLTPEER	1.42667	0.05678	(3) Phospho (ST)
E1 02 1	2	DLADELALVDVIEDK	1.01	0.00892	
E1 01 3	3	DLADELALVDVIEDK	1.02167	0.05615	
E1 02 2	2	DLADELALVDVIEDK	1.04	0.01781	
E1 02	2	DLADELALVDVIEDK	1.05263	0.01001	
E1 01 1	3	DLADELALVDVIEDK	1.075	0.07755	
E2 01 1	2	DLDDFQSWLSR	0.8425	0.077	
E1 03	2	DLDEDELLGNLSETELK	0.74294	0.01956	(12) Phospho (ST)
E1 01 3	3	DLDEEGSEKELHENVLDK	0.865	0.1432	(7) Phospho (ST)
E1 04 3	2	DLFDLNSSEEDDTEGFSER	1.00333	0.03003	(6) Deamidated (NQ);(7) Phospho (ST);(8) Phospho (ST)
E1 04 3	2	DLFDLNSSEEDDTEGFSER	0.96667	0.07738	(7) Phospho (ST)
E2 04 1	2	DLFDLNSSEEDDTEGFSER	1.04083	0.01788	(7) Phospho (ST);(8) Phospho (ST)
E2 04 2	2	DLFDLNSSEEDDTEGFSER	1.0575	0.02458	(7) Phospho (ST);(8) Phospho (ST)
E1 04	2	DLFDLNSSEEDDTEGFSER	1.11857	0.00929	(7) Phospho (ST);(8) Phospho (ST)
E1 04 1	2	DLFDLNSSEEDDTEGFSER	1.14417	0.00791	(7) Phospho (ST);(8) Phospho (ST)
E1 01 3	3	DLFDYSPPLHK	0.91583	0.0104	(6) Phospho (ST)
E1 01 3	2	DLFDYSPPLHK	0.95583	0.01922	(6) Phospho (ST)
E1 01 1	2	DLFDYSPPLHK	0.96917	0.02363	(6) Phospho (ST)
E2 01 2	2	DLFDYSPPLHK	0.97083	0.01472	(6) Phospho (ST)
E2 01 1	2	DLFDYSPPLHK	1.00667	0.00903	(6) Phospho (ST)
E2 01	2	DLFDYSPPLHK	1.02459	0.02112	(6) Phospho (ST)
E1 04	3	DLGHPVEEEDELESGDQEDEDDESEDPGK	0.72046	0.0134	(14) Phospho (ST)
E1 04 3	3	DLGHPVEEEDELESGDQEDEDDESEDPGK	1.1825	0.02733	(14) Phospho (ST)
E2 04 2	3	DLGHPVEEEDELESGDQEDEDDESEDPGK	1.195	0.03667	(14) Phospho (ST)
E1 03 2	3	DLKIESDVQEPTEPEDDLDIMLGNK	1.51917	0.03974	(6) Phospho (ST)
E1 03 1	3	DLKIESDVQEPTEPEDDLDIMLGNK	1.5525	0.04547	(6) Phospho (ST)
E1 03 2	3	DLKIESDVQEPTEPEDDLDIMLGNK	2.00667	0.06261	(6) Phospho (ST);(12) Phospho (ST)
E1 02	2	DLLSDLQDISDSER	0.89552	0.04068	(10) Phospho (ST)
E1 02 1	2	DLLSDLQDISDSER	1.07417	0.01441	(10) Phospho (ST)
E1 02 2	2	DLLSDLQDISDSER	1.10167	0.03195	(10) Phospho (ST)
E1 01 3	3	DMESPTKLDVTLAK	0.75917	0.09274	(2) Oxidation (M);(4) Phospho (ST)
E1 02 2	2	DMESPTKLDVTLAK	1.0375	0.03091	(2) Oxidation (M);(4) Phospho (ST)
E1 02	2	DMESPTKLDVTLAK	1.05116	0.01901	(2) Oxidation (M);(4) Phospho (ST)
E1 02 1	2	DMESPTKLDVTLAK	1.05667	0.03176	(2) Oxidation (M);(4) Phospho (ST)
E1 01 1	3	DMESPTKLDVTLAK	1.07667	0.02562	(2) Oxidation (M);(4) Phospho (ST)
E2 02 2	2	DMESPTKLDVTLAK	1.17667	0.11	(2) Oxidation (M);(4) Phospho (ST)
E2 01 2	3	DMESPTKLDVTLAK	1.22667	0.03482	(2) Oxidation (M);(4) Phospho (ST)
E2 01 1	3	DMESPTKLDVTLAK	1.2275	0.03655	(2) Oxidation (M);(4) Phospho (ST)
E1 02	2	DMESPTKLDVTLAK	0.99469	0.01447	(4) Phospho (ST)
E1 01 1	3	DMESPTKLDVTLAK	1.02667	0.01177	(4) Phospho (ST)
E1 02 1	2	DMESPTKLDVTLAK	1.03417	0.01658	(4) Phospho (ST)
E1 02 2	2	DMESPTKLDVTLAK	1.0375	0.02126	(4) Phospho (ST)
E2 02	2	DMESPTKLDVTLAK	1.05042	0.02721	(4) Phospho (ST)
E1 01 3	3	DMESPTKLDVTLAK	1.05833	0.0145	(4) Phospho (ST)
E1 01	3	DMESPTKLDVTLAK	1.05932	0.01849	(4) Phospho (ST)
E2 01 2	3	DMESPTKLDVTLAK	1.06	0.00964	(4) Phospho (ST)
E2 01 1	3	DMESPTKLDVTLAK	1.065	0.01478	(4) Phospho (ST)
E2 02 2	2	DMESPTKLDVTLAK	1.10167	0.01301	(4) Phospho (ST)
E2 02 1	2	DMESPTKLDVTLAK	1.11833	0.0121	(4) Phospho (ST)
E1 03	3	DMPGGFLFEGLSDDEDDFHPNTR	0.94221	0.03606	(2) Oxidation (M);(12) Phospho (ST)
E1 02 2	3	DMPGGFLFEGLSDDEDDFHPNTR	1.11167	0.04628	(2) Oxidation (M);(12) Phospho (ST)
E1 03 2	3	DMPGGFLFEGLSDDEDDFHPNTR	1.14917	0.05556	(2) Oxidation (M);(12) Phospho (ST)
E1 02	2	DMSPLSETEMALGK	1.06007	0.1005	(3) Phospho (ST)
E1 02 2	2	DMSPLSETEMALGK	1.22833	0.02313	(3) Phospho (ST)
E1 02 2	2	DMSPLSETEMALGK	1.17083	0.02321	(3) Phospho (ST);(6) Phospho (ST)
E2 03 1	3	DMSPLSETEMALGKDVTPPPETEVVLIK	1.17	0.02618	(17) Phospho (ST)
E2 04 2	2	DNLLDTYSADQGDSSEGGTLAR	0.62267	0.02538	(14) Phospho (ST)
E2 04 1	2	DNLLDTYSADQGDSSEGGTLAR	0.62933	0.03214	(14) Phospho (ST)
E2 04	2	DNLLDTYSADQGDSSEGGTLAR	1.28096	0.03691	(14) Phospho (ST)
E1 04	2	DNLLDTYSADQGDSSEGGTLAR	1.35014	0.02432	(14) Phospho (ST)
E1 03 2	3	DNLLDTYSADQGDSSEGGTLARGEEEEK	0.74833	0.01561	(15) Phospho (ST)
E1 03 1	3	DNLLDTYSADQGDSSEGGTLARGEEEEK	0.75183	0.03649	(15) Phospho (ST)
E1 02	2	DNSPPPAFKPEPPK	1.33929	0.05411	(3) Phospho (ST)
E1 01 3	3	DNTFFRESPVGR	0.82475	0.03541	(8) Phospho (ST)
E1 02 2	2	DNTFFRESPVGR	0.828	0.06141	(8) Phospho (ST)
E2 01 1	3	DQSTSMSHINLLFSR	0.68833	0.02693	(5) Phospho (ST)
E2 01 2	3	DQSTSMSHINLLFSR	0.75517	0.02084	(5) Phospho (ST)
E1 01 1	3	DQSTSMSHINLLFSR	0.7575	0.06067	(5) Phospho (ST);(7) Phospho (ST)
E2 01 1	3	DQSTSMSHINLLFSR	0.77175	0.01402	(5) Phospho (ST);(7) Phospho (ST)
E2 01 2	3	DQSTSMSHINLLFSR	0.81667	0.01049	(5) Phospho (ST);(7) Phospho (ST)
E2 03 1	2	DQSTSMSHINLLFSR	0.98417	0.216	(5) Phospho (ST);(7) Phospho (ST)
E1 04 3	2	DSQDASAEQSDHDDEVASLASASGGFGTK	1.15333	0.02463	(10) Phospho (ST)
E1 03 1	3	DSQDASAEQSDHDDEVASLASASGGFGTK	1.18583	0.01829	(10) Phospho (ST)
E1 04 3	2	DSQDASAEQSDHDDEVASLASASGGFGTK	1.15333	0.02463	(6) Phospho (ST)
E1 03 2	3	DSQDASAEQSDHDDEVASLASASGGFGTK	1.15917	0.01482	(6) Phospho (ST)
E1 04 3	3	DSQQTLNIPSLNDSDSEIEDISEIESNR	1.22083	0.01271	(11) Phospho (ST);(15) Phospho (ST)
E1 04 1	3	DSQQTLNIPSLNDSDSEIEDISEIESNR	0.995	0.01484	(15) Phospho (ST);(17) Phospho (ST)
E2 04 2	3	DSQQTLNIPSLNDSDSEIEDISEIESNR	1.06083	0.1077	(15) Phospho (ST);(17) Phospho (ST)
E1 02	2	DVDVSEDSPPPLPER	0.83987	0.0346	(8) Phospho (ST)
E1 01	2	DVLDIEQFSTVK	1.27986	0.02477	(10) Phospho (ST)
E1 03 2	3	DVMSDETNNEETESPSQEFVNITK	1.10333	0.04789	(14) Phospho (ST)
E1 02 1	2	DVTPPPETEVVLIK	1.1375	0.02434	(3) Phospho (ST)
E1 02 2	2	DVTPPPETEVVLIK	1.15833	0.01736	(3) Phospho (ST)
E1 01	3	DVTPPPETEVVLIK	0.98945	0.01519	(8) Phospho (ST)
E2 03	2	DWEDDSDEDMSNFDR	0.83149	0.01283	(6) Phospho (ST)
E1 03	2	DWEDDSDEDMSNFDR	0.86957	0.00416	(6) Phospho (ST)
E1 03 2	2	DWEDDSDEDMSNFDR	1.3925	0.07997	(6) Phospho (ST)
E2 02 2	3	DYEIESQNPLASPTNTLLGSAK	1.14583	0.03055	(12) Phospho (ST)
E1 02 1	3	DYEIESQNPLASPTNTLLGSAK	1.16833	0.03348	(12) Phospho (ST)
E2 02 1	3	DYEIESQNPLASPTNTLLGSAK	1.1775	0.02549	(12) Phospho (ST)
E2 04 2	2	DYEIESQNPLASPTNTLLGSAK	1.24583	0.02417	(12) Phospho (ST)
E1 01 1	2	EAALPPVSPLK	1.05917	0.00893	(8) Phospho (ST)
E1 01 3	2	EAALPPVSPLK	1.16917	0.0074	(8) Phospho (ST)
E2 01 2	3	EALAEAALESPRPALVR	0.83308	0.07836	(10) Phospho (ST)
E2 01 1	3	EALAEAALESPRPALVR	0.87167	0.08061	(10) Phospho (ST)
E1 01 1	3	EALAEAALESPRPALVR	0.89583	0.04639	(10) Phospho (ST)
E1 01 3	3	EALAEAALESPRPALVR	0.92667	0.02254	(10) Phospho (ST)
E1 03 1	3	EDLESMDKEVDDILGEGSDDSDSEK	1.1425	0.02197	(18) Phospho (ST);(21) Phospho (ST)
E1 02 2	3	EEENADSDDEGELQDLLSQDWR	0.9425	0.05316	(7) Phospho (ST)
E1 04	2	EEGSDIEDEDMEELLNDTR	1.37994	0.04319	(4) Phospho (ST)
E1 03 2	2	EELMSSDLEETAGSTSIPK	1.185	0.01054	(5) Phospho (ST)
E1 03 1	2	EELMSSDLEETAGSTSIPK	1.18167	0.01077	(6) Phospho (ST)
E1 03 2	2	EELMSSDLEETAGSTSIPK	1.185	0.01054	(6) Phospho (ST)
E1 02 1	3	EGEEPTVYSDEEEPKDESAR	0.81767	0.03807	(9) Phospho (ST)
E1 02	3	EGEEPTVYSDEEEPKDESAR	1.40713	0.03503	(9) Phospho (ST)
E1 03	3	EGHSLEMENENLVENGADSDEDDNSFLK	1.50845	0.0816	(7) Oxidation (M);(19) Phospho (ST)
E2 03 1	3	EGLRPGDTTSTFCGTPNYIAPEILR	1.05583	0.02414	(11) Phospho (ST)
E2 03	3	EGMNPSYDEYADSDEDQHDAYLER	0.70788	0.01501	(13) Phospho (ST)
E2 03 1	3	EGMNPSYDEYADSDEDQHDAYLER	1.23	0.02083	(13) Phospho (ST)
E2 04 2	2	EGMNPSYDEYADSDEDQHDAYLER	1.31583	0.06691	(13) Phospho (ST)
E2 04 1	2	EGMNPSYDEYADSDEDQHDAYLER	1.32833	0.01601	(13) Phospho (ST)
E2 03	3	EGMNPSYDEYADSDEDQHDAYLER	0.73171	0.00814	(3) Oxidation (M);(13) Phospho (ST)
E2 04 1	2	EGMNPSYDEYADSDEDQHDAYLER	1.16417	0.03029	(3) Oxidation (M);(13) Phospho (ST)
E2 03 1	3	EGMNPSYDEYADSDEDQHDAYLER	1.37167	0.01711	(3) Oxidation (M);(13) Phospho (ST)
E1 01 3	4	EGPGEEHFEDMASDEDMKPK	1.19	0.04748	(13) Phospho (ST)
E1 02 2	3	EGPGEEHFEDMASDEDMKPK	1.24167	0.04448	(13) Phospho (ST)
E1 01 1	4	EGPGEEHFEDMASDEDMKPK	1.25583	0.09679	(13) Phospho (ST)
E1 02 1	3	EGPGEEHFEDMASDEDMKPK	1.31667	0.04194	(13) Phospho (ST)
E1 01 1	4	EGPGEEHFEDMASDEDMKPK	1.23417	0.05845	(13) Phospho (ST);(17) Oxidation (M)

E1 01 3	4	EGPGEEHFEDMASDEDMKPK	1.2425	0.05476	(13) Phospho (ST);(17) Oxidation (M)
E1 04 3	4	EGTGQQERESPRPLQLPGAEGPAISDGEEGGG EPGAGGGAAGAAGAGR	1.08333	0.133	(10) Phospho (ST);(25) Phospho (ST)
E2 01 1	2	EIIDLVLDR	0.96333	0.02557	
E2 01	2	EITALAPSTMK	0.97784	0.03409	
E1 01 1	3	EKEVDGLLTSEPMGSPVSSK	1.065	0.02567	(15) Phospho (ST)
E1 03 1	2	EKEVDGLLTSEPMGSPVSSK	1.10167	0.05525	(15) Phospho (ST)
E1 03 1	2	EKPDSDDDLDIASLVTAK	0.80383	0.1335	(5) Phospho (ST)
E1 03 2	2	EKPDSDDDLDIASLVTAK	0.83	0.1766	(5) Phospho (ST)
E1 03	2	EKPDSDDDLDIASLVTAK	0.90964	0.01094	(5) Phospho (ST)
E1 02 1	3	EKQSDDEVYAPGLDIESSLK	1.3925	0.1046	(4) Phospho (ST)
E2 02 2	3	EKVSSIDLEIDSLSSLLDDMTK	1.095	0.01286	(5) Phospho (ST)
E1 02 2	2	ELDSEFEDLASDVR	0.71642	0.02322	(4) Phospho (ST)
E2 02 2	3	ELEKPIQSKPQSPVIQAAAVSPK	1.09	0.05359	(21) Phospho (ST)
E2 02 1	3	ELEKPIQSKPQSPVIQAAAVSPK	1.1325	0.03501	(21) Phospho (ST)
E1 02 2	3	ELEKPIQSKPQSPVIQAAAVSPK	1.14417	0.1	(21) Phospho (ST)
E1 01	2	ELISNASDALDK	1.20096	0.02861	
E1 02	3	ELSNSPLRENSFGSPLEFR	1.0661	0.02319	(3) Phospho (ST);(5) Phospho (ST)
E1 02 2	3	ELSNSPLRENSFGSPLEFR	1.07417	0.01882	(3) Phospho (ST);(5) Phospho (ST)
E1 02 1	3	ELSNSPLRENSFGSPLEFR	1.22917	0.09614	(3) Phospho (ST);(5) Phospho (ST)
E1 02	3	ELSNSPLRENSFGSPLEFR	1.05189	0.08105	(3) Phospho (ST);(5) Phospho (ST);(14) Phospho (ST)
E2 02 1	3	ELSNSPLRENSFGSPLEFR	0.84833	0.06351	(5) Phospho (ST)
E2 02 2	3	ELSNSPLRENSFGSPLEFR	0.87	0.06953	(5) Phospho (ST)
E1 02 2	3	ELSNSPLRENSFGSPLEFR	0.88917	0.0612	(5) Phospho (ST);(10) Deamidated (NQ);(14) Phospho (ST)
E1 02 2	3	ELSNSPLRENSFGSPLEFR	0.9	0.04016	(5) Phospho (ST);(14) Phospho (ST)
E2 02 1	3	ELSNSPLRENSFGSPLEFR	0.905	0.01401	(5) Phospho (ST);(14) Phospho (ST)
E1 02 1	3	ELSNSPLRENSFGSPLEFR	0.93333	0.00888	(5) Phospho (ST);(14) Phospho (ST)
E2 02 2	3	ELSNSPLRENSFGSPLEFR	0.93417	0.04966	(5) Phospho (ST);(14) Phospho (ST)
E2 02	3	ELSNSPLRENSFGSPLEFR	1.20968	0.06383	(5) Phospho (ST);(14) Phospho (ST)
E1 02	3	ELSNSPLRENSFGSPLEFR	1.23457	0.01151	(5) Phospho (ST);(14) Phospho (ST)
E1 01 3	2	ENSFGSPLEFR	0.75892	0.1327	(6) Phospho (ST)
E1 02 2	3	ENVEYIEREESDGEYDEFGR	0.99	0.01785	(11) Phospho (ST)
E2 04 1	2	ENVEYIEREESDGEYDEFGR	1.02583	0.02416	(11) Phospho (ST)
E1 02 1	3	ENVEYIEREESDGEYDEFGR	1.05333	0.03655	(11) Phospho (ST)
E1 02	3	ENVEYIEREESDGEYDEFGR	1.06232	0.04995	(11) Phospho (ST)
E2 02 2	3	ENVEYIEREESDGEYDEFGR	1.07083	0.02402	(11) Phospho (ST)
E1 04 1	2	ENVEYIEREESDGEYDEFGR	1.12917	0.03095	(11) Phospho (ST)
E1 04 1	2	ENVEYIEREESDGEYDEFGR	1.12917	0.03095	(11) Phospho (ST)
E1 04 3	2	ENVEYIEREESDGEYDEFGR	1.18083	0.06248	(11) Phospho (ST)
E1 02 1	3	ENVEYIEREESDGEYDEFGR	1.05083	0.03647	(2) Deamidated (NQ);(11) Phospho (ST)
E2 02	3	ENVEYIEREESDGEYDEFGRK	0.82508	0.03264	(11) Phospho (ST)
E1 03 1	3	EREESEDELEEANGNNPIDIEVDQNK	0.98083	0.06813	(5) Phospho (ST)
E1 03 2	3	EREESEDELEEANGNNPIDIEVDQNK	1.13417	0.05314	(5) Phospho (ST)
E2 02 2	4	ERGSSLSGTDDGAQEVVKDILEDVVTSAIK	1.21083	0.00789	(7) Phospho (ST)
E1 02 1	3	ERIQQFDDGGSDEEDIWEEK	0.9875	0.1498	(11) Phospho (ST)
E1 04 1	2	ERIQQFDDGGSDEEDIWEEK	1.19167	0.2765	(11) Phospho (ST)
E1 01 3	3	ERSPALKSPLQSVVVR	0.93333	0.0228	(3) Phospho (ST);(8) Phospho (ST)
E1 01 1	3	ERSPALKSPLQSVVVR	0.93583	0.03298	(3) Phospho (ST);(8) Phospho (ST)
E2 03 2	2	ERSPALKSPLQSVVVR	0.94917	0.07713	(3) Phospho (ST);(8) Phospho (ST)
E2 01	3	ERSPALKSPLQSVVVR	0.95178	0.01743	(3) Phospho (ST);(8) Phospho (ST)
E2 01 1	3	ERSPALKSPLQSVVVR	0.96167	0.01837	(3) Phospho (ST);(8) Phospho (ST)
E2 03 1	2	ERSPALKSPLQSVVVR	0.97417	0.08362	(3) Phospho (ST);(8) Phospho (ST)
E2 01 2	3	ERSPALKSPLQSVVVR	0.98083	0.01573	(3) Phospho (ST);(8) Phospho (ST)
E1 01 3	2	ESDQTLAALLSPK	0.80858	0.02179	(11) Phospho (ST)
E1 01 1	2	ESDQTLAALLSPK	0.8575	0.0182	(11) Phospho (ST)
E1 02	3	ESEDKPEIEDVGSDEEEEK	0.92025	0.01391	(13) Phospho (ST)
E1 02	3	ESEDKPEIEDVGSDEEEEKK	0.86207	0.02303	(13) Phospho (ST)
E1 04	3	ESPRPLQLPGAEGPAISDGEEGGGEPGAGGGA AGAAGAGR	0.7768	0.00808	(17) Phospho (ST)
E2 04 2	3	ESPRPLQLPGAEGPAISDGEEGGGEPGAGGGA AGAAGAGR	1.14917	0.03254	(17) Phospho (ST)
E1 04 3	3	ESPRPLQLPGAEGPAISDGEEGGGEPGAGGGA AGAAGAGR	1.1925	0.0252	(17) Phospho (ST)
E1 04 1	3	ESPRPLQLPGAEGPAISDGEEGGGEPGAGGGA AGAAGAGR	1.19667	0.01617	(17) Phospho (ST)
E2 04 1	3	ESPRPLQLPGAEGPAISDGEEGGGEPGAGGGA AGAAGAGR	1.19667	0.02833	(17) Phospho (ST)
E1 01 3	4	ESSPPHSVHSFSGDRDWDR	1.00917	0.01172	(3) Phospho (ST)
E2 01 1	4	ESSPPHSVHSFSGDRDWDR	1.07667	0.02458	(3) Phospho (ST)
E1 04 3	3	EVAATEEDVTRLPSPTSPFSSLSQDQAATSK	1.1425	0.05626	(14) Phospho (ST);(16) Phospho (ST)
E1 04 1	3	EVAATEEDVTRLPSPTSPFSSLSQDQAATSK	1.04167	0.08414	(5) Phospho (ST);(10) Phospho (ST)
E1 03	2	EVDGLLTSEPMGSPVSSK	0.82057	0.01186	(13) Phospho (ST)
E2 03 1	2	EVDGLLTSEPMGSPVSSK	1.075	0.02524	(13) Phospho (ST)
E1 03 2	2	EVDGLLTSEPMGSPVSSK	1.12583	0.01559	(13) Phospho (ST)
E2 03 2	2	EVDGLLTSEPMGSPVSSK	1.13	0.02035	(13) Phospho (ST)
E1 03 1	2	EVDGLLTSEPMGSPVSSK	1.14583	0.01391	(13) Phospho (ST)
E2 03 1	3	EVVEAVTIVETPPMVVVGIVGYVETPR	0.93917	0.0209	
E2 03 2	3	EVVEAVTIVETPPMVVVGIVGYVETPR	0.94	0.01761	
E1 03	2	EYIPGQPPLSQSSDSSPTR	0.75301	0.01364	(16) Phospho (ST)
E1 01 3	3	FCSNSGRLSGPAELR	0.75308	0.03879	(9) Phospho (ST)
E1 04 3	3	FEEESKEPVADEEEEDSDDDVEPITEFR	1.02667	0.02287	(17) Phospho (ST)
E1 04 1	3	FEEESKEPVADEEEEDSDDDVEPITEFR	1.0525	0.02462	(17) Phospho (ST)
E2 04 2	3	FEEESKEPVADEEEEDSDDDVEPITEFR	1.20833	0.00812	(17) Phospho (ST)
E1 03	3	FGESEEVEMEVESDEEDDKQEK	0.94518	0.02032	(9) Oxidation (M);(13) Phospho (ST)
E1 03 2	3	FGESEEVEMEVESDEEDDKQEK	1.025	0.01824	(9) Oxidation (M);(13) Phospho (ST)
E1 02	3	FGESEEVEMEVESDEEDDKQEK	1.07143	0.01713	(9) Oxidation (M);(13) Phospho (ST)
E1 02 2	3	FGESEEVEMEVESDEEDDKQEK	1.075	0.02085	(9) Oxidation (M);(13) Phospho (ST)
E1 02 1	3	FGESEEVEMEVESDEEDDKQEK	1.095	0.01848	(9) Oxidation (M);(13) Phospho (ST)
E1 01 3	2	FGSTLQLDLEK	0.91833	0.03637	(4) Phospho (ST)
E2 03 1	4	FHPEPYGLEDDQRSMGYDDLDYGMMSDYGTAR	1.02917	0.1572	(14) Phospho (ST)
E2 03 1	4	FHPEPYGLEDDQRSMGYDDLDYGMMSDYGTAR	1.02917	0.1572	(17) Phospho (Y)
E2 04 1	2	FIGSVSEDNSEDEISNLVK	1.00833	0.01211	(11) Phospho (ST)
E2 04 2	2	FIGSVSEDNSEDEISNLVK	1.04833	0.00974	(11) Phospho (ST)
E1 04 1	2	FIGSVSEDNSEDEISNLVK	1.13083	0.03634	(7) Phospho (ST);(11) Phospho (ST)
E1 04 3	2	FLESAAADFSDEDEDDDVDGR	0.84	0.07019	(10) Phospho (ST)
E1 02 1	2	FLMECRNSPVTK	1.09417	0.01711	(8) Phospho (ST)
E1 01 3	3	FLNRSPEESFDIK	0.97583	0.03548	(5) Phospho (ST);(9) Phospho (ST)
E1 02 2	3	FNDSEGDDTEETEDYRQFR	0.78875	0.1481	(4) Phospho (ST)
E2 02 1	3	FNDSEGDDTEETEDYRQFR	0.79733	0.2828	(4) Phospho (ST)
E2 03 1	3	FTDKDQQPSGSEGEDDDAEAALKK	1.36583	0.0462	(9) Phospho (ST);(11) Phospho (ST)
E1 03 2	3	GAAEEAELEDSDDEEKPVKQDDFPK	1.13083	0.0398	(11) Phospho (ST)
E1 03 1	3	GAAEEAELEDSDDEEKPVKQDDFPK	1.18833	0.06751	(11) Phospho (ST)
E1 03 1	3	GDLSDVEEEEEEEEMDVDEATGAVKK	0.955	0.06345	(4) Phospho (ST)
E1 03 2	3	GDMSDEDDENEFFDAPEIITMPENLGHK	1.185	0.0378	(4) Phospho (ST)
E1 03 2	2	GDQPAASGDSDDDEPPPLPR	0.74075	0.03091	(10) Phospho (ST)
E1 03 1	2	GDQPAASGDSDDDEPPPLPR	0.75292	0.02946	(10) Phospho (ST)
E1 03	2	GDQPAASGDSDDDEPPPLPR	1.51469	0.01851	(10) Phospho (ST)
E2 03 2	2	GDSETDLEALFNAVMNPK	1.00083	0.01507	(3) Phospho (ST)
E2 03 1	2	GDSETDLEALFNAVMNPK	1.02083	0.0138	(3) Phospho (ST)
E2 03 1	2	GDSETDLEALFNAVMNPK	1.02083	0.0138	(3) Phospho (ST)
E1 04	2	GDSIEEILADSEDEEDNEEEER	0.71225	0.00898	(11) Phospho (ST)
E1 04 3	2	GDSIEEILADSEDEEDNEEEER	1.30167	0.02137	(11) Phospho (ST)
E1 01 3	2	GEFSASPMLK	0.82442	0.02238	(6) Phospho (ST)
E1 02 2	2	GFGFVDFNSEEDAK	1.3825	0.1084	(9) Phospho (ST)
E1 02 1	2	GFGFVDFNSEEDAK	1.53417	0.1132	(9) Phospho (ST)
E2 02	2	GGSISVQVNSIKFDSE	1.0453	0.148	(15) Phospho (ST)
E2 02 1	2	GGSISVQVNSIKFDSE	1.04917	0.03102	(15) Phospho (ST)
E2 02 2	2	GGSISVQVNSIKFDSE	1.18833	0.06252	(15) Phospho (ST)
E2 02 2	3	GHYEVTGSDDETGKLQGSGVSLASK	0.95833	0.02629	(8) Phospho (ST)
E2 02 1	3	GHYEVTGSDDETGKLQGSGVSLASK	0.97417	0.02039	(8) Phospho (ST)
E1 03 1	3	GIEFEDESSDRDARPALETQPQQEK	1.43833	0.02637	(9) Phospho (ST)
E1 03 2	3	GIEFEDESSDRDARPALETQPQQEK	1.5475	0.03489	(9) Phospho (ST)
E1 01 1	2	GIITDSFGR	0.69958	0.02078	(6) Phospho (ST)
E1 01 3	2	GIITDSFGR	0.73542	0.02877	(6) Phospho (ST)
E1 01 3	2	GILAADESTGSIAK	0.79358	0.09475	(11) Phospho (ST)
E1 01	2	GILAADESTGSIAK	1.38122	0.02656	(11) Phospho (ST)
E2 04 1	2	GIPLATGDTSPEPELLPGAPLPPPK	1.17917	0.0068	(10) Phospho (ST)
E2 04 1	2	GIPLATGDTSPEPELLPGAPLPPPK	1.17917	0.0068	(9) Phospho (ST)
E1 01	2	GISPIVFDR	1.05337	0.0578	(3) Phospho (ST)
E1 01 3	2	GISPIVFDR	1.12333	0.02528	(3) Phospho (ST)
E2 04 1	3	GKGNIETSSEDEDDTADLFPEESGFEHAWR	0.84667	0.09159	(7) Phospho (ST);(9) Phospho (ST);(15) Phospho (ST)
E2 01 2	3	GLECSDWKPEAGLSPPR	0.88333	0.03675	(14) Phospho (ST)
E1 04 3	2	GLFSDEEDSEDLFSSQSASK	1.00417	0.03151	(4) Phospho (ST)
E2 01 1	2	GLGSSPDLELLLR	0.82558	0.02997	(4) Phospho (ST)
E2 01	2	GLGSSPDLELLLR	1.21163	0.07874	(4) Phospho (ST)
E1 01	2	GLGSSPDLELLLR	1.43541	0.06842	(4) Phospho (ST)
E2 03 1	2	GLLSDSMTDVPVDTGVAAR	0.885	0.08747	(6) Phospho (ST)
E1 03 2	2	GLLSDSMTDVPVDTGVAAR	0.935	0.04283	(6) Phospho (ST)
E2 03 2	2	GLLSDSMTDVPVDTGVAAR	0.93667	0.0957	(6) Phospho (ST)
E1 03 1	2	GLLSDSMTDVPVDTGVAAR	0.97083	0.04693	(6) Phospho (ST)
E2 03	2	GLLYDSDEEDEERPAR	0.85665	0.0252	(6) Phospho (ST)
E1 03	2	GLLYDSDEEDEERPAR	0.98232	0.04937	(6) Phospho (ST)
E1 01 1	3	GLLYDSDEEDEERPAR	1.00583	0.05004	(6) Phospho (ST)
E1 03 1	2	GLLYDSDEEDEERPAR	1.05667	0.04082	(6) Phospho (ST)
E1 01	3	GLLYDSDEEDEERPAR	1.06232	0.08457	(6) Phospho (ST)
E2 01 2	3	GLLYDSDEEDEERPAR	1.0975	0.0264	(6) Phospho (ST)
E2 01 1	3	GLLYDSDEEDEERPAR	1.09833	0.03235	(6) Phospho (ST)
E1 01 3	3	GLLYDSDEEDEERPAR	1.10833	0.04233	(6) Phospho (ST)
E2 03 2	2	GLLYDSDEEDEERPAR	1.18417	0.01625	(6) Phospho (ST)
E1 03 2	2	GLLYDSDEEDEERPAR	1.19833	0.02381	(6) Phospho (ST)
E2 03 1	2	GLLYDSDEEDEERPAR	1.20167	0.02465	(6) Phospho (ST)
E2 01	3	GLLYDSDEEDEERPARK	0.96277	0.02757	(6) Phospho (ST)
E1 01	3	GLLYDSDEEDEERPARK	1.02249	0.02387	(6) Phospho (ST)
E2 01 2	3	GLLYDSDEEDEERPARK	1.2225	0.04689	(6) Phospho (ST)
E2 03 1	3	GLMAGGRPEGQYSEDEDTDTDEYK	1.16583	0.01472	(12) Phospho (Y);(18) Phospho (ST)
E2 03 2	3	GLMAGGRPEGQYSEDEDTDTDEYK	1.14833	0.01434	(13) Phospho (ST);(18) Phospho (ST)
E2 03 1	3	GLMAGGRPEGQYSEDEDTDTDEYKEAK	1.125	0.02689	(12) Phospho (Y);(18) Phospho (ST)
E2 02 2	2	GLPSPYNMSSAPGSR	0.94667	0.07114	(10) Phospho (ST)
E2 02 1	2	GLPSPYNMSSAPGSR	0.9775	0.03971	(10) Phospho (ST)
E2 03 2	2	GLSASLPDLDSENWIEVK	0.90917	0.02782	(5) Phospho (ST)
E2 03	2	GLSASLPDLDSENWIEVK	0.96712	0.01364	(5) Phospho (ST)
E2 02 1	2	GLYDGPVCEVSVTPK	1.005	0.05794	(13) Phospho (ST)
E2 03	2	GNAEGSSDEEGKLVIDEPAK	0.88968	0.02088	(6) Phospho (ST);(7) Phospho (ST)
E2 04	2	GNAEGSSDEEGKLVIDEPAK	0.92194	0.03641	(6) Phospho (ST);(7) Phospho (ST)
E2 03 2	2	GNAEGSSDEEGKLVIDEPAK	0.93333	0.03762	(6) Phospho (ST);(7) Phospho (ST)
E2 01 1	2	GNSDGYIPINK	0.66558	0.03656	(3) Phospho (ST)

