

TOC1 clock protein phosphorylation controls complex formation with NF-YB/C to repress hypocotyl growth

Jiapei Yan, Shibai Li, Yeon Jeong Kim, Qingning Zeng, Amandine Radziejwoski, Lei Wang, Yuko Nomura, Hirofumi Nakagami and David Somers

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Corresponding author(s): David Somers (somers.24@osu.edu)

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Dear Dr. Somers,

Thank you for submitting your manuscript for consideration by the EMBO Journal. We have now received three referee reports on your manuscript, which are included below for your information

As you will see from the comments, all reviewers find the study interesting, but also highlight a number of issues that would need to be addressed before they can support publication of the manuscript. In particular, reviewers point out concerns with the depth of the analysis, such as the unclear identity of the putative TOC1-targeting kinase, and physiological relevance of a number of findings, including the effect of TOC1 phosphorylation on its interaction with PIF3 or TOC1 interaction with NF-YB/C and HDA15 for circadian clock phenotypes.

Based on the general interest expressed by the reviewers, I would like to invite you to address the comments of the referees in a revised version of your manuscript. Please note that the acceptance of the manuscript will depend on positive reviewer assessment of the revised study.

We have extended our 'scooping protection policy' beyond the usual 3 month revision timeline to cover the period required for a full revision to address the essential experimental issues. This means that competing manuscripts published during revision period will not negatively impact on our assessment of the conceptual advance presented by your study. Please contact me if you see a paper with related content published elsewhere to discuss the appropriate course of action.

When preparing your letter of response to the referees' comments, please bear in mind that this will form part of the Review Process File, and will therefore be available online to the community. For more details on our Transparent Editorial Process, please visit our website: <https://www.embopress.org/page/journal/14602075/authorguide#transparentprocess>

Please note that I will be on maternity leave from June 23, and my colleague Daniel Klimmeck, with whom I have discussed your manuscript and this decision, will take care of your manuscript in my absence. Thank you for the opportunity to consider your work for publication. We look forward to receiving your revised manuscript.

With best regards,

Ieva Gailite

Ieva Gailite, PhD
Scientific Editor
The EMBO Journal
Meyerhofstrasse 1
D-69117 Heidelberg
Tel: +4962218891309
i.gailite@embojournal.org

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9) We replaced Supplementary Information with Expanded View (EV) Figures and Tables that are collapsible/expandable online (see examples in <https://www.embopress.org/doi/10.15252/emboj.201695874>). A maximum of 5 EV Figures can be typeset. EV Figures should be cited as 'Figure EV1, Figure EV2' etc. in the text and their respective legends should be included in the main text after the legends of regular figures.

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- Additional Tables/Datasets should be labelled and referred to as Table EV1, Dataset EV1, etc. Legends have to be provided in a separate tab in case of .xls files. Alternatively, the legend can be supplied as a separate text file (README) and zipped together with the Table/Dataset file.

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Referee #1:

Yan et al., identified phosphorylation sites of Arabidopsis clock transcription factor TOC1 and the phosphorylation is required for full function of TOC1, such as binding to the target genes. Furthermore, TOC1 binds to the target genes as the trimeric complex (NF-TOC1). This is a second case for revealing phosphorylation sites of plant clock proteins. The manuscript also clarified the DNA-binding and transcriptional repression mechanism by TOC1.

The data is convincing to support their idea; however, I have some comments as below.

1. The method for identification of the TOC1 phosphorylation sites was not found in Method section.
2. The authors did not identify kinase responsible for the TOC1 phosphorylation sites; however, could the authors suggest possible kinases based on the amino acid sequences around the phosphorylation sites? Related to this, are TOC1 phosphorylation sites conserved in other Arabidopsis PRR proteins or other plants' TOC1?
3. Early phasing of 5X may involve indirect feedback regulation of TOC1 promoter activity by 5X (e.g., Figure 6). Time course analysis of 5X and WT TOC1 under the constitutive promoter will suggest importance of phosphorylation for TOC1 protein accumulation profile in more detail.

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The manuscript by Yan et al provided a comprehensive set of data to interrogate how the post-translational modification phosphorylation affects the repressor role of a central clock protein TOC1. The story started by the mapping of the 5 phosphorylation sites of TOC1 stimulated by the co-expression of PRR5 in a heterologous system. Evidence shown in this study implied the phosphorylation of TOC1 will enhance the interaction of TOC1 and PIF3 for the repression of PHG genes that promote the pre-dawn hypocotyl elongation. The NF-YB/C complex, on the other hand, can stabilize TOC1 on the PHG promoter- and also recruit HDA15 to achieve a highly coordinated repressing role on PHGs. In general, this study offers multiple angles of experiments to delineate the regulatory roles of TOC1 phosphorylation on rhythmic hypocotyl elongation, as well as how the TOC-NF complex is formed to regulate PHG genes. Before this study is considered for publication, a few points should be addressed or clarified.

1. This study also examined the role of PRR5 in the repressor complex. Although this extended the characterization of the CCT-domain-containing PRR proteins in regulating PHGs, it diffuses the focus on the regulatory role of TOC1 protein phosphorylation. It also raises a question whether the phosphorylation sites discovered on TOC1 are also conserved in the other PRRs?
2. The authors claimed that S175 and 5X share similar physiological impacts and S175 is likely the most important phosphorylation site. However, these two forms seemed to impose different impacts when used to complement *toc1* mutant. For example, despite they partially complement the short period length under free running condition, S175A can well complement the hypocotyl length under most fluences of cR, possibly via rescuing the expressions of some PHGs (Fig. S4), but 5X only partially complement the long hypocotyl phenotype of *toc1* mutant (Fig. 2). As for the early flowering time in *toc1*, 5X appeared to rescue this phenotype more effectively than S175A (Fig. S3). It might be premature for the authors to conclude S175A and 5X are functionally similar. It would be helpful to discuss whether some of the differences were owing to the phosphorylation of the other 4 phosphosites (T135 S194 S201 and S204) under different physiological conditions examined.
3. The authors concluded that "phosphomutants derepress the pre-dawn-phased hypocotyl-growth-related genes (PHGs)". Could this simply reflect the advanced circadian phase in these transgenic lines, considering they cannot complement the early phase phenotype of the parental line *toc1*?
4. In Figure 5, the authors concluded that the phosphorylation of TOC1 enhances the interaction between TOC1 and PIF3, and the binding of TOC1 to the PHGs promoters. These two conclusions were drawn based on experiments conducted in *N. benthamiana* and in protoplasts, both with high levels of exogenous proteins. Whether conclusions drawn stand at the physiological concentration of TOC1, especially for the PIF3-independent association of TOC1 to the PHG promoter, could be confirmed in transgenic lines or at least discussed.
5. Similarly, results in Figure 7 suggested wild-type TOC1 and 5X have comparable interaction affinity with NF-YB/C dimer. These conclusions were based on yeast 2-hybrid or heterologous transient experiments in *N. benthamiana*, both with high protein expression levels and may mask the differential affinities of TOC1 and 5X with the NF-YB/C dimer? A more quantitative yeast 2-hybrid assay or biochemical characterization might be better approaches to reveal if the phosphorylation of TOC1 participate in the interaction of TOC1 with NF-YB/C dimer, in addition to PIF3.

Minor points:

1. The title for Figure 3. "Mutations in 5X and S175A result in shorter period, advanced phase and abnormal photoperiodic hypocotyl growth...". More precisely, it should be "Mutations in 5X and S175 cannot rescue the *toc1* defects in period length, expression phase and".
2. Fig. 6 C and D were not directly relevant to the key element emphasized in this paper.
3. Results obtained for PRR5 could be integrated to Figure 11 to emphasize the sequential repression of PHGs by PRRs?

Referee #3:

In this manuscript, Yan et al set out to investigate the roles of phosphorylation on regulation of the clock protein TOC1. The manuscript is notable for the large number of experiments presented and the care with which they were done. With a few exceptions (see below), the authors are careful in their conclusions and the manuscript should be of interest to plant circadian biologists and photobiologists.

The authors first use mass spectrometry to identify residues phosphorylated on the N-terminus of the clock protein TOC1 when it was transiently expressed in *Nicotiana benthamiana*. The authors state that 5 residues were found to be phosphorylated, but do not indicate whether any other phosphorylated sites were identified. The methods and results of the mass spec experiment are not included in the manuscript, and there is no indication that the mass spec data were uploaded to a public repository. At a minimum, details of the experiment should be included in the methods section and more information about the findings should be presented.

The authors go on to generate versions of TOC1 in which the S and T residues found to be phosphorylated in *N. benthamiana* are mutated to A, and examine the effects of these mutations on: protein mobility in gels; association with NF-Y transcription factors; protein stability; and ability to rescue circadian, hypocotyl, and gene expression phenotypes in *toc1* mutant plants. They find that the S/T to A mutants have reduced ability to complement hypocotyl and circadian phenotypes in *toc1* mutants and commensurately have modest to large effects on a variety of molecular phenotypes as well. For example, they find that the TOC1-S175A mutant protein is degraded slightly faster than wild-type TOC1, leading them to state "These results indicate TOC1 protein stability is enhanced by phosphorylation". However, it is also possible that this mutation has some effect on protein function that is unrelated to the ability of S175 to be phosphorylated. The authors should be more careful in their language, using words such as "suggest" in sentences like the above rather than "indicate". (These types of statements are found throughout the manuscript, including the abstract, and all should be edited.)

Perhaps the finding that will be of greatest interest to the field is the demonstration that TOC1 associates with NF-YB/NF-YC subunits in vivo, confirming previous reports of in vitro associations. Surprisingly, however, the authors do not report whether *nf-yc349* triple mutants have circadian phenotypes (although they do report hypocotyl phenotypes for this mutant). They also do not report the circadian phenotypes of *toc1 nf-yc349* quadruple mutants. These results would help readers evaluate the general importance of TOC1/NF-Y subunit interactions in plants and should be included in the manuscript. Similarly, circadian phenotypes of the *hda15* mutants should be included.

Finally, I am a little disappointed that the authors didn't take advantage of published genomic data (transcriptome and ChIP-seq datasets) to examine the degree of overlap between transcripts regulated by TOC1/PRRs and NF-Y proteins. Although these comparisons would be of great interest, they aren't essential for this manuscript.

Specific comments:

1. The authors conclude that phosphorylation of TOC1 alters its degradation rate (see above), yet they did not actually calculate the degradation rates of the different TOC1 alleles. They should determine the half-lives of the different TOC1 proteins and investigate whether they are significantly different from each other.
2. In the abstract, the authors conclude that the TOC1-5x mutant has de-repressed hypocotyl growth in the middle of the night. They did not actually investigate whether hypocotyl growth is affected at specific times of day; this statement should be removed.
3. on p. 6, "Wild-type TOC1 and T135A fully rescued the long hypocotyl in *toc1-101* at all fluence rates tested, whereas 5X and S175A failed to complement, especially at low fluence rates (Fig. 2a-d)." "failed to complement" should be changed to "partially complemented" or "failed to fully complement"
4. on p. 8, "TOC1:5X failed to repress their expression" should be changed to "failed to fully repress" or "did not repress to wild-type levels"
5. on p. 17, "hypocotyl elongation under constant red light with sequential fluence rates showed slightly longer hypocotyls in *prp5* than Col-0," should be modified, as a (modest) difference was only detected at one of the six fluence rates tested.
6. Figure 8 doesn't have a panel (f); the legend should be changed accordingly.
7. In Figures 10c and 10d, the authors examine gene expression in Col, *toc1*, *prp5*, and *toc1 prp5* mutants at ZT18 and conclude that the *prp5* and *toc1* mutations have synergistic effects on the expression of the three genes assayed. However, they do not report the period phenotype of *prp5 toc1* plants, which is likely significantly shorter than that of *toc1* mutants. If so, the advanced phase of *prp5 toc1* mutants relative to *toc1* mutants could partially or fully account for the observed differences in gene expression. The authors could address this either by showing that *prp5 toc1* and *toc1* have similar clock phenotypes or by examining gene expression in the two mutants over time.

Reply to Reviewer comments.

We greatly appreciate the time and effort the reviewers put into reading and critiquing our manuscript. Below we have addressed each of their comments and queries.

Referee #1:

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The data is convincing to support their idea; however, I have some comments as below.

1. The method for identification of the TOC1 phosphorylation sites was not found in Method section.

The Mass spectrometry methods have been added to the Methods section

2. The authors did not identify kinase responsible for the TOC1 phosphorylation sites; however, could the authors suggest possible kinases based on the amino acid sequences around the phosphorylation sites? Related to this, are TOC1 phosphorylation sites conserved in other Arabidopsis PRR proteins or other plants' TOC1?

We have added comment in the Discussion (lines 478-481) on potential kinases based on the peptide sequences surrounding the sites. Additionally, we have added an expanded view figure (Fig EV5) showing how unique the five sites are to TOC1 and the high degree of conservation of S175 among TOC1 orthologs in other species. We thank this reviewer for making this suggestion as it has strengthened the significance of these sites for TOC1 function.

3. Early phasing of 5X may involve indirect feedback regulation of TOC1 promoter activity by 5X (e.g., Figure 6). Time course analysis of 5X and WT TOC1 under the constitutive promoter will suggest importance of phosphorylation for TOC1 protein accumulation profile in more detail.

Appendix Fig S1 shows the expression level of TOC1 WT and 5X driven by the 35S promoter, and Fig 2E, F and Fig 3 show the effects of constitutive expression of both these TOC1 phosphoforms on hypocotyl (Fig. 2E, 2F, 3A), period (Fig.3B). The different effects of 35S::TOC1 WT and 35S::5X on these 3 phenotypes is extremely similar (except constitutive expression of TOC1 WT drastically suppresses hypocotyl elongation and lengthens period) to what we observed for expression under the native

promoter, suggesting that phasing differences are not responsible for the phenotypic differences between TOC1 WT and 5X.

Referee #2:

The manuscript by Yan et al provided a comprehensive set of data to interrogate how the post-translational modification phosphorylation affects the repressor role of a central clock protein TOC1. The story started by the mapping of the 5 phosphorylation sites of TOC1 stimulated by the co-expression of PRR5 in a heterologous system. Evidence shown in this study implied the phosphorylation of TOC1 will enhance the interaction of TOC1 and PIF3 for the repression of PHG genes that promote the pre-dawn hypocotyl elongation. The NF-YB/C complex, on the other hand, can stabilize TOC1 on the PHG promoter- and also recruit HDA15 to achieve a highly coordinated repressing role on PHGs. In general, this study offers multiple angles of experiments to delineate the regulatory roles of TOC1 phosphorylation on rhythmic hypocotyl elongation, as well as how the TOC-NF complex is formed to regulate PHG genes. Before this study is considered for publication, a few points should be addressed or clarified.

1. This study also examined the role of PRR5 in the repressor complex. Although this extended the characterization of the CCT-domain-containing PRR proteins in regulating PHGs, it diffuses the focus on the regulatory role of TOC1 protein phosphorylation. It also raises a question whether the phosphorylation sites discovered on TOC1 are also conserved in the other PRRs?

We chose to include the role of PRR5 to help explain the results of the continued presence HDA15 and NF-YC9 at the PIL1 target promoter in the *toc1* single mutant (Fig. 9A and B). As we suspected, when PRR5 was also removed (*prp5 toc1* double mutant) both HDA15 and NF-YC9 completely failed to bind to the PIL1 promoter. Thus we were able to better understand how these two PRR proteins, which are expressed so closely in time, are in some cases able to work together. The reviewer makes a good point about conservation of sites, and we have added to the expanded view figure (Fig EV5) an alignment showing that none of the 5 phosphosites are conserved among TOC1 and the other PRRs. However, S175 is absolutely conserved among all TOC1-like genes examined, including the microalgae *Ostreococcus*, supporting our findings on the importance of this residue for TOC1 function.

2. The authors claimed that S175 and 5X share similar physiological impacts and S175 is likely the most important phosphorylation site. However, these two forms seemed to impose different impacts when used to complement *toc1* mutant. For example, despite they partially complement the short period length under free running condition, S175A can well complement the hypocotyl length under most fluences of cR, possibly via rescuing the expressions of some PHGs (Fig. S4), but 5X only partially complement the long hypocotyl phenotype of *toc1* mutant (Fig. 2). As for the early flowering time in *toc1*, 5X appeared to rescue this phenotype more effectively than S175A (Fig. S3). It might

be premature for the authors to conclude S175A and 5X are functionally similar. It would be helpful to discuss whether some of the differences were owing to the phosphorylation of the other 4 phosphosites (T135 S194 S201 and S204) under different physiological conditions examined.

Lines 487-500 discuss the similarities and differences between the S175A mutant phenotypes and the 5X phenotypes. While 5X and S175 are not identical, they are very similar. We have added some extra comments in this section to further emphasize the likelihood that the other sites contribute to TOC1 functionality.

3. The authors concluded that "phosphomutants derepress the pre-dawn-phased hypocotyl-growth-related genes (PHGs)". Could this simply reflect the advanced circadian phase in these transgenic lines, considering they cannot complement the early phase phenotype of the parental line *toc1*?

For the chromatin IP experiments we intentionally chose a time point (ZT 14) where the protein abundance of WT TOC1 and 5X were the same (see Fig 6A) to mitigate against this potential complication. Fig 5C, 7C, 10C and Appendix Fig S8 were all done at ZT14. All consistently show less binding of 5X to the promoters than WT TOC1, consistent with derepression of those genes, since TOC1 is known to act as a repressor of PIF activation.

4. In Figure 5, the authors concluded that the phosphorylation of TOC1 enhances the interaction between TOC1 and PIF3, and the binding of TOC1 to the PHGs promoters. These two conclusions were drawn based on experiments conducted in *N. benthamiana* and in protoplasts, both with high levels of exogenous proteins. Whether conclusions drawn stand at the physiological concentration of TOC1, especially for the PIF3-independent association of TOC1 to the PHG promoter, could be confirmed in transgenic lines or at least discussed.

While the protein-protein interaction tests were done by transient expression in *N. benthamiana*, the ChIPs at the PHGs were all done in stable transgenics at ZT14 to ensure balanced WT TOC1 and 5X protein levels. We also note, that if strong constitutive expression of the two partners results in reproducible and significant differences (as in the case with PIF3-TOC1 WT and 5X tests) then it is likely that these will also bear out at lower levels of expression, when protein densities are lower. All of our results are comparative -- WT vs. 5X -- and high densities of proteins are more likely to result in a loss of sensitivity when such comparative analyses are performed due to the transient nature of the interaction between partners being concentration dependent. We also added a new ChIP results in Fig 5D using native promoter TOC1 transgenics to compare the residence of TOC1 at the physiological concentration on PHG promoters in presence vs. absence of PIF3/4/5. The results suggest that TOC1 binds to the PHG promoter independent to PIF3/4/5, although we can't exclude the possibility that other PIFs, such as PIF1 and PIF7, may anchor TOC1 to the target promoter.

5. Similarly, results in Figure 7 suggested wild-type TOC1 and 5X have comparable interaction affinity with NF-YB/C dimer. These conclusions were based on yeast 2-hybrid or heterologous transient experiments in *N. benthamiana*, both with high protein expression levels and may mask the differential affinities of TOC1 and 5X with the NF-YB/C dimer? A more quantitative yeast 2-hybrid assay or biochemical characterization might be better approaches to reveal if the phosphorylation of TOC1 participate in the interaction of TOC1 with NF-YB/C dimer, in addition to PIF3.

We quantitated the Y2H interaction between the NF-Y subunits and TOC1 WT and 5X (Appendix Fig S6F) and these findings supported the conclusions drawn from the visual assessment in 7A.

Minor points:

1. The title for Figure 3. "Mutations in 5X and S175A result in shorter period, advanced phase and abnormal photoperiodic hypocotyl growth...". More precisely, it should be "Mutations in 5X and S175 cannot rescue the *toc1* defects in period length, expression phase and".

We have adjusted this wording (lines 979-980)

2. Fig. 6 C and D were not directly relevant to the key element emphasized in this paper.

The primary focus of the work was to understand how phosphorylation of TOC1 affects its role in plant development, at the phenotypic and molecular level. Our observation of a reduction in TOC1 homodimerization due to the 5X mutations is relevant to that goal, even though we have not directly tied it to affecting PIF3 function and hypocotyl length. We have moved this section to Appendix Fig S5.

3. Results obtained for PRR5 could be integrated to Figure 11 to emphasize the sequential repression of PHGs by PRRs?

The role of PRR5 in controlling hypocotyl length was not explored as extensively as for TOC1 as we were primarily interested in learning whether it might act together with TOC1 in some cases. This was borne out in Figure 9 where HDA15 and NF-YC9 presence at the PIL1 promoter was enhanced by PRR5, but apparently not so at the two other target genes. Hence, we elected to remain focused on TOC1 alone in Figure 11 since the TOC1-PRR5 relationship appears gene specific and is not so clearly connected to the main theme of a TOC1-PIF3 molecular complex.

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We note in the main text (line 101) that we only focused on the first 242 aa of TOC1, primarily because previously published findings indicated the importance of this region in some protein-protein interactions (Wang et al., doi: 10.1038/emboj.2010.76). We don't have information on downstream regions of TOC1.

The mass spectrometry methods have been added to the Methods section. Additionally, the mass spec data for 4 of the 5 phosphorylated sites have been deposited at the below link for access for editor and reviewers

<https://repository.jpostdb.org/preview/92338156760ad23d4b6673> (Access key: 6074) which will be made available in the final version of the paper as well.

Unfortunately, the raw MS data for T135 is no longer available from the MS facility here at OSU as that work was done too many years ago. We are providing the Mascot files here for the reviewers to peruse and can include them as part of the Supplementary data if the reviewer deems them to be sufficiently informative.

The authors go on to generate versions of TOC1 in which the S and T residues found to be phosphorylated in *N. benthamiana* are mutated to A, and examine the effects of these mutations on: protein mobility in gels; association with NF-Y transcription factors; protein stability; and ability to rescue circadian, hypocotyl, and gene expression phenotypes in *toc1* mutant plants. They find that the S/T to A mutants have reduced ability to complement hypocotyl and circadian phenotypes in *toc1* mutants and commensurately have modest to large effects on a variety of molecular phenotypes as well. For example, they find that the TOC1-S175A mutant protein is degraded slightly faster than wild-type TOC1, leading them to state "These results indicate TOC1 protein stability is enhanced by phosphorylation". However, it is also possible that this mutation has some effect on protein function that is unrelated to the ability of S175 to be phosphorylated. The authors should be more careful in their language, using words such as "suggest" in sentences like the above rather than "indicate". (These types of

statements are found throughout the manuscript, including the abstract, and all should be edited.)

We have adjusted the wording throughout, including changing the wording of the subheadings to remove direct reference to phosphorylations as causative.

Perhaps the finding that will be of greatest interest to the field is the demonstration that TOC1 associates with NF-YB/NF-YC subunits in vivo, confirming previous reports of in vitro associations. Surprisingly, however, the authors do not report whether *nf-yc349* triple mutants have circadian phenotypes (although they do report hypocotyl phenotypes for this mutant). They also do not report the circadian phenotypes of *toc1 nf-yc349* quadruple mutants. These results would help readers evaluate the general importance of TOC1/NF-Y subunit interactions in plants and should be included in the manuscript. Similarly, circadian phenotypes of the *hda15* mutants should be included.

We have conducted new experiments to address the circadian phenotypes of the 3 classes of mutants requested, although the focus of this paper is TOC1 and its molecular role in hypocotyl length control.

The period of the *nf-yc349* and *nf-yc349toc1* are now in Fig 8C. The period of the *hda15* and *toc1hda15* mutants are in Fig 8D. The period results are broadly consistent with the hypocotyl length findings: an additivity (extra period shortening) in the case of *nf-yc349toc1* and little effect on period in the *toc1hda15* mutant compared to *toc1*. This commented on in lines 296-305

Finally, I am a little disappointed that the authors didn't take advantage of published genomic data (transcriptome and ChIP-seq datasets) to examine the degree of overlap between transcripts regulated by TOC1/PRRs and NF-Y proteins. Although these comparisons would be of great interest, they aren't essential for this manuscript.

While we agree with the reviewer that such a comparison would be interesting and potentially fruitful, it is beyond the scope of the already very data-rich manuscript. Additionally, datasets with exactly the same growth conditions are not available among the comparisons requested.

Specific comments:

1. The authors conclude that phosphorylation of TOC1 alters its degradation rate (see above), yet they did not actually calculate the degradation rates of the different TOC1 alleles. They should determine the half-lives of the different TOC1 proteins and investigate whether they are significantly different from each other.

