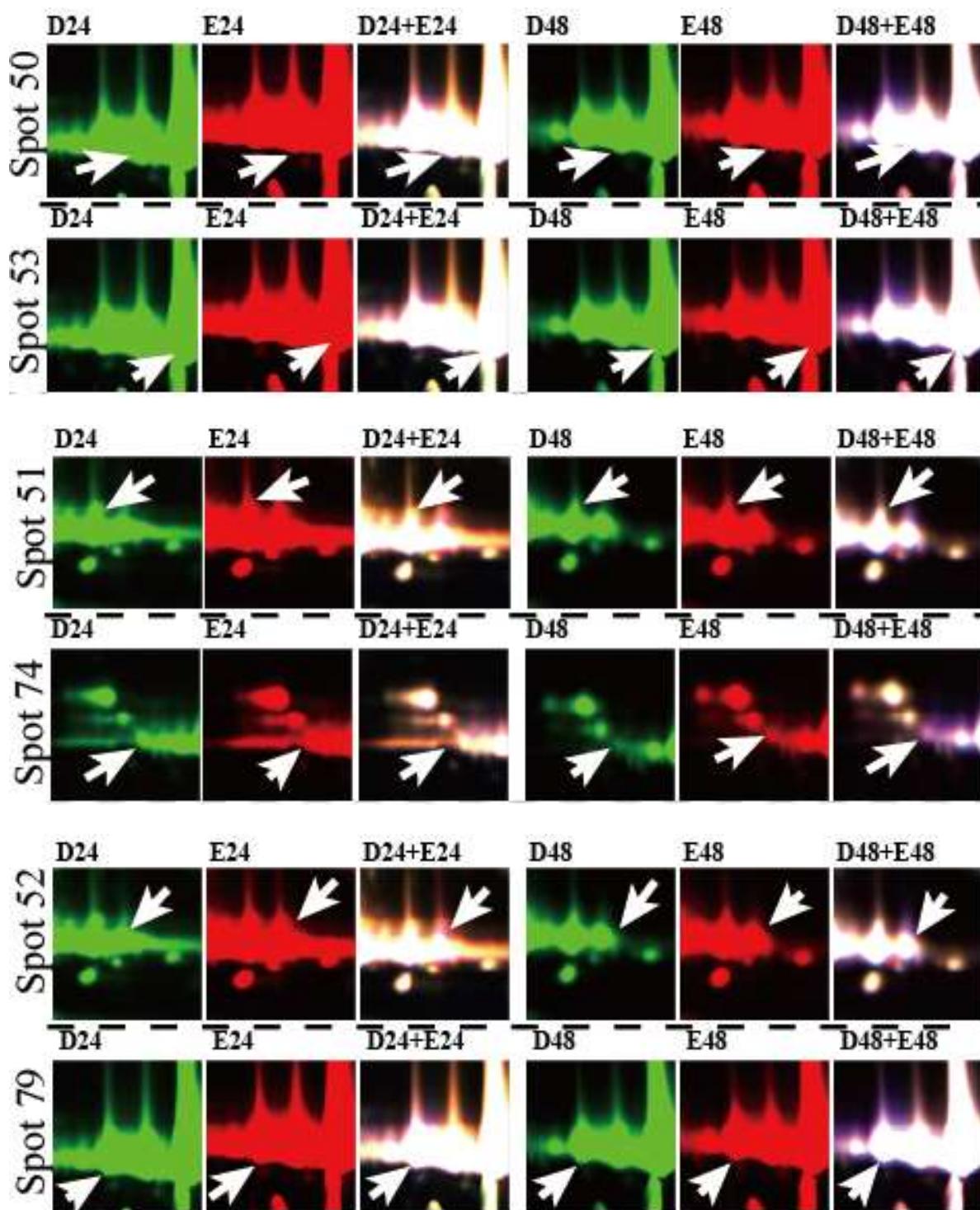


Figure S3: Phosphopeptides and phosphorylation amino acid sites in different REF and SRPP isoforms