E2 01 2	2	GNSDGYIIPINK	0.69833	0.03119	(3) Phospho (ST)
E2 03 1	3	GPPDFSSDEEREPTPVLGSGAAAAGR	0.99833	0.05019	(6) Phospho (ST);(7) Phospho (ST)
E2 03 2	3	GPPDFSSDEEREPTPVLGSGAAAAGR	1.05417	0.05702	(6) Phospho (ST);(7) Phospho (ST)
E2 03	3	GPPDFSSDEEREPTPVLGSGAAAAGR	1.36612	0.05522	(6) Phospho (ST);(7) Phospho (ST)
E1 03 1	2	GPPQSPVFEGVYNNSR	0.81633	0.05944	(5) Phospho (ST)
E1 03 2	2	GPPQSPVFEGVYNNSR	0.90667	0.0476	(5) Phospho (ST)
E2 02 2	2	GPVSPSVSFQPLAR	0.95833	0.04575	(4) Phospho (ST)
E1 02	3	GQTPLTEGSEDLDGHSDPEESFAR	1.38889	0.0281	(16) Phospho (ST)
E1 03	3	GQTPLTEGSEDLDGHSDPEESFAR	1.60479	0.02936	(9) Phospho (ST);(16) Phospho (ST)
E1 01 3	2	GRLGSVDSFER	0.9625	0.01938	(5) Phospho (ST)
E1 01 1	2	GRLGSVDSFER	1.01167	0.01829	(5) Phospho (ST)
E2 01 2	2	GRLSPVPVPR	0.90167	0.03247	(4) Phospho (ST)
E2 01 1	2	GRLSPVPVPR	0.90833	0.03788	(4) Phospho (ST)
E1 01 1	2	GRLSPVPVPR	0.945	0.03051	(4) Phospho (ST)
E1 04 3	3	GSAPHSESDLPEQEEEILGSDDDEQEDPNDYC K	1.24417	0.01126	(20) Phospho (ST)
E2 01 2	3	GSIFPMSVPDVPPSIHPSK	0.77158	0.222	(2) Phospho (ST)
E1 01 1	2	GSLASLDSLR	0.72258	0.02387	(5) Phospho (ST)
E1 01 3	2	GSLASLDSLR	0.72825	0.03288	(5) Phospho (ST)
E1 01 1	2	GSLASLDSLR	0.68358	0.04126	(5) Phospho (ST);(8) Phospho (ST)
E2 01	2	GSLASLDSLRK	0.27203	0.05442	(2) Phospho (ST);(5) Phospho (ST);(8) Phospho (ST)
E2 01 1	2	GSLASLDSLRK	0.87667	0.02344	(2) Phospho (ST);(5) Phospho (ST);(8) Phospho (ST)
E1 01 3	2	GSLASLDSLRK	0.68858	0.02577	(5) Phospho (ST);(8) Phospho (ST)
E1 01 1	2	GSLASLDSLRK	0.71392	0.03408	(5) Phospho (ST);(8) Phospho (ST)
E2 01 1	2	GSLASLDSLRK	0.77108	0.02283	(5) Phospho (ST);(8) Phospho (ST)
E2 01 2	2	GSLASLDSLRK	0.80658	0.02163	(5) Phospho (ST);(8) Phospho (ST)
E1 01	2	GSLASLDSLRK	1.02319	0.02309	(5) Phospho (ST);(8) Phospho (ST)
E2 01	2	GSLASLDSLRK	1.24069	0.02395	(5) Phospho (ST);(8) Phospho (ST)
E2 01	2	GSLASLDSLRK	2.52653	0.04339	(8) Phospho (ST)
E1 02	2	GSPEEELPLPAFEK	1.20676	0.1301	(2) Phospho (ST)
E1 02 1	2	GSPEEELPLPAFEK	1.21	0.1458	(2) Phospho (ST)
E2 02 1	2	GSPHYFSPFRPY	0.85167	0.00759	(2) Phospho (ST)
E2 02 2	2	GSPHYFSPFRPY	0.86667	0.00594	(2) Phospho (ST)
E2 02 2	2	GSPHYFSPFRPY	0.69958	0.02987	(2) Phospho (ST);(7) Phospho (ST)
E2 01 2	3	GSPHYFSPFRPY	0.78983	0.0121	(2) Phospho (ST);(7) Phospho (ST)
E2 02 1	2	GSPHYFSPFRPY	0.83417	0.02105	(2) Phospho (ST);(7) Phospho (ST)
E2 02	2	GSPHYFSPFRPY	1.22449	0.01025	(2) Phospho (ST);(7) Phospho (ST)
E1 01	2	GSPQAGVDLSFATR	1.02529	0.04779	(2) Phospho (ST)
E2 03 2	3	GSSLSGTDDGAQEVVKDILEDVVTSAIK	1.23167	0.01526	(3) Phospho (ST)
E2 03 1	3	GSSLSGTDDGAQEVVKDILEDVVTSAIK	1.23833	0.00591	(3) Phospho (ST)
E2 01 1	4	GSYGSDAEEEEYRQQLSEHSK	0.9825	0.02164	(2) Phospho (ST)
E2 04 1	2	GSYGSDAEEEEYRQQLSEHSK	1.03917	0.01888	(2) Phospho (ST)
E2 02	3	GSYGSDAEEEEYRQQLSEHSK	0.95299	0.01406	(5) Phospho (ST)
E2 02 1	3	GSYGSDAEEEEYRQQLSEHSK	1.10333	0.01179	(5) Phospho (ST)
E2 02 1	3	GSYGSDAEEEEYRQQLSEHSK	1.10333	0.01179	(5) Phospho (ST)
E2 02 2	3	GSYGSDAEEEEYRQQLSEHSK	1.13917	0.01739	(5) Phospho (ST)
E2 03 2	2	GTGQSDDSDIWDDTALIK	0.9875	0.03565	(2) Phospho (ST);(8) Phospho (ST)
E1 03 2	2	GTGQSDDSDIWDDTALIK	1.05333	0.03751	(2) Phospho (ST);(8) Phospho (ST)
E1 03 2	2	GTGQSDDSDIWDDTALIK	0.9375	0.02513	(5) Phospho (ST)
E1 03 2	2	GTGQSDDSDIWDDTALIK	1.05333	0.03751	(5) Phospho (ST);(8) Phospho (ST)
E1 03 1	2	GTGQSDDSDIWDDTALIK	1.07917	0.07112	(8) Phospho (ST)
E1 02 1	3	GTSPRPPEGGLGYSQLGDDDLK	0.9625	0.02172	(3) Phospho (ST)
E1 02 2	3	GTSPRPPEGGLGYSQLGDDDLK	0.965	0.0313	(3) Phospho (ST)
E1 04 3	2	GVDFESSEDDDDDPFMNTSSLR	1.02917	0.05563	(6) Phospho (ST);(7) Phospho (ST)
E1 03 2	3	GVDFESSEDDDDDPFMNTSSLRR	0.86083	0.05331	(6) Phospho (ST);(7) Phospho (ST)
E1 03 1	3	GVDFESSEDDDDDPFMNTSSLRR	0.945	0.04794	(6) Phospho (ST);(7) Phospho (ST)
E2 01 2	2	GVSMPNMLEPK	0.835	0.05402	(3) Phospho (ST)
E1 01 3	2	GVSMPNMLEPK	0.95083	0.01638	(3) Phospho (ST)
E2 02 2	2	GVVDSEDLPLNISR	0.7125	0.06598	
E2 01 2	3	GYTSDSEVYTDHGRPGK	0.83833	0.07071	(4) Phospho (ST)
E2 01 1	3	GYTSDSEVYTDHGRPGK	0.855	0.06643	(4) Phospho (ST)
E1 03 1	3	HDSIPAADTFEDLSDVEGGGSEPTQR	1.14	0.06333	(14) Phospho (ST)
E1 03 2	3	HDSIPAADTFEDLSDVEGGGSEPTQR	1.19833	0.03777	(14) Phospho (ST)
E1 02 2	3	HGSGADSDYENTQSGDPLLGLEGK	0.83917	0.07217	(7) Phospho (ST);(13) Deamidated (NQ)
E2 01 1	4	HGTDLWIDNMSSAVPNHSPEKK	0.92333	0.03735	(12) Phospho (ST)
E1 01 1	4	HIKEEPLSEEEPCTSTAIASPEK	1.00583	0.04094	(8) Phospho (ST)
E1 02	3	HIKEEPLSEEEPCTSTAIASPEK	1.01695	0.00899	(8) Phospho (ST)
E1 01 3	4	HIKEEPLSEEEPCTSTAIASPEK	1.08083	0.03431	(8) Phospho (ST)
E1 02 2	3	HIKEEPLSEEEPCTSTAIASPEK	1.10833	0.01783	(8) Phospho (ST)
E1 02 1	3	HIKEEPLSEEEPCTSTAIASPEK	1.1275	0.01307	(8) Phospho (ST)
E1 04 3	2	HIKEEPLSEEEPCTSTAIASPEK	1.19083	0.0503	(8) Phospho (ST)
E2 03	3	HIKEEPLSEEEPCTSTAIASPEK	0.70456	0.03335	(8) Phospho (ST);(20) Phospho (ST)
E2 03 1	3	HIKEEPLSEEEPCTSTAIASPEK	1.64917	0.03086	(8) Phospho (ST);(20) Phospho (ST)
E2 03 2	3	HIKEEPLSEEEPCTSTAIASPEK	1.66833	0.02973	(8) Phospho (ST);(20) Phospho (ST)
E1 03 1	3	HIKEEPLSEEEPCTSTAIASPEK	1.675	0.01319	(8) Phospho (ST);(20) Phospho (ST)
E1 03 2	3	HIKEEPLSEEEPCTSTAIASPEK	1.71333	0.01195	(8) Phospho (ST);(20) Phospho (ST)
E1 03 2	3	HIKEEPLSEEEPCTSTAIASPEKK	0.865	0.0942	(8) Phospho (ST)
E1 01 3	4	HIKEEPLSEEEPCTSTAIASPEKK	1.90417	0.0471	(8) Phospho (ST);(20) Phospho (ST)
E1 03 2	3	HIKEEPLSEEEPCTSTAIASPEKK	1.98583	0.03645	(8) Phospho (ST);(20) Phospho (ST)
E1 01 1	4	HIKEEPLSEEEPCTSTAIASPEKK	2.0525	0.05144	(8) Phospho (ST);(20) Phospho (ST)
E2 02 1	3	HLDVDLDRQSLSSIDKNPSER	1.31667	0.04691	(10) Phospho (ST);(13) Phospho (ST)
E2 01 2	5	HNDIVDSDSDAEDRGTLSAELTAAHFGGGGGLL HK	0.95917	0.0225	(7) Phospho (ST);(9) Phospho (ST)
E2 02 2	3	HSSISPVRLPLNSSLGAELSR	0.91167	0.01995	(2) Phospho (ST);(5) Phospho (ST)
E2 02 1	3	HSSISPVRLPLNSSLGAELSR	0.93833	0.01655	(2) Phospho (ST);(5) Phospho (ST)
E2 02 1	3	HSSISPVRLPLNSSLGAELSR	0.93833	0.01655	(3) Phospho (ST);(5) Phospho (ST)
E2 01	3	HYEDGYPGGSDNYGSLSR	0.80645	0.05834	(15) Phospho (ST)
E2 03	2	HYEDGYPGGSDNYGSLSR	0.82418	0.01125	(15) Phospho (ST)
E2 01 2	3	HYEDGYPGGSDNYGSLSR	0.86833	0.03341	(15) Phospho (ST)
E2 03 2	2	HYEDGYPGGSDNYGSLSR	0.87333	0.01361	(15) Phospho (ST)
E1 01	2	IAQEIASLSK	1.06686	0.05279	(9) Phospho (ST)
E1 04 1	3	IDEPSTPYHSMMGDDEDACSDTEATEAMAPDIL AR	1.47083	0.03007	(22) Phospho (ST)
E2 02 1	2	IDFSSIAVPGTSSPR	0.91667	0.2063	(13) Phospho (ST)
E2 01	2	IDISPSTFR	0.92365	0.01272	(4) Phospho (ST)
E1 01 1	2	IDISPSTFR	0.9575	0.00422	(4) Phospho (ST)
E1 01	2	IDISPSTFR	0.96031	0.01556	(4) Phospho (ST)
E2 01 1	2	IDISPSTFR	1.01083	0.00672	(4) Phospho (ST)
E1 01 3	2	IDISPSTFR	1.035	0.00985	(4) Phospho (ST)
E2 01 2	2	IDISPSTFR	1.03583	0.01275	(4) Phospho (ST)
E2 01 2	2	IDISPSTFRK	0.84333	0.06835	(4) Phospho (ST)
E1 01 3	3	IDISPSTFRK	0.85417	0.0145	(4) Phospho (ST)
E2 01 2	3	IDISPSTFRK	0.86	0.0196	(4) Phospho (ST)
E1 01	2	IDISPSTLR	0.89659	0.00766	(4) Phospho (ST)
E1 01 1	2	IDISPSTLR	0.9525	0.00584	(4) Phospho (ST)
E1 01 3	2	IDISPSTLR	0.98833	0.01255	(4) Phospho (ST)
E2 01 1	2	IDISPSTLR	0.9925	0.00497	(4) Phospho (ST)
E2 01 2	2	IDISPSTLR	1.00917	0.00738	(4) Phospho (ST)
E1 01 1	3	IDISPSTLRK	0.91417	0.01396	(4) Phospho (ST)
E1 01 3	3	IDISPSTLRK	0.915	0.01473	(4) Phospho (ST)
E2 01 2	3	IDISPSTLRK	0.91667	0.01186	(4) Phospho (ST)
E2 01 1	3	IDISPSTLRK	0.9225	0.01596	(4) Phospho (ST)
E2 01 2	2	IDISPSTLRK	0.98667	0.08264	(4) Phospho (ST)
E2 01 1	2	IDISPSTLRK	1	0.06891	(4) Phospho (ST)
E2 01	2	IDISPSTLRK	1.0274	0.1156	(4) Phospho (ST)
E1 02	3	IEDSEPHIPLIDDTDAEDDAPTK	1.0101	0.09142	(4) Phospho (ST)
E1 03 2	3	IEDSEPHIPLIDDTDAEDDAPTKR	0.72267	0.03058	(4) Phospho (ST)
E1 03 2	3	IEDSEPHIPLIDDTDAEDDAPTKR	0.8115	0.037	(4) Phospho (ST);(14) Phospho (ST)
E2 03 2	3	IEDSEPHIPLIDDTDAEDDAPTKR	0.97583	0.04663	(4) Phospho (ST);(14) Phospho (ST)
E1 03 1	3	IEDSEPHIPLIDDTDAEDDAPTKR	0.99917	0.06677	(4) Phospho (ST);(14) Phospho (ST)
E2 02 1	2	IEDVGSDEEDDSGK	0.94167	0.03881	(6) Phospho (ST)
E1 02	2	IEDVGSDEEDDSGK	0.95359	0.01788	(6) Phospho (ST)
E1 02 2	2	IEDVGSDEEDDSGK	1	0.01254	(6) Phospho (ST)
E2 02 2	2	IEDVGSDEEDDSGK	1.01583	0.04975	(6) Phospho (ST)
E1 03 1	2	IEDVGSDEEDDSGKDK	0.97833	0.02984	(6) Phospho (ST)
E1 01 3	3	IEDVGSDEEDDSGKDK	0.9825	0.0355	(6) Phospho (ST)
E1 03 2	2	IEDVGSDEEDDSGKDK	0.98417	0.02784	(6) Phospho (ST)
E1 01	3	IEEVLSPEGSPSKSPSK	0.97784	0.02567	(14) Phospho (ST)
E1 03 2	2	IEVLPVDTGAGGYSGNSGSPK	0.80142	0.01589	(19) Phospho (ST)
E2 03 2	2	IEVLPVDTGAGGYSGNSGSPK	0.81742	0.03114	(19) Phospho (ST)
E1 03	2	IEVLPVDTGAGGYSGNSGSPK	0.90909	0.08195	(19) Phospho (ST)
E2 04 1	3	IGDLQAAIEDEMESDENEDLINSLQDMVTK	0.92583	0.01661	(14) Phospho (ST)
E2 01 1	2	IGGIGTVPVGR	1.11417	0.02958	
E2 01	2	IGGIGTVPVGR	1.35624	0.02912	
E2 03 2	3	IHDLEDDLEMSSDASDASGEEGGRVPK	1.1475	0.2079	(10) Oxidation (M);(11) Phospho (ST);(12) Phospho (ST);(15) Phospho (ST);(18) Phospho (ST)
E2 03 2	3	IHDLEDDLEMSSDASDASGEEGGRVPK	0.76658	0.3007	(11) Phospho (ST);(12) Phospho (ST);(15) Phospho (ST);(18) Phospho (ST)
E2 03	3	IHDLEDDLEMSSDASDASGEEGGRVPK	0.93985	0.0468	(11) Phospho (ST);(12) Phospho (ST);(15) Phospho (ST);(18) Phospho (ST)
E2 03 1	3	IHDLEDDLEMSSDASDASGEEGGRVPK	1.01333	0.08074	(11) Phospho (ST);(12) Phospho (ST);(15) Phospho (ST);(18) Phospho (ST)
E1 01 3	3	IHRASDPGLPAEEPK	1.04167	0.01209	(5) Phospho (ST)
E1 01 1	3	IHRASDPGLPAEEPK	1.05667	0.01358	(5) Phospho (ST)
E2 01 1	2	ILDLISESPIK	0.8775	0.02897	(9) Phospho (ST)
E2 01 2	2	ILDLISESPIK	0.9175	0.0146	(9) Phospho (ST)
E2 03 2	2	IISNASCTTNCLAPLAK	1.01083	0.03826	
E2 03 1	2	IISNASCTTNCLAPLAK	1.065	0.06355	
E2 02	4	INHTVILDDPFDDPPDLLIPDRSPEPTR	0.85616	0.03199	(23) Phospho (ST)
E2 02 2	4	INHTVILDDPFDDPPDLLIPDRSPEPTR	1.19417	0.0076	(23) Phospho (ST)
E2 02 1	4	INHTVILDDPFDDPPDLLIPDRSPEPTR	1.21167	0.01045	(23) Phospho (ST)
E2 03 1	3	INHTVILDDPFDDPPDLLIPDRSPEPTR	1.23917	0.04061	(23) Phospho (ST)
E1 04 1	2	IQQFDDGGSDEEDIWEEK	1.15833	0.05463	(9) Phospho (ST)
E1 04 3	2	IQQFDDGGSDEEDIWEEK	1.21333	0.04994	(9) Phospho (ST)
E2 04 2	3	ITSVSTGNLCTEEQTPPPRPEAYPIPTQTYTR	1.34667	0.05094	(6) Phospho (ST)
E1 04 3	2	IVEPEVVGESDSEVEGDAWR	1.0225	0.00918	(10) Phospho (ST);(12) Phospho (ST)
E1 04	2	IVEPEVVGESDSEVEGDAWR	1.07604	0.07145	(10) Phospho (ST);(12) Phospho (ST)
E2 04	2	IVEPEVVGESDSEVEGDAWR	1.2987	0.1044	(10) Phospho (ST);(12) Phospho (ST)
E1 02 1	3	IVRGDQPAASGDSDDDEPPPLPR	0.8875	0.00902	(10) Phospho (ST)
E1 02	3	IVRGDQPAASGDSDDDEPPPLPR	1.57596	0.01641	(10) Phospho (ST)
E2 02 2	3	IVRGDQPAASGDSDDDEPPPLPR	0.68667	0.09104	(13) Phospho (ST)
E1 04 1	2	IVRGDQPAASGDSDDDEPPPLPR	0.73658	0.02808	(13) Phospho (ST)
E1 04 3	2	IVRGDQPAASGDSDDDEPPPLPR	0.75775	0.02556	(13) Phospho (ST)
E1 02 1	3	IVRGDQPAASGDSDDDEPPPLPR	0.87583	0.00765	(13) Phospho (ST)
E1 02 2	3	IVRGDQPAASGDSDDDEPPPLPR	0.87583	0.01125	(13) Phospho (ST)
E1 01 1	3	IYHLPDAESDEDEDFK	0.85583	0.01136	(9) Phospho (ST)
E1 03 2	2	IYHLPDAESDEDEDFK	0.9175	0.04014	(9) Phospho (ST)