We have added this data to Fig 6 B and C. The half-life of 5X and S175A mutant proteins are similar to each other and significantly different from WT TOC1 and T135A.

2. In the abstract, the authors conclude that the TOC1-5x mutant has de-repressed hypocotyl growth in the middle of the night. They did not actually investigate whether hypocotyl growth is affected at specific times of day; this statement should be removed.

We have adjusted the abstract to indicate that deficiencies in 5X function leads to a net de-repression of hypocotyl growth, without reference to time of day/night. (line 31)

3. on p. 6, "Wild-type TOC1 and T135A fully rescued the long hypocotyl in *toc1-101* at all fluence rates tested, whereas 5X and S175A failed to complement, especially at low fluence rates (Fig. 2a-d)." "failed to complement" should be changed to "partially complemented" or "failed to fully complement"

The wording has been adjusted. (line 129)

4. on p. 8, "TOC1:5X failed to repress their expression" should be changed to "failed to fully repress" or "did not repress to wild-type levels"

The wording has been adjusted.(line 168)

5. on p. 17, "hypocotyl elongation under constant red light with sequential fluence rates showed slightly longer hypocotyls in *prp5* than Col-0," should be modified, as a (modest) difference was only detected at one of the six fluence rates tested.

We have made this adjustment.(line 383)

6. Figure 8 doesn't have a panel (f); the legend should be changed accordingly.

We apologize for this oversight and have made the adjustment.

7. In Figures 10c and 10d, the authors examine gene expression in Col, *toc1*, *prp5*, and *toc1 prp5* mutants at ZT18 and conclude that the *prp5* and *toc1* mutations have synergistic effects on the expression of the three genes assayed. However, they do not report the period phenotype of *prp5 toc1* plants, which is likely significantly shorter than that of *toc1* mutants. If so, the advanced phase of *prp5 toc1* mutants relative to *toc1* mutants could partially or fully account for the observed differences in gene expression. The authors could address this either by showing that *prp5 toc1* and *toc1* have similar clock phenotypes or by examining gene expression in the two mutants over time.

We now report the period of the *toc1prp5* mutant in Appendix Figure S10. The double mutant period is only 0.7 hrs shorter than the *toc1* single mutant under constant white light. Given that our gene expression and ChIP assays were done under entraining conditions (8:16; light:dark cycles) it is likely that the phasing difference between these

two backgrounds of relevant clock-controlled factors is relatively small and not likely to account for the differences in gene expression in Fig. 10D. This is now noted in lines 382-388.

Figure 10C shows ChIP results (at ZT14 when TOC1 WT and 5X protein levels are similar; Fig. 6A) and the protein blot in Fig EV 4D also shows similar TOC1 abundance in *toc1* vs *prp5toc1* mutant background. The period difference between the TOC1:TOC1/*toc1* and TOC1:TOC1/*p5t1* plants should be approximately the same as the period of the *prp5* mutant, which is close to the period of the 5X and S175A mutants (since TOC1:TOC1 rescues the *toc1* single mutant period phenotype). Therefore the slightly greater chromatin residence of TOC1 WT at these promoters in the *prp5 toc1* double mutant, relative to TOC1 WT residence in the *toc1* single mutant, is unlikely due to the shorter period of the *prp5* mutant background and more likely is due to the absence of PRR5 protein. Meaning it may likely be competing with TOC1 for occupancy at these two promoters.

Mascot File for T135 phosphorylation is appended

Mascot Search Results

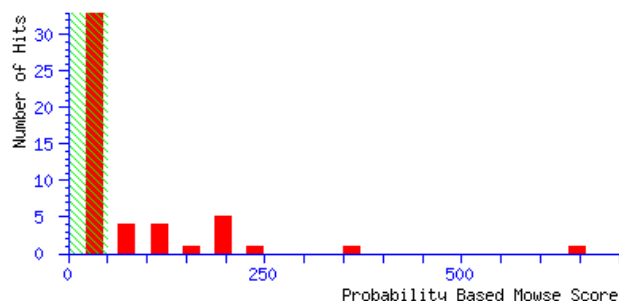
User : Liwen
 Email : zhang.287@osu.edu
 Search title : 12560
 MS data file : E:\mgfs to process\13729_TOC1_TP.mgf
 Database : SwissProt 55.1 (359942 sequences; 129199355 residues)
 Timestamp : 15 Apr 2008 at 14:54:35 GMT
 Protein hits : [APRR1_ARATH](#) Two-component response regulator-like APRR1 - Arabidopsis thaliana (Mouse-ear cress)
 [IGHG1_HUMAN](#) Ig gamma-1 chain C region - Homo sapiens (Human)
 [KAC_HUMAN](#) Ig kappa chain C region - Homo sapiens (Human)
 [TRYP_PIG](#) Trypsin precursor - Sus scrofa (Pig)
 [IGHG4_HUMAN](#) Ig gamma-4 chain C region - Homo sapiens (Human)
 [GST26_SCHJA](#) Glutathione S-transferase class-mu 26 kDa isozyme - Schistosoma japonicum (Blood fluke)
 [POLG_HRV14](#) Genome polyprotein [Contains: Protein VP0 - Human rhinovirus 14 (HRV-14)
 [RBL_NICDE](#) Ribulose biphosphate carboxylase large chain precursor - Nicotiana debneyi (Debney's tobacco)
 [KAC4_RABIT](#) Ig kappa-b4 chain C region - Oryctolagus cuniculus (Rabbit)
 [LAC_HUMAN](#) Ig lambda chain C regions - Homo sapiens (Human)
 [CASA1_BOVIN](#) Alpha-S1-casein precursor - Bos taurus (Bovine)
 [MUCM_RABIT](#) Ig mu chain C region membrane-bound form - Oryctolagus cuniculus (Rabbit)
 [ETV6_HUMAN](#) Transcription factor ETV6 - Homo sapiens (Human)
 [GC_RABIT](#) Ig gamma chain C region - Oryctolagus cuniculus (Rabbit)
 [K2C71_MOUSE](#) Keratin, type II cytoskeletal 71 - Mus musculus (Mouse)
 [ARSG_CANFA](#) Arylsulfatase G precursor - Canis familiaris (Dog)
 [KV302_HUMAN](#) Ig kappa chain V-III region SIE - Homo sapiens (Human)
 [SEC2_ECOLI](#) Protein-export membrane protein secD - Escherichia coli (strain K12)

SwissProt [Decoy](#) False discovery rate

Peptide matches above identity threshold	40	0	0.00 %
Peptide matches above homology or identity threshold	61	4	6.56 %

Probability Based Mowse Score

Ions score is $-10 \cdot \log(P)$, where P is the probability that the observed match is a random event.
 Individual ions scores > 49 indicate identity or extensive homology ($p < 0.05$).
 Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Peptide Summary Report

Format As Peptide Summary [Help](#)
 Significance threshold p< 0.05 Max. number of hits AUTO
 Standard scoring ☒ MudPIT scoring ☐ Ions score or expect cut-off 20 Show sub-sets 0
 Show pop-ups ☒ Suppress pop-ups ☐ Sort unassigned Decreasing Score Require bold red ☒
Select All Select None Search Selected ☐ **Error tolerant** Archive Report

1. [APRR1_ARATH](#) Mass: 69494 Score: 648 Queries matched: 23 emPAI: 0.60
 Two-component response regulator-like APRR1 - Arabidopsis thaliana (Mouse-ear cress)

☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
☒ 485	418.7190	835.4234	835.3824	0.0410	0	53	0.016	1	K.GDGFIDR.S
☒ 486	418.8240	835.6334	835.3824	0.2510	0	(22)	22	1	K.GDGFIDR.S
☒ 487	419.0840	836.1534	835.3824	0.7710	0	(32)	2.3	1	K.GDGFIDR.S

✓	570	474.0540	946.0934	945.5140	0.5795	0	35	1.6	1	R.IPVIMMSR.Q
✓	595	506.7640	1011.5134	1011.5601	-0.0466	0	35	1.3	1	R.QDEVVVVK.C
✓	596	507.0490	1012.0834	1011.5601	0.5234	0	(30)	5.4	1	R.QDEVVVVK.C
✓	632	552.1990	1102.3834	1101.6151	0.7684	1	36	1.1	1	R.RIPVIMMSR.Q
✓	679	624.5540	1247.0934	1246.5942	0.4993	0	(70)	0.00048	1	R.NSNPAQFSSAPK.K
✓	680	624.6040	1247.1934	1246.5942	0.5993	0	73	0.00025	1	R.NSNPAQFSSAPK.K
✓	681	625.1040	1248.1934	1246.5942	1.5993	0	(21)	45	1	R.NSNPAQFSSAPK.K
✓	757	439.5120	1315.5142	1314.7659	0.7482	0	(37)	0.79	1	K.LGAADYLVKPLR.T
✓	758	658.7840	1315.5534	1314.7659	0.7875	0	68	0.00072	1	K.LGAADYLVKPLR.T
✓	759	439.5987	1315.7742	1314.7659	1.0082	0	(35)	1.4	1	K.LGAADYLVKPLR.T
✓	778	675.1190	1348.2234	1347.6711	0.5524	0	(91)	3.8e-006	1	K.IGESSAFFTYVK.S
✓	779	675.1190	1348.2234	1347.6711	0.5524	0	92	3.3e-006	1	K.IGESSAFFTYVK.S
✓	839	703.5790	1405.1434	1405.7201	-0.5767	0	99	6.5e-007	1	K.FQVVASEGINNTK.Q
✓	840	703.8390	1405.6634	1405.7201	-0.0567	0	(95)	1.2e-006	1	K.FQVVASEGINNTK.Q
✓	843	704.1190	1406.2234	1405.7201	0.5033	0	(93)	2.5e-006	1	K.FQVVASEGINNTK.Q
✓	844	704.1690	1406.3234	1405.7201	0.6033	0	(89)	6e-006	1	K.FQVVASEGINNTK.Q
✓	1048	598.7020	1793.0842	1792.8120	0.2722	0	39	0.57	1	R.TNELLNLWIMWR.R + Phospho (ST)
✓	1076	627.1820	1878.5242	1877.8512	0.6730	0	32	3.4	1	R.NYQEGNMNIPQVAMNR.S
✓	1125	676.9320	2027.7742	2025.9981	1.7761	0	38	0.8	1	R.TNGQDPPLVDGNGSLHLHR.G
✓	1203	735.2953	2202.8642	2202.0566	0.8076	0	65	0.0015	1	R.GNLSHQENWSVATAPVHAR.D

2. [IGHG1_HUMAN](#) Mass: 36596 Score: 342 Queries matched: 8 emPAI: 0.63

Ig gamma-1 chain C region - Homo sapiens (Human)

☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
✓ 482	418.5190	835.0234	834.4269	0.5965	0	34	1.7	1	K.DTLMISR.T
✓ 648	581.4340	1160.8534	1160.6223	0.2311	0	50	0.048	1	K.NQVSLTCLVK.G
✓ 658	594.0940	1186.1734	1185.6394	0.5341	0	43	0.28	1	K.GPSVFPLAPSSK.S
✓ 659	594.3690	1186.7234	1185.6394	1.0841	0	(23)	23	1	K.GPSVFPLAPSSK.S
✓ 764	661.6090	1321.2034	1320.6708	0.5327	0	72	0.00031	1	K.STSGGTAALGCLVK.D
✓ 1008	560.3887	1678.1442	1676.7947	1.3495	0	25	16	1	K.FNMYVDGVEVHNAK.T
✓ 1070	937.7140	1873.4134	1872.9146	0.4989	0	73	0.00027	1	K.TTPVLDSGDSFFLYSK.L
✓ 1190	714.0653	2139.1742	2138.0202	1.1540	0	49	0.058	1	R.TPEVTCVVVDVSHEDPEVK.F

3. [KAC_HUMAN](#) Mass: 11773 Score: 238 Queries matched: 6 emPAI: 2.20

Ig kappa chain C region - Homo sapiens (Human)

☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
✓ 903	752.0390	1502.0634	1501.7512	0.3123	0	66	0.0014	1	K.DSTYSLSSTLTLSK.A
✓ 1072	625.8953	1874.6642	1874.9197	-0.2555	0	27	11	1	K.VYACEVTHQLSSPVTK.S
✓ 1103	973.8090	1945.6034	1945.0197	0.5838	0	78	7.7e-005	1	- .TVAAPSVFIFPPSDEQLK.S
✓ 1104	649.7787	1946.3142	1945.0197	1.2945	0	(49)	0.072	1	- .TVAAPSVFIFPPSDEQLK.S
✓ 1184	712.6620	2134.9642	2134.9614	0.0027	0	(28)	6.6	1	K.VDNALQSGNSQESVTEQDSK.D
✓ 1185	713.0253	2136.0542	2134.9614	1.0927	0	67	0.00092	1	K.VDNALQSGNSQESVTEQDSK.D

4. [TRYP_PIG](#) Mass: 25078 Score: 208 Queries matched: 23 emPAI: 1.03

Trypsin precursor - Sus scrofa (Pig)

☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
✓ 491	421.7490	841.4834	841.5022	-0.0187	0	(44)	0.17	1	R.VATVSLPR.S
✓ 492	842.5700	841.5627	841.5022	0.0606	0	(32)	2.6	1	R.VATVSLPR.S
✓ 493	421.8240	841.6334	841.5022	0.1313	0	(43)	0.2	1	R.VATVSLPR.S
✓ 494	421.8390	841.6634	841.5022	0.1613	0	(46)	0.11	1	R.VATVSLPR.S
✓ 495	421.8390	841.6634	841.5022	0.1613	0	55	0.014	1	R.VATVSLPR.S
✓ 496	421.9490	841.8834	841.5022	0.3813	0	(37)	1	1	R.VATVSLPR.S
✓ 497	421.9840	841.9534	841.5022	0.4513	0	(41)	0.44	1	R.VATVSLPR.S
✓ 498	421.9990	841.9834	841.5022	0.4813	0	(34)	2.1	1	R.VATVSLPR.S
✓ 499	422.0340	842.0534	841.5022	0.5513	0	(45)	0.18	1	R.VATVSLPR.S
✓ 500	422.0340	842.0534	841.5022	0.5513	0	(44)	0.21	1	R.VATVSLPR.S

✓	501	422.0490	842.0834	841.5022	0.5813	0	(43)	0.25	1	R.VATVSLPR.S
✓	502	422.0590	842.1034	841.5022	0.6013	0	(55)	0.018	1	R.VATVSLPR.S
✓	503	422.0840	842.1534	841.5022	0.6513	0	(44)	0.2	1	R.VATVSLPR.S
✓	504	422.1040	842.1934	841.5022	0.6913	0	(38)	0.78	1	R.VATVSLPR.S
✓	505	422.1140	842.2134	841.5022	0.7113	0	(51)	0.037	1	R.VATVSLPR.S
✓	506	422.1340	842.2534	841.5022	0.7513	0	(37)	0.88	1	R.VATVSLPR.S
✓	608	522.9290	1043.8434	1044.5564	-0.7129	0	51	0.04	1	K.LSSPATLNSR.V
✓	610	523.5040	1044.9934	1044.5564	0.4371	0	(51)	0.045	1	K.LSSPATLNSR.V
✓	611	523.5090	1045.0034	1044.5564	0.4471	0	(36)	1.2	1	K.LSSPATLNSR.V
✓	612	523.5140	1045.0134	1044.5564	0.4571	0	(36)	1.4	1	K.LSSPATLNSR.V
✓	1204	737.7187	2210.1342	2210.0967	0.0374	0	(73)	0.00025	1	R.LGEHNIDVLEGNEQFINAAK.I
✓	1205	1106.3090	2210.6034	2210.0967	0.5067	0	102	3.4e-007	1	R.LGEHNIDVLEGNEQFINAAK.I
✓	1206	738.0987	2211.2742	2210.0967	1.1774	0	(61)	0.0039	1	R.LGEHNIDVLEGNEQFINAAK.I

5. [IGHG4_HUMAN](#) Mass: 36431 Score: 198 Queries matched: 4 emPAI: 0.34
Ig gamma-4 chain C region - Homo sapiens (Human)

☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
482	418.5190	835.0234	834.4269	0.5965	0	34	1.7	1	K.DTLMISR.T
648	581.4340	1160.8534	1160.6223	0.2311	0	50	0.048	1	K.NQVSLTCLVK.G
✓ 739	644.6090	1287.2034	1286.6442	0.5593	0	40	0.49	1	K.GPSVFPLAPCSR.S
✓ 854	712.3640	1422.7134	1422.7024	0.0110	0	73	0.0002	1	R.STSESTAALGCLVK.D

Proteins matching the same set of peptides:

[IGHG2_HUMAN](#) Mass: 36489 Score: 193 Queries matched: 4
Ig gamma-2 chain C region - Homo sapiens (Human)

6. [GST26_SCHJA](#) Mass: 25710 Score: 184 Queries matched: 4 emPAI: 0.32
Glutathione S-transferase class-mu 26 kDa isozyme - Schistosoma japonicum (Blood fluke)

☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
✓ 576	482.5840	963.1534	962.5225	0.6309	0	43	0.21	1	M.SPILGYWK.I
✓ 607	517.1590	1032.3034	1031.5797	0.7237	0	56	0.011	1	K.LTQSMAIR.Y
✓ 646	575.3740	1148.7334	1148.6328	0.1006	0	48	0.064	1	R.LLLEYLEEK.Y
✓ 657	592.1840	1182.3534	1181.6768	0.6767	1	36	1.1	1	K.RIEAIPQIDK.Y

7. [POLG_HRV14](#) Mass: 245345 Score: 183 Queries matched: 4 emPAI: 0.05
Genome polyprotein [Contains: Protein VP0 - Human rhinovirus 14 (HRV-14)]

☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
473	407.5140	813.0134	812.4068	0.6066	0	27	10	2	K.QYFVEK.Q
✓ 536	440.1040	878.1934	877.4658	0.7277	0	50	0.043	1	R.QGFSALQK.K
✓ 593	504.7990	1007.5834	1007.5321	0.0513	0	37	0.76	1	K.NIMTITTSK.G
✓ 663	601.5640	1201.1134	1200.5887	0.5247	0	83	2.4e-005	1	K.GEFTGLGIHDR.V

8. [RBL_NICDE](#) Mass: 53316 Score: 181 Queries matched: 4 emPAI: 0.14
Ribulose biphosphate carboxylase large chain precursor - Nicotiana debneyi (Debney's tobacco)

☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
✓ 602	511.5290	1021.0434	1020.5240	0.5194	0	55	0.016	1	K.DTDILAAFR.V
✓ 695	629.0940	1256.1734	1255.6520	0.5214	0	63	0.0027	1	R.DLAQEGNQIIR.E
842	704.0840	1406.1534	1405.6765	0.4769	0	40	0.58	2	K.LTYTPEYQTK.D
✓ 1199	724.3953	2170.1642	2168.9797	1.1845	1	28	6.8	1	R.GGLDFTKDDENVNSQPFR.W

Proteins matching the same set of peptides:

[RBL_NOLSP](#) Mass: 52404 Score: 181 Queries matched: 4
Ribulose biphosphate carboxylase large chain - Nolana spathulata

9. [KAC4_RABIT](#) Mass: 11264 Score: 174 Queries matched: 4 emPAI: 1.49

Ig kappa-b4 chain C region - Oryctolagus cuniculus (Rabbit)

☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
☒ 915	762.4090	1522.8034	1522.7740	0.0294	0	100	3.8e-007	1	K.VTQGTTSVVQSFNR.G
☒ 916	508.8020	1523.3842	1522.7740	0.6102	0	(44)	0.21	1	K.VTQGTTSVVQSFNR.G
☒ 917	763.1940	1524.3734	1522.7740	1.5994	0	(95)	1.5e-006	1	K.VTQGTTSVVQSFNR.G
☒ 1221	762.4087	2284.2042	2284.0195	0.1846	1	74	0.0002	1	K.EYTCKVIQGTTSVVQSFNR.G + Phospho (ST)

10. [LAC_HUMAN](#) Mass: 11401 Score: 134 Queries matched: 2 emPAI: 0.82

Ig lambda chain C regions - Homo sapiens (Human)

☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
☒ 1022	571.4287	1711.2642	1710.7519	0.5122	0	34	2.2	1	R.SYSCQVTHEGSTVEK.T
☒ 1032	872.7040	1743.3934	1742.8515	0.5419	0	100	5.4e-007	1	K.YAASSYLSLTPEQWK.S

11. [CASA1_BOVIN](#) Mass: 24570 Score: 124 Queries matched: 3 emPAI: 0.54

Alpha-S1-casein precursor - Bos taurus (Bovine)

☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
☒ 770	446.8887	1337.6442	1336.6735	0.9707	1	38	0.69	1	K.HIQKEDVPSEY.Y
☒ 1035	587.8120	1760.4142	1758.9377	1.4765	0	50	0.061	1	K.HQGLPQEVLENLLR.F
☒ 1105	651.4887	1951.4442	1950.9452	0.4990	1	36	1.3	1	K.YKVPQLEIVPNSAEER.L + Phospho (ST)

12. [MUCM_RABIT](#) Mass: 52945 Score: 119 Queries matched: 3 emPAI: 0.07

Ig mu chain C region membrane-bound form - Oryctolagus cuniculus (Rabbit)

☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
☒ 588	494.7640	987.5134	987.5502	-0.0367	0	28	6.5	1	K.QISVSWLR.D
☒ 671	611.5590	1221.1034	1220.6223	0.4811	0	71	0.00043	1	R.LICQATGFSPK.Q
964	530.0653	1587.1742	1585.8563	1.3179	0	23	28	2	K.VESGVLTKPVEATEK.G

Proteins matching the same set of peptides:

[MUC_RABIT](#) Mass: 50550 Score: 119 Queries matched: 3

Ig mu chain C region secreted form - Oryctolagus cuniculus (Rabbit)

13. [ETV6_HUMAN](#) Mass: 53252 Score: 116 Queries matched: 6 emPAI: 0.14

Transcription factor ETV6 - Homo sapiens (Human)

☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
☒ 577	487.4940	972.9734	973.4869	-0.5134	0	(29)	6.2	1	R.DDVAQWLK.W
578	487.5040	972.9934	973.4869	-0.4934	0	(26)	15	3	R.DDVAQWLK.W
☒ 579	487.5590	973.1034	973.4869	-0.3834	0	45	0.15	1	R.DDVAQWLK.W
581	488.0440	974.0734	973.4869	0.5866	0	(32)	3.6	2	R.DDVAQWLK.W
620	532.0540	1062.0934	1061.5658	0.5277	0	21	42	2	R.LQPIYWSR.D
☒ 1269	829.1053	2484.2942	2484.1379	0.1562	0	52	0.029	1	K.WAENEFLRPIDSNFEMNGK.A

14. [GC_RABIT](#) Mass: 35952 Score: 78 Queries matched: 2 emPAI: 0.10

Ig gamma chain C region - Oryctolagus cuniculus (Rabbit)

☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
482	418.5190	835.0234	834.4269	0.5965	0	34	1.7	1	K.DTLMISR.T
☒ 664	602.0140	1202.0134	1201.6091	0.4043	0	49	0.067	1	K.LSVPTSEWR.G

15. [K2C71_MOUSE](#) Mass: 57860 Score: 62 Queries matched: 1 emPAI: 0.06

Keratin, type II cytoskeletal 71 - Mus musculus (Mouse)

☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
☒ 891	738.6740	1475.3334	1474.7780	0.5555	0	62	0.0037	1	R.FLEQQNQVLQTK.W

Proteins matching the same set of peptides:

[K2C73_MOUSE](#) Mass: 59502 Score: 62 Queries matched: 1
Keratin, type II cytoskeletal 73 - Mus musculus (Mouse)

[K2C73_RAT](#) Mass: 60977 Score: 62 Queries matched: 1
Keratin, type II cytoskeletal 73 - Rattus norvegicus (Rat)

[K2C1_CANFA](#) Mass: 63922 Score: 59 Queries matched: 1
Keratin, type II cytoskeletal 1 - Canis familiaris (Dog)

[K2C1_HUMAN](#) Mass: 66149 Score: 59 Queries matched: 1
Keratin, type II cytoskeletal 1 - Homo sapiens (Human)

[K2C1_MOUSE](#) Mass: 66079 Score: 59 Queries matched: 1
Keratin, type II cytoskeletal 1 - Mus musculus (Mouse)