Protein name: **REF138**

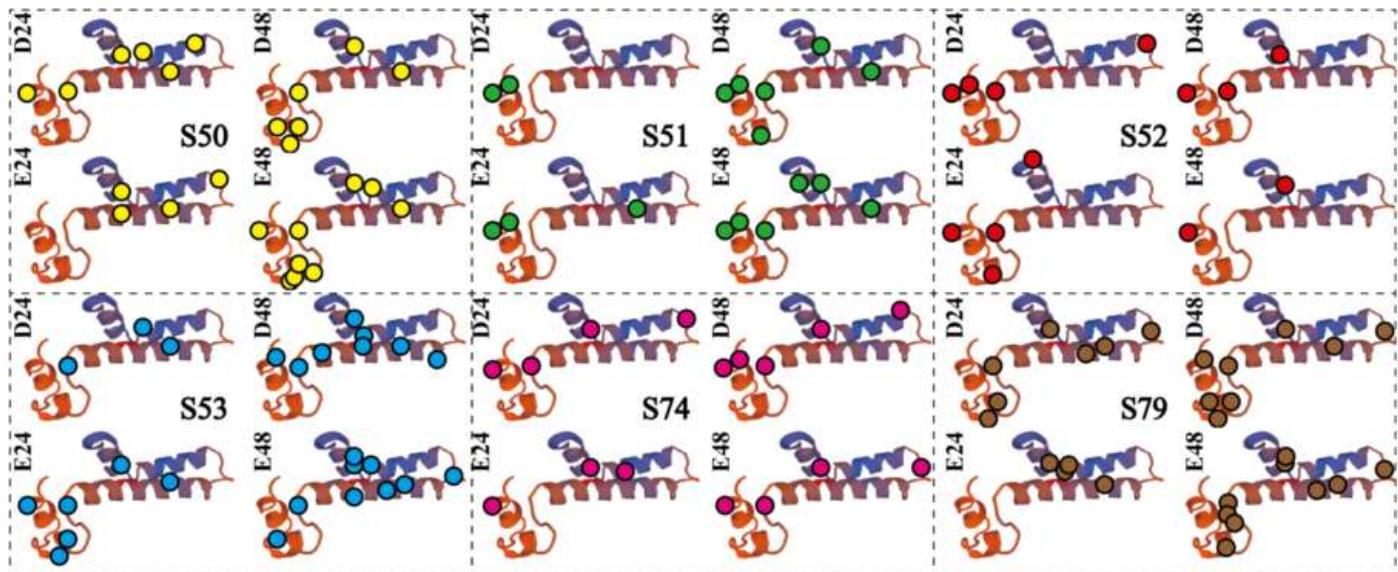
Location of the **six** spots identified as **REF138** by MS from 2-D DIGE gels:



Detail information for phosphorylation of amino acid sites in REF138:

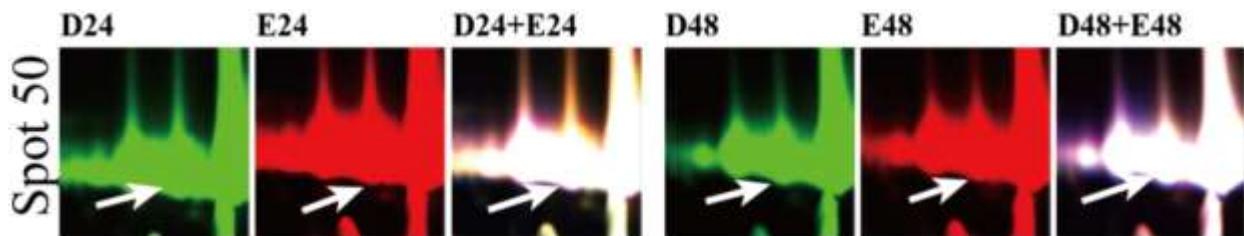
	█ Spot 50	█ Spot 51	█ Spot 52	█ Spot 53	█ Spot 74	█ Spot 79	█ Share
D24h	MAE DE DNQQGQGEGLKYLGFVQDAATYAV T FSNVYLFAKDK S GPLQPGVDIIEGPVKNVAVPLYNRFSYIPNGA						
E24h	MAE DE DNQQGQGEGLKYLGFVQDAATYAV T FSNVYLFAKDK S GPLQPGVDIIEGPVKNVAVPLYNRFSYIPNGA						
D48h	MAE DE DNQQGQGEGLKYLGFVQDAATYAV T FSNVYLFAKDK S GPLQPGVDIIEGPVKNVAVPLYNRFSYIPNGA						
E48h	MAE DE DNQQGQGEGLKYLGFVQDAAT Y AV T FSNVYLFAKDK S GPLQPGVDIIEGPVKNVAVPLYNRFSYIPNGA						
D24h	LKFVD S TVVVASVTIIDRSLLPIVK D ASI Q VVSAIRAAPEAARSLASSLPGQ I KILAKVFYGEN						
E24h	LKFVD S TVVVASVTIIDRSLLPIVK D ASI Q VVSAIRAAPEAARSLASSLPGQ I KILAKVFYGEN						
D48h	LKFVD S TVVVASVTIIDRSLLPIVK D ASI Q VVSAIRAAPEAARSLASSLPGQ I KILAKVFYGEN						
E48h	LKFVD S TVVVASVTIIDRSLLPIVK D ASI Q VVSAIRAAPEAARSLASSLPGQ I KILAKVFYGEN						