E2 03	2	IVHLPDAESDEDEDFK	1.19332	0.01309	(9) Phospho (ST)
E1 01	3	IVHLPDAESDEDEDFK	1.2931	0.00813	(9) Phospho (ST)
E1 04 1	2	IVHLPDAESDEDEDFKEQTR	0.79942	0.06447	(9) Phospho (ST)
E2 01 2	4	IVHLPDAESDEDEDFKEQTR	0.81108	0.02305	(9) Phospho (ST)
E1 02 1	3	IVHLPDAESDEDEDFKEQTR	0.85583	0.04161	(9) Phospho (ST)
E1 04 3	2	IVHLPDAESDEDEDFKEQTR	0.85917	0.1037	(9) Phospho (ST)
E1 01 3	4	IVHLPDAESDEDEDFKEQTR	0.86083	0.00968	(9) Phospho (ST)
E2 02 2	3	IVHLPDAESDEDEDFKEQTR	0.86333	0.1203	(9) Phospho (ST)
E1 02 2	3	IVHLPDAESDEDEDFKEQTR	0.865	0.04911	(9) Phospho (ST)
E2 02 1	3	IVHLPDAESDEDEDFKEQTR	0.8675	0.09575	(9) Phospho (ST)
E1 02	3	IVHLPDAESDEDEDFKEQTR	1.24172	0.02276	(9) Phospho (ST)
E2 02 2	3	KAYSFCGTVEYMAPEVVNR	0.88333	0.07935	(4) Phospho (ST)
E1 03 2	2	KDDSDDDGGGWITPSNIK	1.38583	0.3297	(4) Phospho (ST)
E1 02 1	2	KDSLTQAQEQGNLLN	0.94417	0.04835	(3) Phospho (ST)
E2 04 2	3	KEDSDEEEDDDSEEDEEDDEDEDEDEDEEEPA AMK	1.14	0.02604	(4) Phospho (ST);(12) Phospho (ST);(34) Oxidation (M)
E1 03	3	KEEENADSDDEGELQDLLSQDWR	0.96154	0.02011	(8) Phospho (ST)
E1 03 1	3	KEEENADSDDEGELQDLLSQDWR	0.96917	0.01312	(8) Phospho (ST)
E1 03 2	3	KEEENADSDDEGELQDLLSQDWR	1.03083	0.01998	(8) Phospho (ST)
E1 03 1	2	KEESEESDDDMGFGLFD	0.96917	0.00558	(4) Phospho (ST)
E2 03 2	2	KEESEESDDDMGFGLFD	0.885	0.01186	(4) Phospho (ST);(7) Phospho (ST)
E1 03 2	2	KEESEESDDDMGFGLFD	0.88667	0.00725	(4) Phospho (ST);(7) Phospho (ST)
E1 03 1	2	KEESEESDDDMGFGLFD	0.8875	0.00748	(4) Phospho (ST);(7) Phospho (ST)
E2 03	2	KEESEESDDDMGFGLFD	1.35993	0.01607	(4) Phospho (ST);(7) Phospho (ST)
E1 03 1	2	KEESEESDDDMGFGLFD	0.94083	0.00822	(4) Phospho (ST);(7) Phospho (ST);(11) Oxidation (M)
E2 03 1	2	KEESEESDDDMGFGLFD	0.9525	0.01367	(4) Phospho (ST);(7) Phospho (ST);(11) Oxidation (M)
E1 03 2	2	KEESEESDDDMGFGLFD	0.96667	0.00437	(7) Phospho (ST)
E1 03 1	2	KEESEESDDDMGFGLFD	0.97167	0.00649	(7) Phospho (ST)
E1 03 2	2	KETESEAEDNLDDLEK	0.9325	0.05278	(3) Phospho (ST);(5) Phospho (ST)
E2 03 2	2	KETESEAEDNLDDLEK	1.00333	0.04145	(3) Phospho (ST);(5) Phospho (ST)
E2 03 1	2	KETESEAEDNLDDLEK	1.01083	0.04158	(3) Phospho (ST);(5) Phospho (ST)
E2 03	2	KETESEAEDNLDDLEK	1.05263	0.01736	(3) Phospho (ST);(5) Phospho (ST)
E1 03 2	2	KETESEAEDNLDDLEK	0.79783	0.03529	(5) Phospho (ST)
E2 03 2	2	KETESEAEDNLDDLEK	0.82717	0.02792	(5) Phospho (ST)
E2 03 1	2	KETESEAEDNLDDLEK	0.84167	0.01554	(5) Phospho (ST)
E1 03 1	2	KETESEAEDNLDDLEK	0.85917	0.07175	(5) Phospho (ST)
E2 01 1	3	KETESEAEDNLDDLEK	0.94	0.07073	(5) Phospho (ST)
E1 01 1	3	KFSKEEPVSSGPEEAVGK	1.18667	0.0796	(10) Phospho (ST)
E2 01 2	3	KFSKEEPVSSGPEEAVGK	1.24	0.05001	(9) Phospho (ST);(10) Phospho (ST)
E1 02 2	3	KGGEFDEFVNDDTDDDLPISK	1.13833	0.02937	(13) Phospho (ST)
E2 03 1	3	KGGSYSQAASSDSAQGSDVSLTACKV	0.58775	0.0335	(17) Phospho (ST);(20) Phospho (ST)
E2 03 2	3	KGGSYSQAASSDSAQGSDVSLTACKV	0.61183	0.04316	(17) Phospho (ST);(20) Phospho (ST)
E1 02	3	KGNAEGSSDEEGKLVIDEPAK	0.87209	0.02116	(7) Phospho (ST);(8) Phospho (ST)
E1 02 1	3	KGNAEGSSDEEGKLVIDEPAK	0.8975	0.0632	(7) Phospho (ST);(8) Phospho (ST)
E1 01 1	2	KGSFSALVGR	0.94333	0.04046	(3) Phospho (ST)
E1 01 3	2	KGSFSALVGR	0.94833	0.0326	(3) Phospho (ST)
E2 01 1	2	KGSFSALVGR	1.00667	0.0735	(3) Phospho (ST)
E2 01 2	2	KGSFSALVGR	1.0175	0.04425	(3) Phospho (ST)
E2 01	2	KGSFSALVGR	1.32392	0.3718	(3) Phospho (ST)
E1 02 2	3	KGSVVNVNPTNTRPQSDTPEIR	1.1375	0.01365	(3) Phospho (ST)
E2 02 1	3	KGSVVNVNPTNTRPQSDTPEIR	1.165	0.01728	(3) Phospho (ST)
E2 02 2	3	KGSVVNVNPTNTRPQSDTPEIR	1.17667	0.01985	(3) Phospho (ST)
E2 02	3	KGSVVNVNPTNTRPQSDTPEIR	1.21065	0.0286	(3) Phospho (ST)
E2 02 2	4	KITPPSSPHSLTSTLVSLGHEEALEMAGSK	0.88333	0.01919	(3) Phospho (ST);(6) Phospho (ST)
E2 02 2	3	KKSEPDDELLFDFLNSSQK	0.81958	0.1201	(3) Phospho (ST)
E2 02 1	3	KKSEPDDELLFDFLNSSQK	0.85333	0.09421	(3) Phospho (ST)
E2 01 2	3	KKSPNELVDDLFK	1.0325	0.01634	(3) Phospho (ST)
E2 01 1	3	KKSPNELVDDLFK	1.05333	0.01249	(3) Phospho (ST)
E1 01 3	3	KKSPNELVDDLFK	1.0675	0.00787	(3) Phospho (ST)
E1 01 1	3	KKSPNELVDDLFK	1.09167	0.0117	(3) Phospho (ST)
E2 01 1	3	KLGDVSPTQIDVSQFGSFK	1.19083	0.02069	(6) Phospho (ST)
E1 01 3	2	KLGVSVSPSR	1.11083	0.1137	(7) Phospho (ST)
E2 02 2	3	KLPVDSVFNKFEDEDSDDVPR	0.945	0.1256	(16) Phospho (ST)
E2 02 1	3	KLPVDSVFNKFEDEDSDDVPR	1.07917	0.1589	(16) Phospho (ST)
E1 01 1	3	KLSCSLEDLRSESVDK	1.005	0.02492	(5) Phospho (ST)
E1 01 3	3	KLSCSLEDLRSESVDK	1.0125	0.02614	(5) Phospho (ST)
E2 01 2	3	KLSGDQITLPTTVDYSSVPK	0.68733	0.01418	(3) Phospho (ST)
E1 01 3	3	KLSGDQITLPTTVDYSSVPK	0.75717	0.02108	(3) Phospho (ST)
E2 04 1	2	KLSGDQITLPTTVDYSSVPK	0.79592	0.01702	(3) Phospho (ST)
E1 01	3	KLSGDQITLPTTVDYSSVPK	1.17371	0.01446	(3) Phospho (ST)
E2 01	3	KLSGDQITLPTTVDYSSVPK	1.41376	0.0133	(3) Phospho (ST)
E2 01 2	3	KLSLGQYDNDAGGQLPFSK	1	0.03562	(3) Phospho (ST)
E2 01	3	KLSLGQYDNDAGGQLPFSK	1.03306	0.02341	(3) Phospho (ST)
E2 01 1	3	KLSLPTDLKPDLDVK	1.06833	0.1106	(3) Phospho (ST)
E2 01 1	3	KLSPQDPSEDVSSVDPLK	0.71825	0.05548	(3) Phospho (ST)
E2 01 2	3	KLSPQDPSEDVSSVDPLK	0.79808	0.06899	(3) Phospho (ST)
E1 01 1	3	KLSPQDPSEDVSSVDPLK	0.96167	0.02264	(3) Phospho (ST)
E1 01 3	3	KLSPQDPSEDVSSVDPLK	0.9725	0.0119	(3) Phospho (ST)
E2 01 2	3	KLSPQDPSEDVSSVDPLK	0.79808	0.06899	(8) Phospho (ST)
E1 01 1	3	KLSPQDPSEDVSSVDPLK	0.96167	0.02264	(8) Phospho (ST)
E2 02 1	3	KLSVPTSDEEDEVPAPKPR	1.38	0.01639	(3) Phospho (ST);(6) Phospho (ST);(7) Phospho (ST)
E2 04 2	2	KLSVPTSDEEDEVPAPKPR	1.395	0.01793	(3) Phospho (ST);(6) Phospho (ST);(7) Phospho (ST)
E2 04 1	2	KLSVPTSDEEDEVPAPKPR	1.41083	0.01729	(3) Phospho (ST);(6) Phospho (ST);(7) Phospho (ST)
E2 04	2	KLSVPTSDEEDEVPAPKPR	0.7515	0.01506	(6) Phospho (ST);(7) Phospho (ST)
E2 02	3	KLSVPTSDEEDEVPAPKPR	0.79872	0.01122	(6) Phospho (ST);(7) Phospho (ST)
E1 04	2	KLSVPTSDEEDEVPAPKPR	0.88183	0.09117	(6) Phospho (ST);(7) Phospho (ST)
E1 04 1	2	KLSVPTSDEEDEVPAPKPR	0.9525	0.05833	(6) Phospho (ST);(7) Phospho (ST)
E1 01 3	4	KLSVPTSDEEDEVPAPKPR	1.02083	0.03492	(6) Phospho (ST);(7) Phospho (ST)
E2 04 2	2	KLSVPTSDEEDEVPAPKPR	1.03	0.03721	(6) Phospho (ST);(7) Phospho (ST)
E2 02 1	3	KLSVPTSDEEDEVPAPKPR	1.11917	0.01308	(6) Phospho (ST);(7) Phospho (ST)
E1 02 1	3	KLSVPTSDEEDEVPAPKPR	1.1425	0.01383	(6) Phospho (ST);(7) Phospho (ST)
E1 02 2	3	KLSVPTSDEEDEVPAPKPR	1.15583	0.01556	(6) Phospho (ST);(7) Phospho (ST)
E2 04 1	2	KLSVPTSDEEDEVPAPKPR	1.23333	0.04505	(6) Phospho (ST);(7) Phospho (ST)
E2 03 2	3	KNTFTAWSDEESDYEIDDRDVNK	1.00583	0.0292	(8) Phospho (ST);(12) Phospho (ST)
E1 04	2	KPATPAEDDEDDDIDLFGSDNEEEDK	0.71463	0.01313	(19) Phospho (ST)
E2 03	3	KPATPAEDDEDDDIDLFGSDNEEEDK	0.75605	0.02805	(19) Phospho (ST)
E1 03	3	KPATPAEDDEDDDIDLFGSDNEEEDK	1.05634	0.03902	(19) Phospho (ST)
E2 03 1	3	KPATPAEDDEDDDIDLFGSDNEEEDK	1.14833	0.07305	(19) Phospho (ST)
E1 04 1	2	KPATPAEDDEDDDIDLFGSDNEEEDK	1.19	0.02313	(19) Phospho (ST)
E1 04 3	2	KPATPAEDDEDDDIDLFGSDNEEEDK	1.19083	0.01941	(19) Phospho (ST)
E1 03 1	3	KPATPAEDDEDDDIDLFGSDNEEEDK	1.295	0.02227	(19) Phospho (ST)
E1 03 2	3	KPATPAEDDEDDDIDLFGSDNEEEDK	1.37417	0.027	(19) Phospho (ST)
E1 04	3	KPATPAEDDEDDDIDLFGSDNEEEDKEAAQLR	0.7837	0.00973	(19) Phospho (ST)
E1 03	4	KPATPAEDDEDDDIDLFGSDNEEEDKEAAQLR	0.8161	0.01606	(19) Phospho (ST)
E1 03 2	4	KPATPAEDDEDDDIDLFGSDNEEEDKEAAQLR	1.22083	0.00609	(19) Phospho (ST)
E1 03 1	4	KPATPAEDDEDDDIDLFGSDNEEEDKEAAQLR	1.2475	0.00847	(19) Phospho (ST)
E2 04 2	3	KPATPAEDDEDDDIDLFGSDNEEEDKEAAQLR	1.295	0.01914	(19) Phospho (ST)
E1 04 1	3	KPATPAEDDEDDDIDLFGSDNEEEDKEAAQLR	1.3425	0.01159	(19) Phospho (ST)
E1 03 2	4	KPATPAEDDEDDDIDLFGSDNEEEDKEAAQLR	1.40917	0.0249	(4) Phospho (ST);(19) Phospho (ST)
E2 02 1	3	KPSPAQAAETPALELPLPSVPAPAPL	1.15083	0.0088	(3) Phospho (ST)
E1 02 2	3	KPYRIESDEEEDFENVGK	1.35833	0.04468	(7) Phospho (ST)
E2 02	2	KQSLGELIGTLNAAK	0.90744	0.0216	(3) Phospho (ST)
E2 01 2	3	KQSLGELIGTLNAAK	0.96333	0.01277	(3) Phospho (ST)
E2 02 2	2	KQSLGELIGTLNAAK	0.97	0.0149	(3) Phospho (ST)
E2 01 1	3	KQSLGELIGTLNAAK	0.975	0.0106	(3) Phospho (ST)
E2 02 1	2	KQSLGELIGTLNAAK	1.0025	0.01244	(3) Phospho (ST)
E1 01	3	KTSDANETEDHLESLICK	1.07296	0.04354	(3) Phospho (ST)
E1 01 1	3	KTSDANETEDHLESLICK	1.14	0.0195	(3) Phospho (ST)
E1 01 3	3	KTSDANETEDHLESLICK	1.14583	0.01973	(3) Phospho (ST)
E2 03 2	3	KVEEDLKADEPSSEESDLEIDK	1.1275	0.02354	(12) Phospho (ST);(13) Phospho (ST);(16) Phospho (ST)
E2 03 1	3	KVEEDLKADEPSSEESDLEIDK	1.1325	0.01874	(12) Phospho (ST);(13) Phospho (ST);(16) Phospho (ST)
E1 01 1	3	KVQVAALQASPPLDQDDR	1.19333	0.03861	(10) Phospho (ST)
E2 01 2	3	KVQVAALQASPPLDQDDR	1.45667	0.04439	(10) Phospho (ST)
E2 01 2	3	KVSIVSKPVLYR	0.95417	0.0232	(3) Phospho (ST)
E2 01 1	3	KVSIVSKPVLYR	0.96917	0.04724	(3) Phospho (ST)
E2 02 1	3	KVVDYSQFQESDDADEDYGR	1.08833	0.01685	(11) Phospho (ST)
E2 04 2	2	KVVDYSQFQESDDADEDYGR	1.08917	0.02435	(11) Phospho (ST)
E2 04 1	2	KVVDYSQFQESDDADEDYGR	1.09	0.01869	(11) Phospho (ST)
E2 02 2	3	KVVDYSQFQESDDADEDYGR	1.1025	0.01429	(11) Phospho (ST)
E2 02 2	4	KVVDYSQFQESDDADEDYGRDSGPPTK	0.98917	0.11	(11) Phospho (ST)
E2 03 1	3	KVVDYSQFQESDDADEDYGRDSGPPTK	1.16083	0.0223	(11) Phospho (ST)
E2 03 2	3	KVVDYSQFQESDDADEDYGRDSGPPTK	1.18417	0.02754	(11) Phospho (ST)
E2 02 1	4	KVVDYSQFQESDDADEYYGRDSGPPTK	5.00167	0.196	(11) Phospho (ST);(18) Phospho (Y)
E2 04 1	3	LASPSGSTSSGLEVVAPEGTSAPGGGPGTLDD SATICR	1.275	0.0155	(9) Phospho (ST)
E2 04 2	2	LCDFGSASHVADNDITPYLVSR	1.01833	0.02505	(18) Phospho (Y)
E1 01 1	2	LCLSTVDLEVK	0.7415	0.06058	(4) Phospho (ST)
E1 01 3	2	LCLSTVDLEVK	0.77392	0.05855	(4) Phospho (ST)
E1 01	2	LDIDSPPITAR	0.6643	0.1474	(5) Phospho (ST)
E1 02	3	LDNTPASPPRSPAEPNDIPIAK	0.75113	0.02308	(7) Phospho (ST);(11) Phospho (ST)
E1 03 1	3	LEDSEVRSVASNQSEMEFSSLQDMPK	1.17667	0.01715	(8) Phospho (ST);(11) Phospho (ST);(14) Phospho (ST)
E1 03 2	2	LEEPPELNRQSPNPR	0.90833	0.02838	(11) Phospho (ST)
E2 01 1	3	LEEPPELNRQSPNPR	0.9325	0.02339	(11) Phospho (ST)
E2 01 2	3	LEEPPELNRQSPNPR	0.95083	0.0365	(11) Phospho (ST)
E1 01 1	3	LEEPPELNRQSPNPR	0.9525	0.0395	(11) Phospho (ST)
E1 01	3	LEEPPELNRQSPNPR	0.99867	0.01262	(11) Phospho (ST)
E1 03	3	LESTARPSESSEEFLEEEPEQR	0.80472	0.04336	(10) Phospho (ST);(11) Phospho (ST)
E1 03 2	3	LESTARPSESSEEFLEEEPEQR	1.24083	0.05594	(10) Phospho (ST);(11) Phospho (ST)
E1 03 1	3	LESTARPSESSEEFLEEEPEQR	1.2725	0.0398	(10) Phospho (ST);(11) Phospho (ST)
E1 02 2	3	LESTARPSESSEEFLEEEPEQR	1.42583	0.05776	(11) Phospho (ST)
E1 02 1	3	LESTARPSESSEEFLEEEPEQR	1.43333	0.06375	(11) Phospho (ST)
E1 02 2	3	LESTARPSESSEEFLEEEPEQR	1.42583	0.05776	(4) Phospho (ST)
E1 02 1	3	LESTARPSESSEEFLEEEPEQR	1.43333	0.06375	(4) Phospho (ST)
E2 01 1	3	LETGAPRPPATVTNAVSWR	0.8185	0.03057	(11) Phospho (ST);(13) Phospho (ST)
E2 01 2	3	LETGAPRPPATVTNAVSWR	0.85417	0.05144	(11) Phospho (ST);(13) Phospho (ST)
E2 01	3	LETGAPRPPATVTNAVSWR	1.03878	0.03746	(11) Phospho (ST);(13) Phospho (ST)
E1 01	3	LETGAPRPPATVTNAVSWR	1.41911	0.07886	(11) Phospho (ST);(13) Phospho (ST)

E1 04 3	2	LFPEFDDSDYDEVPEEGPGAPAR	0.915	0.02977	(8) Phospho (ST)
E1 04 1	2	LFPEFDDSDYDEVPEEGPGAPAR	0.96667	0.03011	(8) Phospho (ST)
E2 01 2	3	LFRPPSPAPAAPGAR	1.17833	0.01562	(6) Phospho (ST)
E2 01 1	3	LFRPPSPAPAAPGAR	1.2475	0.02465	(6) Phospho (ST)
E2 02 1	2	LGAGALNAGSYASLGR	1.065	0.0292	(13) Phospho (ST)
E2 02 2	2	LGAGALNAGSYASLGR	1.065	0.02997	(13) Phospho (ST)
E2 02 2	2	LGAPENSGISTLER	0.68267	0.03485	(11) Phospho (ST)
E2 02 1	2	LGAPENSGISTLER	0.71083	0.03675	(11) Phospho (ST)
E1 02 1	2	LGAPENSGISTLER	0.80592	0.01661	(11) Phospho (ST)
E1 02 2	2	LGAPENSGISTLER	0.82142	0.02049	(11) Phospho (ST)
E2 02	2	LGAPENSGISTLER	1.15296	0.01841	(11) Phospho (ST)
E1 02	2	LGAPENSGISTLER	1.16009	0.01151	(11) Phospho (ST)
E1 01 1	3	LGGLRPESPESLTSVSR	1.0925	0.05152	(8) Phospho (ST)
E2 01 2	3	LGGLRPESPESLTSVSR	1.095	0.01808	(8) Phospho (ST)
E1 01 3	3	LGGLRPESPESLTSVSR	1.11333	0.03719	(8) Phospho (ST)
E2 01 1	3	LGGLRPESPESLTSVSR	1.11333	0.01656	(8) Phospho (ST)
E2 03 2	3	LGPGRPLPTFPTSECTSDVEPDTR	0.95417	0.03431	(13) Phospho (ST)
E2 02 1	3	LGPGRPLPTFPTSECTSDVEPDTR	0.89917	0.03817	(17) Phospho (ST)
E2 03 1	3	LGPGRPLPTFPTSECTSDVEPDTR	0.935	0.0623	(17) Phospho (ST)
E2 02 2	3	LGPGRPLPTFPTSECTSDVEPDTR	0.94083	0.05156	(17) Phospho (ST)
E2 03 2	3	LGPGRPLPTFPTSECTSDVEPDTR	0.95417	0.03431	(17) Phospho (ST)
E2 02	3	LGPGRPLPTFPTSECTSDVEPDTR	1.26796	0.02864	(17) Phospho (ST)
E1 03 1	4	LGPQNFIDETSDIENLLKEEEDYKEENNDSK	1.125	0.01579	(11) Phospho (ST)
E1 01 3	2	LGSVDSFER	1.0575	0.07152	(3) Phospho (ST)
E1 01	2	LGVSVSPSR	0.94997	0.06239	(6) Phospho (ST)
E1 01 1	2	LGVSVSPSR	1.21	0.0348	(6) Phospho (ST)
E1 01 3	2	LGVSVSPSR	1.21333	0.03904	(6) Phospho (ST)
E1 03 2	2	LHSSNPNLSTLDFGEEK	0.83583	0.05237	(4) Phospho (ST)
E1 03 1	2	LHSSNPNLSTLDFGEEK	0.84167	0.05357	(4) Phospho (ST)
E1 01 3	3	LHSSNPNLSTLDFGEEK	0.86667	0.01196	(4) Phospho (ST)
E2 01	2	LIPGPLSPVAR	0.91352	0.05286	(7) Phospho (ST)
E2 01 2	2	LIPGPLSPVAR	1.09833	0.00922	(7) Phospho (ST)
E2 01 1	2	LIPGPLSPVAR	1.1225	0.01101	(7) Phospho (ST)
E1 01	2	LISQIVSSITASLR	1.1194	0.0595	
E1 01 1	2	LIVENLSSR	0.96083	0.03454	(8) Phospho (ST)
E2 01 1	2	LIVENLSSR	0.99417	0.02262	(8) Phospho (ST)
E2 01 2	2	LIVENLSSR	1.03583	0.03306	(8) Phospho (ST)
E2 01 2	3	LKDLFDYSPPLHK	0.91583	0.00786	(8) Phospho (ST)
E2 01 1	3	LKDLFDYSPPLHK	0.92417	0.00882	(8) Phospho (ST)
E1 01 3	3	LLDHMAPPPVADQASPR	1.27417	0.05067	(15) Phospho (ST)
E2 01 2	3	LLDHMAPPPVADQASPR	1.38167	0.06083	(15) Phospho (ST)
E1 01 1	2	LLIVQDASER	0.32708	0.1209	(8) Phospho (ST)
E2 01 2	4	LLKEGEEPTVYSDEEEPKDESAR	0.80975	0.04447	(12) Phospho (ST)
E2 03 2	3	LLKEGEEPTVYSDEEEPKDESAR	0.81283	0.009	(12) Phospho (ST)
E2 03 1	3	LLKEGEEPTVYSDEEEPKDESAR	0.82567	0.02254	(12) Phospho (ST)
E1 03 2	3	LLKEGEEPTVYSDEEEPKDESAR	0.84333	0.01564	(12) Phospho (ST)
E1 01 1	3	LLKPGEEPSEYTDEEDTK	0.70108	0.08546	(12) Phospho (ST)
E2 01 1	3	LLKPGEEPSEYTDEEDTK	0.73083	0.04253	(12) Phospho (ST)
E2 01 2	3	LLKPGEEPSEYTDEEDTK	0.73817	0.04722	(12) Phospho (ST)
E1 01 3	3	LLKPGEEPSEYTDEEDTK	0.76725	0.06584	(12) Phospho (ST)
E2 01	3	LLKPGEEPSEYTDEEDTK	1.1839	0.01576	(12) Phospho (ST)
E1 01	3	LLKPGEEPSEYTDEEDTK	1.19522	0.01572	(12) Phospho (ST)
E1 03	2	LLKPGEEPSEYTDEEDTK	1.31349	0.03731	(12) Phospho (ST)
E2 03	2	LLKPGEEPSEYTDEEDTK	1.31579	0.01404	(12) Phospho (ST)
E2 01 1	3	LLLERPSPIRDR	0.91	0.01082	(7) Phospho (ST)
E2 01 1	2	LLSPLSSAR	1.01583	0.07445	(3) Phospho (ST)
E2 01 1	3	LNHVAAGLVSPSLK	0.91917	0.09122	(10) Phospho (ST)
E1 04 3	3	LQEEQDGGSSDEDRAGPAPPGASDGVDIQDVK	1.24667	0.02953	(9) Phospho (ST);(10) Phospho (ST)
E2 01 2	3	LSGQNAMGSQDSLLEITFR	0.80175	0.04075	(9) Phospho (ST);(12) Phospho (ST)
E2 01 1	2	LSSMAMISGLSGR	0.99667	0.07666	(3) Phospho (ST)
E1 01 3	2	LSSPVLHR	0.88583	0.04013	(3) Phospho (ST)
E1 02	2	LSSTDDGYIDLQFK	1.14504	0.06183	(3) Phospho (ST)
E1 02	2	LSSTDDGYIDLQFK	1.14504	0.06183	(4) Phospho (ST)
E1 01 1	3	LSVPTSDEEDEVPAPKPR	0.81933	0.06433	(5) Phospho (ST);(6) Phospho (ST)
E1 01 3	3	LSVPTSDEEDEVPAPKPR	0.89083	0.06353	(5) Phospho (ST);(6) Phospho (ST)
E2 01	3	LSVPTSDEEDEVPAPKPR	0.9772	0.07052	(5) Phospho (ST);(6) Phospho (ST)
E1 01 3	3	LSVPTSDEEDEVPAPKPR	0.7095	0.03094	(6) Phospho (ST)
E1 03	2	LSVPTSDEEDEVPAPKPR	1.28535	0.08185	(6) Phospho (ST)
E2 01 2	3	LSVPYVPQVTDEDRLSR	0.73958	0.1069	(16) Phospho (ST)
E1 01 1	3	LVHDSLEDLQMTR	0.76867	0.03949	(5) Phospho (ST)
E1 01 3	3	LVHDSLEDLQMTR	0.80375	0.05046	(5) Phospho (ST)
E2 02 2	3	LVHSGPGKGSPQAGVDLSFATR	0.68433	0.03216	(10) Phospho (ST)
E2 02 1	3	LVHSGPGKGSPQAGVDLSFATR	0.69492	0.02655	(10) Phospho (ST)
E2 01	3	LVINGNPITIFQERDPSK	1.18297	0.03291	(17) Phospho (ST)
E2 03 1	2	LVINGNPITIFQERDPSK	0.83417	0.3824	(4) Deamidated (NQ);(17) Phospho (ST)
E2 01 2	3	LVINGNPITIFQERDPSK	1.025	0.02369	(4) Deamidated (NQ);(17) Phospho (ST)
E2 01 1	3	LVINGNPITIFQERDPSK	1.0275	0.01881	(4) Deamidated (NQ);(17) Phospho (ST)
E2 01	3	LVINGNPITIFQERDPSK	1.18671	0.02377	(4) Deamidated (NQ);(17) Phospho (ST)
E2 02 2	3	LVINGNPITIFQERDPSKIK	1.3925	0.1067	(4) Deamidated (NQ);(17) Phospho (ST)
E2 03 2	3	MAPTPIPTRSPSDSSTASTPVAEQIER	1.1	0.02967	(1) Oxidation (M);(12) Phospho (ST)
E1 03 1	3	MAPTPIPTRSPSDSSTASTPVAEQIER	1.16583	0.0377	(1) Oxidation (M);(12) Phospho (ST)
E1 03 2	3	MAPTPIPTRSPSDSSTASTPVAEQIER	1.1025	0.02334	(1) Oxidation (M);(16) Phospho (ST)
E2 03 1	3	MAPTPIPTRSPSDSSTASTPVAEQIER	1.15583	0.03486	(1) Oxidation (M);(16) Phospho (ST)
E2 03	3	MEREDSSEEEEEEIDDEEIER	1.07219	0.05421	(6) Phospho (ST);(7) Phospho (ST)
E2 03	3	MGQAPSQSLLPPAQDQPRSPVPSAFSDQSR	1.18203	0.03601	(1) Oxidation (M);(19) Phospho (ST)
E2 03 2	3	MGQAPSQSLLPPAQDQPRSPVPSAFSDQSR	0.98833	0.0291	(19) Phospho (ST)
E2 03	3	MLAESDESGDEESVSQTDKTELQNTLR	0.89286	0.0392	(1) Oxidation (M);(5) Phospho (ST);(8) Phospho (ST)
E1 03	3	MLAESDESGDEESVSQTDKTELQNTLR	0.92025	0.01333	(1) Oxidation (M);(5) Phospho (ST);(8) Phospho (ST)
E1 03 2	3	MLAESDESGDEESVSQTDKTELQNTLR	1.12083	0.01872	(1) Oxidation (M);(5) Phospho (ST);(8) Phospho (ST)
E1 03 1	3	MLAESDESGDEESVSQTDKTELQNTLR	1.12583	0.02019	(1) Oxidation (M);(5) Phospho (ST);(8) Phospho (ST)
E1 03 2	3	MLAESDESGDEESVSQTDKTELQNTLR	1.04167	0.02032	(5) Phospho (ST);(8) Phospho (ST)
E1 01 1	3	MPQDGSDDEDKEWPTLEK	0.8975	0.03286	(6) Phospho (ST)
E1 01 3	3	MPQDGSDDEDKEWPTLEK	0.995	0.03066	(6) Phospho (ST)
E1 01	3	MPQDGSDDEDKEWPTLEK	1.08225	0.05912	(6) Phospho (ST)
E2 01 1	3	MSCFSRPSMSPTPLDR	0.81408	0.08739	(1) Oxidation (M);(5) Phospho (ST);(8) Phospho (ST)
E1 01 1	3	MSCFSRPSMSPTPLDR	0.9475	0.04089	(1) Oxidation (M);(8) Phospho (ST);(10) Phospho (ST)
E1 01 3	3	MSCFSRPSMSPTPLDR	0.98667	0.03376	(1) Oxidation (M);(8) Phospho (ST);(10) Phospho (ST)
E2 01 1	3	MSCFSRPSMSPTPLDR	0.82	0.04817	(8) Phospho (ST);(10) Phospho (ST)
E1 02	2	MYSFDDVLEEGK	0.57099	0.04553	(1) Oxidation (M);(3) Phospho (ST)
E2 03 1	3	NADDLEVSSDIIEAVAISSNSFITTGK	0.85833	0.01878	(9) Phospho (ST)
E2 03 2	3	NADDLEVSSDIIEAVAISSNSFITTGK	0.9175	0.04656	(9) Phospho (ST)
E2 01 1	3	NDARSPGSISYLPSFFTK	0.86917	0.01833	(5) Phospho (ST)
E1 02	3	NDSDLFGLGLEEAGPKESSEEGK	0.79702	0.09954	(19) Phospho (ST)
E1 01 3	2	NDSWGSFDLR	0.86167	0.05111	(3) Phospho (ST)
E2 01 2	2	NDSWGSFDLR	0.8675	0.05924	(3) Phospho (ST)
E1 01	2	NDSWGSFDLR	1.37489	0.01738	(3) Phospho (ST)
E2 01 1	2	NFSAAKSLLK	0.39067	0.265	(3) Phospho (ST);(7) Phospho (ST)
E2 01 2	2	NFSAAKSLLK	0.41383	0.2851	(3) Phospho (ST);(7) Phospho (ST)
E1 01 3	2	NFSAAKSLLK	0.52058	0.1095	(3) Phospho (ST);(7) Phospho (ST)
E1 01 1	2	NFSAAKSLLK	0.53375	0.08464	(3) Phospho (ST);(7) Phospho (ST)
E1 03 1	2	NGILASPQSAPGNLDNSK	0.64517	0.07675	(9) Phospho (ST)
E1 03 2	2	NGILASPQSAPGNLDNSK	0.7415	0.1236	(9) Phospho (ST)
E2 03 2	3	NGLHRPVSTDFAQYNSYGDVSGGVR	0.9725	0.02297	(1) Deamidated (NQ);(16) Phospho (ST)
E2 03 1	3	NGLHRPVSTDFAQYNSYGDVSGGVR	1.0125	0.03395	(1) Deamidated (NQ);(16) Phospho (ST)
E1 01 3	3	NGNGGPGPYVGQAGTATLPR	0.93	0.03534	(1) Deamidated (NQ);(3) Deamidated (NQ);(12) Deamidated (NQ);(17) Phospho (ST)
E1 01 1	3	NGNGGPGPYVGQAGTATLPR	0.86667	0.03586	(1) Deamidated (NQ);(3) Deamidated (NQ);(17) Phospho (ST)
E1 03 2	2	NGNGGPGPYVGQAGTATLPR	0.89583	0.01832	(1) Deamidated (NQ);(3) Deamidated (NQ);(17) Phospho (ST)
E1 03 1	2	NGNGGPGPYVGQAGTATLPR	0.8975	0.02398	(1) Deamidated (NQ);(3) Deamidated (NQ);(17) Phospho (ST)
E1 01 3	3	NGNGGPGPYVGQAGTATLPR	0.93583	0.03458	(1) Deamidated (NQ);(3) Deamidated (NQ);(17) Phospho (ST)
E2 01 1	3	NGRVEIIANDQGNR	0.72317	0.04279	(1) Deamidated (NQ)
E1 01 3	3	NGRVEIIANDQGNR	0.757	0.05777	(1) Deamidated (NQ)
E1 03 1	3	NHSVNEEEQEEQGEGSEDEWEQVGPR	0.93	0.02189	(16) Phospho (ST)
E1 03	3	NHSVNEEEQEEQGEGSEDEWEQVGPR	0.96587	0.01875	(16) Phospho (ST)
E1 03 2	3	NHSVNEEEQEEQGEGSEDEWEQVGPR	0.99583	0.0217	(16) Phospho (ST)
E2 03 1	3	NHSVNEEEQEEQGEGSEDEWEQVGPR	1.09167	0.05182	(16) Phospho (ST)
E2 03 2	3	NHSVNEEEQEEQGEGSEDEWEQVGPR	1.11	0.05116	(16) Phospho (ST)
E2 01 1	2	NIEDVIAQGIGK	0.84667	0.04456	
E2 01 2	2	NIEDVIAQGIGK	0.9	0.0285	
E1 01 3	2	NIGSDFIPR	0.91583	0.0208	(4) Phospho (ST)
E1 02	3	NKLEGDSDVDSELEDRVDGVK	1.01351	0.0925	(7) Phospho (ST)
E2 02 2	3	NKLEGDSDVDSELEDRVDGVK	0.97	0.05021	(7) Phospho (ST);(11) Phospho (ST)
E1 02 2	3	NKLEGDSDVDSELEDRVDGVK	1.02583	0.02565	(7) Phospho (ST);(11) Phospho (ST)
E1 02 1	3	NKLEGDSDVDSELEDRVDGVK	1.02833	0.01665	(7) Phospho (ST);(11) Phospho (ST)
E1 02	3	NKLEGDSDVDSELEDRVDGVK	1.08069	0.02853	(7) Phospho (ST);(11) Phospho (ST)
E2 02	3	NKLEGDSDVDSELEDRVDGVK	1.13895	0.03409	(7) Phospho (ST);(11) Phospho (ST)
E1 03	2	NKPGPNIESGNEDDDASFK	0.78125	0.02043	(9) Phospho (ST)
E1 01	3	NKPGPNIESGNEDDDASFK	0.81655	0.01661	(9) Phospho (ST)
E1 03 1	2	NKPGPNIESGNEDDDASFK	1.09333	0.01308	(9) Phospho (ST)
E1 03 2	2	NKPGPNIESGNEDDDASFK	1.09417	0.02727	(9) Phospho (ST)
E2 03 1	2	NKPGPNIESGNEDDDASFK	1.1225	0.02874	(9) Phospho (ST)
E2 03 2	2	NKPGPNIESGNEDDDASFK	1.1775	0.02773	(9) Phospho (ST)
E1 01 3	2	NLALSRESLVV	0.96167	0.01885	(5) Phospho (ST)
E2 01	3	NLDIERPTYTNLNR	0.94518	0.04332	
E2 01 1	3	NLDIERPTYTNLNR	1.08167	0.09527	
E1 01 3	2	NLEQILNGGESPK	0.895	0.03446	(11) Phospho (ST)