[K2C1_RAT](#) Mass: 65190 Score: 59 Queries matched: 1
Keratin, type II cytoskeletal 1 - Rattus norvegicus (Rat)

[K22E_CANFA](#) Mass: 64812 Score: 59 Queries matched: 1
Keratin, type II cytoskeletal 2 epidermal - Canis familiaris (Dog)

[K22E_HUMAN](#) Mass: 66111 Score: 59 Queries matched: 1
Keratin, type II cytoskeletal 2 epidermal - Homo sapiens (Human)

[K2C1B_MOUSE](#) Mass: 61379 Score: 55 Queries matched: 1
Keratin, type II cytoskeletal 1b - Mus musculus (Mouse)

[K2C1B_RAT](#) Mass: 57391 Score: 55 Queries matched: 1
Keratin, type II cytoskeletal 1b - Rattus norvegicus (Rat)

16. [ARSG_CANFA](#) Mass: 59011 Score: 59 Queries matched: 2

Arylsulfatase G precursor - Canis familiaris (Dog)

☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
☒ 587	490.5690	979.1234	978.4212	0.7023	0	35	1.6	1	K.AFYVSGGAK.A + Phospho (ST)
612	523.5140	1045.0134	1046.4563	-1.4428	0	24	20	4	R.IQLSAVLR.G + 2 Phospho (ST)

17. [KV302_HUMAN](#) Mass: 11882 Score: 55 Queries matched: 1 emPAI: 0.33

Ig kappa chain V-III region SIE - Homo sapiens (Human)

☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
☒ 989	816.3090	1630.6034	1631.7791	-1.1757	0	55	0.014	1	R.FSGSGSGTDFLTISR.L

Proteins matching the same set of peptides:

[KV304_HUMAN](#) Mass: 11895 Score: 55 Queries matched: 1
Ig kappa chain V-III region Ti - Homo sapiens (Human)

[KV305_HUMAN](#) Mass: 11853 Score: 55 Queries matched: 1
Ig kappa chain V-III region WOL - Homo sapiens (Human)

[KV307_HUMAN](#) Mass: 11937 Score: 55 Queries matched: 1
Ig kappa chain V-III region GOL - Homo sapiens (Human)

[KV312_HUMAN](#) Mass: 14178 Score: 55 Queries matched: 1
Ig kappa chain V-III region HAH precursor - Homo sapiens (Human)

[KV313_HUMAN](#) Mass: 14176 Score: 55 Queries matched: 1
Ig kappa chain V-III region HIC precursor - Homo sapiens (Human)

18. [SECD_ECOLI](#) Mass: 66648 Score: 53 Queries matched: 2

Protein-export membrane protein secD - Escherichia coli (strain K12)

☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
☒ 661	599.4390	1196.8634	1197.6102	-0.7467	0	28	7.4	1	R.ITGINNPNEAR.Q
761	440.1020	1317.2842	1316.8068	0.4774	0	27	9.7	6	K.VIILYAVGTGAIK.G

Proteins matching the same set of peptides:

[SECD_SHIFL](#) Mass: 66648 Score: 53 Queries matched: 2

Protein-export membrane protein secD - Shigella flexneri

[SECD_EC057](#) Mass: 66648 Score: 53 Queries matched: 2

Protein-export membrane protein secD - Escherichia coli O157:H7

Peptide matches not assigned to protein hits: (no details means no match)

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
✓ 842	704.0840	1406.1534	1405.6765	0.4769	0	46	0.12	1	LTYYTPQYETK
✓ 528	436.1040	870.1934	871.5603	-1.3669	2	40	0.46	1	KARVASIK
✓ 564	467.5140	933.0134	932.5080	0.5055	0	39	0.59	1	IIGFDNVR
✓ 616	525.1290	1048.2434	1049.4989	-1.2554	1	38	0.79	1	KSESEDSIR
✓ 979	805.4240	1608.8334	1608.7930	0.0404	1	37	0.89	1	GFCAGVSRVETVEK
✓ 523	435.9490	869.8834	869.4971	0.3864	0	36	1.3	1	IGELSVPR
✓ 510	426.4790	850.9434	851.4137	-0.4703	0	36	1.2	1	DTNFISR
✓ 912	508.0720	1521.1942	1522.8402	-1.6460	2	36	1.5	1	CGVVLAVHGEKKAR
✓ 787	679.5940	1357.1734	1356.8228	0.3507	1	35	1.8	1	IISKDLILSIK
✓ 613	523.5290	1045.0434	1045.3518	-0.3084	0	34	1.9	1	ISSSSYSR + 2 Phospho (ST)
✓ 548	459.4540	916.8934	917.5182	-0.6247	1	34	2	1	TQLETAKK
✓ 549	459.4540	916.8934	916.5229	0.3705	1	34	2.2	1	EKLVTAEK
✓ 944	525.1320	1572.3742	1573.6596	-1.2854	0	34	2.4	1	FQGLTIEECQNR + Phospho (ST)
✓ 808	689.6940	1377.3734	1375.8075	1.5660	2	33	2.4	1	FKEGIETLIAKK
✓ 760	659.4290	1316.8434	1316.6377	0.2058	0	33	2.2	1	YASSDILSLIR + Phospho (ST)
✓ 656	591.0840	1180.1534	1179.4825	0.6709	1	33	2.4	1	ELVSTISKEK + 2 Phospho (ST)
✓ 1030	581.4320	1741.2742	1740.7961	0.4781	2	33	2.8	1	KNEPIIKVSSHSSR + 2 Phospho (ST)
✓ 515	429.0390	856.0634	855.5178	0.5457	0	33	2.6	1	VATISLPR
✓ 522	435.8490	869.6834	869.5334	0.1500	0	33	2.3	1	VVSLSIPR
✓ 511	426.5140	851.0134	851.4137	-0.4003	0	33	2.3	1	DTNFISR
✓ 871	482.5820	1444.7242	1444.7707	-0.0465	1	33	2.3	1	AILVSSLLKTIK + 2 Phospho (ST)
✓ 734	428.7420	1283.2042	1281.5725	1.6317	0	33	3	1	SPTEGVTSFDDK
✓ 599	508.0690	1014.1234	1014.4569	-0.3335	1	32	3	1	MSDKVVIR + Phospho (ST)
✓ 581	488.0440	974.0734	973.5920	0.4814	2	32	3	1	TEVTRIKK
✓ 887	490.5687	1468.6842	1469.6973	-1.0131	0	32	2.7	1	FCQPETLSVYAR
✓ 804	459.4553	1375.3442	1375.6943	-0.3502	1	32	3.5	1	RSSTSSEPTPTVK
✓ 563	467.4890	932.9634	932.5304	0.4330	2	32	3.4	1	GAFQRRK
✓ 797	688.1690	1374.3234	1373.5976	0.7258	1	31	3.8	1	RTEGQDLNFSK + Phospho (ST)
✓ 520	435.8340	869.6534	869.5334	0.1200	0	31	3.3	1	VVSLSIPR
✓ 545	458.9440	915.8734	914.5913	1.2822	2	31	4.2	1	VKLQATKK
✓ 1306	961.0787	2880.2142	2878.4466	1.7676	2	31	3.4	1	AVFCVIAGVVLFNAIYSWNSLRRR + Phospho (ST)
✓ 795	458.9453	1373.8142	1373.5976	0.2165	1	30	4.1	1	RTEGQDLNFSK + Phospho (ST)
✓ 761	440.1020	1317.2842	1316.7187	0.5655	1	30	4.8	1	LLTKESEELK
✓ 640	564.4040	1126.7934	1128.4141	-1.6207	0	30	4.4	1	IYDGSISK + 2 Phospho (ST)
✓ 524	436.0090	870.0034	871.4651	-1.4616	0	30	4.8	1	EATVPDLK
✓ 509	426.4340	850.8534	851.4137	-0.5603	0	30	4.2	1	DTNFISR
✓ 850	474.0553	1419.1442	1419.5197	-0.3756	2	30	5.5	1	RTITSKASGGSK + 3 Phospho (ST)
✓ 711	422.0353	1263.0842	1263.5513	-0.4671	0	30	5.4	1	LGTSLLIGGIGK + 2 Phospho (ST)
✓ 1026	575.3753	1723.1042	1723.7107	-0.6065	0	30	5.9	1	IADVDEISIAFER + 2 Phospho (ST)
✓ 931	523.5020	1567.4842	1567.6141	-0.1299	2	29	5.9	1	SQSSSSPSRRSR + 2 Phospho (ST)
✓ 606	514.1290	1026.2434	1026.5822	-0.3387	0	29	5.6	1	IEANLALQR
✓ 1213	743.2253	2226.6542	2225.8571	0.7971	0	29	6.3	1	SSQSSLYLALEFENAAK + 3 Phospho (ST)
✓ 1174	704.1687	2109.4842	2108.0108	1.4733	1	29	6.3	1	SYQPIAGLRAVAVVEK + 2 Phospho (ST)
✓ 895	495.2587	1482.7542	1484.5211	-1.7669	2	29	5	1	SPSGSGREKGGAR + 3 Phospho (ST)
✓ 573	953.8000	952.7927	951.4427	1.3501	0	29	5.9	1	VPDSLVR + Phospho (ST)
✓ 1285	858.8987	2573.6742	2572.2373	1.4369	0	29	6.6	1	NTSALISAGIAICGGSATAAVGPILK + 2 Phospho (ST)
✓ 926	517.1620	1548.4642	1546.7661	1.6981	0	29	6.8	1	GAMLSDDQSELILR
✓ 434	672.4500	671.4427	671.3966	0.0461	0	29	5.6	1	TVSIPR
✓ 1208	738.6720	2212.9942	2213.1279	-0.1338	2	29	5.8	1	CVRPLDFQIVKDSVIKTK + Phospho (ST)
✓ 896	742.5390	1483.0634	1482.4926	0.5708	0	29	7.4	1	SNSNSGAGGWGSSR + 2 Phospho (ST)
✓ 594	504.9740	1007.9334	1007.5287	0.4047	0	29	6.7	1	VTLEDLYR
✓ 514	429.0190	856.0234	854.3357	1.6877	0	28	7.5	1	ADVMPSR + Phospho (ST)
✓ 819	695.0940	1388.1734	1387.7745	0.3990	0	28	7.8	1	LISLDMGSLIAGAK
✓ 762	660.5390	1319.0634	1318.3880	0.6754	0	28	7.7	1	TSGDNLEISR + 3 Phospho (ST)
✓ 642	567.1340	1132.2534	1130.5105	1.7430	0	28	7.2	1	EFDHNSNIR
✓ 473	407.5140	813.0134	813.3909	-0.3774	0	28	7.7	1	EYFVEK
✓ 847	707.1090	1412.2034	1412.6072	-0.4037	0	28	8.1	1	EDQISAIEAIEK + Phospho (ST)

✓	1132	1020.6140	2039.2134	2037.9521	1.2614	1	28	7.4	1	HSDLFSSSSPLDKGTKPR + Phospho (ST)
✓	735	429.0187	1284.0342	1283.6163	0.4179	1	28	8	1	KDDIVTWLŠK + Phospho (ST)
✓	818	462.8820	1385.6242	1385.7779	-0.1537	2	28	6.3	1	IEQKQKWLSAR
✓	1227	785.2420	2352.7042	2351.9811	0.7231	1	28	8	1	QCHSNTCPVGVCQDDKLR + Phospho (ST)
✓	862	714.6390	1427.2634	1427.8058	-0.5424	0	28	8.4	1	VSPIVGMLTGVVEK
✓	1053	602.0120	1803.0142	1801.7818	1.2323	0	28	7.3	1	MTNSTDRPVSVSŠWR + Phospho (ST)
✓	1066	624.5553	1870.6442	1871.0629	-0.4187	2	28	8	1	ETLKAVGQLAPGTFGVKR
✓	1040	589.6753	1766.0042	1765.9314	0.0728	2	28	7.3	1	LVCGSHŠFIKVIKAK + Phospho (ST)
✓	507	423.5240	845.0334	844.4767	0.5568	0	28	8.3	1	TAITGGGLR
✓	550	459.5440	917.0734	917.4971	-0.4236	0	28	8.3	1	FPPTSLR
✓	910	507.5253	1519.5542	1518.4678	1.0864	0	28	7.6	1	TNVVDŠNSDŠSK + 3 Phospho (ST)
✓	513	428.7440	855.4734	855.5178	-0.0443	0	28	6.3	1	VATISLPR
✓	1050	599.4387	1795.2942	1793.7332	1.5610	0	28	9.2	1	DSYHŠVYMVDSGNLK + Phospho (ST)
✓	1067	624.6020	1870.7842	1871.0629	-0.2787	2	28	7.4	1	ETLKAVGQLAPGTFGVKR
✓	716	422.1120	1263.3142	1263.5397	-0.2256	0	28	8.4	1	WGPTAANSGBPAR + Phospho (ST)
✓	1043	592.1853	1773.5342	1772.7982	0.7360	1	28	9.6	1	ŠNŠPPNTTŠKAAYIDK + Phospho (ST)
✓	626	537.9690	1073.9234	1073.4292	0.4943	0	27	9.3	1	QTGGŠGQFGR + Phospho (ST)
✓	1078	629.0953	1884.2642	1884.9532	-0.6890	2	27	10	1	SILNSKGŠŠLLMNKWK + Phospho (ST)
✓	798	688.1690	1374.3234	1373.6228	0.7007	0	27	10	1	YLIANASQAEŠK + Phospho (ST)
✓	805	688.7690	1375.5234	1375.8075	-0.2840	2	27	8.7	1	FKEGIETLIAKK
✓	650	587.8140	1173.6134	1172.6917	0.9217	0	27	7.9	1	GLGGLIFIDLR
✓	707	421.9820	1262.9242	1262.4833	0.4409	0	27	10	1	GVDEAPŠŠILK + 2 Phospho (ST)
✓	652	588.5790	1175.1434	1174.5942	0.5493	1	27	10	1	EIVŠNNRESK
✓	1049	898.1440	1794.2734	1793.9159	0.3575	1	27	11	1	VLVEAHAGIDVKDGDEK
✓	791	683.3540	1364.6934	1364.6684	0.0251	1	27	8.4	1	SQYEQLAEKNR
✓	712	422.0487	1263.1242	1263.5513	-0.4271	0	27	11	1	LGTSLLIGGIGK + 2 Phospho (ST)
✓	790	682.7740	1363.5334	1363.7646	-0.2311	1	27	9	1	LCLSARTIGFVK
✓	706	421.9487	1262.8242	1263.5513	-0.7271	0	27	9.9	1	LGTSLLIGGIGK + 2 Phospho (ST)
✓	1277	841.4987	2521.4742	2519.9123	1.5619	2	27	11	1	AAQHŠEMVŠKETYIFIDKK + 4 Phospho (ST)
✓	980	537.5153	1609.5242	1609.7349	-0.2107	0	27	11	1	TEQSPIVPAATŠŠSR + Phospho (ST)
✓	571	475.5490	949.0834	950.5073	-1.4238	0	26	10	1	NISDYLVK
✓	717	422.1320	1263.3742	1263.5513	-0.1771	0	26	11	1	LGTSLLIGGIGK + 2 Phospho (ST)
✓	848	471.9753	1412.9042	1413.6711	-0.7669	0	26	11	1	NDFLVTCGFSVR
✓	704	421.8353	1262.4842	1262.6475	-0.1633	1	26	9.7	1	IGTPAMTTRGMK
✓	516	432.5240	863.0334	863.4171	-0.3837	0	26	10	1	GVDLMS

✓	529	437.4690	872.9234	873.4109	-0.4875	0	25	18	1	PPINTPR + Phospho (ST)
✓	768	444.4587	1330.3542	1328.7816	1.5726	0	25	16	1	LGAAYLVKPLR
✓	641	565.5190	1129.0234	1128.5200	0.5035	0	25	17	1	YIDPHNDQK
✓	911	508.0387	1521.0942	1519.8011	1.2931	0	25	17	1	ILADADVILVGVSR + Phospho (ST)
✓	933	523.5120	1567.5142	1566.7079	0.8062	0	25	17	1	DASVDGALAASVFHK + Phospho (ST)
✓	490	420.0640	838.1134	836.4392	1.6743	0	25	14	1	LASYLDR
✓	1320	1069.3887	3205.1442	3205.3240	-0.1798	0	25	15	1	TWIEYQLETTIYPNEVMNTTPDGSGAK + 2 Phospho (ST)
✓	852	712.2040	1422.3934	1422.7606	-0.3671	1	25	17	1	YLDKSLDTEVK
✓	702	421.7487	1262.2242	1263.5513	-1.3271	0	25	18	1	LGTSLLIGGIGK + 2 Phospho (ST)
✓	1284	858.6987	2573.0742	2573.9950	-0.9208	1	25	15	1	SMSVGAASGIGASTIICKSVLAOK + 4 Phospho (ST)
✓	1297	925.5453	2773.6142	2772.0834	1.5308	1	25	16	1	VMIYICQQNILSSKIAECCK + 3 Phospho (ST)
✓	929	522.9287	1565.7642	1566.3966	-0.6324	0	25	15	1	SGYSSSSSSSPK + 4 Phospho (ST)
✓	705	421.8420	1262.5042	1263.5513	-1.0471	0	25	14	1	LGTSLLIGGIGK + 2 Phospho (ST)
✓	800	688.3090	1374.6034	1374.6796	-0.0761	1	25	15	1	LISLSLFFEGKK + Phospho (ST)
✓	773	672.2990	1342.5834	1342.6758	-0.0924	0	24	15	1	SGHLLAIPGGVR + Phospho (ST)
✓	820	695.0990	1388.1834	1388.5861	-0.4026	0	24	20	1	DTGGLQDLEFSK + Phospho (ST)
✓	807	688.8190	1375.6234	1375.8075	-0.1840	2	24	15	1	FKEGIETLIAKK
✓	1257	798.1587	2391.4542	2392.0333	-0.5791	1	24	19	1	FFSNDLQPTDVSSRVGGSDER + Phospho (ST)
✓	731	426.5153	1276.5242	1277.6398	-1.1156	1	24	15	1	VKVTDLCSNSR
✓	964	530.0653	1587.1742	1586.7341	0.4401	2	24	21	1	VKNEAWSKTEIK + Phospho (ST)
✓	620	532.0540	1062.0934	1062.5362	-0.4427	0	24	19	1	EIPLPSLSK + Phospho (ST)
✓	715	422.1020	1263.2842	1263.5513	-0.2671	0	24	20	1	LGTSLLIGGIGK + 2 Phospho (ST)
✓	746	435.8487	1304.5242	1303.7360	0.7881	1	24	16	1	QRYNATVIAIR
✓	809	460.2553	1377.7442	1378.8045	-1.0603	1	24	16	1	TTLVHALAREIR
✓	1242	792.9353	2375.7842	2376.0641	-0.2799	1	24	20	1	VDTGRNLVTLPHITATILR + 3 Phospho (ST)
✓	673	411.4453	1231.3142	1230.6680	0.6461	2	24	20	1	DVRAIREGSTK
✓	991	546.0787	1635.2142	1633.9039	1.3103	0	24	22	1	AVLAYSGGLDTSIIVR
✓	714	422.0853	1263.2342	1262.5366	0.6976	0	24	21	1	AYSTTAVMPR + Phospho (ST)
✓	1264	814.5620	2440.6642	2442.1106	-1.4465	1	24	21	1	LESIAMSDIPRTPVLGCCISR + Phospho (ST)
✓	930	523.4787	1567.4142	1568.7018	-1.2876	1	24	22	1	SADGKTQSPGCLLR + Phospho (ST)
✓	970	532.0520	1593.1342	1592.9613	0.1728	1	24	22	1	TRGPAILIDVNAIIR
✓	1036	588.1620	1761.4642	1761.7968	-0.3326	1	24	22	1	QMSRIPISSSSTSSK + Phospho (ST)
✓	1290	875.3487	2623.0242	2624.2288	-1.2046	2	24	19	1	ILEDNFLKSSFPITQAEIDRLR + 2 Phospho (ST)
✓	710	422.0353	1263.0842	1262.6475	0.4367	1	24	22	1	IGTPAMTTRGMK
✓	651	588.1590	1174.3034	1172.5955	1.7080	0	24	21	1	LHGTIPIGAK + Phospho (ST)
✓	1261	805.4220	2413.2442	2414.8569	-1.6127	1	24	19	1	NFSSTEILHAEDKFFCDK + 3 Phospho (ST)
✓	1065	932.7040	1863.3934	1863.7428	-0.3493	0	24	24	1	ETSIDVDPSEEVEVSGK + 2 Phospho (ST)
✓	813	690.4840	1378.9534	1377.7868	1.1667	1	24	23	1	YASIGDKVVTVK
✓	1178	707.1087	2118.3042	2117.8555	0.4487	1	24	23	1	SYSRQSSSDTDLSLTPK + 2 Phospho (ST)
✓	943	525.0953	1572.2642	1573.6881	-1.4239	1	24	24	1	VTSSMSPSMQPKK + Phospho (ST)
✓	1235	788.1253	2361.3542	2360.8393	0.5149	0	24	21	1	TDVTNGGFFSSPEDMSGAEKGK + 2 Phospho (ST)
✓	708	421.9987	1262.9742	1262.5019	0.4723	0	24	23	1	AMSGLEGPLIK + 2 Phospho (ST)
✓	1116	671.4653	2011.3742	2010.8644	0.5098	1	24	24	1	RSASPINTNNSAGDSPDTK + Phospho (ST)
✓	1172	704.0853	2109.2342	2108.0273	1.2069	2	23	22	1	KKAAPTAPAPEDDLDESEK
✓	1280	848.3153	2541.9242	2541.0954	0.8287	1	23	22	1	SIITATAESDRGGFVEATHIK + 3 Phospho (ST)
✓	1263	812.1687	2433.4842	2435.2307	-1.7465	1	23	24	1	WSLVGLSWLLFVASSELKK + 2 Phospho (ST)
✓	901	498.2387	1491.6942	1491.6160	0.0782	0	23	19	1	AFSSANPDAALIR + 2 Phospho (ST)
✓	1073	626.1887	1875.5442	1876.9196	-1.3755	2	23	25	1	TFSITNIRFNVDRK + Phospho (ST)
✓	1055	609.5787	1825.7142	1826.8299	-1.1157	1	23	22	1	TPSVKDADGGTSAVAVSEK + Phospho (ST)
✓	875	487.4920	1459.4542	1458.7256	0.7286	1	23	24	1	DDVPFKLAFDHR
✓	1300	932.7020	2795.0842	2796.2716	-1.1874	1	23	22	1	VDLQSSASEHTEKGNLSGGVQAGFGK + Phospho (ST)
✓	660	598.7040	1195.3934	1194.6373	0.7561	2	23	22	1	KAKEAIGGIK + Phospho (ST)
✓	1051	599.8787	1796.6142	1795.9720	0.6422	1	23	25	1	QYFTDVKKIIDNSIK
✓	1136	1028.9140	2055.8134	2055.9868	-0.1734	2	23	23	1	SVANSPVRSCAQPDQERR
✓	562	466.8540	931.6934	932.5001	-0.8066	1	23	23	1	ILKGMDEK
✓	488	419.8740	837.7334	839.3215	-1.5880	0	23	22	1	WPGIGDK + Phospho (ST)
✓	1295	917.5520	2749.6342	2749.2006	0.4336	1	23	25	1	CRSDSPAVAAVVPAMASYPSSGSGKPK + 2 Phospho (ST)
✓	574	477.5940	953.1734	953.5407	-0.3672	0	23	24	1	TTGARPVPR
✓	1012	561.6487	1681.9242	1682.8141	-0.8899	1	23	23	1	SSVTQLFKNNPVNR + Phospho (ST)
✓	614	524.5240	1047.0334	1045.4805	1.5530	1	23	26	1	ISSIKKTSR + Phospho (ST)
✓	1220	762.0853	2283.2342	2284.9895	-1.7554	1	23	24	1	TSIGFGPRGASLEEDVALLVR + 3 Phospho (ST)
✓	881	488.6453	1462.9142	1462.5659	0.3483	1	23	25	1	QSSASKLLYAR + 3 Phospho (ST)
✓	1207	738.5253	2212.5542	2211.1171	1.4370	1	23	28	1	QFISSLEDAETIKSFNNLR
✓	1004	559.6720	1675.9942	1674.7234	1.2708	0	23	25	1	ATAGDTHLGGEDFDNR
✓	537	443.0540	884.0934	885.4668	-1.3734	1	23	27	1	EATKGQPR

✓	870	481.6887	1442.0442	1440.7378	1.3064	1	23	29	1	IFETTGIPISKR + Phospho (ST)
✓	703	421.8253	1262.4542	1263.5513	-1.0971	0	23	23	1	LGTSLIIGGIGK + 2 Phospho (ST)
✓	766	443.0520	1326.1342	1327.6384	-1.5043	1	23	29	1	GISSKSGSADVLK + Phospho (ST)
✓	669	407.5153	1219.5242	1220.5090	-0.9849	1	23	21	1	EKSLLSQEK + 2 Phospho (ST)
✓	1276	840.9520	2519.8342	2519.2282	0.6060	2	23	27	1	SYSTRISQSARFGVLASPGVNR + Phospho (ST)
✓	967	531.2087	1590.6042	1589.5340	1.0701	0	23	25	1	LIFSPESEPESEK + 3 Phospho (ST)
✓	1175	705.6120	2113.8142	2112.9033	0.9109	2	23	27	1	KFVIEKYGVQDFMFSK + 2 Phospho (ST)
✓	1038	588.6620	1762.9642	1761.9546	1.0096	1	22	26	1	LLTNGSLSEIKEMTVK
✓	1099	961.7490	1921.4834	1921.8264	-0.3429	2	22	31	1	SNFLDSKKSLYSLFN + 2 Phospho (ST)
✓	1191	714.6387	2140.8942	2141.0882	-0.1940	1	22	25	1	TAEVVLVDYGLGNLRSVTR + Phospho (ST)
✓	838	703.4640	1404.9134	1405.6514	-0.7379	0	22	28	1	EEWDQLYPAQK
✓	1061	616.9687	1847.8842	1848.9822	-1.0981	1	22	24	1	GELAAVLGLASSRSALVR + Phospho (ST)
✓	845	705.6140	1409.2134	1407.6114	1.6021	1	22	31	1	DNGASTDDSAAEKK
✓	1141	688.0787	2061.2142	2060.0554	1.1587	2	22	29	1	IVFLANVSTEAISSKSAKK + Phospho (ST)
✓	696	419.8720	1256.5942	1257.7227	-1.1285	1	22	24	1	SLLVAGLCRAAK
✓	747	435.9487	1304.8242	1303.4653	1.3589	0	22	26	1	DSGSSWGNQMR + Phospho (ST)
✓	1309	985.2887	2952.8442	2951.4122	1.4319	1	22	28	1	VSYEDVQAPIHYILKILGIEVNYK + 2 Phospho (ST)
✓	1131	680.5920	2038.7542	2039.6676	-0.9135	2	22	28	1	RDVSSPDESNGQSKSK + 4 Phospho (ST)
✓	786	679.4790	1356.9434	1358.4285	-1.4850	0	22	31	1	MTMATNSGGDSK + 2 Phospho (ST)
✓	718	423.5253	1267.5542	1266.5969	0.9573	0	22	25	1	NLTNALSEAVR + Phospho (ST)
✓	748	436.0087	1305.0042	1303.7360	1.2681	1	22	31	1	QRYNATVIAIR
✓	815	462.7520	1385.2342	1383.7275	1.5066	2	22	33	1	NLLRSGIGKLFSS + Phospho (ST)
✓	888	737.7190	1473.4234	1472.7500	0.6734	2	22	32	1	RVASGELHPKIAK + Phospho (ST)
✓	1122	675.1220	2022.3442	2022.9283	-0.5841	2	22	34	1	SEDKAEWWSGAATRFDK
✓	1216	752.0420	2253.1042	2253.9708	-0.8666	1	22	26	1	SEKLNFEAYINSHGTLISK + 2 Phospho (ST)
✓	624	537.5140	1073.0134	1072.3822	0.6312	0	22	33	1	EAASSGDNSR + Phospho (ST)
✓	923	514.0587	1539.1542	1538.7090	0.4452	1	22	35	1	AELDDAGSLLRGR + Phospho (ST)
✓	1267	817.7087	2450.1042	2451.1885	-1.0843	2	22	26	1	MELKASEFGVVLSDALKLSR + 2 Phospho (ST)
✓	874	729.1390	1456.2634	1456.8250	-0.5615	1	22	35	1	AVGVVVDQLKSNTK
✓	1013	564.4053	1690.1942	1690.7424	-0.5483	0	22	36	1	GARPGGGDAGGTPGEIVR + Phospho (ST)
✓	1197	720.4987	2158.4742	2156.9684	1.5058	0	22	35	1	SDTSSSAFFALALPILEK + 2 Phospho (ST)
✓	521	435.8440	869.6734	871.4512	-1.7777	1	22	29	1	KDGAAGTPR
✓	633	554.0190	1106.0234	1104.6040	1.4195	1	22	33	1	NIKSFLNNR
✓	1118	673.0387	2016.0942	2014.8778	1.2164	2	22	30	1	LKKIATAGAISELTESR + 3 Phospho (ST)
✓	771	670.9290	1339.8434	1338.6221	1.2214	0	22	31	1	ESGQPYIIPQK + Phospho (ST)
✓	744	435.8353	1304.4842	1303.7360	0.7481	1	22	28	1	QRYNATVIAIR
✓	1215	751.6887	2252.0442	2250.8783	1.1659	1	22	28	1	TSIGFSGGGAIVEDVALMRR + 3 Phospho (ST)
✓	685	626.1890	1250.3634	1248.6310	1.7325	1	22	32	1	NAESSKANSITK
✓	1115	670.9287	2009.7642	2008.9305	0.8336	2	22	32	1	QGDILVSGMKTGSSKLK + 2 Phospho (ST)
✓	1153	695.1020	2082.2842	2083.0086	-0.7244	2	22	36	1	VTLEKDEVTKESLEER + Phospho (ST)
✓	615	525.0940	1048.1734	1046.5179	1.6556	0	22	34	1	EASACAAVLR
✓	1268	823.4953	2467.4642	2468.1609	-0.6968	2	22	36	1	LGNGLKISPIVIGCMSYGSKK + 2 Phospho (ST)
✓	994	552.0453	1653.1142	1652.7770	0.3371	1	21	39	1	VLESRLAEEGESVR + Phospho (ST)
✓	1265	815.0753	2442.2042	2441.8137	0.3905	1	21	31	1	KEITGIGPSITITETIVAK + 6 Phospho (ST)
✓	985	541.6653	1621.9742	1622.6855	-0.7113	1	21	36	1	YTDNLSARAIIPR + 2 Phospho (ST)
✓	924	514.1320	1539.3742	1537.7501	1.6241	1	21	42	1	QQPNSAKALSSSIK + Phospho (ST)
✓	919	511.5287	1531.5642	1532.6959	-1.1318	0	21	36	1	VMLDHSGLAAFR + Phospho (ST)
✓	752	436.1020	1305.2842	1305.7881	-0.5039	2	21	39	1	HLLAQAREKIK
✓	655	590.4190	1178.8234	1179.4849	-0.6615	1	21	36	1	EFFADKDIK + Phospho (ST)
✓	1169	703.5787	2107.7142	2106.9843	0.7299	2	21	39	1	KTEMHKAIVIGDTVGDPMK + Phospho (ST)
✓	729	426.4353	1276.2842	1277.6211	-1.3370	1	21	40	1	SETVSQNKETR
✓	556	462.8640	923.7134	923.4589	0.2545	1	21	35	1	LSAERLR + Phospho (ST)
✓	1128	678.6353	2032.8842	2033.7616	-0.8774	1	21	34	1	GDPGESPDGDSLAASERK + 2 Phospho (ST)
✓	939	524.5253	1570.5542	1569.7083	0.8459	2	21	39	1	EVMSPIGSARGRSR + Phospho (ST)
✓	584	489.0440	976.0734	975.4063	0.6672	0	21	39	1	TTFESVGR + Phospho (ST)
✓	1068	625.1020	1872.2842	1872.9247	-0.6405	1	21	45	1	KPPYRSHSLSPSPVNK + Phospho (ST)
✓	1262	810.8453	2429.5142	2428.1934	1.3208	2	21	42	1	SLTLGTRDSVWTGTCRLANLK + Phospho (ST)
✓	1222	763.1953	2286.5642	2287.0022	-0.4380	0	21	43	1	ATPATEESTVPATQSSALPAK + 2 Phospho (ST)
✓	1155	695.7120	2084.1142	2083.9380	0.1761	2	21	36	1	KDLGLNAFIEKNFSSK + 2 Phospho (ST)
✓	908	506.7653	1517.2742	1518.7460	-1.4718	1	21	45	1	GSVSTGVAKIIISK + 2 Phospho (ST)
✓	877	487.5587	1459.6542	1458.7256	0.9286	1	21	35	1	DDVPFKLAFDHR
✓	617	528.1540	1054.2934	1054.5230	-0.2295	0	21	39	1	GDPVNPMAVR
✓	540	444.4590	886.9034	886.4872	0.4162	1	21	46	1	KASTPDLR
✓	1168	703.4653	2107.3742	2105.8143	1.5598	1	21	46	1	SGEGGESLDRIGGCSGNSK + Phospho (ST)
✓	1219	761.8420	2282.5042	2283.1065	-0.6024	2	21	47	1	APIGPVIPLAKSPEPRSPPK + 2 Phospho (ST)

✓	682	625.1140	1248.2134	1247.6063	0.6071	1	21	45	1	AFRY\$ANLVK + Phospho (ST)
✓	694	419.0820	1254.2242	1254.7170	-0.4928	1	21	47	1	RPPSPRRPHR
✓	1098	641.4087	1921.2042	1920.8479	0.3562	1	21	46	1	FSS\$ETNAQRFQGNQIR + Phospho (ST)
✓	527	436.0840	870.1534	871.2960	-1.1426	0	21	44	1	EAQAE\$GI + Phospho (ST)
✓	1187	1069.3940	2136.7734	2136.2266	0.5468	2	20	44	1	VKITGGEPTRLADIIDIIGR
✓	741	649.7790	1297.5434	1297.5720	-0.0286	1	20	38	1	\$FLSLQ\$KIK + 2 Phospho (ST)
✓	1054	603.0987	1806.2742	1805.8366	0.4376	1	20	52	1	INPTTSFPGV\$ILGKK + 2 Phospho (ST)
✓	1062	925.5440	1849.0734	1847.8891	1.1844	1	20	45	1	TRAHEILAATGISADVR + Phospho (ST)
✓	1196	718.7253	2153.1542	2153.1232	0.0310	1	20	43	1	ILTEAATEDKIVITTLNK + Phospho (ST)
✓	561	466.8490	931.6834	931.4052	0.2783	0	20	43	1	JNYVIDK + Phospho (ST)
✓	653	588.6640	1175.3134	1173.7155	1.5979	2	20	46	1	VVDTLKLMK
✓	743	435.7953	1304.3642	1303.6806	0.6836	1	20	48	1	TKGAITEASPMK
✓	1258	800.2887	2397.8442	2399.1482	-1.3040	1	20	48	1	TEIAINEGAVSLGSAAVRFAAER + Phospho (ST)
✓	477	412.9740	823.9334	824.2718	-0.3384	0	20	42	1	T\$ASA\$IK + 2 Phospho (ST)
✓	1060	616.5053	1846.4942	1848.0750	-1.5808	2	20	52	1	ILISRRPPIKLLYK + Phospho (ST)
✓	1198	721.5653	2161.6742	2161.1743	0.4999	2	20	51	1	KSEAQTADVLDGKSFIVVR
✓	983	540.3320	1617.9742	1616.7422	1.2320	2	20	47	1	YQV\$RSYMKTFK + Phospho (ST)
✓	1214	745.6953	2234.0642	2233.9002	0.1640	1	20	41	1	L\$S\$V\$ASNGGGAGGAGNGAGGDKDAK + 2 Phospho (ST)
✓	1107	658.7853	1973.3342	1974.9257	-1.5915	1	20	53	1	HGFLEEFIIPIVKAS\$K + 2 Phospho (ST)
✓	1150	690.4853	2068.4342	2068.8730	-0.4388	1	20	54	1	\$FTFVIKIPPA\$ILLK + 4 Phospho (ST)
✓	1241	792.6053	2374.7942	2374.9478	-0.1536	1	20	50	1	IEENDEPGYGSPKED\$SWEK + Phospho (ST)
✓	1223	767.4620	2299.3642	2300.9633	-1.5991	0	20	50	1	Q\$S\$LG\$L\$FFN\$ILAHGDLR + 3 Phospho (ST)
✓	689	418.5220	1252.5442	1253.7132	-1.1690	0	20	40	1	VLVPPFIGAGER
✓	907	504.9720	1511.8942	1511.6981	0.1961	1	20	46	1	AS\$KAAEIGSDALSR + Phospho (ST)
✓	604	514.0140	1026.0134	1024.4590	1.5544	0	20	50	1	LSGSDIPIR + Phospho (ST)
✓	1317	1053.1353	3156.3842	3157.3701	-0.9859	0	20	38	1	G\$SS\$SSNLT\$T\$S\$AS\$ASLLISNNSSTASSPAPK + 2 Phospho (ST)
✓	1109	660.5387	1978.5942	1977.8308	0.7634	2	20	55	1	T\$KAEAEMLYQTKYR + 2 Phospho (ST)
✓	1134	682.7753	2045.3042	2043.9642	1.3399	0	20	55	1	AL\$INLLDLEAALAIVR + 2 Phospho (ST)
✓	557	462.8790	923.7434	925.3654	-1.6220	0	20	48	1	AD\$QQAAR + Phospho (ST)
✓	667	406.0053	1214.9942	1213.6091	1.3850	0	20	56	1	NVNTFLTYSR
✓	625	537.9590	1073.9034	1073.4292	0.4743	0	20	54	1	QTGG\$GQFGR + Phospho (ST)
✓	816	462.8653	1385.5742	1386.7467	-1.1725	2	20	45	1	ENVKNQTEL\$KK
✓	811	460.3187	1377.9342	1379.7118	-1.7777	1	20	54	1	MKALEEAGAYVAK
✓	1110	660.5520	1978.6342	1979.0275	-0.3933	2	20	56	1	\$GLDPKLLAKILNMSSGR + Phospho (ST)
✓	654	589.6740	1177.3334	1176.4577	0.8757	0	20	50	1	IE\$GGLGASAR + 2 Phospho (ST)
✓	547	459.3090	916.6034	915.5389	1.0646	1	20	45	1	INLEATKK
✓	909	507.0487	1518.1242	1516.5725	1.5517	1	20	59	1	\$S\$AKAAAAV\$T\$SR + 3 Phospho (ST)
✓	941	786.9740	1571.9334	1571.7072	0.2262	1	20	52	1	VMDSTAF\$MARDNK
✓	526	436.0140	870.0134	871.2960	-1.2826	0	20	57	1	EAQAE\$GI + Phospho (ST)
✓	882	489.0453	1464.1142	1462.7052	1.4090	0	19	62	1	YLNEAAGVAAEEAR
✓	725	637.6040	1273.1934	1272.7336	0.4599	2	19	61	1	METINRL\$KK
✓	1230	786.1387	2355.3942	2355.1431	0.2511	2	19	58	1	SQTS\$PKG\$LSR\$SS\$PVTELTAR + Phospho (ST)
✓	934	523.5287	1567.5642	1567.5917	-0.0275	0	19	55	1	VQIES\$STG\$SVG\$NR + 2 Phospho (ST)
✓	719	424.0587	1269.1542	1269.5714	-0.4173	1	19	63	1	KQ\$TATGDGVAR + Phospho (ST)
✓	880	488.2787	1461.8142	1462.6931	-0.8789	0	19	50	1	LIPITIFMEYR + Phospho (ST)
✓	539	444.1340	886.2534	884.5331	1.7203	0	19	56	1	LTVLSQPK
✓	765	662.1040	1322.1934	1320.5550	1.6385	0	19	62	1	IISKPM\$E\$SR + 2 Phospho (ST)
✓	1286	865.7187	2594.1342	2593.0781	1.0561	2	19	49	1	TVP\$K\$W\$V\$V\$S\$T\$TDG\$VKPRR + 4 Phospho (ST)
✓	1314	1047.3487	3139.0242	3137.5629	1.4613	1	19	53	1	TLEAIEGHGGERLGPTEELVEENVQIR
✓	1165	700.1853	2097.5342	2097.6958	-0.1616	1	19	65	1	RVMQ\$PYT\$SS\$F\$SS\$K + 4 Phospho (ST)
✓	817	693.7990	1385.5834	1384.6612	0.9222	1	19	51	1	SPG\$PAVRLHER + Phospho (ST)
✓	1121	675.1187	2022.3342	2022.9283	-0.5941	2	19	66	1	SEDKAE\$W\$SGPAATRFDK
✓	1304	948.4320	2842.2742	2840.8296	1.4446	0	19	48	1	NN\$T\$G\$N\$G\$V\$S\$S\$G\$N\$N\$E\$T\$ILGYK + 6 Phospho (ST)
✓	851	710.8740	1419.7334	1419.6646	0.0688	2	19	50	1	SFVA\$K\$K\$ESTEK + Phospho (ST)
✓	726	637.6240	1273.2334	1274.6871	-1.4536	0	19	66	1	FAETNPVGTVIK
✓	781	676.6790	1351.3434	1349.6228	1.7207	1	19	64	1	DSP\$PQ\$P\$SL\$KK + Phospho (ST)
✓	833	700.1840	1398.3534	1397.7627	0.5908	0	19	66	1	IRPTDTAGDLLAR
✓	812	690.1340	1378.2534	1376.7187	1.5347	0	19	67	1	LL\$FDNEVELAK
✓	1301	937.7153	2810.1242	2810.2394	-0.1153	1	19	54	1	RPL\$K\$CGMEPGGDASLILHGLQNR + 2 Phospho (ST)
✓	1148	689.6953	2066.0642	2065.8597	0.2044	0	19	56	1	LL\$MHPEVEIIT\$ISR + 3 Phospho (ST)
✓	801	459.2853	1374.8342	1374.6456	0.1886	0	19	57	1	NTWTYIF\$SDK
✓	1183	712.3653	2134.0742	2133.9861	0.0881	2	19	54	1	LVQIKKQVSPG\$SGNQ\$G\$LF + 2 Phospho (ST)
✓	1056	610.8553	1829.5442	1827.8097	1.7345	0	19	68	1	TFQIY\$PLVA\$VEVK + 2 Phospho (ST)
✓	512	852.6400	851.6327	853.3807	-1.7480	1	19	51	1	GAE\$VRR + Phospho (ST)
✓	1283	849.3287	2544.9642	2545.1583	-0.1942	2	19	60	1	ATMHKVSTLTERLTHMSV\$ISR + 2 Phospho (ST)

✓	982	537.9687	1610.8842	1610.6647	0.2194	0	19	58	1	CSPGSPIDPNATLSK + Phospho (ST)
✓	1274	839.0587	2514.1542	2512.3600	1.7942	2	19	53	1	RPISADSVIMHPTAKILALSGK + Phospho (ST)
✓	810	460.2853	1377.8342	1379.5371	-1.7029	1	19	58	1	QVEESQKSSAK + 2 Phospho (ST)
✓	471	406.0040	809.9934	811.3225	-1.3291	0	19	58	1	DANVSAR + Phospho (ST)
✓	621	532.0790	1062.1434	1063.5063	-1.3629	0	19	64	1	NLSPGSGKPK + Phospho (ST)
✓	1120	673.8620	2018.5642	2020.0239	-1.4597	1	19	71	1	DAGGHNWIRSVPTQVVR
✓	1101	643.4753	1927.4042	1928.9996	-1.5955	0	19	72	1	IHFLIGDFTAQIGDPTGK
✓	1247	794.0320	2379.0742	2377.9441	1.1301	0	19	56	1	QNNGATTSAGTTTIVGNITIK + 3 Phospho (ST)
✓	772	671.4640	1340.9134	1339.6861	1.2274	2	19	68	1	VRKGDLSLSIAK + Phospho (ST)
✓	876	487.5020	1459.4842	1457.7588	1.7254	1	19	67	1	QFKDLSYMVISK
✓	1143	688.1687	2061.4842	2060.9238	0.5603	0	19	73	1	VPVSAPHLLDTCGIGGDASK + Phospho (ST)
✓	1224	770.8387	2309.4942	2311.0814	-1.5872	2	19	72	1	GPLGGCCGGVKGLLSAKTTADR + Phospho (ST)
✓	879	488.0453	1461.1142	1459.4922	1.6220	0	19	74	1	ETSGISAEDIAK + 3 Phospho (ST)
✓	990	817.7090	1633.4034	1631.7417	1.6618	2	19	75	1	GETASRQSFQRSAK + Phospho (ST)
✓	628	541.6640	1081.3134	1081.6104	-0.2970	2	19	63	1	GLPADARRAR
✓	1279	846.3487	2536.0242	2536.0277	-0.0035	2	19	62	1	AGMLSTDGRCKTFSADANGYVR + 2 Phospho (ST)
✓	1087	636.0787	1905.2142	1904.7417	0.4725	1	19	75	1	RDFSNAIDMADYLVK + 2 Phospho (ST)
✓	1195	717.5520	2149.6342	2148.1685	1.4657	2	19	74	1	GTTVLTRASGISSRTMELLR
✓	1090	637.2653	1908.7742	1908.0155	0.7586	1	19	63	1	ILPTQGSMTIVVKSLGGK + Phospho (ST)
✓	672	616.5040	1230.9934	1230.4084	0.5850	0	19	74	1	VLSSTISAGGGR + 3 Phospho (ST)
✓	677	412.9720	1235.8942	1236.7805	-0.8864	0	19	70	1	LSLVGNPAILLK
✓	883	489.2053	1464.5942	1465.6223	-1.0282	1	19	60	1	MKILMAGGAIASR + 2 Phospho (ST)
✓	1312	1028.9153	3083.7242	3084.6073	-0.8831	1	19	62	1	DPETKPIFVNNYTWLKNLYISFLR
✓	998	554.0187	1659.0342	1660.6859	-1.6517	1	19	72	1	DIPSGLGSESRLDR + 2 Phospho (ST)
✓	1313	1029.7387	3086.1942	3087.3896	-1.1954	1	19	60	1	ASAAAIESLINEAVKTFNNSEYEMSR + Phospho (ST)
✓	591	498.2390	994.4634	994.5464	-0.0829	1	18	52	1	VEKIVISK + Phospho (ST)
✓	582	488.2790	974.5434	973.4869	1.0566	0	18	55	1	DDVAQWLK
✓	627	540.3340	1078.6534	1077.5567	1.0968	0	18	55	1	ALGLSNFNSR
✓	701	631.5990	1261.1834	1259.5659	1.6175	1	18	76	1	KYGIQASGGGR + Phospho (ST)
✓	986	812.1690	1622.3234	1622.6742	-0.3508	1	18	80	1	SILASASWDKIER + 2 Phospho (ST)
✓	755	439.2653	1314.7742	1315.7142	-0.9401	2	18	64	1	LALRRAAMSGDR
✓	721	636.0790	1270.1434	1269.6370	0.5064	1	18	79	1	FSIKGDPVLVK + Phospho (ST)
✓	794	687.8290	1373.6434	1373.6010	0.0424	2	18	61	1	MDSTGTGAGGKGK + Phospho (ST)
✓	1102	644.6087	1930.8042	1929.7200	1.0842	0	18	66	1	VATSFVTVIGHEAEDK + 3 Phospho (ST)
✓	1201	729.1353	2184.3842	2184.0520	0.3322	1	18	79	1	ISTLFPSKYLGAAVSTIEK + 2 Phospho (ST)
✓	1114	667.9220	2000.7442	1999.0520	1.6921	1	18	71	1	VTLSDAILPSQAERIR
✓	1294	898.1453	2691.4142	2691.0268	0.3874	2	18	64	1	TASASEASGSEKAAASAPETPRK + 4 Phospho (ST)
✓	988	815.0740	1628.1334	1628.7494	-0.6160	0	18	85	1	HDIQGSIAHATMLR + Phospho (ST)
✓	1282	848.9853	2543.9342	2543.9081	0.0260	1	18	72	1	VSQSSSSSGGGSSARGIQNQLR + 4 Phospho (ST)
✓	835	467.5153	1399.5242	1397.7683	1.7559	1	18	70	1	IIIIADLIKYR + Phospho (ST)
✓	638	560.3890	1118.7634	1117.4288	1.3346	1	18	69	1	GSKGASSSDDK + Phospho (ST)
✓	1319	1058.1453	3171.4142	3172.4056	-0.9914	2	18	57	1	LRVHTEYNNNALILPDYFIRGFEDK + 2 Phospho (ST)
✓	935	785.2390	1568.4634	1566.7153	1.7481	0	18	82	1	GSI GMPPGPFLGELK + Phospho (ST)
✓	1232	786.9753	2357.9042	2356.1450	1.7592	2	18	73	1	GCKAIYASGGATCIVLRDGMTR
✓	1266	816.3087	2445.9042	2445.1858	0.7184	1	18	75	1	FSLIGKLNSEHNFIPTLSR + 2 Phospho (ST)
✓	1151	693.7987	2078.3742	2078.6938	-0.3197	0	18	85	1	SSSIGHSGSTAPWSSVGR + 4 Phospho (ST)
✓	753	437.4720	1309.3942	1309.6755	-0.2813	2	18	77	1	ISARKLSEAQK + Phospho (ST)
✓	918	509.7687	1526.2842	1524.6514	1.6328	0	18	85	1	DLSEVEQLAYVIK + 2 Phospho (ST)
✓	954	792.9340	1583.8534	1583.7378	0.1156	2	18	70	1	EAPARIASMSKDTK + Phospho (ST)
✓	1239	790.1453	2367.4142	2366.1188	1.2954	0	18	80	1	VIIITGASSGIGEATAILLAEK + 3 Phospho (ST)
✓	974	532.2887	1593.8442	1593.8362	0.0079	0	18	69	1	GVEVVHAETLENAVK
✓	890	738.5240	1475.0334	1474.4779	0.5555	1	18	87	1	SSTESPRAADK + 3 Phospho (ST)
✓	1045	594.3720	1780.0942	1779.7482	0.3460	0	18	81	1	SLPVSDVLSGFEQR + 2 Phospho (ST)
✓	984	810.8440	1619.6734	1620.6933	-1.0199	1	18	71	1	NEDGTWPRGPTPK + Phospho (ST)
✓	1058	917.5490	1833.0834	1834.6060	-1.5226	0	18	79	1	GTVSQGLSDADESSR + 3 Phospho (ST)
✓	1164	700.0953	2097.2642	2095.9163	1.3479	1	18	83	1	TPAQSTHSEAPPSKMVLK + 2 Phospho (ST)
✓	1057	611.5587	1831.6542	1829.8988	1.7553	2	18	81	1	IAEVASAHGCTGKMSRR
✓	1188	713.4820	2137.4242	2136.9705	0.4537	1	18	89	1	VVASDAGTPIKSSTSTLTVR + 2 Phospho (ST)
✓	580	488.0140	974.0134	975.5171	-1.5037	0	18	85	1	TMVANLATR
✓	1181	712.2020	2133.5842	2133.8915	-0.3074	0	18	88	1	AAQNMNTTAAQPVGSLSQK + 2 Phospho (ST)
✓	972	532.0820	1593.2242	1594.6017	-1.3775	1	18	92	1	KLPGCQHITSSK + 3 Phospho (ST)
✓	1108	659.4320	1975.2742	1974.8449	0.4293	1	18	89	1	SSIGHIRDLPSTGSSSSK + 2 Phospho (ST)
✓	1271	833.9253	2498.7542	2499.1213	-0.3671	0	18	87	1	LTGQSSIGVIIGKPVFEGGSLGR + 3 Phospho (ST)
✓	552	460.2840	918.5534	918.4883	0.0652	2	18	62	1	NGDKTRTK
✓	1001	556.7853	1667.3342	1665.9219	1.4123	0	18	95	1	TIALHLIPSGILNPK + Phospho (ST)