E1 01 3	2	NLEQILNGGESPK	0.92167	0.1604	(7) Deamidated (NQ);(11) Phospho (ST)
E1 01	2	NLEQILNGGESPK	1.29534	0.05146	(7) Deamidated (NQ);(11) Phospho (ST)
E1 02 1	2	NLGSINTELQDVQR	0.86667	0.03504	(4) Phospho (ST)
E1 02 2	2	NLGSINTELQDVQR	0.8775	0.02195	(4) Phospho (ST)
E2 02 2	2	NLGSINTELQDVQR	0.91333	0.03759	(4) Phospho (ST)
E1 02	2	NLGSINTELQDVQR	1.53077	0.03517	(4) Phospho (ST)
E1 03	2	NLLEDDSDEEEDFFLR	1.16913	0.02157	(7) Phospho (ST)
E2 02 2	3	NLLLQYNSGEDLAVNIIFPEK	1.0175	0.06014	(1) Deamidated (NQ);(8) Phospho (ST)
E2 02 1	3	NLLLQYNSGEDLAVNIIFPEK	1.16	0.06584	(1) Deamidated (NQ);(8) Phospho (ST)
E2 02 2	3	NLLLQYNSGEDLAVNIIFPEK	0.87	0.02461	(8) Phospho (ST)
E1 01 3	2	NLSSPFIFHEK	0.94167	0.04353	(3) Phospho (ST)
E2 01 2	3	NLSSPFIFHEK	0.98667	0.0205	(3) Phospho (ST)
E2 01 2	2	NLSSPFIFHEK	1.0275	0.0282	(3) Phospho (ST)
E1 01 3	3	NLSSPFIFHEK	1.05333	0.03825	(3) Phospho (ST)
E2 01 1	2	NLSSPFIFHEK	1.07667	0.02555	(3) Phospho (ST)
E2 02 1	3	NMTVEQLLTGSPTSPTVEPEKPTR	0.99083	0.02779	(13) Phospho (ST)
E2 02 2	3	NMTVEQLLTGSPTSPTVEPEKPTR	1.29333	0.2357	(13) Phospho (ST)
E2 02 1	2	NNMTASMFDLSMK	0.788	0.06755	(6) Phospho (ST)
E2 03 2	2	NPVDYMDLPFSSSPSR	0.85417	0.2478	(13) Phospho (ST)
E1 02 1	2	NQLTSNPENTVFDAK	0.683	0.1313	
E1 02 2	2	NQLTSNPENTVFDAK	0.7095	0.1486	
E1 02	2	NQLTSNPENTVFDAK	1.43678	0.01606	
E1 03	2	NQSQSQDALVLEDVEK	0.5083	0.03494	(5) Phospho (ST)
E1 03 1	2	NQSQSQDALVLEDVEK	1.09833	0.01994	(5) Phospho (ST)
E1 03 2	2	NQSQSQDALVLEDVEK	1.11417	0.0214	(5) Phospho (ST)
E1 01 3	3	NQSQSQDALVLEDVEKK	1.1375	0.02406	(5) Phospho (ST)
E2 02 2	2	NRPTSISWDGLDSGK	1.07	0.1064	(5) Phospho (ST)
E1 01	2	NSATFKSFEDR	0.70588	0.09511	(7) Phospho (ST)
E1 01 3	2	NSDLLTVLSR	1.38083	0.1223	(9) Phospho (ST)
E2 01 2	3	NSPTFKSFEEKVENLK	0.72608	0.05507	(7) Phospho (ST)
E2 01 1	3	NSPTFKSFEEKVENLK	0.77692	0.02123	(7) Phospho (ST)
E1 01 3	3	NVAEALGHSPKDPGGGGGPVR	0.945	0.03072	(9) Phospho (ST)
E2 01 1	2	NVFTSAEELER	0.77508	0.01262	(5) Phospho (ST)
E2 01 2	2	NVFTSAEELER	0.79808	0.02105	(5) Phospho (ST)
E1 01 3	2	NVFTSAEELER	0.8525	0.01306	(5) Phospho (ST)
E1 01 1	2	NVFTSAEELER	0.85917	0.01665	(5) Phospho (ST)
E2 01	2	NVFTSAEELER	1.08853	0.01671	(5) Phospho (ST)
E1 01	2	NVFTSAEELER	1.21852	0.01113	(5) Phospho (ST)
E1 03 2	2	NVPQEESLEDSDVDADFK	1.00833	0.01275	(11) Phospho (ST)
E2 03 1	2	NVPQEESLEDSDVDADFK	1.0425	0.09883	(11) Phospho (ST)
E1 03 1	2	NVPQEESLEDSDVDADFK	1.07583	0.01497	(11) Phospho (ST)
E2 03 2	2	NVPQEESLEDSDVDADFK	1.13167	0.05625	(11) Phospho (ST)
E1 03 1	3	NVRSDISDQEEDEESEGCPVSINLSK	1.31083	0.01985	(4) Phospho (ST);(7) Phospho (ST)
E1 04	2	NWEDEDFYDSDDDTFLDR	0.61501	0.04183	(10) Phospho (ST)
E1 04 1	2	NWEDEDFYDSDDDTFLDR	1.345	0.01096	(10) Phospho (ST)
E2 01 1	3	NYSVGSRPLKPLSPLR	1.07333	0.06308	(3) Phospho (ST)
E2 01 2	3	NYSVGSRPLKPLSPLR	1.13167	0.04359	(3) Phospho (ST)
E1 01 1	3	PFSAPKPQTSPSPK	1.0325	0.01725	(10) Phospho (ST)
E1 02 2	2	PFSAPKPQTSPSPK	1.03667	0.02972	(10) Phospho (ST)
E1 01 3	3	PFSAPKPQTSPSPK	1.0475	0.01219	(10) Phospho (ST)
E2 01	3	PIQSKPQSPVIQAAAVSPK	0.90909	0.02878	(17) Phospho (ST)
E2 01 1	3	PIQSKPQSPVIQAAAVSPK	1.0825	0.1537	(17) Phospho (ST)
E2 01 2	3	PIQSKPQSPVIQAAAVSPK	1.08833	0.188	(17) Phospho (ST)
E1 01	2	PQSPVIQAAAVSPK	0.803	0.03534	(12) Phospho (ST)
E1 02	2	PSSSPVIFAGGQDR	7.79626	999	(4) Phospho (ST)
E1 01 3	2	PVPDSPVSVTRL	0.71125	0.05189	(5) Phospho (ST)
E1 01 1	2	PVPDSPVSVTRL	0.75467	0.1025	(5) Phospho (ST)
E1 01 3	2	PVPDSPVSVTRL	0.83008	0.01331	(5) Phospho (ST);(8) Phospho (ST)
E1 01	2	PVPDSPVSVTRL	1.07296	0.01417	(5) Phospho (ST);(8) Phospho (ST)
E2 02 1	2	PVSSAASVYAGAGGSGSR	1.005	0.08981	(7) Phospho (ST)
E2 02 2	2	PVSSAASVYAGAGGSGSR	1.03667	0.07791	(7) Phospho (ST)
E1 03 2	2	QASTDAGTAGALTPQHVR	1.07917	0.03327	(3) Phospho (ST)
E1 03 1	2	QASTDAGTAGALTPQHVR	1.0425	0.04532	(4) Phospho (ST)
E1 03 1	2	QASTDAGTAGALTPQHVR	1.0425	0.04532	(4) Phospho (ST)
E1 03 2	2	QASTDAGTAGALTPQHVR	1.07917	0.03327	(4) Phospho (ST)
E1 01 3	3	QASTDAGTAGALTPQHVR	1.335	0.1143	(4) Phospho (ST)
E2 01 2	3	QDDSPPRPIGPALPPGFIK	1.11917	0.07202	(4) Phospho (ST)
E2 01 1	3	QICLVLMLETLSQSPQGR	0.84667	0.01351	(13) Phospho (ST)
E2 01 1	3	QICLVLMLETLSQSPQGR	0.71133	0.1309	(6) Oxidation (M);(13) Phospho (ST)
E2 03 2	2	QISQDVKLEPDILLR	0.73725	0.05487	(3) Phospho (ST)
E1 01 1	3	QISQDVKLEPDILLR	0.80883	0.02304	(3) Phospho (ST)
E1 01 3	3	QISQDVKLEPDILLR	0.92167	0.01672	(3) Phospho (ST)
E1 01	3	QISQDVKLEPDILLR	0.92194	0.04283	(3) Phospho (ST)
E2 01 2	3	QISQDVKLEPDILLR	0.92417	0.01989	(3) Phospho (ST)
E2 01 1	3	QISQDVKLEPDILLR	0.93	0.01569	(3) Phospho (ST)
E2 01	2	QITVNDLPVGR	0.90964	0.02847	
E2 03	3	QKFNDSEGDDTEETEDYRQFR	0.77963	0.04566	(6) Phospho (ST);(11) Phospho (ST)
E2 03 1	3	QKFNDSEGDDTEETEDYRQFR	1.075	0.02336	(6) Phospho (ST);(11) Phospho (ST)
E1 02 2	2	QLEMENSPLLSPR	0.82017	0.08587	(7) Phospho (ST)
E1 02 1	2	QLEMENSPLLSPR	0.82367	0.02911	(7) Phospho (ST)
E2 01 2	3	QLHLEGASLELSDDDTESK	0.69883	0.03933	(12) Phospho (ST)
E1 01 3	3	QLHLEGASLELSDDDTESK	0.79175	0.01188	(12) Phospho (ST)
E1 01 1	3	QLHLEGASLELSDDDTESK	0.84083	0.03724	(12) Phospho (ST)
E1 01	3	QLHLEGASLELSDDDTESK	1.09569	0.01849	(12) Phospho (ST)
E1 01 3	2	QLSEDLLLTR	0.7905	0.06752	(3) Phospho (ST)
E1 02 2	2	QLSLEGSGLGVEDLK	1.35583	0.2635	(3) Phospho (ST)
E2 01 2	2	QLSLPLTQSK	0.955	0.03514	(3) Phospho (ST)
E2 01 1	2	QLSLPLTQSK	0.96333	0.04363	(3) Phospho (ST)
E1 01 1	2	QLSLPLTQSK	1.0075	0.01623	(3) Phospho (ST)
E1 01	2	QLSLPLTQSK	1.02389	0.04675	(3) Phospho (ST)
E1 01 3	2	QLSLPLTQSK	1.0375	0.01317	(3) Phospho (ST)
E1 01 3	2	QLSSGVSEIR	0.65942	0.1153	(3) Phospho (ST)
E1 02	2	QPLLLSEDEEDTK	0.87668	0.01392	(6) Phospho (ST)
E2 02	2	QPLLLSEDEEDTK	0.89982	0.0109	(6) Phospho (ST)
E2 02 2	2	QPLLLSEDEEDTK	1.09417	0.2242	(6) Phospho (ST)
E1 02 2	2	QPLLLSEDEEDTK	1.10167	0.04085	(6) Phospho (ST)
E1 02 1	2	QPLLLSEDEEDTK	1.13917	0.04385	(6) Phospho (ST)
E2 01 2	3	QPLLLSEDEEDTKR	0.965	0.01172	(6) Phospho (ST)
E2 01 1	3	QPLLLSEDEEDTKR	0.97667	0.00783	(6) Phospho (ST)
E1 01 3	3	QPLLLSEDEEDTKR	1.01917	0.01075	(6) Phospho (ST)
E1 01 1	3	QPLLLSEDEEDTKR	1.03417	0.00803	(6) Phospho (ST)
E1 02 2	2	QPLLLSEDEEDTKR	1.05333	0.02322	(6) Phospho (ST)
E1 02 1	2	QPLLLSEDEEDTKR	1.0575	0.02131	(6) Phospho (ST)
E2 02 1	2	QPLLLSEDEEDTKR	1.1625	0.01972	(6) Phospho (ST)
E2 02 2	2	QPLLLSEDEEDTKR	1.20833	0.02721	(6) Phospho (ST)
E1 02 2	4	QQFHSKPVDSDSDDDPLEAFMAEVEDQAAR	1.07917	0.00992	(10) Phospho (ST);(12) Phospho (ST)
E1 04 3	3	QQFHSKPVDSDSDDDPLEAFMAEVEDQAAR	1.10167	0.01376	(10) Phospho (ST);(12) Phospho (ST)
E2 04 2	3	QQFHSKPVDSDSDDDPLEAFMAEVEDQAAR	1.14333	0.00723	(10) Phospho (ST);(12) Phospho (ST)
E1 02 1	2	QQSEEDLLLQDFSR	0.786	0.06301	(3) Phospho (ST)
E1 02	2	QQSEEDLLLQDFSR	1.58646	0.04391	(3) Phospho (ST)
E1 03 1	3	QSCLRPFTEDDAADPNDSDIDPESR	0.83125	0.02047	(18) Phospho (ST)
E1 03 2	3	QSCLRPFTEDDAADPNDSDIDPESR	0.85667	0.03211	(18) Phospho (ST)
E2 01 1	3	QSGLSSLVNGKSPIR	1.13917	0.04503	(9) Deamidated (NQ);(12) Phospho (ST)
E1 04 3	3	QVLTAPGSAGQPRSEDEDSLEEAGSPAPGPCPR	1.425	0.2051	(14) Phospho (ST);(19) Phospho (ST)
E1 03 2	3	RAADEDWDSELEDDLLGEDLLSGK	0.96917	0.1055	(9) Phospho (ST)
E1 03 1	3	RAADEDWDSELEDDLLGEDLLSGK	1.0175	0.1697	(9) Phospho (ST)
E2 04 2	2	RAASLNYLNQPSAAPLQVSR	1.0425	0.02679	(4) Phospho (ST)
E1 04	3	RADDFPVRDDPSDVTDEDEGPAEPPPPPK	0.74147	0.02154	(12) Phospho (ST);(15) Phospho (ST)
E1 04 3	3	RADDFPVRDDPSDVTDEDEGPAEPPPPPK	1.25083	0.02659	(12) Phospho (ST);(15) Phospho (ST)
E1 01	3	RAPSVANVGSHCDLSLK	1.20968	0.02336	(4) Phospho (ST)
E2 01 1	3	RASGQAFELILSPR	1.16	0.04303	(3) Phospho (ST)
E1 01 3	3	RASLSDLTDLEDIEGLTVR	0.93333	0.05566	(3) Phospho (ST)
E2 02 1	3	RASSKGGGGYTCQSGSGWDEFTK	1.10083	0.02704	(3) Phospho (ST);(4) Phospho (ST)
E2 02 2	3	RASSKGGGGYTCQSGSGWDEFTK	1.10333	0.04136	(3) Phospho (ST);(4) Phospho (ST)
E2 01 2	2	RASSLNVLNVGGK	1.075	0.05529	(4) Phospho (ST)
E2 01 1	2	RASSLNVLNVGGK	1.0775	0.02407	(4) Phospho (ST)
E2 01 2	4	RDSFDDRGPSLNPVLDYDHGSR	1.09167	0.03104	(3) Phospho (ST)
E2 01 1	4	RDSFDDRGPSLNPVLDYDHGSR	1.125	0.02144	(3) Phospho (ST)
E1 02 1	3	RDSSSDDWEIPDGQITVGQR	0.89583	0.07191	(3) Phospho (ST)
E1 01 3	3	RESGPGIAPGPEPHGLTNK	0.895	0.05527	(3) Phospho (ST)
E2 01 2	2	RFSFSQR	0.82425	0.2638	(3) Phospho (ST)
E1 01 1	2	RFSFSQR	0.91083	0.3012	(3) Phospho (ST)
E1 01 3	3	RGLLYDSDEEDEERPAR	1.26083	0.02627	(7) Phospho (ST)
E2 01 2	3	RGLLYDSDEEDEERPAR	1.34917	0.03	(7) Phospho (ST)
E2 01 1	3	RGLLYDSDEEDEERPAR	1.3675	0.02962	(7) Phospho (ST)
E2 01 2	3	RGSGDTSSLDPDTSLSELR	0.89417	0.1157	(3) Phospho (ST)
E1 01 3	3	RGSGDTSSLDPDTSLSELR	0.95583	0.01553	(3) Phospho (ST)
E1 01	3	RGSGDTSSLDPDTSLSELR	1.12444	0.01225	(3) Phospho (ST)
E2 01 1	3	RGSGDTSSLDPDTSLSELR	1.15333	0.3173	(3) Phospho (ST)
E1 01	3	RGSGDTSSLDPDTSLSELR	1.12444	0.01225	(6) Phospho (ST)
E2 01 2	4	RGSGDTSSLDPDTSLSELRDIYDLK	1.2425	0.05657	(3) Phospho (ST)
E1 01 3	3	RGSPSAAFTFPDTDDFGK	0.70542	0.03482	(3) Phospho (ST)
E1 01 3	3	RGTGQSDDSDWDDTALIK	0.96167	0.01836	(6) Phospho (ST)
E2 04 1	2	RGTGQSDDSDWDDTALIK	0.9525	0.05206	(6) Phospho (ST);(9) Phospho (ST)
E1 04	2	RGTGQSDDSDWDDTALIK	0.95541	0.04989	(6) Phospho (ST);(9) Phospho (ST)
E1 04 1	2	RGTGQSDDSDWDDTALIK	1.04083	0.01068	(6) Phospho (ST);(9) Phospho (ST)
E1 04 3	2	RGTGQSDDSDWDDTALIK	1.04083	0.01302	(6) Phospho (ST);(9) Phospho (ST)
E1 02	3	RGTGQSDDSDWDDTALIK	1.04239	0.02284	(6) Phospho (ST);(9) Phospho (ST)
E1 02 2	3	RGTGQSDDSDWDDTALIK	1.04417	0.00723	(6) Phospho (ST);(9) Phospho (ST)
E2 02	3	RGTGQSDDSDWDDTALIK	1.05411	0.00718	(6) Phospho (ST);(9) Phospho (ST)
E2 02 1	3	RGTGQSDDSDWDDTALIK	1.05417	0.01442	(6) Phospho (ST);(9) Phospho (ST)
E2 02 2	3	RGTGQSDDSDWDDTALIK	1.09167	0.03538	(6) Phospho (ST);(9) Phospho (ST)
E2 04	2	RGTGQSDDSDWDDTALIK	1.28977	0.01797	(6) Phospho (ST);(9) Phospho (ST)
E2 01 2	4	RHSASNLHALAHPAPSPGSCSPK	1.08667	0.05038	(5) Phospho (ST)
E1 01 3	3	RHSSDINHLVTQGR	0.895	0.03883	(3) Phospho (ST)
E2 01 1	4	RHSSDINHLVTQGR	0.90333	0.021	(3) Phospho (ST)
E1 01 1	3	RHSSDINHLVTQGR	0.93083	0.05471	(3) Phospho (ST)
E2 01 2	4	RHSSDINHLVTQGR	0.94667	0.02305	(3) Phospho (ST)
E2 01 2	3	RHSSDINHLVTQGR	0.95917	0.04983	(3) Phospho (ST)
E1 01 3	4	RHSSDINHLVTQGR	0.975	0.01341	(3) Phospho (ST)
E2 01 1	3	RHSSDINHLVTQGR	1	0.04588	(3) Phospho (ST)
E1 01 1	4	RHSSDINHLVTQGR	1.02583	0.0493	(3) Phospho (ST)
E1 01	2	RIDISPSTFR	0.74813	0.07564	(5) Phospho (ST)
E2 01	2	RIDISPSTFR	0.75	0.116	(5) Phospho (ST)
E1 01 1	2	RIDISPSTFR	1.0525	0.0275	(5) Phospho (ST)
E1 01 3	2	RIDISPSTFR	1.12333	0.02705	(5) Phospho (ST)
E2 01 2	2	RIDISPSTFR	1.1425	0.06156	(5) Phospho (ST)
E2 01 1	2	RIDISPSTFR	1.14833	0.05588	(5) Phospho (ST)
E2 01 1	3	RIDISPSTFRK	0.9625	0.01292	(5) Phospho (ST)
E2 01 2	3	RIDISPSTFRK	0.96333	0.01213	(5) Phospho (ST)
E2 01 1	2	RIDISPSTLR	0.90917	0.03354	(5) Phospho (ST)
E1 01 1	2	RIDISPSTLR	0.93583	0.02733	(5) Phospho (ST)
E1 01	2	RIDISPSTLR	0.95541	0.01467	(5) Phospho (ST)
E2 01	2	RIDISPSTLR	0.97025	0.02728	(5) Phospho (ST)
E1 01 3	2	RIDISPSTLR	1.01	0.02607	(5) Phospho (ST)
E2 01 2	3	RILSDVTHSAVFGVPASK	0.98333	0.05118	(4) Phospho (ST)
E2 01 1	3	RIPSIVSSPLNSPLDR	0.87667	0.02458	(8) Phospho (ST);(12) Phospho (ST)
E2 01 2	3	RIPSIVSSPLNSPLDR	0.91	0.0298	(8) Phospho (ST);(12) Phospho (ST)
E1 01 3	2	RISDPQVFSK	0.91333	0.02445	(3) Phospho (ST)
E1 01 1	2	RISDPQVFSK	0.9325	0.03612	(3) Phospho (ST)
E1 03 2	3	RISSSSVQPCSEEVSTPQDSLAQCK	0.9875	0.03763	(3) Phospho (ST)
E1 03 2	3	RISSSSVQPCSEEVSTPQDSLAQCK	0.9875	0.03763	(6) Phospho (ST)
E1 01 3	3	RKPEDVLDDDDAGSAPLK	0.81858	0.03354	(14) Phospho (ST)
E1 01 1	3	RKPEDVLDDDDAGSAPLK	0.84333	0.02994	(14) Phospho (ST)
E1 01	3	RKPEDVLDDDDAGSAPLK	1.01078	0.02378	(14) Phospho (ST)
E2 01 1	3	RLSEVIYEPFQLLSK	0.815	0.03109	(3) Phospho (ST)
E2 01 2	3	RLSGDLSSMPGPGTLSVR	0.89	0.198	(3) Phospho (ST)
E2 01 1	3	RLSGDLSSMPGPGTLSVR	0.92167	0.07421	(3) Phospho (ST)
E2 01 2	3	RLSLPGLLSQVSPR	0.86417	0.01016	(3) Phospho (ST);(12) Phospho (ST)
E2 01 1	3	RLSLPGLLSQVSPR	0.88917	0.0192	(3) Phospho (ST);(12) Phospho (ST)