✓	1112	662.1020	1983.2842	1984.9530	-1.6689	2	18	92	1	FWDKETSLDKDVFR
✓	1288	872.7053	2615.0942	2615.2655	-0.1714	2	18	73	1	SGAPTLLPSSVQVAR\$MATARLR + 2 Phospho (ST)
✓	665	401.7353	1202.1842	1202.7387	-0.5545	1	18	89	1	LGVGFLVKTAAK
✓	693	418.8220	1253.4442	1252.5853	0.8589	0	18	75	1	LQ\$PTPFLDR + Phospho (ST)
✓	849	710.2040	1418.3934	1417.6434	0.7501	2	18	89	1	QKDGAGGDDAKDK
✓	525	436.0140	870.0134	871.5491	-1.5356	1	18	87	1	KATVVLNK
✓	675	411.6120	1231.8142	1231.5710	0.2431	0	18	80	1	RP\$DPG\$IPLR + Phospho (ST)
✓	957	793.9890	1585.9634	1584.6278	1.3357	0	18	84	1	\$NGSSRPNESNGSGR + Phospho (ST)
✓	1179	710.2020	2127.5842	2125.8540	1.7302	1	18	93	1	EVG\$AGKAVLVF\$TAAIAK + 4 Phospho (ST)
✓	868	720.4990	1438.9834	1438.7681	0.2154	2	18	89	1	NNIRYAGNKYVK
✓	1252	795.9520	2384.8342	2383.1897	1.6445	1	18	86	1	YGKPVAAVG\$G\$VALKNAGIDSSR + Phospho (ST)
✓	999	556.1320	1665.3742	1665.7449	-0.3708	1	18	95	1	\$TALMTISQKLGKEK + 2 Phospho (ST)
✓	1044	594.0953	1779.2642	1780.5744	-1.3102	0	18	95	1	EAV\$SSHG\$DPIDR + 3 Phospho (ST)
✓	569	471.9740	941.9334	941.3978	0.5357	0	18	91	1	EYGETESK
✓	709	632.5490	1263.0834	1262.5881	0.4954	1	18	90	1	AAGTHARLGSSR + Phospho (ST)
✓	1042	591.0853	1770.2342	1771.5730	-1.3388	2	18	97	1	GG\$LE\$RSS\$SR\$R + 4 Phospho (ST)
✓	1093	638.1120	1911.3142	1910.9519	0.3623	1	18	95	1	\$KDLPLIIPVVVSNAAK + 2 Phospho (ST)
✓	1275	839.8387	2516.4942	2515.1843	1.3099	0	18	87	1	LTS\$YAGNIDSIGGIVLENER + Phospho (ST)
✓	1303	948.1653	2841.4742	2841.0179	0.4563	1	18	73	1	KCICCPQPTCCVQPTCCSENK + Phospho (ST)
✓	1310	992.8087	2975.4042	2975.5085	-0.1044	0	18	68	1	STEYASSIG\$AATLVQYILVFFIIFR + Phospho (ST)
✓	995	552.1987	1653.5742	1653.6913	-0.1171	0	18	87	1	RPSP\$ASAPETAAPR + 2 Phospho (ST)
✓	683	625.5790	1249.1434	1249.5939	-0.4504	1	18	90	1	DSPDRVGDYVK
✓	856	475.5520	1423.6342	1424.6701	-1.0359	0	18	74	1	ALGI\$DAAVSQWK + Phospho (ST)
✓	1094	638.1320	1911.3742	1912.6322	-1.2580	1	18	98	1	GGCGSCG\$KGGCG\$G\$K + Phospho (ST)
✓	697	420.0653	1257.1742	1257.4080	-0.2339	1	17	98	1	LK\$DEP\$SR + 3 Phospho (ST)
✓	1226	783.2520	2346.7342	2346.1441	0.5901	2	17	93	1	SASLLGV\$IDGGAHEIARR\$R + Phospho (ST)
✓	1308	973.8087	2918.4042	2920.1872	-1.7831	2	17	70	1	\$LTLNLIT\$EMGRLPITFMTQKAR + 5 Phospho (ST)
✓	1085	948.4290	1894.8434	1894.7863	0.0571	1	17	77	1	SPPDLEAH\$S\$ANKGPTK + 2 Phospho (ST)
✓	869	721.5640	1441.1134	1442.6919	-1.5784	0	17	98	1	AFATLQSV\$GVGAR + Phospho (ST)
✓	806	459.5420	1375.6042	1376.4663	-0.8621	2	17	74	1	D\$KK\$TASDAK + 3 Phospho (ST)
✓	959	794.0340	1586.0534	1584.8334	1.2201	1	17	98	1	GFLSSLNLFGMGKK
✓	1321	1069.3920	3205.1542	3203.7571	1.3971	0	17	79	1	AVLVG\$PTINN\$ILPVV\$PLLDLVLGRPK + Phospho (ST)
✓	649	581.7340	1161.4534	1161.5819	-0.1284	1	17	72	1	TFSVRFDYK
✓	1130	679.5920	2035.7542	2034.8941	0.8601	1	17	89	1	IIS\$N\$THAIKLENLR + 3 Phospho (ST)
✓	484	418.5540	835.0934	833.5123	1.5811	1	17	78	1	VKTAFLR
✓	865	716.9840	1431.9534	1431.7180	0.2354	1	17	96	1	ECAKNGDWLVLK
✓	1024	858.8990	1715.7834	1714.8655	0.9180	1	17	80	1	HPEITIVLATGNKDK + Phospho (ST)
✓	1244	793.7553	2378.2442	2377.0968	1.1474	2	17	82	1	TEF\$K\$T\$PLLDTIRTPDDL + 2 Phospho (ST)
✓	592	999.8100	998.8027	998.4182	0.3845	1	17	97	1	AARE\$SNGK + Phospho (ST)
✓	830	466.8487	1397.5242	1397.7279	-0.2037	2	17	84	1	G\$ISLKTSLREK + Phospho (ST)
✓	1074	626.7620	1877.2642	1877.8942	-0.6300	1	17	1e+002	1	DFAEVRADGAINGDVAMK
✓	1299	930.3853	2788.1342	2788.4038	-0.2696	1	17	82	1	V\$GGLHGVGV\$VVNALSSKLELTIHR + 2 Phospho (ST)
✓	1302	941.2620	2820.7642	2820.1293	0.6348	2	17	93	1	TGVLPGDV\$D\$ATSDSAK\$K\$G\$G\$K + 3 Phospho (ST)
✓	1180	710.8720	2129.5942	2129.9443	-0.3501	2	17	1e+002	1	VGIGRVMVG\$G\$GVRGAPDAR + 2 Phospho (ST)
✓	1028	867.6290	1733.2434	1734.8553	-1.6119	1	17	1.1e+002	1	AEDNLIVK\$VNPIQK + Phospho (ST)
✓	448	688.3700	687.3627	687.3738	-0.0110	1	17	87	1	GKAMPGK
✓	728	638.1340	1274.2534	1272.6149	1.6386	1	17	1e+002	1	LMSSVVK\$GTGK + Phospho (ST)
✓	861	476.5720	1426.6942	1426.8031	-0.1089	2	17	80	1	LLSGEEPKIGEEK
✓	1069	625.1153	1872.3242	1871.7816	0.5426	2	17	1.1e+002	1	\$STPKVFSKNSS\$NR\$R + 2 Phospho (ST)
✓	1189	713.7620	2138.2642	2138.1517	0.1125	2	17	96	1	KITLT\$TPKLVILAANAPK + 2 Phospho (ST)
✓	750	436.0120	1305.0142	1305.5714	-0.5573	0	17	1e+002	1	NHLVVGNSGD\$K + Phospho (ST)
✓	1182	712.3387	2133.9942	2133.1056	0.8886	2	17	81	1	RGRG\$SAVAGPTVVA\$INGSVK + Phospho (ST)
✓	634	556.1340	1110.2534	1110.4069	-0.1535	0	17	95	1	\$MELGITVK + 2 Phospho (ST)
✓	1006	560.0587	1677.1542	1678.8791	-1.7249	0	17	1.1e+002	1	HAQFGISLSDLHLNK
✓	1091	637.6053	1909.7942	1908.9054	0.8887	1	17	87	1	TQSSHLS\$ISSGALLER + Phospho (ST)
✓	832	700.0990	1398.1834	1396.6613	1.5222	0	17	1.1e+002	1	HGH\$TRPVEGLK + Phospho (ST)
✓	824	698.4890	1394.9634	1393.6966	1.2668	1	17	1e+002	1	LQVLAR\$SPTDK + Phospho (ST)
✓	467	777.4800	776.4727	776.4796	-0.0069	0	17	65	1	FLGLSLK
✓	643	569.5740	1137.1334	1136.4557	0.6778	0	17	1e+002	1	GADPDMFDNR
✓	647	578.8290	1155.6434	1156.6452	-1.0017	1	17	83	1	EIIVDKIGDR
✓	1097	961.0790	1920.1434	1918.8859	1.2576	1	17	98	1	K\$SIV\$FLSLLGSLTK + 3 Phospho (ST)
✓	1296	917.6853	2750.0342	2749.5143	0.5199	1	17	92	1	VAPARIVVGASTGGPPALEIL\$SLPK + Phospho (ST)
✓	1305	960.1153	2877.3242	2876.2681	1.0561	1	17	78	1	ITEVNGLSLESTIMG\$AVKVLIGSSR + 3 Phospho (ST)
✓	1088	636.3187	1905.9342	1906.9319	-0.9977	0	17	87	1	IGGLTILHG\$LAPGGAVVK + 2 Phospho (ST)
✓	1250	794.1753	2379.5042	2378.9473	0.5568	2	17	1.1e+002	1	DDWLEAI\$S\$IEEYAKKR + 3 Phospho (ST)

866	717.5540	1433.0934	1433.6204	-0.5270	1	17	1.1e+002	1	IIVEEGERIIIK + 2 Phospho (ST)
1023	858.6990	1715.3834	1716.8253	-1.4418	0	17	1.1e+002	1	YIIVPVLVGS_LPGSR + 2 Phospho (ST)
567	941.2800	940.2727	941.4444	-1.1716	2	17	85	1	TNKT_SRR + Phospho (ST)
740	432.5253	1294.5542	1294.5741	-0.0199	0	17	82	1	_SLGLDNPVMR + Phospho (ST)
1123	676.3820	2026.1242	2025.9124	0.2117	1	17	96	1	QKV_SILVL_SAMGS_NLR + 3 Phospho (ST)
361	546.4400	545.4327	546.1922	-0.7594	0	17	1e+002	1	DPNSD
565	469.2440	936.4734	937.5709	-1.0974	0	17	70	1	KPQAAAKPK
603	512.9940	1023.9734	1024.5318	-0.5583	2	17	1e+002	1	VEAVGS_KKK + Phospho (ST)
355	546.3000	545.2927	546.1922	-0.8994	0	17	1e+002	1	DPNSD
922	514.0153	1539.0242	1537.7137	1.3104	0	17	1.1e+002	1	VLEGSSASIIANGR + Phospho (ST)
1228	785.9420	2354.8042	2353.0726	1.7316	0	17	1.1e+002	1	TEDLSSNFLSLQEIQI_TAYSK + Phospho (ST)
774	673.0390	1344.0634	1345.6837	-1.6203	1	17	1.2e+002	1	QTESVLEEQKR
751	436.0853	1305.2342	1305.6751	-0.4409	1	17	1.1e+002	1	MVKDVVAEPYR
1113	992.8090	1983.6034	1985.0887	-1.4852	2	17	1.1e+002	1	ISYYIFKIRYLQHNK
1160	699.3953	2095.1642	2093.7510	1.4131	1	17	1e+002	1	AGDGGRSGSPSTPSTSVITK + 4 Phospho (ST)
992	546.9353	1637.7842	1638.7890	-1.0048	0	17	91	1	TPEELFHPLGADSVQ
1307	961.7453	2882.2142	2881.1374	1.0767	0	17	90	1	_SGISDDAS_VPAIVHEIPPNASI_SAAR + 4 Phospho (ST)
745	435.8453	1304.5142	1304.7201	-0.2059	2	17	90	1	FEKTGAVRELR
1211	742.5387	2224.5942	2226.0794	-1.4852	2	17	1.2e+002	1	VDRPAITGGKGEGLTEQTFKR + Phospho (ST)
645	573.4640	1144.9134	1145.5192	-0.6057	0	17	1.1e+002	1	YLNTIS_PMK + Phospho (ST)
1157	698.4887	2092.4442	2092.5837	-0.1395	1	17	1.2e+002	1	SNSSSSSSSDEEGEEKK + 4 Phospho (ST)
733	641.4090	1280.8034	1280.5146	0.2888	1	17	98	1	LRTDSHDDSR + Phospho (ST)
789	681.9590	1361.9034	1361.5517	0.3518	1	17	1.1e+002	1	_IGEDVT_PDKLK + 2 Phospho (ST)
354	546.2800	545.2727	545.2809	-0.0082	0	17	1.1e+002	1	AALNAS
375	573.1800	572.1727	571.1639	1.0088	0	17	1.1e+002	1	ANGSGS_ + Phospho (ST)
1234	787.4987	2359.4742	2358.9829	0.4912	0	17	1.2e+002	1	GTTTNATSTTTTASTAVADAQK + 2 Phospho (ST)
1077	941.2640	1880.5134	1880.8557	-0.3423	0	16	1.2e+002	1	VYSGVINS_GDIVYNSVK + Phospho (ST)
390	590.4700	589.4627	589.2708	0.1920	0	16	94	1	DPSGSK
1019	849.3290	1696.6434	1695.8944	0.7491	2	16	1e+002	1	TNSEALKRPFKYDK
853	712.3390	1422.6634	1422.6157	0.0478	1	16	94	1	_SITNLGTGNSKK + 2 Phospho (ST)
1225	782.0753	2343.2042	2344.0359	-0.8318	0	16	99	1	DDADSETVALGEGYVAVI_PLK + Phospho (ST)
886	735.2940	1468.5734	1467.7082	0.8652	1	16	1e+002	1	RSAP_SATTSSKPAK + Phospho (ST)
519	435.7940	869.5734	870.5109	-0.9375	1	16	93	1	KLGVAPMR
637	560.0590	1118.1034	1117.6316	0.4719	2	16	1.2e+002	1	RLRTASSTAR
1273	835.9320	2504.7742	2505.1358	-0.3617	0	16	1.2e+002	1	QEFGLILIQATSLISAAFISR + 3 Phospho (ST)
1029	578.8287	1733.4642	1732.9696	0.4946	1	16	1.3e+002	1	NALQVALAEHVRVSAR
629	546.0790	1090.1434	1090.5479	-0.4044	2	16	1.2e+002	1	ERSKGASSNR
754	437.5787	1309.7142	1310.6496	-0.9355	0	16	1e+002	1	FARPTVGALGS_ + Phospho (ST)
1291	883.2020	2646.5842	2646.2140	0.3702	2	16	1.2e+002	1	GARSVYHQLFMSSLLMDLYK + 2 Phospho (ST)
517	869.4300	868.4227	869.3756	-0.9529	1	16	88	1	VDSGTRR + Phospho (ST)
368	556.4800	555.4727	556.2969	-0.8242	1	16	95	1	KAGNPA
756	439.3853	1315.1342	1313.6646	1.4696	0	16	1.3e+002	1	AVIHIVGPVWR + Phospho (ST)
981	537.9620	1610.8642	1610.7189	0.1453	1	16	1.1e+002	1	TKAAPVEIVDETR + Phospho (ST)
369	556.5200	555.5127	556.2969	-0.7842	1	16	97	1	KAGNPA
1253	796.0920	2385.2542	2386.9193	-1.6651	2	16	1.1e+002	1	SRSRPT_SILDAAGSGSGSGSGSP + 3 Phospho (ST)
993	823.4940	1644.9734	1643.7780	1.1954	1	16	1.2e+002	1	RPAANADDVAPPSKR + Phospho (ST)
836	701.3790	1400.7434	1399.6748	1.0686	0	16	1.1e+002	1	S_LFTAPASASALQK + Phospho (ST)
1117	672.2987	2013.8742	2014.9262	-1.0520	1	16	1.1e+002	1	YQGGANAGHTV_IAKGQTFK + Phospho (ST)
385	590.4500	589.4427	590.3136	-0.8709	1	16	99	1	GSRS GK
546	459.2840	916.5534	917.4131	-0.8596	0	16	1e+002	1	FSTYASDK
900	745.6940	1489.3734	1489.4289	-0.0555	1	16	1.3e+002	1	SISR_SSTTSR + 4 Phospho (ST)
1009	840.9540	1679.8934	1680.8083	-0.9149	2	16	1.1e+002	1	VRDLEDKLE_SIER + Phospho (ST)
623	532.2890	1062.5634	1061.5658	0.9977	0	16	93	1	LQPIYWSR
1176	1058.1290	2114.2434	2116.0215	-1.7781	2	16	1.3e+002	1	TTRFHPTRQS_SLYTVSR + Phospho (ST)
566	937.6600	936.6527	938.4296	-1.7769	0	16	98	1	MV_SALGGPK + Phospho (ST)
1133	681.9620	2042.8642	2043.1282	-0.2640	0	16	1.1e+002	1	LAAQVIS_SGTFLGAGVILHK + Phospho (ST)
670	610.8540	1219.6934	1219.4870	0.2064	0	16	1e+002	1	LADTDDHPIR + Phospho (ST)
767	444.1353	1329.3842	1330.6223	-1.2382	1	16	1.3e+002	1	WNGLRV_SYGK + Phospho (ST)
1106	985.2890	1968.5634	1968.9744	-0.4109	0	16	1.4e+002	1	MTL_SAPSDALVIAGKPYP + Phospho (ST)
749	436.0120	1305.0142	1306.7010	-1.6868	1	16	1.3e+002	1	KLVIAT_INNGLGK + Phospho (ST)
829	466.8420	1397.5042	1397.6439	-0.1397	2	16	1.2e+002	1	QKK_SLDDLEDK + Phospho (ST)
987	814.5640	1627.1134	1626.7551	0.3584	0	16	1.5e+002	1	YSDHITVPIMMIK + Phospho (ST)
1159	699.0953	2094.2642	2093.1286	1.1356	1	16	1.3e+002	1	LIVATGSSPHILPIPADKK + Phospho (ST)
541	446.8890	891.7634	893.4008	-1.6373	0	16	1.2e+002	1	AAPSELAR + Phospho (ST)
1177	1058.1440	2114.2734	2114.9173	-0.6439	0	16	1.4e+002	1	AENPELISGENSAAALLEK + 2 Phospho (ST)

✓	727	638.1140	1274.2134	1273.6180	0.5955	2	16	1.4e+002	1	ISYKKGASNR + Phospho (ST)
✓	1071	625.5787	1873.7142	1873.8740	-0.1598	1	16	1.3e+002	1	KTSSGSLPPLSLFGAR + 2 Phospho (ST)
✓	978	804.3840	1606.7534	1605.7463	1.0071	2	16	1.1e+002	1	RIARTVCGSSLVK + 2 Phospho (ST)
✓	1318	1058.1287	3171.3642	3171.0398	0.3244	1	16	1e+002	1	TSLLSSTSSDPHHLRPIIDRSPK + 8 Phospho (ST)
✓	831	466.8553	1397.5442	1398.4070	-0.8629	0	16	1.2e+002	1	EIAFEFLSSE + 3 Phospho (ST)
✓	973	532.2153	1593.6242	1593.6647	-0.0406	0	16	1.2e+002	1	VGFTCEAGGFGIGVR + Phospho (ST)
✓	699	629.8090	1257.6034	1257.5364	0.0670	2	16	1.1e+002	1	GGRSGGRDFGGR + Phospho (ST)
✓	899	496.3253	1485.9542	1486.7909	-0.8367	0	16	1.4e+002	1	SIPHIIVISATLR + Phospho (ST)
✓	1298	927.9220	2780.7442	2779.0697	1.6744	0	16	1.4e+002	1	IIMQSIISDSNNSSTDPISSGEIR + 3 Phospho (ST)
✓	889	738.0990	1474.1834	1473.4939	0.6896	0	16	1.5e+002	1	STNLSSANGGAAGSK + 3 Phospho (ST)
✓	920	767.4640	1532.9134	1531.8206	1.0929	1	16	1.3e+002	1	ATETLKATGISGDLR
✓	676	616.9690	1231.9234	1233.5503	-1.6268	1	16	1.4e+002	1	SSSHSLSHKGGK + Phospho (ST)
✓	837	469.2420	1404.7042	1405.6966	-0.9925	0	16	1.2e+002	1	VPLIAGVGTNEIR + Phospho (ST)
✓	878	488.0153	1461.0242	1461.6581	-0.6339	0	16	1.5e+002	1	SFPLWYEEALK + Phospho (ST)
✓	1293	891.7520	2672.2342	2673.1367	-0.9025	1	15	1.1e+002	1	AGRSSSVAGTLPAGVVGSPAGVTIR + 4 Phospho (ST)
✓	814	461.1887	1380.5442	1379.6698	0.8744	0	15	1.2e+002	1	APVLVSGTDGVGVIK + Phospho (ST)
✓	1031	581.7353	1742.1842	1740.7971	1.3870	1	15	1.6e+002	1	EQFPKETVVESSGPK + Phospho (ST)
✓	1200	725.3920	2173.1542	2174.0749	-0.9207	2	15	1.3e+002	1	KIVIIQAAGKDQGVVLGTTK + 2 Phospho (ST)
✓	1171	703.8953	2108.6642	2109.9272	-1.2631	1	15	1.5e+002	1	ALSGKDYIAETDPGVLVVK + 2 Phospho (ST)
✓	1249	794.1320	2379.3742	2379.0178	0.3564	1	15	1.4e+002	1	GMGTNEAAIIEILSGRTSDER + 2 Phospho (ST)
✓	921	512.9953	1535.9642	1535.7820	0.1821	2	15	1.4e+002	1	AQEEARIARIK + Phospho (ST)
✓	1119	673.6187	2017.8342	2016.1554	1.6788	2	15	1.3e+002	1	KTPVFLESLVTNMLRLR
✓	609	523.4790	1044.9434	1044.6040	0.3395	2	15	1.5e+002	1	ISIRASDKR
✓	1237	789.6920	2366.0542	2364.8640	1.1901	0	15	1.2e+002	1	DTECLLDSSDIEAMEGHR + 2 Phospho (ST)
✓	867	718.7240	1435.4334	1436.5408	-1.1074	0	15	1.5e+002	1	VPSIMTGSVDAR + 2 Phospho (ST)
✓	1082	631.5987	1891.7742	1890.6695	1.1047	1	15	1.3e+002	1	DMSGADITTPSRLCK + 3 Phospho (ST)
✓	1254	796.3820	2386.1242	2385.0767	1.0475	0	15	1.2e+002	1	NLLDSEPVHQVGNFITSSLR + 2 Phospho (ST)
✓	622	532.2140	1062.4134	1062.5305	-0.1171	1	15	1.1e+002	1	KLTDGAESSR
✓	969	797.1340	1592.2534	1591.5596	0.6938	0	15	1.6e+002	1	EEETSNIADMEEK + Phospho (ST)
✓	884	489.5920	1465.7542	1464.5786	1.1756	0	15	1.2e+002	1	TIEELNEALSAAK + 2 Phospho (ST)
✓	1137	686.3553	2056.0442	2056.8884	-0.8442	1	15	1.3e+002	1	LDGNLKAVASSSQSLVIK + 3 Phospho (ST)
✓	1144	688.2820	2061.8242	2060.0667	1.7575	1	15	1.4e+002	1	ILLGKESTGGLGAGGIPDIGR + Phospho (ST)
✓	1156	698.3053	2091.8942	2092.9500	-1.0559	1	15	1.3e+002	1	TSTGFSTGGATAEDIALMRK + Phospho (ST)
✓	555	462.7490	923.4834	923.4937	-0.0103	0	15	1.1e+002	1	AIGSNHGLR
✓	945	787.4990	1572.9834	1571.6327	1.3508	1	15	1.5e+002	1	MSESSTYFEKQR + Phospho (ST)
✓	598	508.0390	1014.0634	1012.5665	1.4969	0	15	1.6e+002	1	KPQGTVDLR
✓	1089	636.5820	1906.7242	1906.0384	0.6857	2	15	1.5e+002	1	IPVSSASIAVNEGRKHGGK
✓	927	782.0790	1562.1434	1563.6705	-1.5270	1	15	1.7e+002	1	GGCAGGQCCGPLRSK
✓	1142	688.1687	2061.4842	2059.8904	1.5937	2	15	1.7e+002	1	EVVIVKTEELSDGFKR + 2 Phospho (ST)
✓	1202	735.0487	2202.1242	2203.0262	-0.9020	1	15	1.3e+002	1	RDIVAIIAAMPGPTGLSAFR + 2 Phospho (ST)
✓	1138	1029.7390	2057.4634	2057.9201	-0.4567	2	15	1.7e+002	1	SRSEINPGSMEGTQTLKR + Phospho (ST)
✓	1323	1106.3120	3315.9142	3314.4771	1.4371	2	15	1.3e+002	1	YSDAMGATVLDENGREKSVIMGCVGIGVSR + Phospho (ST)
✓	1233	787.0753	2358.2042	2358.8929	-0.6887	1	15	1.4e+002	1	CRKPCSVTSYQLSAGYSR + 3 Phospho (ST)
✓	619	531.2090	1060.4034	1061.5757	-1.1722	0	15	1.3e+002	1	EEFINALVK
✓	780	676.3790	1350.7434	1351.6190	-0.8755	1	15	1.3e+002	1	STGDKLAIFIK + 2 Phospho (ST)
✓	1149	690.1353	2067.3842	2066.8751	0.5091	1	15	1.7e+002	1	KEQTAFAESIDLNQWK + 2 Phospho (ST)
✓	902	751.6890	1501.3634	1501.7929	-0.4295	0	15	1.7e+002	1	AGFEPHTAFVSVLK
✓	873	725.3940	1448.7734	1448.6952	0.0782	0	15	1.3e+002	1	SLISQLYPSFSK + Phospho (ST)
✓	1124	676.6787	2027.0142	2025.9984	1.0158	1	15	1.4e+002	1	TDVTVKILAAEIQTSDVR + Phospho (ST)
✓	1147	688.8187	2063.4342	2061.8544	1.5797	2	15	1.8e+002	1	KADPTSSDISEPSESPKK + 2 Phospho (ST)
✓	965	795.9540	1589.8934	1588.6075	1.2859	0	15	1.4e+002	1	EITLSDTLVSGSK + 3 Phospho (ST)
✓	222	461.3600	460.3527	460.2394	0.1133	0	15	1.6e+002	1	ATGGR
✓	775	673.6190	1345.2234	1345.5526	-0.3292	0	15	1.8e+002	1	MDTYHFLPSR + Phospho (ST)
✓	1037	588.5753	1762.7042	1762.7977	-0.0936	0	15	1.5e+002	1	SLTALGMVINALTDGK + 2 Phospho (ST)
✓	1245	793.9887	2378.9442	2379.2466	-0.3024	0	15	1.5e+002	1	MVDAFFQIIVLLFSLFLGAR + Phospho (ST)
✓	938	786.1390	1570.2634	1571.7072	-1.4438	1	15	1.8e+002	1	VMDSTAFSMARDNK
✓	1015	565.5220	1693.5442	1694.6161	-1.0719	1	15	1.7e+002	1	EFSDIDCNHERK + 2 Phospho (ST)
✓	1059	917.6840	1833.3534	1832.8016	0.5519	0	15	1.8e+002	1	TSCGSLNYAAPEVISGK + Phospho (ST)
✓	572	476.5740	951.1334	949.5457	1.5877	2	15	1.5e+002	1	SVYAARKR
✓	1003	835.9290	1669.8434	1669.6637	0.1797	1	15	1.4e+002	1	GGKIAIYDSNSEEK + 2 Phospho (ST)
✓	1096	640.5453	1918.6142	1916.8405	1.7737	0	15	1.7e+002	1	VVPGSEPAAPQETAETSA + Phospho (ST)
✓	892	740.8290	1479.6434	1480.7221	-1.0787	2	15	1.4e+002	1	DMVGKVRSKPR + Phospho (ST)
✓	1238	789.9753	2366.9042	2368.1269	-1.2227	1	15	1.6e+002	1	AQFSINLIDKWIQIAYGK + 2 Phospho (ST)
✓	1146	688.7687	2063.2842	2064.1295	-0.8453	1	15	1.8e+002	1	LIAYNLVKEAFDLWLEK
✓	533	439.5140	877.0134	876.4552	0.5582	1	15	1.5e+002	1	IKDSASEK

✓	1052	601.5620	1801.6642	1801.8764	-0.2122	0	15	1.7e+002	1	FIDLIPSNLPHEA <u>IR</u> + Phospho (ST)
✓	1154	695.4387	2083.2942	2081.9159	1.3783	1	15	1.8e+002	1	VA <u>IN</u> LARNMVTQWGF <u>SK</u> + 2 Phospho (ST)
✓	446	686.3200	685.3127	685.3143	-0.0016	0	15	1.4e+002	1	NGSSHGK
✓	601	509.7690	1017.5234	1017.5567	-0.0332	1	15	1.3e+002	1	KSQALSGTAR
✓	905	756.4090	1510.8034	1510.7769	0.0265	1	15	1.5e+002	1	IH <u>ILL</u> IGH <u>SERR</u> + Phospho (ST)
✓	1243	793.6120	2377.8142	2379.0356	-1.2214	2	15	1.7e+002	1	KDQIGKGTQGATAGASS <u>ELDA</u> <u>SK</u> + 2 Phospho (ST)
✓	955	793.6090	1585.2034	1583.7944	1.4091	1	15	1.9e+002	1	GDKSTDFYIVINGR
✓	65	421.2600	420.2527	421.1809	-0.9282	0	15	66	1	TSSAG
✓	777	450.1853	1347.5342	1346.4710	1.0632	1	15	1.5e+002	1	LGFI <u>S</u> KDPS <u>R</u> + 3 Phospho (ST)
✓	690	418.5520	1252.6342	1251.3611	1.2731	0	15	1.4e+002	1	<u>S</u> ASSDGFV <u>S</u> R + 3 Phospho (ST)
✓	1135	683.3553	2047.0442	2045.9895	1.0546	1	15	1.5e+002	1	AGGAY <u>S</u> LNLTGGSVTVRST <u>IR</u> + Phospho (ST)
✓	456	743.4200	742.4127	742.3974	0.0154	0	15	1.4e+002	1	GDVTVPR
✓	962	794.1740	1586.3334	1584.7120	1.6215	1	15	2e+002	1	ETW <u>N</u> IRLLGCQK + Phospho (ST)
✓	928	783.2490	1564.4834	1562.9297	1.5538	2	15	1.8e+002	1	HKNPFTIQLPIKK
✓	952	528.1553	1581.4442	1582.5904	-1.1463	1	14	1.9e+002	1	<u>S</u> ISKSITSMF <u>S</u> R + 3 Phospho (ST)
✓	202	460.8500	459.8427	460.2394	-0.3967	0	14	2.7e+002	1	AASGR
✓	457	744.4200	743.4127	742.3973	1.0154	0	14	1.5e+002	1	AAESLPR
✓	864	477.5953	1429.7642	1429.7078	0.0563	2	14	1.5e+002	1	FESLSKQR <u>S</u> L + Phospho (ST)
✓	1127	677.3253	2028.9542	2029.8499	-0.8958	2	14	1.5e+002	1	<u>T</u> SMRCQGRAYGTGSSGFK + Phospho (ST)
✓	1260	804.3820	2410.1242	2409.0090	1.1152	0	14	1.5e+002	1	VSDGTTIPLHLSMQGGSAAIVK + 3 Phospho (ST)
✓	1100	643.0353	1926.0842	1925.8577	0.2264	0	14	1.7e+002	1	YALGDAFGLPVGI <u>VT</u> IGK + 2 Phospho (ST)
✓	575	481.6890	961.3634	961.4746	-0.1112	0	14	1.4e+002	1	GVV <u>I</u> THLR + Phospho (ST)
✓	1086	635.7087	1904.1042	1904.9609	-0.8567	1	14	1.8e+002	1	LVLGGAPAGPAGI <u>GK</u> TETTK + Phospho (ST)
✓	1251	794.2020	2379.5842	2380.0591	-0.4749	2	14	2e+002	1	MSDENNKGVGI <u>AV</u> GVGGPRDGR + Phospho (ST)
✓	1046	891.4590	1780.9034	1779.7247	1.1788	0	14	1.6e+002	1	ATHVGAD <u>IT</u> L <u>S</u> QIVK + 3 Phospho (ST)
✓	1209	740.8287	2219.4642	2219.0347	0.4294	1	14	2e+002	1	CHPFHPGGVDPVPEL <u>I</u> PKR + Phospho (ST)
✓	1212	742.6020	2224.7842	2225.7403	-0.9561	2	14	1.9e+002	1	<u>S</u> SRGTRNGGT <u>S</u> GGGGGGSGQR + 4 Phospho (ST)
✓	1025	573.4620	1717.3642	1718.6590	-1.2948	1	14	2.1e+002	1	DKYALF <u>S</u> SSSDP <u>S</u> R + 2 Phospho (ST)
✓	1311	1020.6153	3058.8242	3060.2667	-1.4425	1	14	1.8e+002	1	MAWPEDHVFISIPSFNYIGRDFQR + 2 Phospho (ST)
✓	1034	875.3490	1748.6834	1748.7635	-0.0800	0	14	1.8e+002	1	DIV <u>ST</u> IIPASSEITR + 2 Phospho (ST)
✓	872	724.3940	1446.7734	1447.7062	-0.9328	2	14	1.6e+002	1	SGGRNCGRITTR
✓	1231	786.5120	2356.5142	2356.9273	-0.4132	1	14	2.1e+002	1	GSSNPQGVTCGAA <u>IL</u> SAERVR + 3 Phospho (ST)
✓	1322	1071.8487	3212.5242	3211.2852	1.2390	0	14	1.4e+002	1	CLMCWRPTVPETQPD <u>T</u> DQGG <u>S</u> FLQA + 2 Phospho (ST)
✓	686	626.7640	1251.5134	1250.6102	0.9032	2	14	1.6e+002	1	KDEASGSQSKSK
✓	279	470.4300	469.4227	470.2853	-0.8626	0	14	1.3e+002	1	AGVPK
✓	1064	930.3840	1858.7534	1859.7509	-0.9974	0	14	1.8e+002	1	VIV <u>L</u> DLTNPATF <u>S</u> R + 3 Phospho (ST)
✓	365	548.3900	547.3827	547.2966	0.0862	1	14	1.2e+002	1	QKATT
✓	1240	790.1987	2367.5742	2366.1470	1.4272	1	14	2.1e+002	1	MHIVLIGPGIGKGIQAELLSK + 2 Phospho (ST)
✓	475	411.5540	821.0934	821.3796	-0.2862	1	14	1.6e+002	1	KSPAP <u>S</u> R + Phospho (ST)
✓	1315	1048.6587	3142.9542	3142.4771	0.4771	2	14	1.8e+002	1	IAR <u>S</u> AGTSVTISGLDGNYSLIKMT <u>S</u> GEVR + 2 Phospho (ST)
✓	1166	701.3787	2101.1142	2100.8400	0.2742	1	14	1.8e+002	1	Y <u>S</u> ITFIKW <u>S</u> QTAFPK + 3 Phospho (ST)
✓	860	714.0640	1426.1134	1426.8144	-0.7009	1	14	2.2e+002	1	SVDVAALKDAGIIR
✓	383	590.4300	589.4227	590.3136	-0.8909	1	14	1.6e+002	1	GSRSGK
✓	639	561.6490	1121.2834	1120.6353	0.6482	2	14	1.9e+002	1	EPPKVPNRGK
✓	1246	794.0253	2379.0542	2379.0834	-0.0292	1	14	1.7e+002	1	DDKIVAITAAMP <u>S</u> GIGLDLFGK + 2 Phospho (ST)
✓	380	590.3900	589.3827	590.3136	-0.9309	1	14	1.6e+002	1	GSRSGK
✓	698	629.7140	1257.4134	1257.5364	-0.1230	2	14	2e+002	1	GGR <u>S</u> GGRDFGGR + Phospho (ST)
✓	1193	715.6753	2144.0042	2144.9277	-0.9235	1	14	1.8e+002	1	FERTTTQLNDENGHF <u>IR</u> + Phospho (ST)
✓	466	777.0500	776.0427	777.3691	-1.3263	0	14	1.7e+002	1	TAQEAMK
✓	674	411.5520	1231.6342	1231.4904	0.1438	1	14	1.6e+002	1	TDGVSC <u>I</u> REK + Phospho (ST)
✓	937	786.0640	1570.1134	1571.7692	-1.6558	0	14	2.3e+002	1	VGASATDVHIFGADGR
✓	605	514.0590	1026.1034	1025.5311	0.5724	0	14	2.1e+002	1	ISFLPL <u>IR</u> + Phospho (ST)
✓	1021	569.5720	1705.6942	1706.6300	-0.9358	1	14	1.8e+002	1	KEYA <u>S</u> MYGP <u>IT</u> GDK + 2 Phospho (ST)
✓	422	636.4300	635.4227	635.3391	0.0836	1	14	1.1e+002	1	GRSGFL
✓	1316	1049.4253	3145.2542	3145.4887	-0.2345	1	14	1.7e+002	1	LHGTVPVIFERDGTAIT <u>S</u> YVDITPIQR + 2 Phospho (ST)
✓	483	418.5540	835.0934	835.3672	-0.2737	0	14	1.7e+002	1	DADTATSR
✓	382	590.4200	589.4127	590.3136	-0.9009	1	14	1.7e+002	1	GSRSGK
✓	1129	679.4787	2035.4142	2033.8190	1.5951	0	14	2.3e+002	1	DGETVWFCDVGQL <u>S</u> ER + Phospho (ST)
✓	391	590.4800	589.4727	590.3136	-0.8409	1	14	1.8e+002	1	GSRSGK
✓	936	785.9390	1569.8634	1571.6325	-1.7691	2	14	1.9e+002	1	DDD <u>S</u> QSRSPSR + Phospho (ST)
✓	1111	661.6120	1981.8142	1982.9020	-1.0878	0	14	1.9e+002	1	I <u>I</u> IGTNEECDLVAEALR + Phospho (ST)
✓	1229	786.0620	2355.1642	2354.9797	0.1844	1	14	1.8e+002	1	IVEGGE <u>S</u> ELLIKAVINQDGR + 3 Phospho (ST)
✓	1011	841.4990	1680.9834	1681.8036	-0.8202	1	14	2e+002	1	VEAVSDVRADVVT <u>S</u> R + Phospho (ST)
✓	1210	741.1487	2220.4242	2222.0385	-1.6143	2	14	2.3e+002	1	<u>I</u> ADALAAKYGNESIKLELR + 2 Phospho (ST)
✓	678	416.2520	1245.7342	1245.6707	0.0635	2	14	1.8e+002	1	HIRI <u>S</u> ASKVR + Phospho (ST)

✓	1270	829.7653	2486.2742	2485.3289	0.9453	1	14	1.9e+002	1	EQANVAISTLDGHVLDGHKLQLK
✓	388	590.4700	589.4627	590.3136	-0.8509	1	14	1.8e+002	1	GSRS GK
✓	1080	629.8087	1886.4042	1884.8642	1.5399	0	14	2.4e+002	1	FHGYAVQNDYETVQSK
✓	402	600.7100	599.7027	600.2867	-0.5840	0	14	2.3e+002	1	ADNPGK
✓	384	590.4500	589.4427	590.3136	-0.8709	1	14	1.7e+002	1	GSRS GK
✓	1092	637.6220	1909.8442	1909.9799	-0.1357	2	14	1.9e+002	1	TFPYHHAPTKDVAKNGK
✓	386	590.4500	589.4427	590.3136	-0.8709	1	14	1.8e+002	1	GSRS GK
✓	785	678.6340	1355.2534	1355.6169	-0.3635	2	14	2.4e+002	1	KCLWDSRVGR + Phospho (ST)
✓	428	661.3000	660.2927	659.3490	0.9437	0	13	1.7e+002	1	GDDIIK
✓	914	762.0890	1522.1634	1520.7600	1.4035	0	13	2.4e+002	1	LVSTSNVTAAHIK + Phospho (ST)
✓	401	600.4100	599.4027	600.2867	-0.8840	0	13	1.6e+002	1	ADNPGK
✓	381	590.4200	589.4127	590.3136	-0.9009	1	13	1.8e+002	1	GSRS GK
✓	961	794.1290	1586.2434	1584.7120	1.5315	1	13	2.6e+002	1	ETWNTRLGCGK + Phospho (ST)
✓	585	489.2090	976.4034	975.4410	0.9624	0	13	1.7e+002	1	AGFAGDDAPR
✓	1139	686.8920	2057.6542	2056.9103	0.7439	0	13	2.4e+002	1	LTNTAAIDTAPSYSPDGQR + Phospho (ST)
✓	389	590.4700	589.4627	590.3136	-0.8509	1	13	1.9e+002	1	GSRS GK
✓	1007	839.8390	1677.6634	1676.7732	0.8902	0	13	2.1e+002	1	GTVIYVGMEEGITIK + Phospho (ST)
✓	956	793.7540	1585.4934	1586.6031	-1.1096	1	13	2.4e+002	1	LAKSLSVSEER + 3 Phospho (ST)
✓	958	794.0240	1586.0334	1584.3725	1.6610	0	13	2.5e+002	1	STASTIIDITST + 5 Phospho (ST)
✓	1002	835.1340	1668.2534	1666.8179	1.4356	0	13	2.6e+002	1	SISVPISSSALLDNGK + Phospho (ST)
✓	688	627.1840	1252.3534	1252.6428	-0.2894	0	13	2.3e+002	1	TSILLVTSSPR + Phospho (ST)
✓	691	418.5553	1252.6442	1253.5653	-0.9211	0	13	1.9e+002	1	QTTTIGNNIPK + Phospho (ST)
✓	963	794.2040	1586.3934	1584.6250	1.7684	0	13	2.6e+002	1	SQGESDDDMGFLLD
✓	1152	695.0953	2082.2642	2083.9364	-1.6722	2	13	2.4e+002	1	ATYKSPQAYERSQNSFK + Phospho (ST)
✓	414	634.3800	633.3727	634.3221	-0.9493	1	13	1.4e+002	1	GRMGSK
✓	1016	848.3140	1694.6134	1693.7719	0.8416	2	13	2.3e+002	1	ETRLPVITRLIR + 3 Phospho (ST)
✓	1075	626.7920	1877.3542	1878.0284	-0.6743	0	13	2.6e+002	1	MNITTALPLPHLLSEK
✓	618	530.0640	1058.1134	1059.6149	-1.5014	2	13	2.6e+002	1	RTAAGTSKIR
✓	424	644.5100	643.5027	644.2419	-0.7391	0	13	2.2e+002	1	SVTGTI + Phospho (ST)
✓	940	786.5140	1571.0134	1570.8566	0.1568	1	13	2.5e+002	1	DDTADVLIQNLVKK
✓	1256	797.5887	2389.7442	2388.0154	1.7288	2	13	2.5e+002	1	NSSAKIVRPGISLGVRSPSR + 4 Phospho (ST)
✓	841	703.8940	1405.7734	1404.6666	1.1068	1	13	2.1e+002	1	LVLLIAKDSAK + 2 Phospho (ST)
✓	906	504.7987	1511.3742	1512.5915	-1.2173	0	13	2.6e+002	1	STSSLLPLPGSSK + 3 Phospho (ST)
✓	421	634.7100	633.7027	633.2970	0.4058	0	13	1.9e+002	1	DLDGSK
✓	1079	629.7153	1886.1242	1884.8642	1.2599	0	13	2.4e+002	1	FHGYAVQNDYETVQSK
✓	476	411.6090	821.2034	822.4963	-1.2929	0	13	1.8e+002	1	IPDIPLR
✓	742	651.4890	1300.9634	1301.6050	-0.6416	0	13	2.6e+002	1	TMTSVISLLNR + Phospho (ST)
✓	1289	874.6987	2621.0742	2621.2634	-0.1893	0	13	2.1e+002	1	YGPLMHLQLGEVSAVVVTSPDMAK + Phospho (ST)
✓	589	495.2590	988.5034	989.5393	-1.0359	0	13	1.9e+002	1	ATAIDIATSK
✓	1272	835.1320	2502.3742	2501.3060	1.0682	2	13	2.3e+002	1	EAAEIAQKAMDGHVLDGHKLQLK
✓	387	590.4500	589.4427	590.3136	-0.8709	1	13	2e+002	1	GSRS GK
✓	827	699.3940	1396.7734	1396.6599	0.1136	1	13	2.1e+002	1	KLIESGEINQAK + Phospho (ST)
✓	415	634.3800	633.3727	634.3286	-0.9559	0	13	1.5e+002	1	GSISGSK
✓	1081	629.8387	1886.4942	1884.8690	1.6251	2	13	2.8e+002	1	DRTSQASATESLDLRR + Phospho (ST)
✓	976	800.2890	1598.5634	1598.6491	-0.0857	0	13	2.5e+002	1	VVNITSPGHDASSR + 2 Phospho (ST)
✓	738	643.4740	1284.9334	1285.6683	-0.7348	0	13	2.7e+002	1	QDVSIIPPLPK + Phospho (ST)
✓	418	634.4700	633.4627	633.2970	0.1658	0	13	1.6e+002	1	DLDGSK
✓	432	671.2000	670.1927	669.4173	0.7754	1	13	2e+002	1	NAPKLK
✓	897	742.5990	1483.1834	1483.6764	-0.4929	0	13	2.8e+002	1	VHAGSQASQDSQGGR
✓	925	770.8390	1539.6634	1539.5061	0.1573	1	13	2.3e+002	1	SAKTATIGPGITK + 4 Phospho (ST)
✓	417	634.4500	633.4427	634.3286	-0.8859	0	13	1.6e+002	1	GSISGSK
✓	855	712.6640	1423.3134	1423.7184	-0.4050	1	13	2.8e+002	1	LKSNVLSAVNSGR + Phospho (ST)
✓	1145	688.3087	2061.9042	2063.0412	-1.1370	2	13	2.2e+002	1	SSAIPAAKVSSKHSKPSK + Phospho (ST)
✓	416	634.4100	633.4027	634.3286	-0.9259	0	13	1.5e+002	1	GSISGSK
✓	489	838.8400	837.8327	836.4028	1.4299	0	13	2.3e+002	1	DNYNAIK
✓	996	829.1040	1656.1934	1654.9155	1.2780	2	13	3e+002	1	ESSIPGAGLGVAKRK
✓	1033	874.6990	1747.3834	1745.7903	1.5932	1	13	3e+002	1	RAIFSVNEPSPPIR + 2 Phospho (ST)
✓	443	684.0400	683.0327	682.4014	0.6314	0	13	2.5e+002	1	ALASPPK
✓	1218	756.4053	2266.1942	2265.0994	1.0948	2	13	2.4e+002	1	MANNTRFGLSCGLVSPEREK
✓	583	488.6440	975.2734	973.4845	1.7889	2	13	2.5e+002	1	SKTKTTIK + Phospho (ST)
✓	91	429.2300	428.2227	428.2383	-0.0156	0	13	1.4e+002	1	AGPGK
✓	1041	590.4220	1768.2442	1768.7070	-0.4628	0	13	3.1e+002	1	LYPAGATINSDSGVTR + 2 Phospho (ST)
✓	668	609.5790	1217.1434	1217.7496	-0.6061	2	13	2.9e+002	1	KVIRGYEILK
✓	977	804.1790	1606.3434	1605.6742	0.6692	1	13	3e+002	1	GVRTFFSAFGITR + 2 Phospho (ST)
✓	1248	794.1287	2379.3642	2378.0620	1.3022	2	13	2.7e+002	1	DIKIVVPQILSSRHTGLMR + 3 Phospho (ST)