E2 01 2	3	RLSTSPDVIQGHQPR	0.79367	0.02454	(3) Phospho (ST)
E1 01 1	3	RLSTSPDVIQGHQPR	0.845	0.01668	(3) Phospho (ST)
E1 01	3	RLSTSPDVIQGHQPR	1.34288	0.0325	(3) Phospho (ST)
E2 01 1	3	RLSTSPDVIQGHQPR	0.78425	0.03317	(5) Phospho (ST)
E1 01 3	3	RLSTSPDVIQGHQPR	0.82117	0.03132	(5) Phospho (ST)
E1 01 1	3	RLSTSPDVIQGHQPR	0.845	0.01668	(5) Phospho (ST)
E1 01	3	RLSTSPDVIQGHQPR	1.34288	0.0325	(5) Phospho (ST)
E1 02 1	3	RNDDISELEDLSELEDLK	0.83008	0.8368	(6) Phospho (ST);(12) Phospho (ST)
E2 01 2	3	RNLGSINTELQDVQR	0.72133	0.2545	(5) Phospho (ST)
E2 01 1	3	RNLGSINTELQDVQR	0.79692	0.09528	(5) Phospho (ST)
E1 01 3	3	RNLLEDDSDEEEDFFLR	0.74375	0.172	(8) Phospho (ST)
E1 02	2	RNSSEASSGDFLDLK	0.95299	0.02089	(3) Phospho (ST)
E1 01	3	RNSSEASSGDFLDLK	1.11193	0.0174	(3) Phospho (ST)
E2 03 1	3	RPDYAPMESSDEEDEEFQFIK	0.87	0.2234	(9) Phospho (ST);(10) Phospho (ST)
E2 03 1	3	RPDYAPMESSDEEDEEFQFIKK	0.95417	0.04211	(9) Phospho (ST);(10) Phospho (ST)
E2 03 2	3	RPDYAPMESSDEEDEEFQFIKK	1.00417	0.04747	(9) Phospho (ST);(10) Phospho (ST)
E2 03 1	3	RPLFLAPDFDRWLDESDAEMELR	0.79525	0.03956	(16) Phospho (ST)
E2 03 1	3	RPLFLAPDFDRWLDESDAEMELR	1.0075	0.03274	(16) Phospho (ST);(20) Oxidation (M)
E2 01 1	3	RQQPPLGPSSSLLSLPGLK	0.85333	0.04211	(11) Phospho (ST);(14) Phospho (ST)
E2 01 1	3	RQQPPLGPSSSLLSLPGLK	0.85333	0.04211	(9) Phospho (ST);(14) Phospho (ST)
E2 02 1	3	RRSIQDLTVTGTEPGQVSSR	1.115	0.02452	(3) Phospho (ST)
E2 01 2	3	RRSSLPNGEGLQLK	0.86917	0.04867	(4) Phospho (ST);(7) Deamidated (NQ)
E1 02 1	3	RSASPDDDLGSSNWEAADLGNEER	1.0325	0.02109	(12) Phospho (ST)
E1 04 1	2	RSASPDDDLGSSNWEAADLGNEER	1.11167	0.02543	(12) Phospho (ST)
E1 02 2	3	RSASPDDDLGSSNWEAADLGNEER	1.00167	0.01804	(4) Phospho (ST)
E1 04 3	2	RSASPDDDLGSSNWEAADLGNEER	1.10667	0.01437	(4) Phospho (ST)
E1 04 1	2	RSASPDDDLGSSNWEAADLGNEER	1.11167	0.02543	(4) Phospho (ST)
E1 02 2	3	RSASPDDDLGSSNWEAADLGNEER	0.99667	0.01874	(4) Phospho (ST);(13) Deamidated (NQ)
E2 03	3	RSASPDDDLGSSNWEAADLGNEERK	0.77801	0.03411	(4) Phospho (ST)
E1 03	3	RSASPDDDLGSSNWEAADLGNEERK	0.79702	0.01858	(4) Phospho (ST)
E1 01	4	RSASPDDDLGSSNWEAADLGNEERK	0.90799	0.02317	(4) Phospho (ST)
E2 01 2	4	RSHSGPAGSFNKPAIR	1.62833	0.0256	(4) Phospho (ST)
E2 01 1	4	RSHSGPAGSFNKPAIR	1.77417	0.02113	(4) Phospho (ST)
E2 01 1	3	RSPVPAQIAITVPK	0.79167	0.09054	(2) Phospho (ST)
E2 01 1	2	RSSLLSLMTGK	0.81425	0.03077	(3) Phospho (ST)
E2 01 1	3	RSSSETILSSLAGSDIVK	0.73575	0.01945	(4) Phospho (ST)
E2 03	2	RSSSETILSSLAGSDIVK	1.19522	0.06227	(4) Phospho (ST)
E2 01 1	3	RSSSETILSSLAGSDIVK	0.73575	0.01945	(6) Phospho (ST)
E2 01 2	3	RSSVFAAEIMDAFDR	0.6535	0.08229	(3) Phospho (ST)
E2 02 1	3	RSSVFAAEIMDAFDRSPTDK	0.7095	0.08114	(3) Phospho (ST)
E2 02 2	3	RSSVFAAEIMDAFDRSPTDK	0.71375	0.05229	(3) Phospho (ST)
E1 01	3	RSYSSPDITQAIQEEEK	1.23967	0.03141	(4) Phospho (ST)
E1 01 3	3	RSYSSPDITQAIQEEEK	0.92583	0.01895	(5) Phospho (ST)
E1 01	3	RSYSSPDITQAIQEEEK	1.23967	0.03141	(5) Phospho (ST)
E2 01 2	3	RTSMGGTQQQFVEGVR	1	0.01236	(2) Phospho (ST)
E2 01	3	RTSMGGTQQQFVEGVR	1.06458	0.02265	(2) Phospho (ST)
E1 01 1	3	RTSMGGTQQQFVEGVR	1.095	0.03344	(2) Phospho (ST)
E1 03 1	2	RTSMGGTQQQFVEGVR	0.845	0.2429	(3) Phospho (ST)
E1 03 2	2	RTSMGGTQQQFVEGVR	0.85583	0.2023	(3) Phospho (ST)
E2 03 2	2	RTSMGGTQQQFVEGVR	0.89083	0.04628	(3) Phospho (ST)
E2 01	3	RTSMGGTQQQFVEGVR	1.06458	0.02265	(3) Phospho (ST)
E2 01 1	3	RTSMGGTQQQFVEGVR	1.00083	0.02486	(7) Phospho (ST)
E1 01 1	3	RTSMGGTQQQFVEGVR	1.095	0.03344	(7) Phospho (ST)
E1 01 3	3	RTSMGGTQQQFVEGVR	1.1325	0.03874	(7) Phospho (ST)
E2 01 2	2	RTSPQVLGSILK	0.96917	0.031	(3) Phospho (ST)
E2 01 1	2	RTSPQVLGSILK	1.0125	0.05648	(3) Phospho (ST)
E2 01 1	3	RVQSLPSVPLSCAAYR	0.72225	0.07478	(4) Phospho (ST)
E2 01 2	3	RVQSLPSVPLSCAAYR	0.789	0.03577	(4) Phospho (ST)
E1 02 1	3	RVSSDEEHTVDSCISDMK	1.17417	0.04389	(3) Phospho (ST);(4) Phospho (ST)
E2 02 2	4	RVSSSSELDLPSGDHCEAGLLQLDVPLLR	0.85417	0.07501	(5) Phospho (ST)
E2 04 2	3	RYGLLANTEDPTEMASLDSDEETVFESR	1.0225	0.02021	(12) Phospho (ST);(19) Phospho (ST)
E1 04 3	3	RYGLLANTEDPTEMASLDSDEETVFESR	0.86667	0.07776	(16) Phospho (ST);(19) Phospho (ST)
E2 01 1	3	RYSLIDPSSAPELLR	1.02333	0.03183	(3) Phospho (ST)
E1 01 3	2	SASFAFEFPK	0.711	0.04572	(3) Phospho (ST)
E2 01 1	2	SASFAFEFPK	0.77742	0.03606	(3) Phospho (ST)
E2 04 2	2	SASPDDDLGSSNWEAADLGNEER	1.12333	0.00843	(10) Phospho (ST)
E1 02 2	3	SASPDDDLGSSNWEAADLGNEER	1.00167	0.01356	(3) Phospho (ST)
E2 02 1	3	SASPDDDLGSSNWEAADLGNEER	1.015	0.05929	(3) Phospho (ST)
E1 04 3	2	SASPDDDLGSSNWEAADLGNEER	1.10083	0.00781	(3) Phospho (ST)
E1 04 1	2	SASPDDDLGSSNWEAADLGNEER	1.12083	0.01489	(3) Phospho (ST)
E2 04 2	2	SASPDDDLGSSNWEAADLGNEER	1.12333	0.00843	(3) Phospho (ST)
E2 04 1	2	SASPDDDLGSSNWEAADLGNEER	1.1425	0.01793	(3) Phospho (ST)
E1 02 2	3	SASPDDDLGSSNWEAADLGNEER	1.00833	0.01441	(3) Phospho (ST);(12) Deamidated (NQ)
E1 02 2	3	SASPDDDLGSSNWEAADLGNEERK	0.88083	0.06847	(3) Phospho (ST)
E1 04 1	2	SASPDDDLGSSNWEAADLGNEERK	0.9325	0.0666	(3) Phospho (ST)
E2 02 2	3	SASPDDDLGSSNWEAADLGNEERK	0.99417	0.03705	(3) Phospho (ST)
E1 02 1	3	SASPDDDLGSSNWEAADLGNEERK	1.025	0.05337	(3) Phospho (ST)
E2 03	2	SASQSSLDKLDQELK	0.91463	0.01058	(3) Phospho (ST);(6) Phospho (ST)
E1 03 1	2	SASQSSLDKLDQELK	0.945	0.05102	(3) Phospho (ST);(6) Phospho (ST)
E1 03 2	2	SASQSSLDKLDQELK	0.97	0.06729	(3) Phospho (ST);(6) Phospho (ST)
E1 01 1	3	SASQSSLDKLDQELK	1.05083	0.02006	(3) Phospho (ST);(6) Phospho (ST)
E2 03 2	2	SASQSSLDKLDQELK	1.12167	0.01317	(3) Phospho (ST);(6) Phospho (ST)
E2 03 2	2	SASQSSLDKLDQELK	1.12167	0.01317	(3) Phospho (ST);(6) Phospho (ST)
E1 01 1	3	SASQSSLDKLDQELK	1.05083	0.02006	(5) Phospho (ST);(6) Phospho (ST)
E2 01 1	3	SASQSSLDKLDQELK	1.10167	0.01301	(5) Phospho (ST);(6) Phospho (ST)
E2 01 1	3	SASQSSLDKLDQELK	1.10167	0.01301	(5) Phospho (ST);(6) Phospho (ST)
E1 01 3	3	SASQSSLDKLDQELK	1.11333	0.01715	(5) Phospho (ST);(6) Phospho (ST)
E2 03 2	2	SASQSSLDKLDQELK	1.12167	0.01317	(5) Phospho (ST);(6) Phospho (ST)
E2 03 2	2	SASQSSLDKLDQELK	1.12167	0.01317	(5) Phospho (ST);(6) Phospho (ST)
E2 01 2	3	SASQSSLDKLDQELK	1.12667	0.01153	(5) Phospho (ST);(6) Phospho (ST)
E2 03 1	2	SASQSSLDKLDQELK	1.14	0.01432	(5) Phospho (ST);(6) Phospho (ST)
E2 01 2	3	SASTLCLPSVGAARPQVK	1.12917	0.02571	(3) Phospho (ST)
E2 01 1	3	SASTLCLPSVGAARPQVK	1.16583	0.03799	(3) Phospho (ST)
E2 03 2	3	SATRPSPSPERSSTGPEPPAPTPLLAER	1.2475	0.01263	(6) Phospho (ST);(8) Phospho (ST)
E2 01 1	3	SAYQEYDSDSDVPEELKR	1.005	0.1443	(10) Phospho (ST)
E1 01 3	2	SCFESSPDPELK	0.97833	0.04319	(6) Phospho (ST)
E1 03 1	2	SDKSPDLAPTPAPQSTPR	1.255	0.04198	(1) Phospho (ST)
E1 03 2	2	SDKSPDLAPTPAPQSTPR	1.0775	0.06083	(4) Phospho (ST)
E1 01 3	3	SDKSPDLAPTPAPQSTPR	1.0825	0.05817	(4) Phospho (ST)
E1 01 1	3	SDKSPDLAPTPAPQSTPR	1.11	0.05687	(4) Phospho (ST)
E1 02 2	2	SDVLELTDDNFESR	0.75508	0.04247	
E1 02	2	SDVLELTDDNFESR	1.46915	0.09344	
E1 03 2	3	SEPVKEESSELEQPFAQDTSSVGPDR	0.78167	0.08369	(9) Phospho (ST)
E1 03 1	2	SESLIDASEDSQLEAAIR	1.11	0.01425	(11) Phospho (ST)
E1 03 2	2	SESLIDASEDSQLEAAIR	1.15167	0.00855	(11) Phospho (ST)
E1 03	2	SESLIDASEDSQLEAAIR	1.29758	0.02259	(11) Phospho (ST)
E1 03	2	SFEVEEVETPNSTPPR	1.2215	0.02845	(1) Phospho (ST)
E1 01 1	2	SFSADNFIGIQR	0.69817	0.01131	(3) Phospho (ST)
E2 01 2	2	SFSADNFIGIQR	0.72917	0.0154	(3) Phospho (ST)
E1 01 3	2	SFSADNFIGIQR	0.77375	0.05538	(3) Phospho (ST)
E2 01	2	SFSADNFIGIQR	1.23967	0.02502	(3) Phospho (ST)
E1 01	2	SFSADNFIGIQR	1.41643	0.2568	(3) Phospho (ST)
E1 02 2	3	SFSKEELMSSDLEETAGSTSIPK	1.09083	0.03557	(10) Phospho (ST)
E2 02 1	3	SFSKEELMSSDLEETAGSTSIPK	1.09667	0.0216	(10) Phospho (ST)
E2 02 2	3	SFSKEELMSSDLEETAGSTSIPK	1.1125	0.00832	(10) Phospho (ST)
E1 02 2	3	SFSKEELMSSDLEETAGSTSIPK	1.07667	0.06813	(8) Oxidation (M);(10) Phospho (ST)
E2 02 1	3	SFSKEELMSSDLEETAGSTSIPK	1.09333	0.06867	(8) Oxidation (M);(10) Phospho (ST)
E1 02 1	3	SFSKEELMSSDLEETAGSTSIPK	1.1075	0.04649	(8) Oxidation (M);(10) Phospho (ST)
E2 02 2	3	SFSKEELMSSDLEETAGSTSIPK	1.13	0.06848	(8) Oxidation (M);(10) Phospho (ST)
E2 01 2	2	SFSKEVEER	1.135	0.0161	(3) Phospho (ST)
E2 02 1	2	SFSLASSSNSPISQR	1.06167	0.1294	(3) Phospho (ST)
E2 02 2	2	SFSLASSSNSPISQR	1.23667	0.1773	(3) Phospho (ST)
E1 01 1	2	SFSLDPLMER	0.9	0.04701	(3) Phospho (ST)
E1 01 3	2	SFSMQDLR	0.91583	0.03732	(3) Phospho (ST)
E2 01 2	2	SFTGGLGQLVVPSK	0.70017	0.05863	(1) Phospho (ST)
E2 01 1	2	SFTGGLGQLVVPSK	0.72092	0.0331	(1) Phospho (ST)
E2 01 2	2	SFTGGLGQLVVPSK	0.70017	0.05863	(3) Phospho (ST)
E2 01 1	2	SFTGGLGQLVVPSK	0.72092	0.0331	(3) Phospho (ST)
E1 04 1	3	SGLELTELQNMTVPEDDNISNDSNDFTEVENGQI NSK	0.965	0.03547	(12) Phospho (ST);(20) Phospho (ST);(24) Deamidated (NQ)
E1 04 1	3	SGLELTELQNMTVPEDDNISNDSNDFTEVENGQI NSK	0.965	0.03547	(20) Phospho (ST);(23) Phospho (ST);(31) Deamidated (NQ)
E1 01 1	2	SGLSLEELR	0.8825	0.0386	(4) Phospho (ST)
E2 01 1	2	SGLSLEELR	0.88417	0.03577	(4) Phospho (ST)
E1 01	2	SGLSLEELR	0.90416	0.07019	(4) Phospho (ST)
E1 01 3	2	SGLSLEELR	0.99917	0.05281	(4) Phospho (ST)
E2 01	4	SGSGSVGNGSSRYSPSQNSPIHHIPSR	0.88339	0.02602	(8) Deamidated (NQ);(13) Phospho (Y);(19) Phospho (ST)
E2 02 2	4	SGSGSVGNGSSRYSPSQNSPIHHIPSRR	1.23333	0.0238	(8) Deamidated (NQ);(13) Phospho (Y);(19) Phospho (ST)
E2 02 1	3	SGSPRPTEPTDFLMLFEGSPSGK	1.20167	0.03572	(3) Phospho (ST)
E2 02 2	3	SGSPRPTEPTDFLMLFEGSPSGK	1.205	0.04897	(7) Phospho (ST)
E2 02 1	3	SGSPRPTEPTDFLMLFEGSPSGK	0.86583	0.08745	(7) Phospho (ST);(14) Oxidation (M)
E1 02 2	3	SGSSSPDSEITELKFPSINHD	1.01583	0.03676	(4) Phospho (ST);(5) Phospho (ST)
E2 02 1	3	SGSSSPDSEITELKFPSINHD	1.06583	0.03433	(4) Phospho (ST);(5) Phospho (ST)
E1 02 2	3	SGSSSPDSEITELKFPSINHD	0.86083	0.02162	(5) Phospho (ST)
E2 02 1	3	SGSSSPDSEITELKFPSINHD	0.95167	0.02055	(5) Phospho (ST)
E2 01 1	3	SHSGPAGSFNKPAIR	1.37333	0.01691	(3) Phospho (ST)
E2 01 2	3	SHSGPAGSFNKPAIR	1.375	0.024	(3) Phospho (ST)
E2 02 2	3	SHSRQASTDAGTAGALTPQHVR	1.09583	0.02839	(3) Phospho (ST);(12) Phospho (ST)
E1 02 1	3	SHSRQASTDAGTAGALTPQHVR	1.11	0.02481	(3) Phospho (ST);(8) Phospho (ST)
E2 01 2	4	SHSSPASLQLGTGAGAAGSPAQQHAHLR	1.15167	0.02829	(4) Phospho (ST)
E2 01 1	4	SHSSPASLQLGTGAGAAGSPAQQHAHLR	1.17583	0.02586	(4) Phospho (ST)
E2 01 2	3	SHTITRPLESDEDEK	1.04833	0.2322	(10) Phospho (ST)
E1 02 2	2	SIEVENDFLPVEK	0.9275	0.07332	(1) Phospho (ST)
E1 02	2	SIEVENDFLPVEK	1.29646	0.03364	(1) Phospho (ST)
E1 03 2	3	SILKPSTPPPQEGEEVGESSEEQDNAPK	1.20083	0.02805	(20) Phospho (ST)
E2 02 2	2	SIQFVDWCPTGFK	0.96	0.02626	(1) Phospho (ST)
E2 02 1	2	SIQFVDWCPTGFK	1.11333	0.032	(1) Phospho (ST)
E2 03 1	3	SISQDSLDELSMEDYWIELENIK	0.89167	0.04346	(3) Phospho (ST)
E2 03 1	3	SISQDSLDELSMEDYWIELENIKK	0.97417	0.02847	(3) Phospho (ST)
E2 03 2	3	SISQDSLDELSMEDYWIELENIKK	0.97583	0.033	(3) Phospho (ST)
E2 01 2	4	SLAPDRSDDEHDPLDNTSRPR	0.97833	0.02293	(7) Phospho (ST)
E2 01 1	4	SLAPDRSDDEHDPLDNTSRPR	1.005	0.01889	(7) Phospho (ST)
E1 01	4	SLAPDRSDDEHDPLDNTSRPR	1.0211	0.0365	(7) Phospho (ST)
E1 01 3	4	SLAPDRSDDEHDPLDNTSRPR	1.04	0.02019	(7) Phospho (ST)
E1 01 1	4	SLAPDRSDDEHDPLDNTSRPR	1.08083	0.01898	(7) Phospho (ST)
E1 01	2	SLDMDSIIAEVK	1.34048	0.4557	(1) Phospho (ST)
E1 01 3	2	SLEDLRAPK	0.96667	0.02588	(1) Phospho (ST)
E1 03 1	2	SLEGLNQELEEVFVK	0.99167	0.02701	(1) Phospho (ST)
E1 03 2	2	SLEGLNQELEEVFVK	1.06417	0.04325	(1) Phospho (ST)
E2 01 2	3	SLGNILQAKPTSSPAK	1.1775	0.03655	(13) Phospho (ST)
E2 01 1	3	SLGNILQAKPTSSPAK	1.21	0.04744	(13) Phospho (ST)
E2 03	3	SLGSVQAPSYGARPVSSAASVYAGAGGSGSR	0.67054	0.01095	(20) Phospho (ST)
E2 03 2	3	SLGSVQAPSYGARPVSSAASVYAGAGGSGSR	1.20583	0.04352	(20) Phospho (ST)
E2 03 1	3	SLGSVQAPSYGARPVSSAASVYAGAGGSGSR	1.21167	0.05261	(20) Phospho (ST)

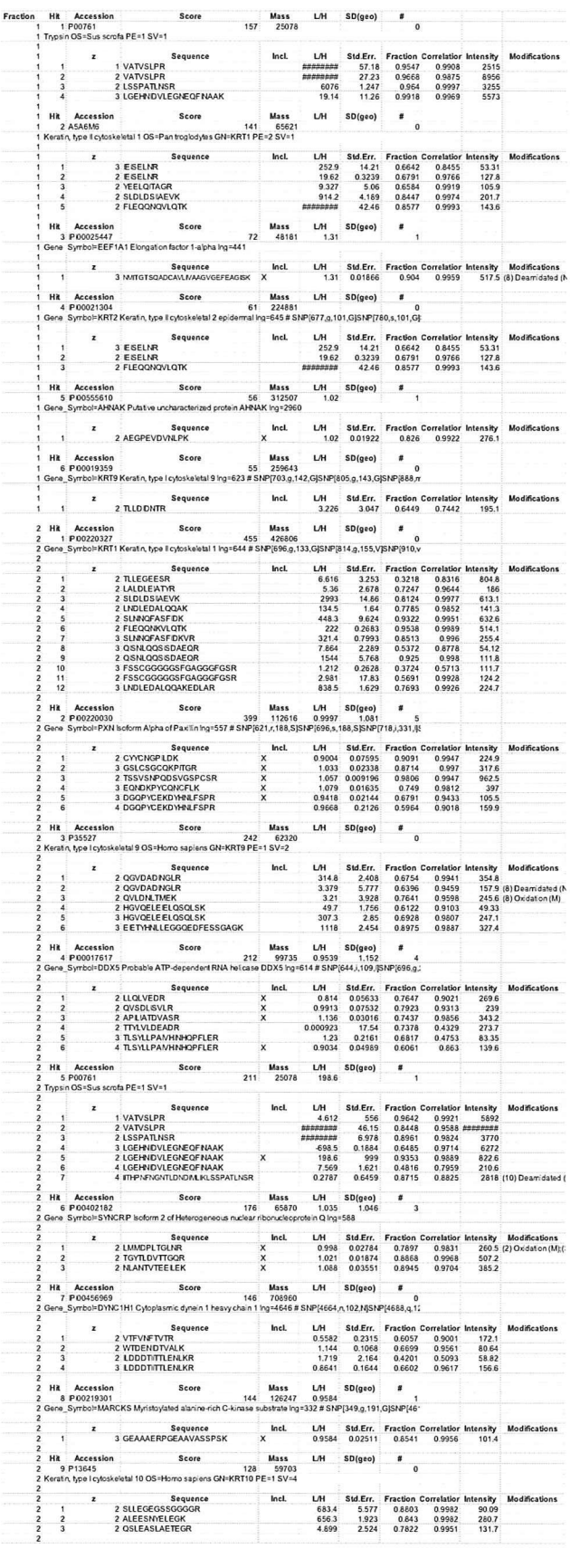
E1 01 3	2	SLIYTDTLVR	1.2825	0.1204	(1) Phospho (ST)
E2 02 1	3	SLKESEQESEEEILAQKK	1.09	0.02309	(5) Phospho (ST);(9) Phospho (ST)
E2 02 2	3	SLKESEQESEEEILAQKK	1.10667	0.04664	(5) Phospho (ST);(9) Phospho (ST)
E1 01	2	SLLDASEEAIKK	1.21852	0.0935	(1) Phospho (ST)
E2 02 2	3	SLLGDSAPTLHLNKGTPSQSPVVGR	0.82783	0.01994	(16) Phospho (ST);(20) Phospho (ST)
E2 02	3	SLLGDSAPTLHLNKGTPSQSPVVGR	1.03878	0.02594	(6) Phospho (ST);(20) Phospho (ST)
E2 03 1	3	SLLSHEFQDETDTEEETLYSSK	0.72575	0.3891	(11) Phospho (ST);(13) Phospho (ST)
E2 03 2	3	SLLSHEFQDETDTEEETLYSSK	0.93667	0.1673	(11) Phospho (ST);(13) Phospho (ST)
E2 03 1	3	SLLSHEFQDETDTEEETLYSSKH	0.92167	0.01711	(11) Phospho (ST);(13) Phospho (ST)
E2 03 2	3	SLLSHEFQDETDTEEETLYSSKH	0.94167	0.01344	(11) Phospho (ST);(13) Phospho (ST)
E1 01 1	2	SLMSSPEDLTK	1.02417	0.05975	(4) Phospho (ST);(5) Phospho (ST)
E1 03 2	3	SLMSSPEDLTKDFEELKAEEVDVTK	1.29167	0.1624	(3) Oxidation (M);(4) Phospho (ST);(5) Phospho (ST)
E2 02 1	3	SLPELDRDKSDSDTEGLLFSR	0.865	0.01811	(1) Phospho (ST);(12) Phospho (ST)
E2 02 2	3	SLPELDRDKSDSDTEGLLFSR	0.83417	0.02655	(10) Phospho (ST);(12) Phospho (ST)
E2 02	3	SLPELDRDKSDSDTEGLLFSR	1.20482	0.01678	(10) Phospho (ST);(12) Phospho (ST)
E2 02 2	3	SLPELDRDKSDSDTEGLLFSR	0.87833	0.101	(12) Phospho (ST)
E2 02 1	3	SLPELDRDKSDSDTEGLLFSR	0.96833	0.04595	(12) Phospho (ST)
E2 01 2	2	SLPVSVPVWGFK	0.9625	0.01087	(1) Phospho (ST)
E2 01 1	2	SLPVSVPVWGFK	0.98417	0.01984	(1) Phospho (ST)
E2 03 2	3	SLQENEEEEIGNLELAWDMLDLAK	0.945	0.02251	(1) Phospho (ST)
E2 03 1	3	SLQENEEEEIGNLELAWDMLDLAK	0.95167	0.02058	(1) Phospho (ST)
E2 03	3	SLQENEEEEIGNLELAWDMLDLAK	1.10051	0.02205	(1) Phospho (ST)
E2 02 1	3	SLSKSDSDLLTCSPTEDATMGSR	1.005	0.0262	(7) Phospho (ST)
E2 02 2	3	SLSKSDSDLLTCSPTEDATMGSR	1.01417	0.03973	(7) Phospho (ST)
E1 02 2	3	SLSKSDSDLLTCSPTEDATMGSR	1.06833	0.06211	(7) Phospho (ST)
E1 02 1	3	SLSKSDSDLLTCSPTEDATMGSR	1.11167	0.05208	(7) Phospho (ST)
E1 02 2	3	SLSKSDSDLLTCSPTEDATMGSR	1.1	0.05323	(7) Phospho (ST);(20) Oxidation (M)
E1 04 3	2	SLSNSNPDISGTPTSPDDEVR	0.9825	0.03274	(3) Phospho (ST)
E2 04 2	2	SLSNSNPDISGTPTSPDDEVR	1.06583	0.05727	(3) Phospho (ST)
E1 04 1	2	SLSNSNPDISGTPTSPDDEVR	0.97917	0.01824	(5) Phospho (ST)
E1 04 3	2	SLSNSNPDISGTPTSPDDEVR	0.9825	0.03274	(5) Phospho (ST)
E2 01 1	2	SLSPGGAALGYR	0.80292	0.04404	(3) Phospho (ST)
E1 01 3	3	SLSPGKENVSALDMEK	0.7735	0.05912	(3) Phospho (ST)
E1 02 1	2	SLSPGKENVSALDMEK	0.86333	0.05169	(3) Phospho (ST)
E1 02 2	2	SLSPGKENVSALDMEK	0.9175	0.06106	(3) Phospho (ST)
E2 04 2	2	SLSQSFENLLDEPAYGLIQK	1.1675	0.05118	(5) Phospho (ST)
E2 04 1	2	SLSQSFENLLDEPAYGLIQK	1.23833	0.0415	(5) Phospho (ST)
E2 02 1	2	SLSSPTDNLELSLR	1.4275	0.06259	(4) Phospho (ST)
E1 02 2	2	SLSSPTDNLELSLR	1.43667	0.1635	(4) Phospho (ST)
E1 02 1	2	SLSSPTDNLELSLR	1.7675	0.08338	(4) Phospho (ST)
E1 02	2	SLSSPTVTLSAPLEGAK	0.77519	0.01614	(3) Phospho (ST)
E2 02	2	SLSSPTVTLSAPLEGAK	0.88287	0.02788	(3) Phospho (ST)
E1 02 1	2	SLSSPTVTLSAPLEGAK	1.02	0.00874	(3) Phospho (ST)
E1 02	2	SLSSPTVTLSAPLEGAK	0.77519	0.01614	(4) Phospho (ST)
E2 02	2	SLSSPTVTLSAPLEGAK	0.88287	0.02788	(4) Phospho (ST)
E2 02 2	2	SLSSPTVTLSAPLEGAK	1.0175	0.0181	(4) Phospho (ST)
E1 02 1	2	SLSSPTVTLSAPLEGAK	1.02	0.00874	(4) Phospho (ST)
E1 02 2	2	SLSSPTVTLSAPLEGAK	1.03917	0.01535	(4) Phospho (ST)
E2 02 1	2	SLSSPTVTLSAPLEGAK	1.07667	0.01986	(4) Phospho (ST)
E2 03 2	2	SLSTSGESLYHVLGLDK	0.79017	0.01789	(3) Phospho (ST)
E2 03 1	2	SLSTSGESLYHVLGLDK	0.79967	0.01824	(3) Phospho (ST)
E2 01 2	3	SLSTSGESLYHVLGLDK	0.82483	0.00862	(3) Phospho (ST)
E2 01 1	3	SLSTSGESLYHVLGLDK	0.87833	0.02267	(3) Phospho (ST)
E2 03	2	SLSTSGESLYHVLGLDK	1.25523	0.01565	(3) Phospho (ST)
E2 03 1	2	SLSTSGESLYHVLGLDK	0.79967	0.01824	(4) Phospho (ST)
E2 01 1	3	SLSTSGESLYHVLGLDK	0.6525	0.02962	(5) Phospho (ST)
E2 01 2	3	SLSTSGESLYHVLGLDK	0.658	0.02204	(5) Phospho (ST);(8) Phospho (ST)
E2 01 1	3	SLSTSGESLYHVLGLDK	0.67208	0.01726	(5) Phospho (ST);(8) Phospho (ST)
E2 01 1	3	SLSTSGESLYHVLGLDK	0.6515	0.02048	(8) Phospho (ST)
E1 01 3	2	SLSVPVDLSR	1.07	0.1383	(3) Phospho (ST)
E2 02 1	3	SLTETELTKPNYLYLLPTEK	1.1625	0.1557	(3) Phospho (ST)
E2 01 2	2	SLTSSLENIFSR	1.01333	0.0629	(1) Phospho (ST)
E2 01 1	2	SLTSSLENIFSR	1.06083	0.02545	(1) Phospho (ST)
E2 01 1	2	SLTSSLENIFSR	0.96583	0.00594	(4) Phospho (ST)
E1 01 1	2	SLTSSLENIFSR	0.97167	0.02063	(5) Phospho (ST)
E2 01 2	2	SLTSSLENIFSR	0.97583	0.00717	(5) Phospho (ST)
E1 01	2	SLTSSLENIFSR	1.13122	0.03882	(5) Phospho (ST)
E1 01 1	3	SMDELNHDFQALALEGR	0.89667	0.05141	(1) Phospho (ST)
E1 01 3	3	SMDELNHDFQALALEGR	0.88333	0.02516	(1) Phospho (ST);(6) Deamidated (NQ)
E2 01	2	SMPVLGSVSSVTK	0.84842	0.05867	(1) Phospho (ST)
E1 01 3	2	SMSAPVIFDR	0.62175	0.07761	(3) Phospho (ST)
E1 02	2	SMSDVSAEDVQNLR	0.82147	0.03466	(1) Phospho (ST)
E2 04	2	SNISPNFNFMGQLLDFER	0.76687	0.03007	(4) Phospho (ST);(10) Oxidation (M)
E2 04 1	2	SNISPNFNFMGQLLDFER	1.0025	0.105	(4) Phospho (ST);(10) Oxidation (M)
E2 01 2	3	SNISPNFNFMGQLLDFER	1.07333	0.03134	(4) Phospho (ST);(10) Oxidation (M)
E2 02 1	3	SNSAPLIHGLSDTSPVFQAEAPSAR	0.9475	0.02623	(3) Phospho (ST)
E2 02 2	3	SNSAPLIHGLSDTSPVFQAEAPSAR	0.9675	0.02469	(3) Phospho (ST)
E1 02 2	2	SNSELEDEILCLEK	0.61242	0.04156	(3) Phospho (ST)
E1 02 1	2	SNSELEDEILCLEK	0.62808	0.03929	(3) Phospho (ST)
E1 01 3	3	SNSELEDEILCLEK	0.66508	0.03518	(3) Phospho (ST)
E1 01 1	3	SNSELEDEILCLEK	0.68158	0.07014	(3) Phospho (ST)
E1 02	2	SNSELEDEILCLEK	1.67729	0.01733	(3) Phospho (ST)
E1 04 1	3	SNSFSDEREFSGPSTPTGTLEFEGGEVSLEGGK	0.92417	0.06858	(3) Phospho (ST)
E2 04 1	3	SNSFSDEREFSGPSTPTGTLEFEGGEVSLEGGK	1.0925	0.09587	(3) Phospho (ST)
E1 03 2	2	SPAVATSTAAPPPPSSPLPSK	0.99667	0.01284	(16) Phospho (ST)
E2 03	3	SPDVISSASTALSQDIPEIASEALSR	1.00267	0.0155	(1) Phospho (ST)
E2 02 1	3	SPEKIEEVLSPEGSPSKSPSK	0.99333	0.08586	(14) Phospho (ST);(18) Phospho (ST)
E2 02 2	3	SPEKIEEVLSPEGSPSKSPSK	1.03833	0.0545	(14) Phospho (ST);(18) Phospho (ST)
E2 02 2	3	SPEKIEEVLSPEGSPSKSPSK	1.02917	0.02164	(18) Phospho (ST)
E1 02 1	3	SPEKIEEVLSPEGSPSKSPSK	0.97833	0.02652	(20) Phospho (ST)
E1 02 2	3	SPEKIEEVLSPEGSPSKSPSK	0.9825	0.03214	(20) Phospho (ST)
E2 02 2	3	SPEKIEEVLSPEGSPSKSPSK	1.02917	0.02164	(20) Phospho (ST)
E2 01 2	3	SPGETSKPRPFAGGGYR	1.32667	0.05483	(1) Phospho (ST)
E2 01 1	3	SPGETSKPRPFAGGGYR	1.39667	0.02794	(1) Phospho (ST)
E1 01 1	2	SPGHMVILDQTK	0.88417	0.08718	(1) Phospho (ST)
E1 01 3	2	SPGHMVILDQTK	0.935	0.11	(1) Phospho (ST)
E1 01 1	3	SPGKCDQEKPAPSFACLK	0.74592	0.09224	(1) Phospho (ST)
E2 04 1	4	SPLGEAPEPDSDAEVAEAAKPHLSEVTTEGYPS EPLGGLEQK	1.00583	0.02864	(11) Phospho (ST)
E2 02 2	3	SPPYTAFLGNLPYDVTEESIK	1.335	0.08443	(1) Phospho (ST)
E1 02 2	2	SPSFASEWDEIEK	0.80975	0.2162	(3) Phospho (ST)
E1 02	2	SPSFASEWDEIEK	0.95724	0.03811	(3) Phospho (ST)
E1 02 1	2	SPSFASEWDEIEK	0.99667	0.0282	(3) Phospho (ST)
E1 01 3	3	SPSKEPHFTDFEGK	0.7535	0.07631	(3) Phospho (ST)
E2 02 1	3	SPSPPTQHTGQPPGQPSAPSQLSAPR	1.14917	0.01953	(3) Phospho (ST)
E1 04 1	3	SPSSDLDTDAEGDDFELLDQSELSQLDPASSR	0.975	0.02768	(4) Phospho (ST);(8) Phospho (ST)
E1 04 3	3	SPSSDLDTDAEGDDFELLDQSELSQLDPASSR	1.02333	0.0358	(4) Phospho (ST);(8) Phospho (ST)
E2 02 1	3	SPTMEQAVQTASAHLPAPAAVGR	0.75817	0.03512	(1) Phospho (ST)
E2 02 1	3	SPTMEQAVQTASAHLPAPAAVGR	0.75817	0.03512	(3) Phospho (ST)
E1 01	3	SPVSTRPLPSASQK	1.24688	0.05092	(1) Phospho (ST)
E1 02	3	SQDATFSPGSEQAEKSPGPIVSR	0.70356	0.07994	(16) Phospho (ST)
E1 03 2	3	SQLDDHPESDDEENFIDANDDEDMEK	1.0425	0.1359	(9) Phospho (ST)
E1 03 1	3	SQLDDHPESDDEENFIDANDDEDMEK	1.06083	0.07458	(9) Phospho (ST)
E2 03 1	3	SQSDLDDQHDYDSVASDEDTDQEPLR	1.05167	0.03697	(13) Phospho (ST);(16) Phospho (ST)
E2 01 2	2	SQSLPTTLLSPVR	0.79608	0.02317	(3) Phospho (ST)
E2 01 1	2	SQSLPTTLLSPVR	0.81067	0.03185	(3) Phospho (ST)
E2 01	2	SQSLPTTLLSPVR	1.2087	0.03457	(3) Phospho (ST)
E2 01 1	3	SQSSHSYDDSTLPLIDR	0.8975	0.02159	(11) Phospho (ST)
E2 01 2	3	SQSSHSYDDSTLPLIDR	0.925	0.02855	(11) Phospho (ST)
E2 01 2	3	SRDDLYDQDDSRDFPR	1.10083	0.08222	(1) Phospho (ST)
E2 04 2	2	SRINSSGESGDESDEFLQSR	1.06917	0.08955	(5) Phospho (ST);(6) Phospho (ST);(9) Phospho (ST);(13) Phospho (ST)
E2 01 1	3	SRLSAIEIDIPVVSHTT	0.9025	0.00941	(4) Phospho (ST)
E2 01 1	2	SRSPLAIR	1.00083	0.0438	(1) Phospho (ST);(3) Phospho (ST)
E2 01 1	3	SRTHSTSSSLGSGESPFSR	1.16833	0.04666	(6) Phospho (ST)
E2 01 2	3	SRTHSTSSSLGSGESPFSR	1.17417	0.0537	(7) Phospho (ST)
E2 01 1	3	SRTHSTSSSLGSGESPFSR	1.16833	0.04666	(9) Phospho (ST)
E1 04 3	3	SSGDVLETFNFLENADDSDEDEENDMIEGIPEG K	1.12083	0.01763	(18) Phospho (ST)
E1 04 3	3	SSGDVLETFNFLENADDSDEDEENDMIEGIPEG K	1.12417	0.03161	(8) Phospho (ST);(26) Oxidation (M)
E2 01 1	3	SSIHNFMTHPEFR	0.92583	0.05491	(2) Phospho (ST)
E2 01 1	3	SSKASLGSLEGEAEAEASSPK	0.74617	0.04471	(5) Phospho (ST);(8) Phospho (ST)
E2 01	3	SSKASLGSLEGEAEAEASSPK	0.94697	0.02759	(5) Phospho (ST);(8) Phospho (ST)
E2 01 2	3	SSKASLGSLEGEAEAEASSPK	0.95333	0.04201	(5) Phospho (ST);(8) Phospho (ST)
E2 03	2	SSLAETLDSTGSLDPQR	2.18468	0.03533	(10) Phospho (ST);(12) Phospho (ST)
E1 01 3	3	SSLETLEDIEENAPLRR	0.63058	0.05316	(2) Phospho (ST)
E1 01 1	3	SSLETLEDIEENAPLRR	0.70625	0.07838	(2) Phospho (ST)
E2 02 2	2	SSLSGDEEDELFK	0.9425	0.1623	(2) Phospho (ST);(4) Phospho (ST)
E2 02 1	2	SSLSGDEEDELFK	0.965	0.1248	(2) Phospho (ST);(4) Phospho (ST)
E1 01 3	2	SSMSGLHLVK	0.80325	0.03083	(3) Oxidation (M);(4) Phospho (ST)
E2 01 1	2	SSMSGLHLVK	0.79667	0.1021	(4) Phospho (ST)
E2 02 1	2	SSSETILSSLAGSDIVK	0.77417	0.00526	(1) Phospho (ST)
E1 02 2	2	SSSETILSSLAGSDIVK	0.7565	0.01153	(3) Phospho (ST)
E2 02 1	2	SSSETILSSLAGSDIVK	0.77417	0.00526	(3) Phospho (ST)
E2 02 2	2	SSSETILSSLAGSDIVK	0.77758	0.00634	(3) Phospho (ST)
E1 02 1	2	SSSETILSSLAGSDIVK	0.81258	0.02301	(3) Phospho (ST)
E2 03 2	2	SSSPAPADIAQTVQEDLR	0.92417	0.00916	(3) Phospho (ST)
E2 03 1	2	SSSPAPADIAQTVQEDLR	0.92583	0.00879	(3) Phospho (ST)
E1 03 1	2	SSSPAPADIAQTVQEDLR	0.95083	0.01143	(3) Phospho (ST)
E1 03 2	2	SSSPAPADIAQTVQEDLR	0.95083	0.01465	(3) Phospho (ST)
E1 01 3	3	SSSPAPADIAQTVQEDLR	0.98167	0.00905	(3) Phospho (ST)
E2 01 1	3	SSSPAPADIAQTVQEDLR	1.0275	0.00323	(3) Phospho (ST)
E2 03	2	SSSPAPADIAQTVQEDLR	1.13636	0.01772	(3) Phospho (ST)
E1 03	2	SSSPAPADIAQTVQEDLR	1.26582	0.02563	(3) Phospho (ST)
E1 03 2	2	SSSPAPADIAQTVQEDLR	0.9525	0.09847	(3) Phospho (ST);(11) Deamidated (NQ)
E1 03 2	2	SSSPAPADIAQTVQEDLR	0.9925	0.05946	(3) Phospho (ST);(14) Deamidated (NQ)
E1 03 1	2	SSSPAPADIAQTVQEDLR	1.07667	0.06738	(3) Phospho (ST);(14) Deamidated (NQ)
E2 01 2	2	SSSPELVTHLK	1.17417	0.01958	(3) Phospho (ST)
E2 01 1	2	SSSPELVTHLK	1.20833	0.0091	(3) Phospho (ST)
E1 01 3	2	SSSPELVTHLK	1.25583	0.02383	(3) Phospho (ST)
E1 01 1	2	SSSPELVTHLK	1.29	0.02625	(3) Phospho (ST)
E2 01 1	3	SSSPVTELASRSPIRQDR	1.03333	0.01234	(3) Phospho (ST);(12) Phospho (ST)
E2 02 2	3	SSSSPELQTLQDILGDPGDKADVGR	0.82692	0.07163	(4) Phospho (ST)
E2 03 2	2	SSSVGSSSSYPISPAVSR	0.74617	0.9428	(3) Phospho (ST)
E2 01 1	3	SSSVPHPFQVTLLR	0.88833	0.04089	(2) Phospho (ST)
E2 01 1	3	SSSVSLTHHVGLR	0.78858	0.05398	(3) Phospho (ST)
E2 03 2	3	STAQQELDGKPASPTPVIVASHTANK	1.3475	0.2899	(13) Phospho (ST)
E1 03	3	STAQQELDGKPASPTPVIVASHTANK	0.94103	0.028	(15) Phospho (ST)
E2 03 2	3	STAQQELDGKPASPTPVIVASHTANK	1.3475	0.2899	(15) Phospho (ST)
E2 03 1	3	STAQQELDGKPASPTPVIVASHTANK	1.365	0.2864	(15) Phospho (ST)
E2 02 1	4	STAQQELDGKPASPTPVIVASHTANKEEK	1.24333	0.04334	(13) Phospho (ST)
E2 02 2	4	STAQQELDGKPASPTPVIVASHTANKEEK	1.27917	0.04815	(13) Phospho (ST)
E2 01 2	3	STFREESPLR	0.87167	0.01724	(7) Phospho (ST)
E2 01 1	3	STFREESPLR	0.89667	0.02119	(7) Phospho (ST)
E2 01 1	2	STFREESPLR	1.00833	0.0284	(7) Phospho (ST)
E2 01 2	2	STFREESPLR	1.03	0.02702	(7) Phospho (ST)
E2 01 1	3	STIGVMVTASHNPEEDNGVK	1.06667	0.1081	(10) Phospho (ST);(17) Deamidated (NQ)
E1 03 2	3	STLESEKPGSPEAAETSPPSNIDHCEK	0.99167	0.1617	(16) Phospho (ST);(17) Phospho (ST)
E1 03 1	3	STLESEKPGSPEAAETSPPSNIDHCEK	1.03417	0.1513	(16) Phospho (ST);(17) Phospho (ST)
E2 02 2	2	STLNPQWNESFTFK	0.92	0.0892	(10) Phospho (ST)
E2 01 2	3	STSRDRLDDIIVLTK	0.71433	0.06836	(3) Phospho (ST)