✓	474	411.4440	820.8734	822.4712	-1.5977	2	12	2.4e+002	1	AKSSFRK
✓	825	466.2487	1395.7242	1394.7058	1.0184	0	12	2.3e+002	1	SLALLGLSLEDGK + Phospho (ST)
✓	1292	891.4587	2671.3542	2672.3033	-0.9491	2	12	2.4e+002	1	YEILARAELKSLVCVESHYANK + Phospho (ST)
✓	1000	833.9240	1665.8334	1664.8803	0.9531	2	12	2.5e+002	1	SFIHPLYKIKVPR + Phospho (ST)
✓	784	677.3290	1352.6434	1352.4066	0.2368	0	12	2.4e+002	1	DSSMSAYMSSK + 2 Phospho (ST)
✓	1083	948.1690	1894.3234	1894.8980	-0.5746	1	12	3.2e+002	1	SNSDSARLPISSGSTSSSR
✓	1063	927.9240	1853.8334	1853.9247	-0.0912	1	12	2.5e+002	1	HIEVHDKLWVCQK
✓	419	634.5800	633.5727	634.3286	-0.7559	0	12	2.2e+002	1	GSISGSK
✓	788	680.5890	1359.1634	1358.7293	0.4342	1	12	3.2e+002	1	SLLEEDKVDLAK
✓	1095	960.1140	1918.2134	1918.0710	0.1425	2	12	3.1e+002	1	QENVKCAFKLLIQSIK
✓	586	489.5890	977.1634	977.5797	-0.4162	0	12	2.8e+002	1	IISEILYK
✓	1186	1069.3890	2136.7634	2135.8143	0.9491	0	12	3e+002	1	FFCHDESNIAETQEDSK + Phospho (ST)
✓	590	496.3240	990.6334	989.4818	1.1517	1	12	2.4e+002	1	DDWAKDLK
✓	859	713.7640	1425.5134	1425.7688	-0.2554	1	12	2.8e+002	1	TINKPRVAQEDR
✓	535	439.5990	877.1834	876.5069	0.6766	1	12	2.6e+002	1	IGFGKVEK
✓	468	780.5900	779.5827	780.3515	-0.7687	0	12	2.2e+002	1	HSSNVHT
✓	662	599.8790	1197.7434	1199.5071	-1.7636	0	12	2.7e+002	1	DJEINISNSK + Phospho (ST)
✓	425	658.7300	657.7227	657.3446	0.3781	0	12	3.5e+002	1	GISEPR
✓	1167	1053.1340	2104.2534	2105.8830	-1.6296	0	12	3.2e+002	1	QSENSLFDPAIAIFEDDK + Phospho (ST)
✓	769	667.9240	1333.8334	1335.5191	-1.6856	1	12	2.9e+002	1	EEKNSSSSSSSK + Phospho (ST)
✓	1255	797.1353	2388.3842	2388.0706	0.3135	2	12	3.1e+002	1	STENAFGRSNLGAANAEGSEK + Phospho (ST)
✓	968	796.3840	1590.7534	1592.5146	-1.7612	0	12	2.7e+002	1	CGSGCCTLGNCTC
✓	359	546.3900	545.3827	545.2809	0.1018	0	12	3.2e+002	1	AALNAS
✓	966	796.0890	1590.1634	1589.6399	0.5236	0	12	3.5e+002	1	SFGAEQEVSHYK + Phospho (ST)
✓	1259	804.1787	2409.5142	2409.1379	0.3763	2	12	3.5e+002	1	RNQEVLRYFLNTHSSYFR + Phospho (ST)
✓	1281	848.4553	2542.3442	2541.4196	0.9246	2	12	2.9e+002	1	LPFIQDSAVAALKHSLTRLRLR + Phospho (ST)
✓	858	713.4790	1424.9434	1424.5867	0.3568	1	12	3.4e+002	1	SVIIATIGGSPKR + 3 Phospho (ST)
✓	470	401.7340	801.4534	802.4548	-1.0014	1	12	2.8e+002	1	GDIKTAAK
✓	1140	687.8287	2060.4642	2061.0127	-0.5485	1	12	3.7e+002	1	DGLIGYAEGRDDQVGAIQK
✓	1027	865.7190	1729.4234	1728.8097	0.6138	0	12	3.8e+002	1	HAFASHLQNGADLR + Phospho (ST)
✓	48	415.3500	414.3427	415.2431	-0.9004	0	12	2.4e+002	1	IGGVA
✓	863	715.6740	1429.3334	1428.6902	0.6433	1	12	3.8e+002	1	VKFTPTAIDLEK + Phospho (ST)
✓	1126	677.0887	2028.2442	2028.9446	-0.7004	0	12	3.6e+002	1	ASGVSLGSPEQVPVIFVEF + Phospho (ST)
✓	357	546.3600	545.3527	545.2809	0.0718	0	12	3.5e+002	1	AALNAS
✓	666	603.0990	1204.1834	1202.6619	1.5216	2	12	3.7e+002	1	AVKKDGSASAAK
✓	950	790.1440	1578.2734	1579.8875	-1.6140	1	11	3.9e+002	1	FFLTPKNLNAFLR
✓	542	450.1840	898.3534	897.3957	0.9577	0	11	2.8e+002	1	GAIVTSDR + Phospho (ST)
✓	420	634.6100	633.6027	634.2969	-0.6942	1	11	2.7e+002	1	GSRCR
✓	631	552.0440	1102.0734	1101.5220	0.5515	1	11	3.8e+002	1	RSVSGELFK + Phospho (ST)
✓	946	788.1290	1574.2434	1573.7362	0.5072	1	11	4e+002	1	HRAPGSIGSITTPGR + Phospho (ST)
✓	644	571.4290	1140.8434	1142.4791	-1.6357	0	11	3.7e+002	1	GVGIGISAMDR + Phospho (ST)
✓	722	636.3190	1270.6234	1269.7768	0.8466	2	11	3.1e+002	1	KTARPKDLITK
✓	553	460.3190	918.6234	919.4164	-0.7930	0	11	3e+002	1	APAAPQASK + Phospho (ST)
✓	953	792.6040	1583.1934	1583.5614	-0.3680	1	11	4.2e+002	1	SSSGSSHSGSRSSSK + 2 Phospho (ST)
✓	1236	789.6387	2365.8942	2365.9382	-0.0440	0	11	3.6e+002	1	QYDSNIIIVGGGFANSQLR + 3 Phospho (ST)
✓	1192	1071.8490	2141.6834	2143.0261	-1.3427	2	11	4e+002	1	SPVVAVKELMSRSAPKPER + 2 Phospho (ST)
✓	600	508.8040	1015.5934	1015.3794	0.2140	0	11	3.2e+002	1	GSPSVSCSR + Phospho (ST)
✓	947	789.6390	1577.2634	1576.9552	0.3082	2	11	4.2e+002	1	QIIITGSVYKISKK
✓	1014	846.3490	1690.6834	1689.7641	0.9194	1	11	3.5e+002	1	VGTVHISYNQVAKR + 2 Phospho (ST)
✓	532	439.3840	876.7534	877.4059	-0.6524	0	11	3.5e+002	1	SHVLGASK + Phospho (ST)
✓	782	676.9290	1351.8434	1352.6701	-0.8266	1	11	3.7e+002	1	NTGILKEITER + Phospho (ST)
✓	1163	1049.4240	2096.8334	2097.7880	-0.9546	1	11	3.7e+002	1	ELSKMDGGLVSSDPHER + 3 Phospho (ST)
✓	450	716.1300	715.1227	715.3864	-0.2637	0	11	4.2e+002	1	NVAGEVK
✓	317	502.4000	501.3927	502.3115	-0.9188	0	11	4.6e+002	1	SGIVK
✓	531	439.2640	876.5134	876.4427	0.0708	1	11	2.8e+002	1	RHQGSHR
✓	948	789.6890	1577.3634	1577.7984	-0.4350	1	11	4.4e+002	1	MYPSVPVNSRTATR
✓	635	556.7840	1111.5534	1112.5267	-0.9733	2	11	3.2e+002	1	INPFGKKEI + Phospho (ST)
✓	426	659.3400	658.3327	657.3670	0.9657	1	11	3.7e+002	1	GAAGRAR
✓	630	546.9340	1091.8534	1092.3750	-0.5216	1	11	4e+002	1	DNSQIRGR + 2 Phospho (ST)
✓	684	625.8940	1249.7734	1248.6268	1.1467	0	11	3.5e+002	1	VYLPPSAPVAR + Phospho (ST)
✓	1047	891.7540	1781.4934	1780.8105	0.6830	2	11	4.6e+002	1	VKAATRDGGELGEQDR + Phospho (ST)
✓	333	517.2700	516.2627	516.2656	-0.0029	0	11	4.6e+002	1	APSSR
✓	358	546.3900	545.3827	546.1922	-0.8094	0	11	4.2e+002	1	DPNSD
✓	560	466.8440	931.6734	932.5403	-0.8669	2	11	3.8e+002	1	AKKGSISSR
✓	199	460.4400	459.4327	460.2394	-0.8067	0	11	5.6e+002	1	ASAGR

✓	732	640.5440	1279.0734	1278.6932	0.3803	0	11	4.5e+002	1	AQIHVLEGGVEK
✓	362	546.4400	545.4327	546.1922	-0.7594	0	11	4.3e+002	1	DPNSD
✓	636	559.6740	1117.3334	1118.5597	-1.2263	1	11	4e+002	1	IPREGSRPK + Phospho (ST)
✓	356	546.3500	545.3427	546.1922	-0.8494	0	11	4.3e+002	1	DPNSD
✓	724	637.2690	1272.5234	1272.5897	-0.0663	2	11	3.7e+002	1	MRKTVNTIDK + Phospho (ST)
✓	792	686.3540	1370.6934	1370.6078	0.0856	1	11	3.6e+002	1	SKGESDKPSASAK + Phospho (ST)
✓	480	416.2490	830.4834	829.3219	1.1616	1	11	3.7e+002	1	DTKGDSK + Phospho (ST)
✓	554	461.1890	920.3634	919.3688	0.9946	1	11	3e+002	1	YDEKITGK + Phospho (ST)
✓	436	677.0100	676.0027	675.3122	0.6905	0	11	3.7e+002	1	GLCGNR
✓	353	546.2700	545.2627	546.1922	-0.9294	0	11	4.3e+002	1	DPNSD
✓	360	546.4100	545.4027	546.1922	-0.7894	0	11	4.3e+002	1	DPNSD
✓	363	546.4500	545.4427	546.1922	-0.7494	0	11	4.5e+002	1	DPNSD
✓	309	502.2600	501.2527	502.2751	-1.0224	0	11	5e+002	1	VIANIS
✓	464	766.4600	765.4527	766.2300	-0.7772	0	11	2.7e+002	1	ASIGSGK + 2 Phospho (ST)
✓	828	699.5490	1397.0834	1397.4779	-0.3944	0	11	4.8e+002	1	QSSVPIAAQNR + 3 Phospho (ST)
✓	410	615.3900	614.3827	614.2313	0.1515	0	11	3.7e+002	1	SAIVAS + Phospho (ST)
✓	191	458.8500	457.8427	458.2125	-0.3698	0	11	5.7e+002	1	APASN
✓	1020	567.1320	1698.3742	1697.7410	0.6332	0	11	4.9e+002	1	SEIVNGENFPAVAAR + Phospho (ST)
✓	1039	883.1990	1764.3834	1762.6617	1.7217	1	11	4.9e+002	1	STVKQVDFSEVER + 3 Phospho (ST)
✓	949	789.9740	1577.9334	1576.7845	1.1489	1	11	4.2e+002	1	ETNDFGIAQNKVNK
✓	597	507.5290	1013.0434	1013.1946	-0.1512	0	10	4.7e+002	1	SGTINSK + 4 Phospho (ST)
✓	776	673.8640	1345.7134	1344.5962	1.1172	1	10	3.8e+002	1	GSEKETNPLYK + Phospho (ST)
✓	396	592.8500	591.8427	592.2340	-0.3913	0	10	2.8e+002	1	LGSSDD
✓	1278	841.5020	2521.4842	2521.0395	0.4447	1	10	4.7e+002	1	ITLGITTVLTMTITLTIARK + 5 Phospho (ST)
✓	997	829.7640	1657.5134	1658.8505	-1.3370	1	10	5e+002	1	LPPRPLGRSASTAEK + Phospho (ST)
✓	783	677.0890	1352.1634	1352.6602	-0.4967	2	10	5.2e+002	1	FKHSVVREGSK + Phospho (ST)
✓	543	901.9600	900.9527	901.4981	-0.5454	2	10	5.4e+002	1	IRDGGKEK
✓	1217	754.6587	2260.9542	2261.0664	-0.1122	0	10	4.3e+002	1	WVLTAAHCIQGLDPSSSLAVR + Phospho (ST)
✓	857	713.0240	1424.0334	1423.5633	0.4701	1	10	5.3e+002	1	GTSTIVAPSSKDSK + 2 Phospho (ST)
✓	441	682.7600	681.7527	682.2687	-0.5160	0	10	4.1e+002	1	SPQGSK + Phospho (ST)
✓	898	743.2240	1484.4334	1483.6764	0.7571	0	10	5.3e+002	1	VHAGSQASQDSQGGR
✓	364	546.4700	545.4627	545.2809	0.1818	0	10	5.3e+002	1	AALNAS
✓	700	629.8390	1257.6634	1256.6716	0.9919	1	10	4.3e+002	1	GILFRMLIK + Phospho (ST)
✓	559	466.2490	930.4834	931.4723	-0.9889	1	10	4.3e+002	1	GDIKADGTR
✓	154	447.1600	446.1527	447.1965	-1.0438	0	10	4.2e+002	1	EAAAS
✓	151	447.1100	446.1027	447.1965	-1.0938	0	10	4.5e+002	1	EAAAS
✓	793	686.8890	1371.7634	1370.6846	1.0788	1	10	4.6e+002	1	KSDLYVPAAIK + Phospho (ST)
✓	1158	1047.3490	2092.6834	2092.0718	0.6117	1	10	5.5e+002	1	EGSLGPLPGPSTQPHKGILK + Phospho (ST)
✓	392	592.4700	591.4627	591.2136	0.2491	0	10	2.9e+002	1	GENGES
✓	33	413.7700	412.7627	413.2274	-0.4647	0	10	2.3e+002	1	IAGPG
✓	885	735.0490	1468.0834	1468.7569	-0.6734	1	10	6.1e+002	1	MTSIQQRALHR
✓	1018	848.9840	1695.9534	1696.0247	-0.0712	2	9	5.2e+002	1	AVNAVIVITLKNKEGK
✓	399	597.1300	596.1227	595.2367	0.8861	0	9	3.1e+002	1	ANPSK + Phospho (ST)
✓	92	429.3700	428.3627	429.2224	-0.8596	0	9	3.2e+002	1	SGVPA
✓	1005	839.0590	1676.1034	1674.8164	1.2870	0	9	6.5e+002	1	HNIVGNLIMEQVIK + Phospho (ST)
✓	960	794.1290	1586.2434	1587.7732	-1.5297	1	9	6.8e+002	1	IIGFGICLSKGIDK + Phospho (ST)
✓	278	469.4800	468.4727	469.2285	-0.7558	0	9	4.2e+002	1	TGVGH
✓	430	662.5600	661.5527	660.3806	1.1721	0	9	4.6e+002	1	LNVSTK
✓	538	885.5600	884.5527	883.3801	1.1727	1	9	5.2e+002	1	EDGRIVK + Phospho (ST)
✓	736	643.0340	1284.0534	1284.6132	-0.5597	0	9	7e+002	1	PTLPGLTLVK + 2 Phospho (ST)
✓	942	787.0740	1572.1334	1571.7800	0.3535	0	9	7.2e+002	1	AQMENGQVNPMLK
✓	687	626.7940	1251.5734	1250.6496	0.9239	1	9	5.3e+002	1	NSSLTIKRPR + Phospho (ST)
✓	442	684.0200	683.0127	684.4170	-1.4043	0	9	6.1e+002	1	LGSAPLK
✓	723	636.5790	1271.1434	1270.5959	0.5476	0	9	7.3e+002	1	IKPGSPSYVQK + Phospho (ST)
✓	93	429.5300	428.5227	428.2383	0.2844	0	8	6.9e+002	1	APGGK
✓	371	563.1300	562.1227	561.2832	0.8395	0	8	4.1e+002	1	ELGLM
✓	111	433.0000	431.9927	431.2380	0.7547	0	8	9.7e+002	1	ATAGI
✓	318	502.4000	501.3927	502.2387	-0.8460	0	8	8.6e+002	1	GSDKP
✓	412	628.4800	627.4727	627.2014	0.2714	0	8	5.3e+002	1	SDNGR + Phospho (ST)
✓	481	833.7200	832.7127	834.3607	-1.6480	0	8	7.1e+002	1	EEDDVTK
✓	435	676.2100	675.2027	674.2871	0.9156	0	8	5.7e+002	1	GTPAAGDS
✓	185	458.3200	457.3127	458.2125	-0.8998	0	8	6.6e+002	1	APASN
✓	971	797.5890	1593.1634	1592.7893	0.3741	0	8	8.7e+002	1	SSSNINSSETIVDLK
✓	35	414.3100	413.3027	413.2274	0.0753	0	8	2.7e+002	1	IAGPG
✓	975	798.1590	1594.3034	1592.8295	1.4739	2	8	8.8e+002	1	MAKMIPVSRGKPAK + Phospho (ST)

✓	534	878.1800	877.1727	876.4375	0.7353	1	8	6.9e+002	1	KAAEEAMK
✓	397	595.5200	594.5127	595.1292	-0.6165	0	8	4.5e+002	1	SVSGS + 2 Phospho (ST)
✓	215	461.2800	460.2727	460.2394	0.0333	0	8	8.2e+002	1	GSAAR
✓	181	458.1900	457.1827	458.2489	-1.0661	0	8	7.1e+002	1	LAAAN
✓	951	790.1990	1578.3834	1579.7520	-1.3686	1	8	9.4e+002	1	TMNICEVGAVKCAK
✓	394	592.7700	591.7627	592.2340	-0.4713	0	8	5.4e+002	1	LGSSDD
✓	307	501.3900	500.3827	500.3322	0.0505	1	7	7.2e+002	1	ALKGL
✓	451	716.4000	715.3927	716.4432	-1.0505	0	7	7.9e+002	1	IITATAK
✓	393	592.7500	591.7427	592.2857	-0.5429	0	7	5.6e+002	1	APDYK
✓	444	684.0600	683.0527	683.3255	-0.2728	0	7	8.4e+002	1	ASSIVK + Phospho (ST)
✓	431	666.7700	665.7627	664.2234	1.5393	1	7	6.8e+002	1	IGKSI + 2 Phospho (ST)
✓	904	754.6590	1507.3034	1508.7358	-1.4324	1	7	1e+003	1	VERLEDYEESLK
✓	1010	841.4990	1680.9834	1682.7447	-1.7613	0	7	9.1e+002	1	SESDVVARPGAICR + Phospho (ST)
✓	544	907.1900	906.1827	907.3510	-1.1683	0	7	8.6e+002	1	MNVYSK + Phospho (ST)
✓	370	556.8400	555.8327	556.1894	-0.3567	1	7	9.8e+002	1	GKDA + Phospho (ST)
✓	340	523.0200	522.0127	523.1762	-1.1635	0	7	5.3e+002	1	DESSS
✓	720	635.7090	1269.4034	1269.6846	-0.2812	1	7	9.8e+002	1	VYAKLGIVAR + Phospho (ST)
✓	1161	1048.6590	2095.3034	2094.7221	0.5813	0	7	1.1e+003	1	NGIDSQNDYSSSIGSPK + 3 Phospho (ST)
✓	463	766.3400	765.3327	766.4450	-1.1122	0	7	6e+002	1	TIAAVHR
✓	374	572.5500	571.5427	571.2003	0.3424	0	7	1.1e+003	1	GSSGGK + Phospho (ST)
✓	332	516.8800	515.8727	515.3067	0.5660	0	7	1.4e+003	1	AAGGIK
✓	427	660.5300	659.5227	659.3827	0.1400	2	7	1e+003	1	GGSRRK
✓	1017	848.4540	1694.8934	1693.8859	1.0075	2	7	9.5e+002	1	GEKRDINGSPLNPAAR
✓	405	607.5800	606.5727	606.2973	0.2754	0	7	7.3e+002	1	SSATNK
✓	413	628.6000	627.5927	628.3293	-0.7365	0	7	1e+003	1	ASAAGPR
✓	445	684.2900	683.2827	682.4014	0.8814	0	6	7.9e+002	1	APSIAPK
✓	893	741.1490	1480.2834	1481.7351	-1.4517	1	6	1.2e+003	1	RLSSQVANVSSR + Phospho (ST)
✓	34	414.2700	413.2627	413.2274	0.0353	0	6	3.9e+002	1	IAGPG
✓	429	662.0500	661.0427	661.3031	-0.2604	0	6	1.1e+003	1	NSEANK
✓	192	459.2200	458.2127	459.2329	-1.0202	0	6	1.3e+003	1	EAAGL
✓	433	672.4400	671.4327	671.3425	0.0902	0	6	1e+003	1	GTVMHK
✓	280	472.7800	471.7727	472.2758	-0.5030	0	6	1.2e+003	1	AVAGR
✓	400	599.4400	598.4327	599.3027	-0.8700	0	6	8.3e+002	1	TNTHK
✓	461	755.4200	754.4127	754.2626	0.1502	0	6	8.4e+002	1	MDDCSK
✓	347	537.1300	536.1227	535.3118	0.8109	0	6	5.7e+002	1	LAPHV
✓	110	432.1500	431.1427	431.2380	-0.0953	0	6	1.4e+003	1	AASLA
✓	411	617.3100	616.3027	615.3340	0.9687	1	6	1.3e+003	1	AAARDL
✓	398	595.5400	594.5327	596.2918	-1.7591	1	6	7.3e+002	1	KEPSH
✓	447	687.8900	686.8827	687.2225	-0.3398	0	6	1.6e+003	1	GDSSSR + Phospho (ST)
✓	95	430.4100	429.4027	431.2016	-1.7989	0	5	1.2e+003	1	SAGTP
✓	349	537.1500	536.1427	535.2061	0.9367	0	5	6.4e+002	1	GGCDK
✓	59	419.3800	418.3727	417.1860	1.1868	0	5	1.2e+003	1	GPSAS
✓	478	825.4400	824.4327	826.2082	-1.7754	0	5	1.1e+003	1	SSCSAR + 2 Phospho (ST)
✓	320	504.4400	503.4327	503.2777	0.1550	0	5	1.7e+003	1	VLAMA
✓	221	461.3600	460.3527	460.2030	0.1497	0	5	1.6e+003	1	GDGGR
✓	157	449.1900	448.1827	449.1758	-0.9931	0	5	7.9e+002	1	GESSA
✓	454	736.6700	735.6627	735.3551	0.3076	0	5	1.2e+003	1	NVDNFK
✓	187	458.3700	457.3627	458.2489	-0.8862	0	5	1.4e+003	1	GSAPK
✓	62	420.0700	419.0627	418.2176	0.8451	0	5	7.4e+002	1	GSGAK
✓	328	512.3500	511.3427	512.1632	-0.8204	0	5	6.9e+002	1	ANASA + Phospho (ST)
✓	337	520.1400	519.1327	519.2541	-0.1213	0	5	1e+003	1	TVVDS
✓	282	476.1200	475.1127	474.2551	0.8577	0	5	1.5e+003	1	GVGSR
✓	313	502.3400	501.3327	502.2751	-0.9424	1	4	2e+003	1	KEGIG
✓	336	520.1300	519.1227	518.2336	0.8891	0	4	1.1e+003	1	AINDS
✓	327	510.7900	509.7827	511.1679	-1.3852	0	4	9.2e+002	1	ASAPS + Phospho (ST)
✓	286	482.3400	481.3327	482.2853	-0.9525	0	4	2.9e+002	1	APAPK
✓	439	678.4800	677.4727	678.3119	-0.8392	0	4	1.1e+003	1	GSSICR
✓	195	460.2600	459.2527	459.2441	0.0086	0	4	2.4e+003	1	GANAK
✓	51	418.1300	417.1227	417.2223	-0.0996	0	4	2e+003	1	AVSAA
✓	472	811.8500	810.8427	812.3867	-1.5440	0	4	1.8e+003	1	AMIGLIK + Phospho (ST)
✓	558	930.3500	929.3427	928.5454	0.7973	1	4	1.8e+003	1	KPVKTNSR
✓	438	678.4200	677.4127	678.3119	-0.8992	0	4	1.1e+003	1	GSSICR
✓	455	743.1800	742.1727	740.4545	1.7183	0	4	1.7e+003	1	SIGIPVR
✓	403	600.7900	599.7827	600.2520	-0.4693	1	4	2.1e+003	1	SSSKL + Phospho (ST)
✓	437	678.3400	677.3327	678.3119	-0.9792	0	4	1.1e+003	1	GSSICR