E2 01 1	3	STSRDRLDDIIVLTK	0.73417	0.08374	(3) Phospho (ST)
E1 03 1	2	STTPPPAEPVSLPQEPPK	1.0425	0.1628	(3) Phospho (ST)
E1 01	3	STTPPPAEPVSLPQEPPKPR	0.97339	0.01054	(3) Phospho (ST)
E1 01 1	3	STTPPPAEPVSLPQEPPKPR	1.02167	0.01243	(3) Phospho (ST)
E1 04 1	2	STTPPPAEPVSLPQEPPKPR	1.02333	0.03334	(3) Phospho (ST)
E1 03 2	2	STTPPPAEPVSLPQEPPKPR	1.03417	0.04282	(3) Phospho (ST)
E2 01	3	STTPPPAEPVSLPQEPPKPR	1.03663	0.02344	(3) Phospho (ST)
E2 01 1	3	STTPPPAEPVSLPQEPPKPR	1.09083	0.03969	(3) Phospho (ST)
E1 01 3	3	STTPPPAEPVSLPQEPPKPR	1.1625	0.0317	(3) Phospho (ST)
E1 04 3	2	STTPPPAEPVSLPQEPPKPR	1.17833	0.05934	(3) Phospho (ST)
E1 01 3	2	SVDFDSLTVR	1.0275	0.01674	(1) Phospho (ST)
E1 01 1	2	SVDFDSLTVR	1.04167	0.04592	(1) Phospho (ST)
E1 03 2	3	SVEDVRPHHTDANNQSACFEAPDQK	1.04917	0.02763	(1) Phospho (ST)
E1 01 3	4	SVEDVRPHHTDANNQSACFEAPDQK	1.04417	0.01559	(10) Phospho (ST)
E1 02 2	2	SVSSDSLGPPRPAPAR	1.20583	0.04658	(3) Phospho (ST)
E2 01 1	2	SVWGSLAVQNSPK	1.21417	0.09005	(11) Phospho (ST)
E1 03 2	2	SWASPVYTEADGTFSR	0.86917	0.01997	(1) Phospho (ST)
E2 03 2	2	SWASPVYTEADGTFSR	0.87833	0.04481	(1) Phospho (ST)
E2 03 1	2	SWASPVYTEADGTFSR	0.88	0.03145	(1) Phospho (ST)
E1 03 1	2	SWASPVYTEADGTFSR	0.88083	0.0336	(1) Phospho (ST)
E1 03	2	SWASPVYTEADGTFSR	1.23153	0.07951	(1) Phospho (ST)
E1 01 3	2	SWSPPPEVSR	1.06083	0.1274	(3) Phospho (ST)
E1 03 2	2	SYSSPDITQAIQEEEK	0.87167	0.0496	(4) Phospho (ST)
E1 03 1	3	TASISSSPSEGTPTVGSYGCTPQSLPK	0.79058	0.04524	(3) Phospho (ST)
E1 03 2	3	TASISSSPSEGTPTVGSYGCTPQSLPK	0.79367	0.0466	(3) Phospho (ST)
E2 03 2	3	TASISSSPSEGTPTVGSYGCTPQSLPK	0.83917	0.03311	(3) Phospho (ST)
E1 01 3	3	TDGFAEAIHSPQVAGVPR	0.75817	0.03218	(10) Phospho (ST)
E1 01 3	3	TDSREDEISPPPPNPVVK	1.525	0.03097	(9) Phospho (ST)
E1 03 1	2	TDSREDEISPPPPNPVVK	1.56083	0.04852	(9) Phospho (ST)
E1 01 3	3	TESPATAAETASEELDNR	0.9775	0.01715	(10) Phospho (ST)
E1 01	3	TESPATAAETASEELDNR	1.1811	0.01964	(10) Phospho (ST)
E1 01 3	2	TFDEIASGFR	1.01167	0.03197	(7) Phospho (ST)
E1 04 1	3	TFQQIQEEEDDDYPGSYSPQDPSAGPLLTEELIK	0.9625	0.01932	(18) Phospho (ST)
E2 03 2	3	TGPAATTLPDGAAAESLVESSEVAVIGFFK	0.74142	0.02758	
E2 03 1	3	TGPAATTLPDGAAAESLVESSEVAVIGFFK	0.76417	0.01892	
E2 02 2	3	TGSGSPFAGNSPAREGEQDAASLK	1.09833	0.04059	(3) Phospho (ST);(11) Phospho (ST)
E1 04 1	2	TGSGSPFAGNSPAREGEQDAASLK	1.12917	0.02101	(5) Phospho (ST);(11) Phospho (ST)
E1 02 2	3	TGSGSPFAGNSPAREGEQDAASLK	1.15167	0.03402	(5) Phospho (ST);(11) Phospho (ST)
E2 04 2	2	TGSGSPFAGNSPAREGEQDAASLK	1.30417	0.0873	(5) Phospho (ST);(11) Phospho (ST)
E2 03 2	3	TGSSSPPGGPPKPGSQLDSMLGSLQSDLNK	1.105	0.04531	(5) Phospho (ST)
E2 03 1	3	TGSSSPPGGPPKPGSQLDSMLGSLQSDLNK	1.1125	0.03849	(5) Phospho (ST)
E2 03 2	2	THSTSSSLGSGESPFSR	1.26333	0.08774	(3) Phospho (ST)
E1 03 1	2	TIGGGDDSFNTFFSETGAGK	0.69242	0.08605	(8) Phospho (ST)
E1 01 1	3	TIQEVLEEQSEDEDREAK	1.19333	0.03276	(10) Phospho (ST)
E2 01 1	3	TISAQDTLAYATALLNEK	0.99833	0.02175	(3) Phospho (ST)
E1 01 1	4	TKFASDDEHDEHDENGATGPVK	1.0125	0.04296	(5) Phospho (ST)
E1 01 3	4	TKFASDDEHDEHDENGATGPVK	1.01417	0.05313	(5) Phospho (ST)
E1 01 3	4	TKFASDDEHDEHDENGATGPVK	1.06583	0.0825	(5) Phospho (ST);(15) Deamidated (NQ)
E1 01 1	4	TKFASDDEHDEHDENGATGPVK	1.11833	0.08905	(5) Phospho (ST);(15) Deamidated (NQ)
E1 01 3	3	TLDRSGDLGDMEPLK	0.8675	0.02624	(5) Phospho (ST)
E1 02 1	4	TLHCEGTEINSDDEQESKEVEETATAK	1.10083	0.1112	(11) Phospho (ST)
E1 03 1	3	TLHCEGTEINSDDEQESKEVEETATAK	1.11583	0.02224	(11) Phospho (ST)
E2 01 1	3	TLLSESSSQSSKSPSLSSK	0.98583	0.09028	(10) Phospho (ST)
E2 01 2	3	TLLSESSSQSSKSPSLSSK	1	0.07164	(13) Phospho (ST)
E2 01 1	2	TLMLPLTEGSLR	0.83333	0.05438	(10) Phospho (ST)
E2 02 2	3	TLVLSNLSYSATEETLQEVFEK	1.03583	0.02262	
E2 02 1	3	TLVLSNLSYSATEETLQEVFEK	1.04417	0.01287	
E2 04	2	TPEELDDSDFETEDFDVR	0.73099	0.02008	(8) Phospho (ST)
E1 04	2	TPEELDDSDFETEDFDVR	0.8547	0.01612	(8) Phospho (ST)
E1 01 1	3	TPEELDDSDFETEDFDVR	0.98583	0.04373	(8) Phospho (ST)
E1 01 3	3	TPEELDDSDFETEDFDVR	1.00167	0.02813	(8) Phospho (ST)
E2 04 1	2	TPEELDDSDFETEDFDVR	1.04833	0.01778	(8) Phospho (ST)
E2 04 2	2	TPEELDDSDFETEDFDVR	1.05	0.01513	(8) Phospho (ST)
E1 04 3	2	TPEELDDSDFETEDFDVR	1.06	0.00968	(8) Phospho (ST)
E1 04 1	2	TPEELDDSDFETEDFDVR	1.06917	0.00849	(8) Phospho (ST)
E2 01 2	3	TPKDSPGIPPSANAHQLFR	1.05333	0.04272	(5) Phospho (ST)
E2 01 1	3	TPKDSPGIPPSANAHQLFR	1.07	0.03382	(5) Phospho (ST)
E2 04 2	3	TPLSFTNPLHSDDSDSDERNSDGAVTQNK	1.09917	0.04505	(11) Phospho (ST);(14) Phospho (ST)
E2 04 1	3	TPLSFTNPLHSDDSDSDERNSDGAVTQNK	1.10917	0.02855	(11) Phospho (ST);(14) Phospho (ST)
E2 01 1	3	TPSSEEISPTKFPGLYR	0.75567	0.02431	(3) Phospho (ST)
E2 01 2	3	TPSSEEISPTKFPGLYR	0.7805	0.01966	(3) Phospho (ST)
E2 02	2	TQTPPLGQTPQLGLK	0.80472	0.05101	(3) Phospho (ST)
E2 02 2	2	TQTPPLGQTPQLGLK	1.01333	0.03321	(3) Phospho (ST)
E2 02 1	2	TQTPPLGQTPQLGLK	1.01417	0.05517	(3) Phospho (ST)
E2 03 1	3	TQTPPVSPAPQPTEERLPSSPVYEDAASFK	1.38667	0.03424	(20) Phospho (ST)
E2 04 2	3	TQTPPVSPAPQPTEERLPSSPVYEDAASFK	1.48583	0.04421	(20) Phospho (ST)
E2 03 1	3	TQTPPVSPAPQPTEERLPSSPVYEDAASFK	1.16167	0.0579	(3) Phospho (ST)
E2 04 2	3	TQTPPVSPAPQPTEERLPSSPVYEDAASFK	1.46917	0.02276	(3) Phospho (ST);(23) Phospho (Y)
E1 04	3	TQTPPVSPAPQPTEERLPSSPVYEDAASFK	0.70389	0.03586	(3) Phospho (ST);(7) Phospho (ST)
E2 04	3	TQTPPVSPAPQPTEERLPSSPVYEDAASFK	0.71667	0.04912	(3) Phospho (ST);(7) Phospho (ST)
E1 04 3	3	TQTPPVSPAPQPTEERLPSSPVYEDAASFK	1.34917	0.02346	(7) Phospho (ST);(13) Phospho (ST)
E2 03 1	3	TRSPDVISSASTALSQDIPEIASEALSR	1.14333	0.00533	(3) Phospho (ST)
E2 03 2	3	TRSPDVISSASTALSQDIPEIASEALSR	1.15583	0.00574	(3) Phospho (ST)
E2 04 1	2	TSAAACAVTDLSDDSDFDEK	0.95583	0.0407	(12) Phospho (ST);(15) Phospho (ST)
E2 02 2	2	TSFSVGSDDELGPIR	0.87667	0.09628	(7) Phospho (ST)
E2 02 1	2	TSFSVGSDDELGPIR	0.90417	0.04915	(7) Phospho (ST)
E1 02 2	2	TSFSVGSDDELGPIR	0.98333	0.06555	(7) Phospho (ST)
E1 04 1	2	TSLITEEEDSTSEVLDEELK	1.24833	0.02625	(12) Phospho (ST)
E2 02 1	2	TSMGGTQQQFVEGVR	1.025	0.04655	(2) Phospho (ST)
E2 02 1	4	TSPKPAVVETVTTAKPQQIQALMDEVTK	1.21	0.03371	(2) Phospho (ST)
E2 03 2	3	TSPKPAVVETVTTAKPQQIQALMDEVTK	1.27917	0.02262	(2) Phospho (ST)
E2 02 1	3	TSSESIYSRPGSSIPGSPGHTIYAK	1.03583	0.03575	(3) Phospho (ST)
E2 02 1	3	TSSESIYSRPGSSIPGSPGHTIYAK	1.03583	0.03575	(3) Phospho (ST)
E2 02 2	3	TSSESIYSRPGSSIPGSPGHTIYAK	1.0775	0.03553	(3) Phospho (ST)
E1 03 2	3	TTQSMQDFPVVDSEEEAEEEFQK	1.0475	0.07977	(13) Phospho (ST)
E2 01 1	3	TVANLLSGKSPR	1.1175	0.05985	(10) Phospho (ST)
E2 02 2	4	TVSLGAGAKDELHIVEAEAMNYEGSPIK	1.05833	0.02484	(20) Oxidation (M);(21) Deamidated (NQ);(25) Phospho (ST)
E2 02 1	4	TVSLGAGAKDELHIVEAEAMNYEGSPIK	1.03917	0.01748	(20) Oxidation (M);(25) Phospho (ST)
E2 02 2	4	TVSLGAGAKDELHIVEAEAMNYEGSPIK	1.0575	0.0227	(20) Oxidation (M);(25) Phospho (ST)
E2 02 1	4	TVSLGAGAKDELHIVEAEAMNYEGSPIK	0.85167	0.06658	(21) Deamidated (NQ);(25) Phospho (ST)
E2 02 2	4	TVSLGAGAKDELHIVEAEAMNYEGSPIK	1.13583	0.03131	(21) Deamidated (NQ);(25) Phospho (ST)
E1 02 1	4	TVSLGAGAKDELHIVEAEAMNYEGSPIK	1.19	0.04637	(21) Deamidated (NQ);(25) Phospho (ST)
E2 02 1	4	TVSLGAGAKDELHIVEAEAMNYEGSPIK	1.0475	0.02221	(25) Phospho (ST)
E2 02 2	4	TVSLGAGAKDELHIVEAEAMNYEGSPIK	1.06083	0.01881	(25) Phospho (ST)
E2 03 1	3	TVSLGAGAKDELHIVEAEAMNYEGSPIK	1.14667	0.01246	(25) Phospho (ST)
E2 03 2	3	TVSLGAGAKDELHIVEAEAMNYEGSPIK	1.18	0.01005	(25) Phospho (ST)
E2 03 1	3	TVSSPPTSPRPGSAATVSASTSNIPPR	1.52333	0.0591	(3) Phospho (ST);(4) Phospho (ST)
E2 03 1	3	TVSSPPTSPRPGSAATVSASTSNIPPR	1.45583	0.04959	(4) Phospho (ST);(7) Phospho (ST)
E2 03 2	3	TVSSPPTSPRPGSAATVSASTSNIPPR	1.52667	0.06192	(4) Phospho (ST);(7) Phospho (ST)
E2 02 1	3	TWTLCGTPEYLAPEILSK	0.8675	0.00556	(3) Phospho (ST)
E2 04 2	2	VADAKGDSESEEDEDLEVPVPSR	0.95667	0.01706	(8) Phospho (ST);(10) Phospho (ST)
E1 02 2	3	VADAKGDSESEEDEDLEVPVPSR	0.96667	0.0193	(8) Phospho (ST);(10) Phospho (ST)
E2 04 1	2	VADAKGDSESEEDEDLEVPVPSR	0.9675	0.01398	(8) Phospho (ST);(10) Phospho (ST)
E1 02	3	VADAKGDSESEEDEDLEVPVPSR	0.98945	0.01179	(8) Phospho (ST);(10) Phospho (ST)
E1 04 1	2	VADAKGDSESEEDEDLEVPVPSR	1.00583	0.0254	(8) Phospho (ST);(10) Phospho (ST)
E2 02 2	3	VADAKGDSESEEDEDLEVPVPSR	1.02333	0.01553	(8) Phospho (ST);(10) Phospho (ST)
E1 04 3	2	VADAKGDSESEEDEDLEVPVPSR	1.03167	0.02666	(8) Phospho (ST);(10) Phospho (ST)
E1 01 3	3	VASGSDLHLTDIDSDSNR	0.79692	0.08504	(5) Phospho (ST)
E1 01	3	VASGSDLHLTDIDSDSNR	1.47348	0.03621	(5) Phospho (ST)
E1 01 1	3	VDNLTYRTSPDTLR	0.935	0.03913	(9) Phospho (ST)
E1 01	3	VDNLTYRTSPDTLR	0.94578	0.0349	(9) Phospho (ST)
E2 01 2	3	VDNLTYRTSPDTLR	0.9625	0.02081	(9) Phospho (ST)
E2 01 1	3	VDNLTYRTSPDTLR	0.98417	0.02853	(9) Phospho (ST)
E1 03 2	2	VDPSLMEDSDDGPSLPTK	0.74067	0.02949	(6) Oxidation (M);(9) Phospho (ST)
E2 03 2	2	VDPSLMEDSDDGPSLPTK	0.69042	0.02816	(9) Phospho (ST)
E1 03 1	2	VDPSLMEDSDDGPSLPTK	0.83667	0.01877	(9) Phospho (ST)
E1 03 2	2	VDPSLMEDSDDGPSLPTK	0.84917	0.01717	(9) Phospho (ST)
E1 02 2	2	VDSTTCLFPVEEK	0.905	0.0129	(3) Phospho (ST)
E2 02 1	2	VDSTTCLFPVEEK	0.94417	0.01412	(3) Phospho (ST)
E1 02 1	2	VDSTTCLFPVEEK	0.8925	0.01225	(4) Phospho (ST)
E1 02 2	2	VDSTTCLFPVEEK	0.905	0.0129	(4) Phospho (ST)
E2 02 1	2	VDSTTCLFPVEEK	0.94417	0.01412	(4) Phospho (ST)
E2 02	2	VDSTTCLFPVEEK	1.22649	0.06705	(4) Phospho (ST)
E1 02	2	VDSTTCLFPVEEK	1.25839	0.02474	(4) Phospho (ST)
E1 01 3	2	VEIIANDQGNR	1.135	0.07967	
E1 01	2	VEIIANDQGNR	1.31926	0.04147	
E2 04 2	3	VEMGTSSQNDVDMSWIPQETLNQINKASPR	0.82983	0.02055	(13) Oxidation (M);(28) Phospho (ST)
E2 04 2	3	VEMGTSSQNDVDMSWIPQETLNQINKASPR	0.9525	0.09182	(28) Phospho (ST)
E2 02 2	3	VEMYSGSDDDDDFNKLPK	1.10417	0.01995	(3) Oxidation (M);(5) Phospho (ST);(7) Phospho (ST)
E2 02 1	3	VEMYSGSDDDDDFNKLPK	1.11167	0.02995	(3) Oxidation (M);(5) Phospho (ST);(7) Phospho (ST)
E2 04 1	2	VEMYSGSDDDDDFNKLPK	1.07833	0.01752	(5) Phospho (ST);(7) Phospho (ST)
E2 04 2	2	VEMYSGSDDDDDFNKLPK	1.09917	0.01435	(5) Phospho (ST);(7) Phospho (ST)
E2 02 2	3	VEMYSGSDDDDDFNKLPKK	1.27583	0.04398	(5) Phospho (ST);(7) Phospho (ST)
E2 02 1	3	VEMYSGSDDDDDFNKLPKK	1.28333	0.04092	(5) Phospho (ST);(7) Phospho (ST)
E1 02 1	3	VGDGDLSAEEIPENEVSLRR	1.07417	0.04554	(7) Phospho (ST)
E2 01 1	2	VGGSSVDLHR	0.80567	0.0771	(4) Phospho (ST)
E1 01 1	2	VGGSSVDLHR	0.8295	0.01769	(4) Phospho (ST)
E1 01 3	2	VGGSSVDLHR	0.85833	0.0314	(4) Phospho (ST)
E1 01	2	VGGSSVDLHR	1	0.05682	(4) Phospho (ST)
E2 02	2	VGSLDNVGHLPAGGAVK	0.68997	0.0523	(3) Phospho (ST)
E1 02	2	VGSLDNVGHLPAGGAVK	0.69284	0.03633	(3) Phospho (ST)
E1 01	3	VGSLDNVGHLPAGGAVK	0.79281	0.06886	(3) Phospho (ST)
E2 02 2	2	VGSLDNVGHLPAGGAVK	1.185	0.04342	(3) Phospho (ST)
E2 02 1	2	VGSLDNVGHLPAGGAVK	1.20417	0.02734	(3) Phospho (ST)
E1 02 1	2	VGSLDNVGHLPAGGAVK	1.37667	0.01666	(3) Phospho (ST)
E1 02 2	2	VGSLDNVGHLPAGGAVK	1.38833	0.01621	(3) Phospho (ST)
E1 03 2	2	VLGSEGEEEDEALSPAK	0.925	0.05645	(4) Phospho (ST)
E1 02	2	VLNTGSDVEEAVADALK	0.9009	0.0391	(6) Phospho (ST)
E1 03 2	2	VLNTGSDVEEAVADALK	0.98417	0.07531	(6) Phospho (ST)
E2 02 1	2	VLNTGSDVEEAVADALK	1.00583	0.01588	(6) Phospho (ST)
E1 03 1	2	VLNTGSDVEEAVADALK	1.02667	0.04793	(6) Phospho (ST)
E1 02 1	2	VLNTGSDVEEAVADALK	1.02917	0.03862	(6) Phospho (ST)
E2 01 2	3	VLNTGSDVEEAVADALK	1.04583	0.02518	(6) Phospho (ST)
E2 03 1	2	VLNTGSDVEEAVADALK	1.0525	0.03095	(6) Phospho (ST)
E2 02 2	2	VLNTGSDVEEAVADALK	1.10083	0.03173	(6) Phospho (ST)
E2 01 1	3	VLNTGSDVEEAVADALKK	1.05333	0.08375	(6) Phospho (ST)
E2 01 1	3	VLSPPKLNEVSSDANR	1.19083	0.09024	(3) Phospho (ST)