✓	316	502.3900	501.3827	501.2659	0.1168	0	4	2.3e+003	1	AGGAAR
✓	395	592.7800	591.7727	592.3333	-0.5605	1	4	1.3e+003	1	RIAAY
✓	310	502.3100	501.3027	502.2863	-0.9836	0	4	2.4e+003	1	GSIAR
✓	298	488.9700	487.9627	488.2594	-0.2967	0	4	3.2e+003	1	SSAPK
✓	330	513.1400	512.1327	513.2911	-1.1584	0	4	1.2e+003	1	GPVVK
✓	319	502.5500	501.5427	502.2863	-0.7436	0	4	3e+003	1	AVTGR
✓	449	705.6600	704.6527	705.3211	-0.6684	0	4	1.8e+003	1	AIHGIK + Phospho (ST)
✓	311	502.3100	501.3027	501.2659	0.0368	0	4	2.5e+003	1	AGGAAR
✓	197	460.3800	459.3727	460.2394	-0.8667	0	3	2.8e+003	1	ATGGR
✓	329	512.4300	511.4227	512.1996	-0.7768	1	3	1.2e+003	1	AKGGI + Phospho (ST)
✓	97	430.8600	429.8527	431.2380	-1.3853	0	3	3.1e+003	1	AALSA
✓	379	584.3600	583.3527	584.1843	-0.8316	0	3	1.6e+003	1	SGSASP + Phospho (ST)
✓	225	461.3900	460.3827	460.2394	0.1433	0	3	2.3e+003	1	AGSAR
✓	458	744.5200	743.5127	742.5065	1.0062	2	3	2e+003	1	GKKVALK
✓	407	611.2000	610.1927	609.2887	0.9040	1	3	1.1e+003	1	KPKIG + Phospho (ST)
✓	453	722.4000	721.3927	722.3000	-0.9073	0	3	1.4e+003	1	SAPPGSK + Phospho (ST)
✓	452	722.3900	721.3827	722.3000	-0.9173	0	3	1.4e+003	1	SAPPGSK + Phospho (ST)
✓	155	447.2300	446.2227	447.1965	-0.9738	0	3	1.9e+003	1	EAAAS
✓	183	458.2900	457.2827	458.2601	-0.9774	0	3	2e+003	1	AGVGR
✓	314	502.3600	501.3527	502.2863	-0.9336	0	3	2.8e+003	1	ATGVR
✓	198	460.4200	459.4127	460.2394	-0.8267	0	3	3.1e+003	1	ATGGR
✓	37	414.4000	413.3927	413.2274	0.1653	0	3	8.6e+002	1	IAGPG
✓	69	421.4200	420.4127	419.2016	1.2111	0	3	9.6e+002	1	VTSGG
✓	404	606.9900	605.9827	606.2544	-0.2717	0	3	1.8e+003	1	ANSCR
✓	217	461.3300	460.3227	460.2645	0.0582	0	3	2.6e+003	1	VSAGK
✓	376	573.3600	572.3527	572.1479	0.2048	0	3	2.7e+003	1	IGNDS + Phospho (ST)
✓	465	774.1100	773.1027	772.4079	0.6948	0	3	2.9e+003	1	VDLSSPR
✓	153	447.1500	446.1427	447.2329	-1.0902	0	3	2.2e+003	1	LSAAS
✓	469	783.1200	782.1127	783.2023	-1.0896	0	2	2.5e+003	1	SGS S MR + 2 Phospho (ST)
✓	19	407.3800	406.3727	405.1859	1.1868	0	2	1.4e+003	1	SAAAS
✓	90	428.1500	427.1427	427.2431	-0.1004	0	2	1.8e+003	1	VVGGP
✓	373	570.3000	569.2927	570.2050	-0.9123	0	2	2e+003	1	AAAI S A + Phospho (ST)
✓	296	486.4100	485.4027	485.2598	0.1429	0	2	2.2e+003	1	GGAPGK
✓	158	449.2000	448.1927	449.1758	-0.9831	0	2	1.5e+003	1	GESSA
✓	70	421.5200	420.5127	419.2016	1.3111	0	2	1.7e+003	1	VTSGG
✓	46	415.2600	414.2527	413.0948	1.1579	0	2	2.4e+003	1	S G GGG + Phospho (ST)
✓	38	414.6400	413.6327	413.0948	0.5379	0	2	3.2e+003	1	S G GGG + Phospho (ST)
✓	223	461.3800	460.3727	460.2645	0.1082	0	2	3.4e+003	1	GSGIK
✓	339	522.8400	521.8327	520.2493	1.5834	0	2	1.9e+003	1	TASDK
✓	43	415.2300	414.2227	413.0948	1.1279	0	2	2.5e+003	1	S G GGG + Phospho (ST)
✓	285	482.2500	481.2427	482.2853	-1.0425	0	2	5.5e+002	1	APAPK
✓	152	447.1400	446.1327	447.1965	-1.0638	0	2	2.8e+003	1	EAAAS
✓	216	461.3100	460.3027	461.2486	-0.9458	0	1	3.6e+003	1	SSLVG
✓	18	407.3700	406.3627	407.1652	-0.8025	0	1	1.8e+003	1	SGSAS
✓	233	463.4000	462.3927	463.2278	-0.8351	0	1	2e+003	1	SSLSA
✓	459	748.4300	747.4227	747.4313	-0.0085	1	1	2.5e+003	1	AMAKLSK
✓	479	826.3000	825.2927	824.4617	0.8311	0	1	3e+003	1	RPSAAPAR
✓	224	461.3900	460.3827	459.2693	1.1134	0	1	4e+003	1	ATVIG
✓	147	444.4500	443.4427	443.2380	0.2047	0	1	4.1e+003	1	AGPSI
✓	334	517.4700	516.4627	516.3020	0.1607	0	1	5e+003	1	ATAVR
✓	31	413.5100	412.5027	413.2274	-0.7247	0	1	1.8e+003	1	IAGPG
✓	460	748.9000	747.8927	749.3221	-1.4294	0	1	3.7e+003	1	I H SGIR + Phospho (ST)
✓	207	461.0300	460.0227	459.2693	0.7534	0	0	6.7e+003	1	GAILS
✓	423	639.4000	638.3927	639.1554	-0.7627	0	0	2.4e+003	1	SV S TS + 2 Phospho (ST)
✓	148	444.4600	443.4527	444.2696	-0.8169	1	0	4.8e+003	1	IAKGG
✓	281	473.3800	472.3727	472.2394	0.1333	0	0	4.2e+003	1	GSGPR
✓	17	407.3400	406.3327	405.1859	1.1468	0	0	2.3e+003	1	SAAAS
✓	201	460.7000	459.6927	458.2601	1.4326	0	0	7.5e+003	1	GVAGR
✓	1	400.3300	399.3227							
✓	2	400.4000	399.3927							
✓	3	400.5000	399.4927							
✓	4	400.5300	399.5227							
✓	5	402.3200	401.3127							
✓	6	402.4800	401.4727							
✓	7	402.7700	401.7627							

☒	8	402.9300	401.9227
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✓	440	682.2900	681.2827
✓	462	760.8200	759.8127
✓	518	870.0600	869.0527

Search Parameters

Type of search : MS/MS Ion Search
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Phospho (ST)
Mass values : Monoisotopic
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 1.8 Da
Fragment Mass Tolerance : ± 0.8 Da
Max Missed Cleavages : 2
Instrument type : ESI-TRAP
Number of queries : 1323

Mascot: <http://www.matrixscience.com/>

Dear Dr Somers,

Thank you for submitting your revised manuscript (EMBOJ-2021-108684R) to The EMBO Journal. Your amended study was sent back to the referees for re-evaluation and we have received re-reports from two of them, which I share below. As you will see, the reviewer stated that his/her issues have been comprehensively resolved and s/he is now broadly in favour of publication. Please note that while reviewer #3 was unfortunately not able to reassess the revised work at this time, we have carefully editorially evaluated your response to the issues raised and found these to be satisfactorily addressed.

Thus, we are pleased to inform you that your manuscript has been accepted in principle for publication in The EMBO Journal.

We need you to take care of a number of minor points related to formatting and data representation as detailed below, which should be addressed at re-submission.

Please contact me at any time if you have additional questions related to below points.

Thank you for giving us the chance to consider your manuscript for The EMBO Journal. I look forward to your final revision.

Again, please contact me at any time if you need any help or have further questions.

Kind regards,

Daniel Klimmeck

Daniel Klimmeck PhD
Senior Editor
The EMBO Journal

Formatting changes required for the revised version of the manuscript:

>> Please add a separate 'Statistical analysis' section to your manuscript, detailing the algorithms applied.

>> Introduce a separate 'Data availability section' with dataset identifier and http link to the jpostdb database. Ensure the data privacy is released.

>> Update the author checklist with the dataset information.

>> Recheck callouts and their correct order in the main text for Figures 11A, 11B.

>> Include Table EV1 as 'Appendix Table S1' into the appendix file and adjust callouts accordingly.

>> Update email addresses for H. N. and Y. N. in our online system.

>> Please update your funding information in our online portal. Currently - Rural Development Administration, Republic of Korea, is missing.

>> The number of replicates are missing from Figures 2, 3A, 6C; Fig EV2+4 "Biological duplicates". Please make the suggested changes in the attached Data Edited manuscript leaving track changes activated. Please upload this edited manuscript as the main manuscript.

>> Please consider additional changes and comments from our production team as indicated by the .doc file enclosed and leave changes in track mode.

Please remember: Digital image enhancement is acceptable practice, as long as it accurately represents the original data and conforms to community standards. If a figure has been subjected to significant electronic manipulation, this must be noted in the figure legend or in the 'Materials and Methods' section. The editors reserve the right to request original versions of figures and the original images that were used to assemble the figure.

Further information is available in our Guide For Authors: <https://www.embopress.org/page/journal/14602075/authorguide>

The revision must be submitted online within 90 days; please click on the link below to submit the revision online before 1st Jan 2022.

<https://emboj.msubmit.net/cgi-bin/main.plex>

Referee #1:

The major concerns raised during the first round of review have been well addressed.

Referee #2:

Adding Figure EV5 does help to strengthen the unique significance of the 5 phosphorylation sites of TOC1. This reviewer also appreciate the authors' efforts in comprehensively responding to the previous comments and in improving the manuscript. No further comments remain to be addressed.

Dear Dr Somers,

Thank you for submitting the revised version of your manuscript. I have now evaluated your amended manuscript and concluded that the remaining minor concerns have been sufficiently addressed.

Thus, I am pleased to inform you that your manuscript has been accepted for publication in the EMBO Journal.

Please note that it is EMBO Journal policy for the transcript of the editorial process (containing referee reports and your response letter) to be published as an online supplement to each paper. I would thus like to ask for your consent on keeping the additional referee figure content included in this file.

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On a different note, I would like to alert you that EMBO Press is currently developing a new format for a video-synopsis of work published with us, which essentially is a short, author-generated film explaining the core findings in hand drawings, and, as we believe, can be very useful to increase visibility of the work. This has proven to offer a nice opportunity for exposure i.p. for the first author(s) of the study. Please see the following link for representative examples and their integration into the article web page:

https://www.embopress.org/video_synopses

<https://www.embopress.org/doi/full/10.15252/emboj.2019103932>

Please let me know, should you be interested to engage in commissioning a similar video synopsis for your work. According operation instructions are available and intuitive.

If you have any questions, please do not hesitate to call or email the Editorial Office.

Thank you again for this contribution to The EMBO Journal and congratulations on a successful publication! Please consider us again in the future for your most exciting work.

Kind regards,

Daniel Klimmeck

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Senior Editor
The EMBO Journal
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PLEASE NOTE THAT THIS CHECKLIST WILL BE PUBLISHED ALONGSIDE YOUR PAPER

Corresponding Author Name: David Somers

Journal Submitted to: EMBO J

Manuscript Number: EMBOJ-2021-108684

Reporting Checklist For Life Sciences Articles (Rev. June 2017)

This checklist is used to ensure good reporting standards and to improve the reproducibility of published results. These guidelines are consistent with the Principles and Guidelines for Reporting Preclinical Research issued by the NIH in 2014. Please follow the journal's authorship guidelines in preparing your manuscript.

A- Figures

1. Data

The data shown in figures should satisfy the following conditions:

- the data were obtained and processed according to the field's best practice and are presented to reflect the results of the experiments in an accurate and unbiased manner.
- figure panels include only data points, measurements or observations that can be compared to each other in a scientifically meaningful way.
- graphs include clearly labeled error bars for independent experiments and sample sizes. Unless justified, error bars should not be shown for technical replicates.
- if $n < 5$, the individual data points from each experiment should be plotted and any statistical test employed should be justified
- Source Data should be included to report the data underlying graphs. Please follow the guidelines set out in the author ship guidelines on Data Presentation.

2. Captions

Each figure caption should contain the following information, for each panel where they are relevant:

- a specification of the experimental system investigated (eg cell line, species name).
- the assay(s) and method(s) used to carry out the reported observations and measurements
- an explicit mention of the biological and chemical entity(ies) that are being measured.
- an explicit mention of the biological and chemical entity(ies) that are altered/varied/perturbed in a controlled manner.
- the exact sample size (n) for each experimental group/condition, given as a number, not a range;
- a description of the sample collection allowing the reader to understand whether the samples represent technical or biological replicates (including how many animals, litters, cultures, etc.).
- a statement of how many times the experiment shown was independently replicated in the laboratory.
- definitions of statistical methods and measures:
 - common tests, such as t-test (please specify whether paired vs. unpaired), simple χ^2 tests, Wilcoxon and Mann-Whitney tests, can be unambiguously identified by name only, but more complex techniques should be described in the methods section;
 - are tests one-sided or two-sided?
 - are there adjustments for multiple comparisons?
 - exact statistical test results, e.g., P values = x but not P values < x;
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 - definition of error bars as s.d. or s.e.m.

Any descriptions too long for the figure legend should be included in the methods section and/or with the source data.

In the pink boxes below, please ensure that the answers to the following questions are reported in the manuscript itself. Every question should be answered. If the question is not relevant to your research, please write NA (non applicable). We encourage you to include a specific subsection in the methods section for statistics, reagents, animal models and human subjects.

B- Statistics and general methods

Please fill out these boxes ↓ (Do not worry if you cannot see all your text once you press return)

1.a. How was the sample size chosen to ensure adequate power to detect a pre-specified effect size?	No sample size test was performed. All quantitative measurements were done using at least three independent trials, at least 15 biological samples were combined for each trial of RT-qPCR, protein abundance quantitation and ChIP-qPCR assays.
1.b. For animal studies, include a statement about sample size estimate even if no statistical methods were used.	NA
2. Describe inclusion/exclusion criteria if samples or animals were excluded from the analysis. Were the criteria pre-established?	No data were excluded from the analyses.
3. Were any steps taken to minimize the effects of subjective bias when allocating animals/samples to treatment (e.g. randomization procedure)? If yes, please describe.	NA
For animal studies, include a statement about randomization even if no randomization was used.	NA
4.a. Were any steps taken to minimize the effects of subjective bias during group allocation or/and when assessing results (e.g. blinding of the investigator)? If yes please describe.	No
4.b. For animal studies, include a statement about blinding even if no blinding was done	NA
5. For every figure, are statistical tests justified as appropriate?	Yes. Statistical tests used in the study were applied according to standard mean comparison procedures, involving ANOVA followed by Tukey or t tests and non-parametric tests. Statistical tests are described in details in figure legends and source data files.
Do the data meet the assumptions of the tests (e.g., normal distribution)? Describe any methods used to assess it.	Normality distribution of %input values of ChIP-qPCR assays and band-intensity quantification values were tested with Shapiro-Wilk tests. Statistical analysis of RT-qPCR expressions were performed using nonparametric Wilcoxon tests.

USEFUL LINKS FOR COMPLETING THIS FORM

<http://www.antibodypedia.com>

<http://1degreebio.org>

<http://www.equator-network.org/reporting-guidelines/improving-bioscience-research-repo>

<http://grants.nih.gov/grants/olaw/olaw.htm>

<http://www.mrc.ac.uk/Ourresearch/Ethicsresearchguidance/Useofanimals/index.htm>

<http://ClinicalTrials.gov>

<http://www.consort-statement.org>

<http://www.consort-statement.org/checklists/view/32-consort/66-title>

<http://www.equator-network.org/reporting-guidelines/reporting-recommendations-for-tun>

<http://datadryad.org>

<http://figshare.com>

<http://www.ncbi.nlm.nih.gov/gap>

<http://www.ebi.ac.uk/ega>

<http://biomodels.net/>

<http://biomodels.net/miriam/>

<http://jij.biochem.sun.ac.za>

<https://osp.od.nih.gov/biosafety-biosecurity-and-emerging-biotechnology/>

<http://www.selectagents.gov/>

Is there an estimate of variation within each group of data?	Standard error bars were indicated as estimates in each barplot presenting averages of data from each group.
Is the variance similar between the groups that are being statistically compared?	Homogeneity of variances were assessed with Fisher tests.

C- Reagents

6. To show that antibodies were profiled for use in the system under study (assay and species), provide a citation, catalog number and/or clone number, supplementary information or reference to an antibody validation profile. e.g., Antibodypedia (see link list at top right), IDegreeBio (see link list at top right).	Informations of the antibodies used in this manuscript, including the clone number and manufacturer, are provided and can be found in material and method section. All commercial antibodies were validated by their manufacturers as specified on their website. Anti-ADK is a gift from David Bisaro lab.
7. Identify the source of cell lines and report if they were recently authenticated (e.g., by STR profiling) and tested for mycoplasma contamination.	NA

* for all hyperlinks, please see the table at the top right of the document

D- Animal Models

8. Report species, strain, gender, age of animals and genetic modification status where applicable. Please detail housing and husbandry conditions and the source of animals.	NA
9. For experiments involving live vertebrates, include a statement of compliance with ethical regulations and identify the committee(s) approving the experiments.	NA
10. We recommend consulting the ARRIVE guidelines (see link list at top right) (PLoS Biol. 8(6), e1000412, 2010) to ensure that other relevant aspects of animal studies are adequately reported. See author guidelines, under 'Reporting Guidelines'. See also: NIH (see link list at top right) and MRC (see link list at top right) recommendations. Please confirm compliance.	NA

E- Human Subjects

11. Identify the committee(s) approving the study protocol.	NA
12. Include a statement confirming that informed consent was obtained from all subjects and that the experiments conformed to the principles set out in the WMA Declaration of Helsinki and the Department of Health and Human Services Belmont Report.	NA
13. For publication of patient photos, include a statement confirming that consent to publish was obtained.	NA
14. Report any restrictions on the availability (and/or on the use) of human data or samples.	NA
15. Report the clinical trial registration number (at ClinicalTrials.gov or equivalent), where applicable.	NA
16. For phase II and III randomized controlled trials, please refer to the CONSORT flow diagram (see link list at top right) and submit the CONSORT checklist (see link list at top right) with your submission. See author guidelines, under 'Reporting Guidelines'. Please confirm you have submitted this list.	NA
17. For tumor marker prognostic studies, we recommend that you follow the REMARK reporting guidelines (see link list at top right). See author guidelines, under 'Reporting Guidelines'. Please confirm you have followed these guidelines.	NA

F- Data Accessibility

18: Provide a "Data Availability" section at the end of the Materials & Methods, listing the accession codes for data generated in this study and deposited in a public database (e.g. RNA-Seq data: Gene Expression Omnibus GSE39462, Proteomics data: PRIDE PXD000208 etc.) Please refer to our author guidelines for 'Data Deposition'. Data deposition in a public repository is mandatory for: a. Protein, DNA and RNA sequences b. Macromolecular structures c. Crystallographic data for small molecules d. Functional genomics data e. Proteomics and molecular interactions	Raw MS data has been made available via an accession code
19. Deposition is strongly recommended for any datasets that are central and integral to the study; please consider the journal's data policy. If no structured public repository exists for a given data type, we encourage the provision of datasets in the manuscript as a Supplementary Document (see author guidelines under 'Expanded View' or in unstructured repositories such as Dryad (see link list at top right) or Figshare (see link list at top right).	NA
20. Access to human clinical and genomic datasets should be provided with as few restrictions as possible while respecting ethical obligations to the patients and relevant medical and legal issues. If practically possible and compatible with the individual consent agreement used in the study, such data should be deposited in one of the major public access-controlled repositories such as dbGAP (see link list at top right) or EGA (see link list at top right).	NA
21. Computational models that are central and integral to a study should be shared without restrictions and provided in a machine-readable form. The relevant accession numbers or links should be provided. When possible, standardized format (SBML, CellML) should be used instead of scripts (e.g. MATLAB). Authors are strongly encouraged to follow the MIRIAM guidelines (see link list at top right) and deposit their model in a public database such as Biomodels (see link list at top right) or JWS Online (see link list at top right). If computer source code is provided with the paper, it should be deposited in a public repository or included in supplementary information.	NA

G- Dual use research of concern

22. Could your study fall under dual use research restrictions? Please check biosecurity documents (see link list at top right) and list of select agents and toxins (APHIS/CDC) (see link list at top right). According to our biosecurity guidelines, provide a statement only if it could.	NA
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