E2 02 2	2	VLSTSTDLEAAVADALK	1.14083	0.1398	(5) Phospho (ST)
E2 01 2	3	VLSTSTDLEAAVADALK	0.98917	0.04711	(6) Phospho (ST)
E2 02 2	3	VLSTSTDLEAAVADALLLGDSR	1.05417	0.06557	(6) Phospho (ST)
E2 02 1	3	VMTIPYQPMPASSPVICAGGQDR	1.0125	0.03294	(2) Oxidation (M);(13) Phospho (ST)
E2 03 1	2	VNQSALEAVTPSPSFQQR	1.04083	0.09045	(12) Phospho (ST)
E1 04 1	2	VPAEDETQSIDSEDSFVPGR	1.115	0.05524	(9) Phospho (ST);(12) Phospho (ST)
E1 01	3	VPKPEPIPEPKEPSPEK	0.88863	0.1616	(14) Phospho (ST)
E1 01 3	3	VPKPEPIPEPKEPSPEK	1.0275	0.0956	(14) Phospho (ST)
E1 01 1	3	VPKPEPIPEPKEPSPEK	1.03917	0.09165	(14) Phospho (ST)
E2 01 2	2	VPSVESLFR	0.69633	0.05177	(3) Phospho (ST)
E2 01 1	2	VPSVESLFR	0.76133	0.06328	(3) Phospho (ST)
E1 01 1	2	VPSVESLFR	0.76333	0.0368	(3) Phospho (ST)
E1 01 3	2	VPSVESLFR	0.84	0.01329	(3) Phospho (ST)
E1 04	3	VQGEAVSNIQENTQTPTVQEESEEEEVDETGVE VK	0.76648	0.01233	(22) Phospho (ST)
E1 04 3	3	VQGEAVSNIQENTQTPTVQEESEEEEVDETGVE VK	1.2075	0.00767	(22) Phospho (ST)
E1 04 1	3	VQGEAVSNIQENTQTPTVQEESEEEEVDETGVE VK	1.21167	0.00944	(22) Phospho (ST)
E2 04 1	3	VQIPVSRPDPEPVSDNEEDSYDEEIHDPR	1.23833	0.04767	(14) Phospho (ST);(20) Phospho (ST)
E1 03 2	3	VSALEEDMDDVESSEEEEEEDEKLER	0.94083	0.01693	(13) Phospho (ST);(14) Phospho (ST)
E1 01 3	3	VSGRTSPPLLDR	0.87167	0.01461	(6) Phospho (ST)
E1 01 3	2	VSGRTSPPLLDR	0.9075	0.02983	(6) Phospho (ST)
E1 02	3	VTFFEPGSGDENGTSNKEDEFR	0.87413	0.05979	(8) Phospho (ST);(12) Deamidated (NQ)
E1 02 1	3	VTFFEPGSGDENGTSNKEDEFR	1.27667	0.1126	(8) Phospho (ST);(12) Deamidated (NQ)
E1 03 2	3	VTLQDYRLPDSDDDEDEETAIQR	1.12417	0.0096	(11) Phospho (ST)
E1 03 1	3	VTLQDYRLPDSDDDEDEETAIQR	1.13417	0.02405	(11) Phospho (ST)
E2 03 2	3	VTTEIQLPSQSPVEEQSPASLSSLR	1.18833	0.06081	(11) Phospho (ST)
E2 04	2	VVDYSQFQESDDADEDYGR	0.84746	0.01498	(10) Phospho (ST)
E1 04 3	2	VVDYSQFQESDDADEDYGR	1.025	0.02971	(10) Phospho (ST)
E1 04 1	2	VVDYSQFQESDDADEDYGR	1.14333	0.02794	(10) Phospho (ST)
E2 04 1	2	VVDYSQFQESDDADEDYGR	1.1625	0.01436	(10) Phospho (ST)
E1 03	3	VVDYSQFQESDDADEDYGRDSGPPTK	0.83011	0.01607	(10) Phospho (ST)
E1 03 1	3	VVDYSQFQESDDADEDYGRDSGPPTK	1.0725	0.02038	(10) Phospho (ST)
E1 03 2	3	VVDYSQFQESDDADEDYGRDSGPPTK	1.13583	0.01579	(10) Phospho (ST)
E2 03 2	3	VVDYSQFQESDDADEDYGRDSGPPTK	1.175	0.01866	(10) Phospho (ST)
E2 03 1	3	VVDYSQFQESDDADEDYGRDSGPPTK	1.21833	0.01075	(10) Phospho (ST)
E2 02 1	2	VVPSFLPVDQGGSLVGR	0.77225	0.06857	(13) Phospho (ST)
E2 02 2	2	VVPSFLPVDQGGSLVGR	0.78217	0.01795	(13) Phospho (ST)
E2 03	2	VVPSFLPVDQGGSLVGR	1.23762	0.1723	(13) Phospho (ST)
E2 02	2	VVPSFLPVDQGGSLVGR	1.28205	0.1305	(13) Phospho (ST)
E2 02	4	WAHDKFSGEEGEIEDDESGTENREEK	0.83519	0.02074	(7) Phospho (ST);(18) Phospho (ST)
E2 03 2	3	WAHDKFSGEEGEIEDDESGTENREEK	1.1775	0.03558	(7) Phospho (ST);(18) Phospho (ST)
E1 03 1	3	WAHDKFSGEEGEIEDDESGTENREEK	1.18417	0.02906	(7) Phospho (ST);(18) Phospho (ST)
E1 03 2	3	WAHDKFSGEEGEIEDDESGTENREEK	1.2425	0.02654	(7) Phospho (ST);(20) Phospho (ST)
E1 02 2	3	WEDGSRDGVSLGAVSSTEEASR	0.58092	0.04699	(10) Phospho (ST);(15) Phospho (ST)
E1 02 1	3	WEDGSRDGVSLGAVSSTEEASR	0.609	0.03812	(10) Phospho (ST);(15) Phospho (ST)
E2 02 2	2	WLDESDAEMELR	0.7045	0.1604	(5) Phospho (ST)
E2 02 1	2	WLDESDAEMELR	0.75525	0.08471	(5) Phospho (ST)
E1 02 2	2	WLDESDAEMELR	0.78167	0.01753	(5) Phospho (ST)
E1 02	2	WLDESDAEMELR	1.26582	0.09083	(5) Phospho (ST)
E1 02 2	2	WLDESDAEMELR	0.82925	0.06799	(5) Phospho (ST);(9) Oxidation (M)
E2 03	3	WVEENVPSSVTDVALPALLDSDEER	0.7222	0.03087	(21) Phospho (ST)
E2 04	2	WVEENVPSSVTDVALPALLDSDEER	0.73565	0.03134	(21) Phospho (ST)
E2 04 1	2	WVEENVPSSVTDVALPALLDSDEER	1.02667	0.022	(21) Phospho (ST)
E2 03 1	3	WVEENVPSSVTDVALPALLDSDEER	1.12083	0.04097	(21) Phospho (ST)
E2 04 1	3	YAFMPLIDDSDDEIEEFMVTSENLTEGIK	0.88167	0.01659	(10) Phospho (ST)
E2 03 1	3	YGLLANTEDPTEMASLDSDEETVFESR	0.5865	0.1053	(15) Phospho (ST);(18) Phospho (ST)
E1 01 1	3	YGSIVDDERLSAEEMDER	0.86667	0.0651	(3) Phospho (ST)
E1 01	3	YGSIVDDERLSAEEMDER	1.18859	0.08796	(3) Phospho (ST)
E1 02 1	3	YKDLDEDELLGNLSETELK	0.93667	0.01231	(14) Phospho (ST)
E1 02 2	2	YLLGDAPVSPSSQK	1.21833	0.01255	(9) Phospho (ST)
E1 02 1	2	YLLGDAPVSPSSQK	1.23917	0.01602	(9) Phospho (ST)
E1 01 1	2	YLSFTPPEK	0.90167	0.00924	(3) Phospho (ST)
E2 01 2	2	YLSFTPPEK	0.92333	0.00884	(3) Phospho (ST)
E2 01 1	2	YLSFTPPEK	0.9375	0.00915	(3) Phospho (ST)
E2 03 2	3	YLVDGTKPNAGSEEISSEDDELVEEK	0.98167	0.0226	(12) Phospho (ST);(16) Phospho (ST);(17) Phospho (ST)
E2 03 1	3	YLVDGTKPNAGSEEISSEDDELVEEKK	1.17333	0.04994	(12) Phospho (ST);(16) Phospho (ST);(17) Phospho (ST)
E2 03 2	3	YLVDGTKPNAGSEEISSEDDELVEEKK	1.20417	0.0389	(12) Phospho (ST);(16) Phospho (ST);(17) Phospho (ST)
E1 04	3	YMAENPTAGVVQEEEEDNLEYDSDGNPIAPTK	0.86705	0.02428	(2) Oxidation (M);(23) Phospho (ST)
E1 04 1	3	YMAENPTAGVVQEEEEDNLEYDSDGNPIAPTKK	1.09167	0.01263	(2) Oxidation (M);(23) Phospho (ST)
E1 04 3	3	YMAENPTAGVVQEEEEDNLEYDSDGNPIAPTKK	1.13167	0.01291	(2) Oxidation (M);(23) Phospho (ST)
E1 03	3	YQDEVFGGFVTEPQEESEEEVEEPEER	1.00536	0.03166	(17) Phospho (ST)
E1 03 2	3	YQDEVFGGFVTEPQEESEEEVEEPEER	1.15417	0.02281	(17) Phospho (ST)
E2 02 1	3	YRIQEQESSGEEDSDLSPEER	1.215	0.03652	(8) Phospho (ST);(9) Phospho (ST)
E2 04 1	2	YRIQEQESSGEEDSDLSPEER	1.3825	0.04189	(8) Phospho (ST);(9) Phospho (ST)
E2 02 2	3	YSHSYLSDSDTEAKLTETNA	0.89833	0.01585	(7) Phospho (ST);(9) Phospho (ST)
E2 02 1	3	YSHSYLSDSDTEAKLTETNA	0.91583	0.01287	(7) Phospho (ST);(9) Phospho (ST)
E2 01 1	3	YSPSQNSPIHHIPSR	0.845	0.3137	(1) Phospho (Y);(7) Phospho (ST)
E2 01 2	3	YSPSQNSPIHHIPSRR	1.02917	0.01628	(1) Phospho (Y);(7) Phospho (ST)
E2 01 1	3	YSPSQNSPIHHIPSRR	1.04083	0.01276	(1) Phospho (Y);(7) Phospho (ST)
E2 01 1	4	YSPSQNSPIHHIPSRR	1.05833	0.04166	(1) Phospho (Y);(7) Phospho (ST)
E2 01 2	4	YSPSQNSPIHHIPSRR	1.07417	0.04812	(1) Phospho (Y);(7) Phospho (ST)
E2 01 2	3	YSPSQNSPIHHIPSRR	1.02917	0.01628	(2) Phospho (ST);(7) Phospho (ST)
E2 01 2	4	YSPSQNSPIHHIPSRR	1.07167	0.05158	(2) Phospho (ST);(7) Phospho (ST)
E2 03 2	3	YYDDIYFDSDSEDEDRAVQVTK	1.1975	0.1717	(9) Phospho (ST);(11) Phospho (ST)
E2 03 1	3	YYDDIYFDSDSEDEDRAVQVTK	1.20583	0.04174	(9) Phospho (ST);(11) Phospho (ST)

表２　リン酸化プロテオーム解析結果

（抗チロシンリン酸化抗体による濃縮法を使用）



Fraction Hit Accession Score Mass L/H SD(geo) #
1 1 P00761 157 25078 0
1 Trypsin OS=Sus scrofa PE=1 SV=1
1
1 z Sequence Incl. L/H Std.Err. Fraction Correlation Intensity Modifications
1 1 1 VATVSLPR ######## 57.18 0.9547 0.9908 2315
1 2 2 VATVSLPR ######## 27.23 0.9668 0.9875 8956
1 3 2 LSSPATLNSR 6076 1.247 0.964 0.9997 3255
1 4 3 LGEHNDVLEGNEQFNAAK 19.14 11.26 0.9918 0.9969 5573
1
1 Hit Accession Score Mass L/H SD(geo) #
1 2 A5A6M6 141 65621 0
1 Keratin, type II cytoskeletal 1 OS=Pan troglodytes GN=KRT1 PE=2 SV=1
1
1 z Sequence Incl. L/H Std.Err. Fraction Correlation Intensity Modifications
1 1 3 IESELNR 252.9 14.21 0.6642 0.8455 53.31
1 2 2 IESELNR 19.62 0.3239 0.6791 0.9766 127.8
1 3 2 YEELQITAGR 9.327 5.06 0.6584 0.9919 105.9
1 4 2 SLDLDSIAEVK 914.2 4.169 0.8447 0.9974 201.7
1 5 2 FLEQQNQVLQTK ######## 42.46 0.8577 0.9993 143.6
1
1 Hit Accession Score Mass L/H SD(geo) #
1 3 P00025447 72 48181 1.31 1
1 Gene_Symbol=EEF1A1 Elongation factor 1-alpha 1 ng=441
1
1 z Sequence Incl. L/H Std.Err. Fraction Correlation Intensity Modifications
1 1 3 NMTGTSQADCAVLIVAAGVGEFEAGISK X 1.31 0.01866 0.904 0.9959 517.5 (8) Deamidated (N
1
1 Hit Accession Score Mass L/H SD(geo) #
1 4 P00021304 61 224881 0
1 Gene_Symbol=KRT2 Keratin, type II cytoskeletal 2 epidermal ng=645 # SNP(677,g,101,G|SNP(780,s,101,G|
1
1 z Sequence Incl. L/H Std.Err. Fraction Correlation Intensity Modifications
1 1 3 IESELNR 252.9 14.21 0.6642 0.8455 53.31
1 2 2 IESELNR 19.62 0.3239 0.6791 0.9766 127.8
1 3 2 FLEQQNQVLQTK ######## 42.46 0.8577 0.9993 143.6
1
1 Hit Accession Score Mass L/H SD(geo) #
1 5 P00555610 56 312507 1.02 1
1 Gene_Symbol=AHNAK Putative uncharacterized protein AHNAK ng=2960
1
1 z Sequence Incl. L/H Std.Err. Fraction Correlation Intensity Modifications
1 1 2 AEGPEVDVNLPK X 1.02 0.01922 0.826 0.9922 276.1
1
1 Hit Accession Score Mass L/H SD(geo) #
1 6 P00019359 55 259643 0
1 Gene_Symbol=KRT9 Keratin, type I cytoskeletal 9 ng=623 # SNP(703,g,142,G|SNP(805,g,143,G|SNP(888,m
1
1 z Sequence Incl. L/H Std.Err. Fraction Correlation Intensity Modifications
1 1 2 TLLDIDNTR 3.226 3.047 0.6449 0.7442 195.1

2 Hit Accession Score Mass L/H SD(geo) #
2 1 P00220327 455 426806 0
2 Gene_Symbol=KRT1 Keratin, type II cytoskeletal 1 ng=644 # SNP(696,g,133,G|SNP(814,g,155,V|SNP(910,v
2
2 z Sequence Incl. L/H Std.Err. Fraction Correlation Intensity Modifications
2 1 2 TLLEGEESR 6.616 3.253 0.3218 0.8316 804.8
2 2 2 LALDLEIATYR 5.36 2.678 0.7247 0.9644 186
2 3 2 SLDLDSIAEVK 2993 14.66 0.8124 0.9977 613.1
2 4 2 LNDLEDALQQAK 134.5 1.64 0.7785 0.9852 141.3
2 5 2 SLNNQFASFIDK 448.3 9.624 0.9322 0.9951 632.6
2 6 2 FLEQQNKVLQTK 222 0.2683 0.9538 0.9989 514.1
2 7 3 SLNNQFASFIDKVR 321.4 0.7993 0.8513 0.996 255.4
2 8 3 QSNLQQSISDAEQR 7.864 2.289 0.5372 0.8778 54.12
2 9 2 QSNLQQSISDAEQR 1544 5.768 0.925 0.998 111.8
2 10 3 FSSCGGGGGSFGAGGGFGSR 1.212 0.2628 0.3724 0.5713 111.7
2 11 2 FSSCGGGGGSFGAGGGFGSR 2.981 17.83 0.5691 0.9928 124.2
2 12 3 LNDLEDALQQAKEDLAR 838.5 1.629 0.7693 0.9926 224.7

2 Hit Accession Score Mass L/H SD(geo) #
2 2 P00220030 399 112616 0.9997 1.081 5
2 Gene_Symbol=PXN Isoform Alpha of Paxillin ng=557 # SNP(621,r,188,S|SNP(696,s,188,S|SNP(718,i,331,I|S
2
2 z Sequence Incl. L/H Std.Err. Fraction Correlation Intensity Modifications
2 1 2 CYYCNGPLDK X 0.9004 0.07595 0.9091 0.9947 224.9
2 2 3 GSLCSGCQKPITGR X 1.033 0.02338 0.8714 0.997 317.6
2 3 2 TSSVSNPQDSVGSPCSR X 1.057 0.009196 0.9806 0.9947 962.5
2 4 3 EQNDKPYQQNCFLK X 1.079 0.01635 0.749 0.9812 397
2 5 3 DGGPYCEKDYHNLFSPR X 0.9418 0.02144 0.6791 0.9433 105.5
2 6 4 DGGPYCEKDYHNLFSPR 0.9668 0.2126 0.5964 0.9018 159.9

2 Hit Accession Score Mass L/H SD(geo) #
2 3 P35527 242 62320 0
2 Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=2
2
2 z Sequence Incl. L/H Std.Err. Fraction Correlation Intensity Modifications
2 1 2 QGVDADNGLR 314.8 2.408 0.6754 0.9941 354.8
2 2 2 QGVDADNGLR 3.379 5.777 0.6396 0.9459 157.9 (8) Deamidated (N
2 3 2 QVLDNLTMEK 3.21 3.928 0.7641 0.9598 245.6 (8) Oxidation (M)
2 4 2 HGVQELEELQSQLSK 49.7 1.756 0.6122 0.9103 49.33
2 5 3 HGVQELEELQSQLSK 307.3 2.85 0.6928 0.9807 247.1
2 6 3 EETYNNLLEGGQEDFESSGAGK 1118 2.454 0.8975 0.9887 327.4

2 Hit Accession Score Mass L/H SD(geo) #
2 4 P00017617 212 99735 0.9539 1.152 4
2 Gene_Symbol=DDX5 Probable ATP-dependent RNA helicase DDX5 ng=614 # SNP(644,i,109,I|SNP(696,g,
2
2 z Sequence Incl. L/H Std.Err. Fraction Correlation Intensity Modifications
2 1 2 LLQLVEDR X 0.814 0.05633 0.7647 0.9021 269.6
2 2 2 QVSDLSVLR X 0.9913 0.07532 0.7923 0.9313 239
2 3 2 APLIATDVASR X 1.136 0.03016 0.7437 0.9856 343.2
2 4 2 TTYLVLDEADR 0.000923 17.54 0.7378 0.4329 273.7
2 5 3 TLSYLLPAIVHINHQPFLER 1.23 0.2161 0.6817 0.4753 83.35
2 6 4 TLSYLLPAIVHINHQPFLER X 0.9034 0.04989 0.6061 0.863 139.6

2 Hit Accession Score Mass L/H SD(geo) #
2 5 P00761 211 25078 198.6 1
2 Trypsin OS=Sus scrofa PE=1 SV=1
2
2 z Sequence Incl. L/H Std.Err. Fraction Correlation Intensity Modifications
2 1 1 VATVSLPR 4.612 556 0.6562 0.9921 5892
2 2 2 VATVSLPR ######## 46.15 0.8448 0.9588 ########
2 3 2 LSSPATLNSR ######## 6.978 0.8961 0.9824 3770
2 4 3 LGEHNDVLEGNEQFNAAK -698.5 0.1884 0.6485 0.9714 6272
2 5 2 LGEHNDVLEGNEQFNAAK X 198.6 999 0.9353 0.9889 822.6
2 6 4 LGEHNDVLEGNEQFNAAK 7.569 1.621 0.4816 0.7959 210.6
2 7 4 IIHPNFNGNTLDNDIMLIKLSSPATLNSR 0.2787 0.6459 0.8715 0.8825 2818 (10) Deamidated (

2 Hit Accession Score Mass L/H SD(geo) #
2 6 P00402182 176 65870 1.035 1.046 3
2 Gene_Symbol=SYNCRP Isoform 2 of Heterogeneous nuclear ribonucleoprotein Q ng=588
2
2 z Sequence Incl. L/H Std.Err. Fraction Correlation Intensity Modifications
2 1 2 LLMDPLTGLNR X 0.998 0.02784 0.7897 0.9831 260.5 (2) Oxidation (M)
2 2 2 TGYTLDVTTGQR X 1.021 0.01874 0.8868 0.9968 507.2
2 3 2 NLANTVTEELEK X 1.088 0.03551 0.8945 0.9704 385.2

2 Hit Accession Score Mass L/H SD(geo) #
2 7 P00456969 146 708960 0
2 Gene_Symbol=DYNC1H1 Cytoplasmic dynein 1 heavy chain 1 ng=4648 # SNP(4664,n,102,M|SNP(4688,q,1
2
2 z Sequence Incl. L/H Std.Err. Fraction Correlation Intensity Modifications
2 1 2 VTFVNFTVTR 0.5582 0.2315 0.6057 0.9001 172.1
2 2 2 WTDENDTVALK 1.144 0.1068 0.6699 0.9561 80.64
2 3 2 LDDDTITTLENLKR 1.719 2.164 0.4201 0.5093 58.82
2 4 3 LDDDTITTLENLKR 0.8641 0.1644 0.6602 0.9617 156.6

2 Hit Accession Score Mass L/H SD(geo) #
2 8 P00219301 144 126247 0.9584 1
2 Gene_Symbol=MARCKS Myristoylated alanine-rich C-kinase substrate ng=332 # SNP(349,g,191,G|SNP(46
2
2 z Sequence Incl. L/H Std.Err. Fraction Correlation Intensity Modifications
2 1 3 GEAAAERPGEAAVASSPSK X 0.9584 0.02511 0.8541 0.9956 101.4

2 Hit Accession Score Mass L/H SD(geo) #
2 9 P13645 128 59703 0
2 Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 SV=4
2
2 z Sequence Incl. L/H Std.Err. Fraction Correlation Intensity Modifications
2 1 2 SLLEGEGSSGGGGR 683.4 5.577 0.8803 0.9982 90.09
2 2 2 ALEESNYELEGK 656.3 1.923 0.843 0.9982 280.7
2 3 2 QSLEASLAETEGR 4.699 2.524 0.7822 0.9951 131.7
2

2 Hit Accession Score Mass L/H SD(geo) #
2 10 P00644087 98 69492 0.7942 1.024 2
2 Gene_Symbol=LMNA Lamin A/C ng=614
2
2 z Sequence Incl. L/H Std.Err. Fraction Correlation Intensity Modifications
2 1 2 SGAQASSTPLSPTR X 0.8077 0.02184 0.9192 0.9978 243.7
2 2 3 NSNLVGAAHEELQQSR X 0.781 0.03687 0.3721 0.9583 111.5

2 Hit Accession Score Mass L/H SD(geo) #
2 11 P00011134 93 56165 0.9574 1.025 2
2 Gene_Symbol=HSPA7 Putative heat shock 70 kDa protein 7 ng=367 # CON(376,N,59,S|CON(408,K,95,Q|C
2
2 z Sequence Incl. L/H Std.Err. Fraction Correlation Intensity Modifications
2 1 2 VELANDQGNR X 0.974 0.0401 0.7228 0.9876 99.6
2 2 2 TTPSYVAFTDTER X 0.9411 0.02722 0.8713 0.99 144.2

2 Hit Accession Score Mass L/H SD(geo) #
2 12 P00045921 85 65303 1.047 1.109 2
2 Gene_Symbol=ATAD3B TOB3 ng=578
2
2 z Sequence Incl. L/H Std.Err. Fraction Correlation Intensity Modifications
2 1 2 QTVLESR 1.426 0.1134 0.6004 0.8853 191.7
2 2 2 TAGTLFGEGFR X 0.973 0.05331 0.612 0.9212 197.2
2 3 3 QQQLLNEENLR 1.69 0.6604 0.413 0.621 42.89
2 4 2 QQQLLNEENLR X 1.127 0.02735 0.7836 0.9926 69.4

2 Hit Accession Score Mass L/H SD(geo) #
2 13 P00791086 77 64490 0.9036 1
2 Gene_Symbol=EIF3D Putative uncharacterized protein EIF3D ng=548
2
2 z Sequence Incl. L/H Std.Err. Fraction Correlation Intensity Modifications
2 1 3 VADWTGATYQDKR X 0.9036 0.05219 0.5591 0.8851 111.5

2 Hit Accession Score Mass L/H SD(geo) #
2 14 P00103525 64 70246 0
2 Gene_Symbol=PSPC1 Isoform 1 of Paraspeckle component 1 ng=523 # SNP(537,k,161,K|SNP(582,n,161,K
2
2 z Sequence Incl. L/H Std.Err. Fraction Correlation Intensity Modifications
2 1 4 LFVGNLPTDITEEDFKR 0.1905 1.021 0.433 0.3201 101.6
2 2 3 LFVGNLPTDITEEDFKR 1.165 0.1147 0.6257 0.9625 157.8

2 Hit Accession Score Mass L/H SD(geo) #
2 15 P00141318 59 86080 0
2 Gene_Symbol=CKAP4 Isoform 1 of Cytoskeleton-associated protein 4 ng=602 # SNP(611,i,111,L|SNP(650,r
2
2 z Sequence Incl. L/H Std.Err. Fraction Correlation Intensity Modifications
2
2 Hit Accession Score Mass L/H SD(geo) #
2 16 P00003886 51 61020 0
2 Gene_Symbol=GNL3 Isoform 2 of Guanine nucleotide-binding protein-like 3 ng=537
2
2 z Sequence Incl. L/H Std.Err. Fraction Correlation Intensity Modifications
2
2 Hit Accession Score Mass L/H SD(geo) #
2 17 P00221354 48 53551 0
2 Gene_Symbol=FUS Isoform Short of RNA-binding protein FUS ng=525
2
2 z Sequence Incl. L/H Std.Err. Fraction Correlation Intensity Modifications
2
2 Hit Accession Score Mass L/H SD(geo) #
2 18 P00017578 48 114175 0.8968 1
2 Gene_Symbol=SHB SH2 domain-containing adapter protein B ng=596 # SNP(611,a,133,Q|SNP(665,v,133,C
2
2 z Sequence Incl. L/H Std.Err. Fraction Correlation Intensity Modifications
2 1 3 VESAAGGGAGDPLGGACAGGR 0.5932 0.1662 0.5214 0.8093 58.75
2 2 2 VESAAGGGAGDPLGGACAGGR X 0.8968 0.02563 0.9417 0.9963 252.9

2 Hit Accession Score Mass L/H SD(geo) #
2 19 P00910316 45 57103 0.8337 1
2 Gene_Symbol=--cDNA FLJ54333, highly similar to T-complex protein 1 subunit epsilon ng=514
2
2 z Sequence Incl. L/H Std.Err. Fraction Correlation Intensity Modifications
2 1 2 IADGYEQAAR X 0.8337 0.04429 0.7029 0.9953 66.08

3 Hit Accession Score Mass L/H SD(geo) #
3 1 P00413961 2239 215760 1.081 32
3 Gene_Symbol=PTK2 PTK2 protein tyrosine kinase 2 isoform b ng=1074 # SNP(1066,h,111,H|SNP(1117,p,1
3
3 z Sequence Incl. L/H Std.Err. Fraction Correlation Intensity Modifications
3 1 2 LGDFGLSR X 1.046 0.02117 0.7684 0.9898 1586
3 2 2 LIQQTFR X 1.033 0.02114 0.8395 0.9913 905.7
3 3 2 KLIQQTFR 0.005469 6.039 0.8058 0.9733 1661
3 4 2 NLLDVDQAR X 1.039 0.007673 0.9251 0.9938 4170
3 5 2 NVLVSSNDCVK X 1.054 0.01233 0.9075 0.9964 3177
3 6 2 AQLSTLEEEEK X 1.142 0.02042 0.9062 0.9916 2189
3 7 2 LLNSDLGELINK X 1.04 0.01384 0.9511 0.998 4154
3 8 3 QMLTAAHALAVDAK X 0.9828 0.008165 0.8399 0.9975 1244
3 9 2 QMLTAAHALAVDAK X 1.493 0.03769 0.7625 0.9665 451.8
3 10 2 SNVEVLEKDVGLK 1.176 0.2032 0.2682 0.7939 102.8
3 11 3 SNVEVLEKDVGLK X 0.9755 0.02566 0.5569 0.9525 182.8
3 12 3 SNDKVYENVTGLVK X 1.109 0.03992 0.7473 0.9965 2848
3 13 2 SNDKVYENVTGLVK 0.6092 0.2166 0.8808 0.9843 792.2
3 14 3 GGQVLPTHLMEER X 1.128 0.09003 0.907 0.8496 3321
3 15 2 GIGQVLPTHLMEER X 0.8781 0.07579 0.9204 0.9859 769.6
3 16 2 IQPAPPEEVVPMVK X 1.072 0.01652 0.9649 0.9909 2338
3 17 3 GIGQVLPTHLMEER X 1.119 0.02985 0.7938 0.9853 2119 (11) Oxidation (M)
3 18 2 GIGQVLPTHLMEER X 1.015 0.01765 0.7969 0.9896 484.2 (11) Oxidation (M)
3 19 3 LVNGTSQSFIRPQK 1.003 0.1286 0.8419 0.9918 2461
3 20 3 LVNGTSQSFIRPQK X 1.068 0.04916 0.7199 0.9915 745.1 (3) Deamidated (N
3 21 3 LAQQYVMTSLQQEYKK 0.7891 0.1484 0.7796 0.9672 1981
3 22 3 LAQQYVMTSLQQEYKK X 1.089 0.02476 0.8406 0.9753 2336 (7) Oxidation (M)
3 23 3 SEEVHVVLHVDMGVSSVR X 0.9934 0.01389 0.8519 0.9902 457.7 (11) Oxidation (M)
3 24 4 SEEVHVVLHVDMGVSSVR X 0.9774 0.01496 0.8231 0.9788 597.6 (11) Oxidation (M)
3 25 3 AQLSTLEEEKAQQEER X 1.066 0.02307 0.9043 0.9945 4709
3 26 3 TLLATVDETPLLPASTHR X 1.058 0.01681 0.8208 0.9942 6143
3 27 2 TLLATVDETPLLPASTHR X 0.9708 0.01549 0.8868 0.9794 660.1
3 28 3 MAAAYLDPNLNHTPNSSTK X 1.021 0.02627 0.6587 0.9943 730.4
3 29 3 GFLMQFTEDVVDTKYSNSEDKDR X 1.097 0.0123 0.9156 0.9902 4036
3 30 4 QATVSWDSGGSDEAPPKPSRPGYPSPR X 1.106 0.05222 0.6975 0.9765 595.1
3 31 4 KPPRPGAPGHLGSLASLSSPADSYNEGVK X 1.187 0.03207 0.7522 0.9714 2258
3 32 5 KPPRPGAPGHLGSLASLSSPADSYNEGVK X 1.185 0.02045 0.4936 0.9262 786.2
3 33 3 CKGEGQFGDVHQGIYMSPENPALAVAK X 1.2 0.02323 0.9214 0.9815 1189
3 34 4 GCNPTHLADFTQGVQTKQYSNSEDKDR X 1.093 0.01673 0.9088 0.9735 1359
3 35 3 IAGAPEPLTVTAPSLTAENMADLIDGYCR X 1.259 0.01497 0.977 0.9764 2770
3 36 4 GSDREDGSLGGPKGYNQHVGPVGKPDPAPPK X 1.188 0.07599 0.6139 0.9481 219.8
3 37 5 GSDREDGSLGGPKGYNQHVGPVGKPDPAPPK X 1.066 0.01948 0.7823 0.9793 736.8
3
3 Hit Accession Score Mass L/H SD(geo) #
3 2 P00021267 569 112476 0.9441 1.062 9
3 Gene_Symbol=EPHA2 Ephrin type-A receptor 2 ng=976 # SP(978,A,24,A|
3
3 z Sequence Incl. L/H Std.Err. Fraction Correlation Intensity Modifications
3 1 2 VSDFGLSR X 1 0.03478 0.8129 0.9972 537.8
3 2 2 FADVSLDK X 0.9556 0.01757 0.8567 0.9972 1640
3 3 2 TVSEWLESK X 0.9262 0.02368 0.8595 0.9906 1146
3 4 2 QSPEDVYFSK X 0.9041 0.02677 0.8317 0.9906 611.7
3 5 2 WTAPEAISYR X 1.034 0.08643 0.8042 0.9857 781.9
3 6 2 NLVNSNLVCK X 0.8375 0.02105 0.9369 0.9835 1897
3 7 2 VGAGEFGEVYK X 0.9476 0.08304 0.8836 0.9947 1566
3 8 2 LPSTSGSEGVPFR X 0.9371 0.01912 0.9139 0.9928 1425
3 9 2 TASVSNQTEPPK 1.414 0.2377 0.8209 0.7927 636.1
3 10 2 VLEDDPEATYTTSGGK X 0.968 0.02221 0.972 0.9952 348.4
3
3 Hit Accession Score Mass L/H SD(geo) #
3 3 P00745296 569 295006 0.9441 1.062 9
3 Gene_Symbol=EPHA2 ephrin receptor EphA2 ng=976 # SP(978,A,24,A|SNP(1020,a,190,A|SNP(1046,i,191
3
3 z Sequence Incl. L/H Std.Err. Fraction Correlation Intensity Modifications
3 1 2 VSDFGLSR X 1 0.03478 0.8129 0.9972 537.8
3 2 2 FADVSLDK X 0.9556 0.01757 0.8567 0.9972 1640
3 3 2 TVSEWLESK X 0.9262 0.02368 0.8595 0.9906 1146
3 4 2 QSPEDVYFSK X 0.9041 0.02677 0.8317 0.9906 611.7
3 5 2 WTAPEAISYR X 1.034 0.08643 0.8042 0.9857 781.9
3 6 2 NLVNSNLVCK X 0.8375 0.02105 0.9369 0.9835 1897
3 7 2 VGAGEFGEVYK X 0.9476 0.08304 0.8836 0.9947 1566
3 8 2 LPSTSGSEGVPFR X 0.9371 0.01912 0.9139 0.9928 1425
3 9 2 TASVSNQTEPPK 1.414 0.2377 0.8209 0.7927 636.1
3 10 2 VLEDDPEATYTTSGGK X 0.968 0.02221 0.972 0.9952 348.4
3
3 Hit Accession Score Mass L/H SD(geo) #
3 4 P13645 447 59703 0
3 Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 SV=4
3
3 z Sequence Incl. L/H Std.Err. Fraction Correlation Intensity Modifications
3 1 2 SLLEGEGSSGGGGR 8028 15.43 0.9096 0.9988 720.5
3 2 3 QSVEADNGLRR 135 2.592 0.534 0.9834 346.1
3 3 2 QSVEADNGLRR 3.435 2.818 0.6185 0.9541 261.3
3 4 3 SQYEQLAEQNR 0.00866 11.72 0.3215 0.4651 223.8
3 5 2 SQYEQLAEQNR 169.7 2.746 0.8537 0.9814 338
3 6 2 ALEESNVELEGK 2.84 12.68 0.8934 0.9964 868.4
3 7 2 QSLEASLAETEGR 2.438 53.01 0.8857 0.9977 562.6
3 8 2 GSLGGGFSSGGFSGGSFSR ######## 76.95 0.9239 0.9947 726.4
3 9 2 GSSGGGCFGGSSGGYGGLGGFGGGSFR 3076 19.88 0.8481 0.9778 368.5
3 10 3 GSSGGGCFGGSSGGYGGLGGFGGGSFR 111.5 28.37 0.6819 0.7746 327.2
3 11 3 NVSTGDVNVEMNAAPGVDLTQLLNNMR 268.4 2.336 0.8561 0.9688 387 (11) Oxidation (M)

3	Hit		Accession	Score	Mass	L/H	SD(geo)	#			
3	5		IPI00021290	427	249896	0.894	1.065	5			
3	Gene_Symbol=ACLY ATP-citrate synthase lng=1101 # SNP[1120,a,1056,A]SNP[1156,a,111,V]SNP[1208,v,·										
3											
3			z	Sequence	Incl.	L/H	Std.Err.	Fraction	Correlation	Intensity	Modifications
3	1		2	VTPDTDWAR	X	0.8362	0.07638	0.306	0.9421	297	
3	2		2	VDATADYICK		1.051	0.1331	0.7699	0.9653	452.2	
3	3		2	FICTTSAIQNR	X	0.8777	0.03979	0.8913	0.9895	471.4	
3	4		2	LGLVGVNLTLDGVK		0.7727	0.2084	0.4841	0.9693	526	
3	5		3	SGGMSNELNNIISR		0.03531	1.95	0.508	0.5689	164.8	(4) Oxidation (M)
3	6		2	SGGMSNELNNIISR	X	0.9579	0.06186	0.7749	0.9709	318	(4) Oxidation (M)
3	7		2	TAIAEGIPEALTR	X	0.8525	0.06595	0.7202	0.9501	645.9	
3	8		2	DLVSSLTSGLLTIGDR	X	0.9528	0.02616	0.8333	0.9904	527.7	
3											
3	Hit		Accession	Score	Mass	L/H	SD(geo)	#			
3	6		P04264	375	66149			0			
3	Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV=5										
3											
3			z	Sequence	Incl.	L/H	Std.Err.	Fraction	Correlation	Intensity	Modifications
3	1		2	EISELNR		2.464	12.94	0.7858	0.9968	661.7	
3	2		2	YEELQITAGR		5.904	1.922	0.6209	0.9651	791.4	
3	3		2	TNAENEFVTIK		55.3	0.7471	0.8315	0.9944	564.8	
3	4		2	LALDLEIATYR		2.983	4.796	0.7242	0.9637	472.8	
3	5		2	LNDLEDALQQAK		4.695	0.1755	0.4384	0.9155	336.7	
3	6		2	FLEQQNQVLQTK		2366	6.7	0.9349	0.9987	1176	
3	7		3	SLNNQFASFIDKVR		140.8	2.236	0.7337	0.9878	411.4	
3	8		3	QISNLQQSISDAEQR		40.76	0.8717	0.5244	0.8034	196.6	
3	9		2	QISNLQQSISDAEQR		9.384	5.781	0.8906	0.9966	155.8	
3	10		2	LNDLEDALQQAKEDLAR		41.79	16.66	0.3821	0.5677	143.9	
3	11		3	LNDLEDALQQAKEDLAR		3.42	2.941	0.6454	0.9691	272.2	
3	12		4	LDSELKNMQDMVEDYR		1.17	0.2732	0.4378	0.476	154	(8) Oxidation (M);(
3	13		3	LDSELKNMQDMVEDYR		4.806	1.696	0.6793	0.8591	235.2	(8) Oxidation (M);(
3											
3	Hit		Accession	Score	Mass	L/H	SD(geo)	#			
3	7		IPI00641339	318	95638	0.9852	1.039	2			
3	Gene_Symbol=BCAR1 cDNA FLJ55515, highly similar to Breast cancer anti-estrogen resistanceprotein 1 lng										
3											
3			z	Sequence	Incl.	L/H	Std.Err.	Fraction	Correlation	Intensity	Modifications
3	1		2	GGSGATLEDLDR	X	1.013	0.01911	0.8401	0.9953	383.3	
3	2		3	ATAPGPEGGGTLHPNPTDK		1.136	0.1028	0.6924	0.9437	714.1	
3	3		3	ALYDNVAESPDELSFR		5.755	1.627	0.3901	0.4768	358	
3	4		2	ALYDNVAESPDELSFR		1.104	0.1087	0.9265	0.9899	879.6	
3	5		2	GGSGATLEDLDRLVACSR		6.112	12.03	0.793	0.7549	690.3	
3	6		3	GGSGATLEDLDRLVACSR	X	0.9586	0.01941	0.6254	0.9642	694.4	
3											
3	Hit		Accession	Score	Mass	L/H	SD(geo)	#			
3	8		IPI00001466	317	166157	1.029	1.031	3			
3	Gene_Symbol=EML4 Echinoderm microtubule-associated protein-like 4 lng=981 # SNP[995,e,283,E]SNP[10										
3											
3			z	Sequence	Incl.	L/H	Std.Err.	Fraction	Correlation	Intensity	Modifications
3	1		2	AALADVLR	X	1.047	0.02379	0.6555	0.8321	179.6	
3	2		2	VQQQEDEITVLK	X	1.086	0.02757	0.9256	0.9919	628	
3	3		2	LSLPQNETVADTTLTK	X	1.048	0.01638	0.9534	0.993	482.9	
3	4		3	ASPSPQPSSQPLQIHR	X	0.993	0.02635	0.7909	0.9898	321.1	
3											
3	Hit		Accession	Score	Mass	L/H	SD(geo)	#			
3	9		P35908	296	66111	5.167		1			
3	Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KRT2 PE=1 SV=1										
3											
3			z	Sequence	Incl.	L/H	Std.Err.	Fraction	Correlation	Intensity	Modifications
3	1		2	EISELNR		2.464	12.94	0.7858	0.9968	661.7	
3	2		2	TAAENDFVTLK		3.385	5.876	0.6902	0.9819	438.2	
3	3		2	GFSSGSAVVSGGSR		54.79	0.4288	0.8773	0.9938	572	
3	4		2	NLDLDSIIAEVK		5055	7.211	0.8354	0.9953	813.6	
3	5		2	VDLLNQEIEFLK	X	5.167	999	0.3541	0.9782	367.1	
3	6		2	FLEQQNQVLQTK		2366	6.7	0.9349	0.9987	1176	
3	7		3	GGSGGGGSISGGGYGSGGGSGGR		0.1062	0.7024	0.05892	0.3398	119.5	
3	8		2	GGSGGGGSISGGGYGSGGGSGGR		1141	12.12	0.6722	0.995	95.15	
3											
3	Hit		Accession	Score	Mass	L/H	SD(geo)	#			
3	10		IPI00293464	282	291098	0.9525	1.045	4			
3	Gene_Symbol=DDB1 DNA damage-binding protein 1 lng=1140 # SNP[1148,h,1070,H]SNP[1177,r,1122,R]S										
3											
3			z	Sequence	Incl.	L/H	Std.Err.	Fraction	Correlation	Intensity	Modifications
3	1		2	VVEELTR		93	13.63	0.5117	0.9075	623.3	
3	2		2	LLASINSTVR	X	0.8985	0.03296	0.7244	0.9952	614.7	
3	3		2	VTLGTQPTVLR	X	0.9608	0.02059	0.7891	0.9945	574.3	
3	4		3	QGQGQLVTCSGAFK		0.02436	1.172	0.2125	0.7489	175.7	
3	5		2	QGQGQLVTCSGAFK	X	0.954	0.02709	0.8679	0.995	393.7	
3	6		3	KTEPATGFIDGDLIESFLDISRPK	X	0.9993	0.06981	0.5936	0.9801	199.9	
3	7		4	KTEPATGFIDGDLIESFLDISRPK		3.934	0.499	0.588	0.7622	533.2	
3											
3	Hit		Accession	Score	Mass	L/H	SD(geo)	#			
3	11		P00761	189	25078			0			
3	Trypsin OS=Sus scrofa PE=1 SV=1										
3											
3			z	Sequence	Incl.	L/H	Std.Err.	Fraction	Correlation	Intensity	Modifications
3	1		1	VATVSLPR		-2590	0.4474	0.9562	0.9953	3491	
3	2		2	VATVSLPR		-37.46	0.06769	0.7066	0.9339	4663	
3	3		3	LGEHNIDVLEGNEQFINAAK		-395.9	0.2093	0.6408	0.9459	5660	
3	4		2	LGEHNIDVLEGNEQFINAAK		509.7	0.6599	0.8885	0.9798	1661	
3	5		2	LGEHNIDVLEGNEQFINAAK		1.308	0.05062	0.6169	0.557	102.7	(17) Deamidated (
3	6		3	LGEHNIDVLEGNEQFINAAK		63.23	3.16	0.5273	0.8829	447	(17) Deamidated (
3	7		3	IITHPNFNGNTLDNDIMLIK		10.25	2.03	0.796	0.9707	833.3	(8) Deamidated (N
3	8		3	IITHPNFNGNTLDNDIMLIK		3.353	11.49	0.8671	0.9886	1518	(17) Oxidation (M)
3											
3	Hit		Accession	Score	Mass	L/H	SD(geo)	#			
3	12		IPI00910003	119	88790	1.026	1.093	4			
3	Gene_Symbol=- cDNA FLJ53378, highly similar to Eukaryotic translation initiation factor 3 subunit 8 lng=761										
3											
3			z	Sequence	Incl.	L/H	Std.Err.	Fraction	Correlation	Intensity	Modifications
3	1		2	ELLGQGLLLR	X	1.162	0.09529	0.6912	0.7976	519.5	
3	2		2	LGSLVENNER	X	1.024	0.03363	0.839	0.993	418.1	
3	3		1	FEELTNLIR		1.265	0.1786	0.3459	0.05773	255.3	
3	4		2	FEELTNLIR	X	0.9821	0.09868	0.8108	0.9789	117.2	
3	5		2	CLEEFELLGK		0.8974	0.1272	0.7035	0.9446	665.3	
3	6		4	RLDEEEEDNEGGEWER		0.8905	0.2709	0.3275	0.6342	140.2	
3	7		3	RLDEEEEDNEGGEWER	X	0.9472	0.02958	0.7402	0.9862	190.7	
3											
3	Hit		Accession	Score	Mass	L/H	SD(geo)	#			
3	13		IPI00640106	111	83774	0.9278	1.048	2			
3	Gene_Symbol=HNRNPU cDNA FLJ44920 fis, clone BRAMY3011501, highly similar to Heterogeneous nuclea										
3											
3			z	Sequence	Incl.	L/H	Std.Err.	Fraction	Correlation	Intensity	Modifications
3	1		1	FEIAAR		17.12	1.52	0.5266	0.8977	45.33	
3	2		2	FEIAAR	X	0.8977	0.06875	0.56	0.9749	157.7	
3	3		3	NFILDQTNVSAAAQR		0.703	0.1115	0.3659	0.5452	214.2	
3	4		2	NFILDQTNVSAAAQR	X	0.9588	0.01858	0.664	0.9905	320.8	
3											
3	Hit		Accession	Score	Mass	L/H	SD(geo)	#			
3	14		IPI00786995	102	470127	1.241	1.094	2			
3	Gene_Symbol=LOC731751 similar to DNA dependent protein kinase catalytic subunit lng=4096										
3											
3			z	Sequence	Incl.	L/H	Std.Err.	Fraction	Correlation	Intensity	Modifications
3	1		2	VTELALTASDR	X	1.323	0.09163	0.6333	0.8635	377.4	
3	2		2	LVINTEEVFRPYAK		2.612	0.3737	0.2363	0.4109	135.6	
3	3		3	LVINTEEVFRPYAK	X	1.165	0.08429	0.5117	0.8492	429.2	
3											
3	Hit		Accession	Score	Mass	L/H	SD(geo)	#			
3	15		P13647	98	62568			0			
3	Keratin, type II cytoskeletal 5 OS=Homo sapiens GN=KRT5 PE=1 SV=3										
3											
3			z	Sequence	Incl.	L/H	Std.Err.	Fraction	Correlation	Intensity	Modifications
3	1		2	ISISTSGGSFR		249.1	4.226	0.7223	0.9779	467.1	
3	2		2	NLDLDSIIAEVK		5055	7.211	0.8354	0.9953	813.6	
3											
3	Hit		Accession	Score	Mass	L/H	SD(geo)	#			
3	16		IPI00022353	93	421374	0.6053	1.005	2			
3	Gene_Symbol=TYK2 Non-receptor tyrosine-protein kinase TYK2 lng=1187 # SNP[1217,a,1016,A]SNP[1258,ε										
3											
3			z	Sequence	Incl.	L/H	Std.Err.	Fraction	Correlation	Intensity	Modifications
3	1		2	ELGAALQGCLLR	X	0.603	0.03114	0.6806	0.9821	281	
3	2		3	AAALSFVSLVDGYFR		0.3954	0.4023	0.4124	0.5674	192	
3	3		2	AAALSFVSLVDGYFR	X	0.6076	0.04431	0.588	0.8704	290.5	
3											
3	Hit		Accession	Score	Mass	L/H	SD(geo)	#			
3	17		P35527	90	62320			0			
3	Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=2										
3											
3			z	Sequence	Incl.	L/H	Std.Err.	Fraction	Correlation	Intensity	Modifications
3	1		2	QGVDADINGLR		57.63	1.468	0.4066	0.8796	285.6	
3											
3	Hit		Accession	Score	Mass	L/H	SD(geo)	#			
3	18		IPI00106495	88	188666			0			
3	Gene_Symbol=NCAPG Condensin complex subunit 3 lng=1015 # SNP[1028,h,251,Q]SNP[1053,d,259,D]SNI										
3											
3			z	Sequence	Incl.	L/H	Std.Err.	Fraction	Correlation	Intensity	Modifications
3	1		2	LLSDFLDSEVSELR		1.091	0.4108	0.509	0.6057	202.6	
3	Hit		Accession	Score	Mass	L/H	SD(geo)	#			
3	19		IPI00449049	78	272500	0.9139		1			
3	Gene_Symbol=PARP1 Poly [ADP-ribose] polymerase 1 lng=1014 # SNP[1023,f,113,F]SNP[1040,p,174,P]SI										
3											
3			z	Sequence	Incl.	L/H	Std.Err.	Fraction	Correlation	Intensity	Modifications
3	1		2	TTNFAGILSQGLR	X	0.9139	0.0704	0.1016	0.9047	387	
3											
3	Hit		Accession	Score	Mass	L/H	SD(geo)	#			
3	20		IPI00332841	77	185035	0.9181		1			
3	Gene_Symbol=RAPGEF1 guanine nucleotide-releasing factor 2 isoform b lng=1095 # SNP[1098,n,1053,N]SI										
3											
3			z	Sequence	Incl.	L/H	Std.Err.	Fraction	Correlation	Intensity	Modifications
3	1		2	ATSGSSLPVGINR	X	0.9181	0.03512	0.7657	0.9912	211.2	
3											
3	Hit		Accession	Score	Mass	L/H	SD(geo)	#			
3	21		P08730	75	48066			0			
3	Keratin, type I cytoskeletal 13 OS=Mus musculus GN=Krt13 PE=2 SV=2										
3											
3			z	Sequence	Incl.	L/H	Std.Err.	Fraction	Correlation	Intensity	Modifications
3	1		2	LEQEIATYR		6.208	1.206	0.6237	0.6025	325.7	
3	2		3	QSVEADINGLRR		135	2.592	0.534	0.9834	346.1	
3	3		2	QSVEADINGLRR		3.435	2.818	0.6185	0.9541	261.3	
3											
3	Hit		Accession	Score	Mass	L/H	SD(geo)	#			
3	22		IPI00747119	69	199704	1.052		1			
3	Gene_Symbol=PKP4 plakophilin 4 isoform b lng=1149 # SNP[1162,s,223,S]SNP[1190,y,223,S]SNP[1223,g,										
3											
3			z	Sequence	Incl.	L/H	Std.Err.	Fraction	Correlation	Intensity	Modifications
3	1		3	AEGQTLVQPSVANR		135.2	8.444	0.4608	0.6127	148.1	
3	2		2	AEGQTLVQPSVANR	X	1.052	0.02402	0.864	0.9928	194.1	
3											
3	Hit		Accession	Score	Mass	L/H	SD(geo)	#			
3	23		IPI00003519	69	171026			0			
3	Gene_Symbol=EFTUD2 116 kDa U5 small nuclear ribonucleoprotein component lng=972 # SNP[983,t,254,T]										
3											
3			z	Sequence	Incl.	L/H	Std.Err.	Fraction	Correlation	Intensity	Modifications
3	1		3	EGPLCDELIR		15.21	0.9598	0.5813	0.7051	137.6	
3	2		2	EGPLCDELIR		0.8282	0.1395	0.5461	0.8705	414.9	
3											
3	Hit		Accession	Score	Mass	L/H	SD(geo)	#			
3	24		IPI00012837	64	157217			0			
3	Gene_Symbol=KIF5B Kinesin-1 heavy chain lng=963 # SNP[978,e,236,E]SNP[993,c,291,G]SNP[1026,g,291										
3											
3			z	Sequence	Incl.	L/H	Std.Err.	Fraction	Correlation	Intensity	Modifications
3	1		2	LITDLQDQNQK		2.84	0.2154	0.2976	0.9678	529.9	
3											
3	Hit		Accession	Score	Mass	L/H	SD(geo)	#			
3	25		IPI00221106	60	149611			0			
3	Gene_Symbol=SF3B2 splicing factor 3B subunit 2 lng=895 # SNP[936,l,111,P]SNP[1012,p,111,P]SNP[1071										
3											
3			z	Sequence	Incl.	L/H	Std.Err.	Fraction	Correlation	Intensity	Modifications
3	1		2	KPGDLSDELR		0.001251	33.28	0.8244	0.8617	5374	
3	2		4	LAEIGAPIQGNREELVER		3.568	0.6226	0.4565	0.4658	129.3	
3	3		3	LAEIGAPIQGNREELVER		0.5314	0.4903	0.1917	0.9356	439.9	
3											
3	Hit		Accession	Score	Mass	L/H	SD(geo)	#			
3	26		P02533	58	51875			0			
3	Keratin, type I cytoskeletal 14 OS=Homo sapiens GN=KRT14 PE=1 SV=3										
3											
3			z	Sequence	Incl.	L/H	Std.Err.	Fraction	Correlation	Intensity	Modifications
3	1		2	LEQEIATYR		6.208	1.206	0.6237	0.6025	325.7	
3											
3	Hit		Accession	Score	Mass	L/H	SD(geo)	#			
3	27		IPI00217449	57	125953	0.6655		1			
3	Gene_Symbol=GTF2I Isoform 3 of General transcription factor II-I lng=978 # SNP[992,r,143,R]SNP[1035,l,174										
3											
3			z	Sequence	Incl.	L/H	Std.Err.	Fraction	Correlation	Intensity	Modifications
3	1		2	QVEELFER	X	0.6655	0.06554	0.5268	0.8548	301.9	
3											
3	Hit		Accession	Score	Mass	L/H	SD(geo)	#			
3	28		IPI00644231	52	198441	0.7429		1			
3	Gene_Symbol=CYFIP1 Isoform 1 of Cytoplasmic FMR1-interacting protein 1 lng=1253 # SNP[1262,a,1200,P]										
3											
3			z	Sequence	Incl.	L/H	Std.Err.	Fraction	Correlation	Intensity	Modifications
3	1		2	NVIQSVLQAIR	X	0.7429	0.05851	0.5738	0.7821	199.4	
3											
3	Hit		Accession	Score	Mass	L/H	SD(geo)	#			
3	29		IPI00007402	47	191272			0			
3	Gene_Symbol=IPO7 Importin-7 lng=1038 # SNP[1058,n,111,T]SNP[1092,l,111,T]SNP[1113,a,239,D]SNP[12										
3											
3			z	Sequence	Incl.	L/H	Std.Err.	Fraction	Correlation	Intensity	Modifications
3	1		2	AIFQTIQNR		60.86	3.763	0.4717	0.5632	293.8	
3											
3	Hit		Accession	Score	Mass	L/H	SD(geo)	#			
3	30		P02769	46	71244			0			
3	Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4										
3											
3			z	Sequence	Incl.	L/H	Std.Err.	Fraction	Correlation	Intensity	Modifications
3	1		2	LVNELTEFAK		207.6	11.07	0.4916	0.8978	334.5	
3											
3	Hit		Accession	Score	Mass	L/H	SD(geo)	#			
3	31		IPI00034049	45	138953	0.8791		1			
3	Gene_Symbol=UPF1 Isoform 1 of Regulator of nonsense transcripts 1 lng=1129 # CON[1157,T,466,I]CON[11										
3											
3			z	Sequence	Incl.	L/H	Std.Err.	Fraction	Correlation	Intensity	Modifications
3	1		2	AGLSQSLFER	X	0.8791	0.03485	0.6395	0.9215	254.2	
4	Hit		Accession	Score	Mass	L/H	SD(geo)	#			
4	1		IPI00871932	244	276767	1.076	1.032	2			
4	Gene_Symbol=SPTBN1 276 kDa protein lng=2377										
4											
4			z	Sequence	Incl.	L/H	Std.Err.	Fraction	Correlation	Intensity	Modifications
4	1		2	LVSDGNINSDR	X	1.052	0.03552	0.7888	0.9909	82.41	
4	2		2	TALPAQSAATLPAR	X	1.1	0.017	0.8824	0.9969	153.9	
4	3		3	AQTLPTSVVTITSESSPGKR		0.4879	0.3267	0.7411	0.6899	99.64	(2) Deamidated (N
4											
4	Hit		Accession	Score	Mass	L/H	SD(geo)	#			
4	2		P00761	194	25078			0			
4	Trypsin OS=Sus scrofa PE=1 SV=1										
4											
4			z	Sequence	Incl.	L/H	Std.Err.	Fraction	Correlation	Intensity	Modifications
4	1		1	VATVSLPR		########	36.08	0.9602	0.9903	3379	
4	2		2	VATVSLPR		########	17.37	0.9025	0.969	8787	
4	3		2	LSSPATLNSR		641.1	0.574	0.9334	0.995	2827	
4	4		3	LGEHNIDVLEGNEQFINAAK		-461	0.3506	0.6889	0.9761	5291	
4	5		3	IITHPNFNGNTLDNDIMLIK		5.98	14.04	0.9041	0.9951	1311	(8) Deamidated (N
4											
4	Hit		Accession	Score	Mass	L/H	SD(geo)	#			
4	3		IPI00333541	154	297575	1.039	1.105	3			
4	Gene_Symbol=FLNA Isoform 1 of Filamin-A lng=2647 # CON[2650,T,44,I]CON[2682,L,695,F]CON[2739,G,1										
4											
4			z	Sequence	Incl.	L/H	Std.Err.	Fraction	Correlation	Intensity	Modifications
4	1		2	LIALLEVLSQK	X	0.9269	0.02211	0.5821	0.9946	132	
4	2		2	EATTEFSVDAR	X	1.082	0.02222	0.8335	0.9919	122.1	
4	3		3	AFGPGLQGGSAGSPAR		14.55	0.5805	0.2497	0.7118	45.21	
4	4		2	AFGPGLQGGSAGSPAR	X	1.117	0.03509	0.909	0.9972	107.3	
4											
4	Hit		Accession	Score	Mass	L/H	SD(geo)	#			
4	4		IPI00382696	93	277637	0.9838	1.088	2			
4	Gene_Symbol=FLNB Isoform 2 of Filamin-B lng=2578										
4											
4			z	Sequence	Incl.	L/H	Std.Err.	Fraction	Correlation	Intensity	Modifications
4	1		2	LIALLEVLSQK	X	0.9269	0.02211	0.5821	0.9946	132	
4	2		2	IGNLQTDLSDGLR	X	1.044	0.0215	0.5717	0.9782	124.5	
4											
4	Hit		Accession	Score	Mass	L/H	SD(geo)	#			
4	5		IPI00744706	89	282828			0			
4	Gene_Symbol=SPTAN1 cDNA FLJ61399, highly similar to Spectrin alpha chain, brain lng=2452										
4											
4			z	Sequence	Incl.	L/H	Std.Err.	Fraction	Correlation	Intensity	Modifications
4	1		4	LSDDNTIGKEEIQQR		0.5645	0.3248	0.5898	0.6839	141.1	
4	2		3	LSDDNTIGKEEIQQR		0.02575	0.881	0.8389	0.74	441.4	
4											
4	Hit		Accession	Score	Mass	L/H	SD(geo)	#			
4	6		IPI00787743	80	232096	0.9108		1			
4	Gene_Symbol=RICS Isoform 1 of Rho/Cdc42/Rac GTPase-activating protein RICS lng=2087										
4											
4			z	Sequence	Incl.	L/H	Std.Err.	Fraction	Correlation	Intensity	Modifications
4	1		2	FSDAVSAATDEER	X	0.9108	0.02373	0.8996	0.9973	80.61	
4											
4	Hit		Accession	Score	Mass	L/H	SD(geo)	#			
4	7		IPI00217182	72	399948	0.9955		1			
4	Gene_Symbol=DSP Isoform DPII of Desmoplakin lng=2271 # SNP[2282,k,1094,K]SNP[2304,n,1094,K]SNP[										
4											
4			z	Sequence	Incl.	L/H	Std.Err.	Fraction	Correlation	Intensity	Modifications
4	1		2	AITGFDDPFSGK	X	0.9955	0.0479	0.6509	0.9762	106.1	
4											
4	Hit		Accession	Score	Mass	L/H	SD(geo)	#			
4	8		P35908	63	66111			0			
4	Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KRT2 PE=1 SV=1										
4											
4			z	Sequence	Incl.	L/H	Std.Err.	Fraction	Correlation	Intensity	Modifications
4	1		2	GFSSGSAVVSGGSR		24.51	0.2319	0.5799	0.9925	122.9	
4											
4	Hit		Accession	Score	Mass	L/H	SD(geo)	#			
4	9		P13645	60	59703			0			
4	Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 SV=4										
4											
4			z	Sequence	Incl.	L/H	Std.Err.	Fraction	Correlation	Intensity	Modifications
4	1		3	ALEESNYELEGK		20.23	1.341	0.1329	0.5161	73.27	
4	2		2	ALEESNYELEGK		669.7	2.621	0.7885	0.9958	85.96	