Predicted 3-D structure and phosphorylated amino acids in different REF138 isoforms:



Spot No. 50

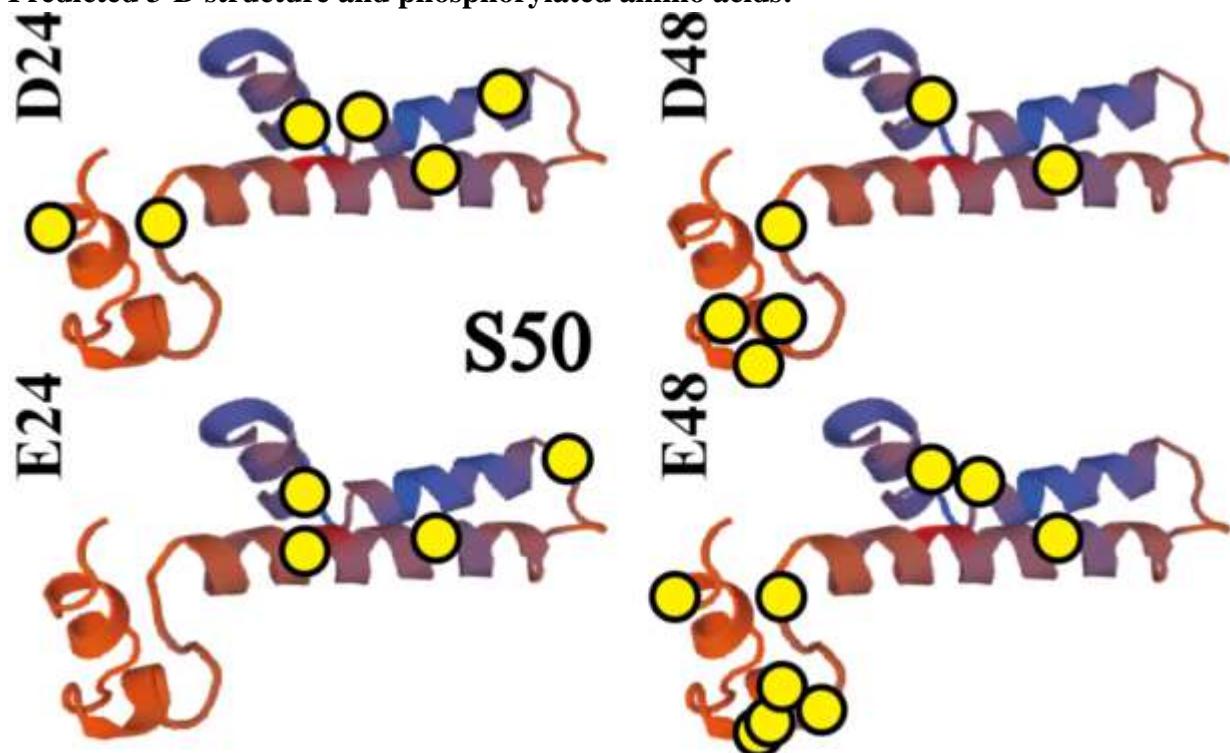
Changed pattern on DIGE gel:



Location in rubber genome: scaffold1222_136753.mRNA1

Protein name: Rubber elongation factor protein/REF138

Predicted 3-D structure and phosphorylated amino acids:



Detail information for phosphorylation of amino acid sites:

D24: MAEDEDDNQQGQGEGLKYLGFVQDAATYAVTTFSNVYLFAKDKSGPLQPGVDIIEGPVKNVAVPLYNRFSYIPNGA

E24: MAEDEDNQQGQGEGLKYLGFVQDAATYAVTTFSNVYLFAKDKSGPLQPGVDIIEGPVKNVAVPLYNRFSYIPNGA

D48: MAEDEDNQQGQGEGLKYLGFVQDAATTYAVTTFSNVYLFAKDKSGPLQPGVDIIEGPVKNVAVPLYNRFSYIPNGA

E48: MAEDEDDNQQGQGEGLKYLGFVQDAATYAVTTFSNVYLFAKDKSGPLQPGVDIIEGPVKNVAVPLYNRFSYIPNGA

D24: LKFVDSTVVASVTIIDRSLPIVKDASIQVVSAIRAAPEAARSLASSLPGQTKILAKVFYGEN

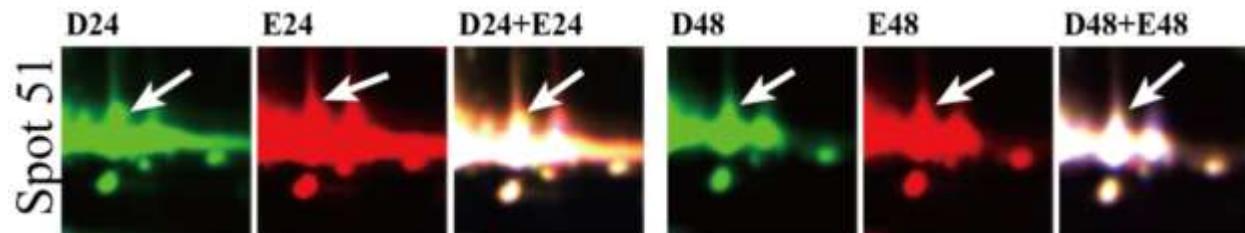
E24: LKFVDSTVVASVTIIDRSLPIVKDASQVVSAIRAAPEAARSLASSLPGQTKILAKVFYGEN

D48: LKFVDSTVVASVTIIDRSLPIVKDASIQVVSAIRAAPEAARSLASSLPGQTKILAKVFYGEN

E48: LKFVDSTVVASVTIIDRSLPIVKDASIQVVSAIRAAPEAARSLASSLPGQTKILAKVFYGEN

Spot No. 51

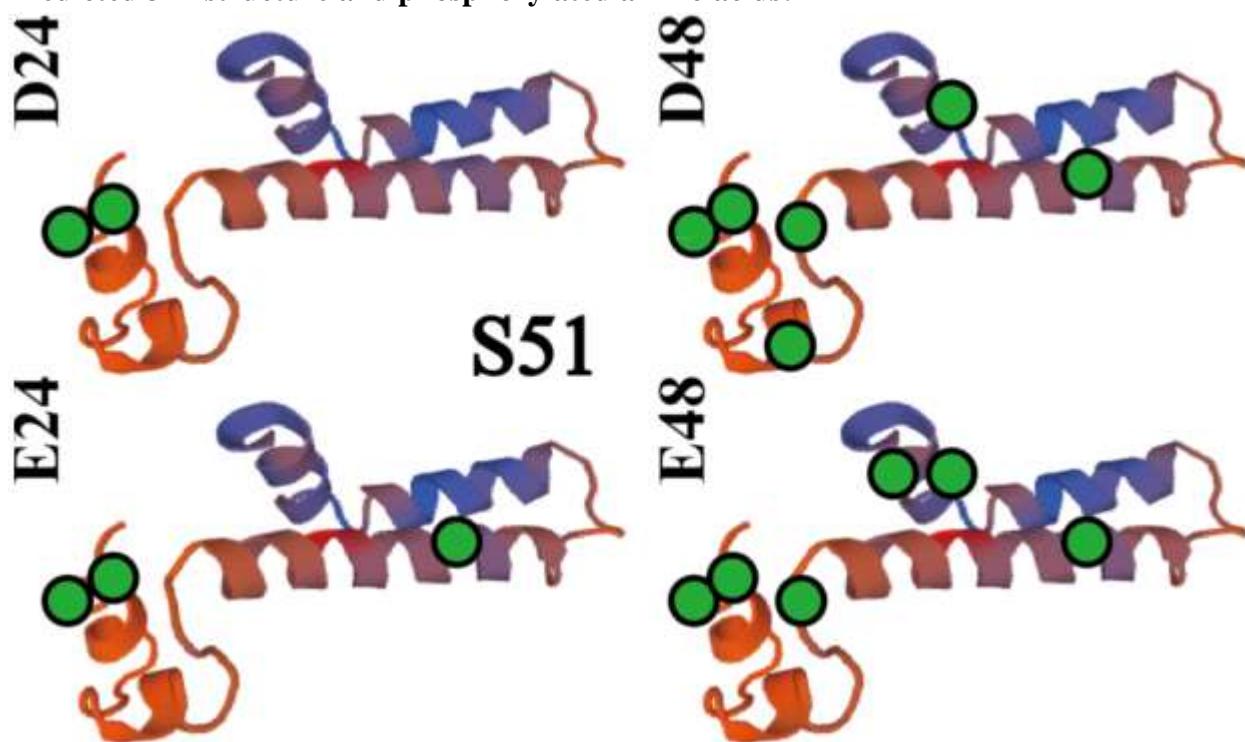
Changed pattern on DIGE gel:



Location in rubber genome: scaffold1222_136753.mRNA1

Protein name: Rubber elongation factor protein/REF138

Predicted 3-D structure and phosphorylated amino acids:



Detail information for phosphorylation of amino acid sites:

D24: MAEDEDNQQGQGEGLKYLGFVQDAATYAVTTFSNVYLFAKDKSGPLQPGVDIIEGPVKNVAVPLYNRFSYIPNGA

E24: MAEDEDNQQGQGEGLKYLGFVQDAATYAVTTFSNVYLFAKDKSGPLQPGVDIIEGPVKNVAVPLYNRFSYIPNGA

D48: MAEDEDNQQGQGEGLKYLGFVQDAATYAVTTFSNVYLFAKDKSGPLQPGVDIIEGPVKNVAVPLYNRFSYIPNGA

E48: MAEDEDNQQGQGEGLKYLGFVQDAATYAVTTFSNVYLFAKDKSGPLQPGVDIIEGPVKNVAVPLYNRFSYIPNGA

D24: LKFV DSTVVASVTIIDRSLPIVKDASIQVVS AIRAAPEAARS LASSLPGQT KILAKV FYGEN

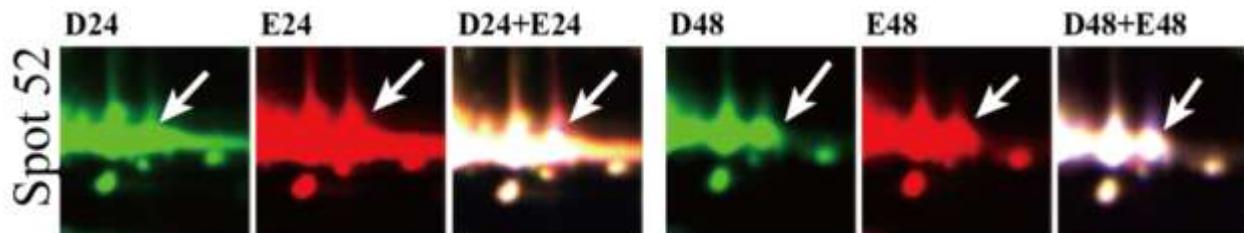
E24: LKFV DSTVVASVTIIDRSLPIVKDASIQVVS AIRAAPEAARS LASSLPGQT KILAKV FYGEN

D48: LKFV DSTVVASVTIIDRSLPIVKDASIQVVS AIRAAPEAARS LASSLPGQTKI LAKV FYGEN

E48: LKFV DSTVVASVTIIDRSLPIVKDASIQVVS AIRAAPEAARS LASSLPGQTKI LAKV FYGEN

Spot No. 52

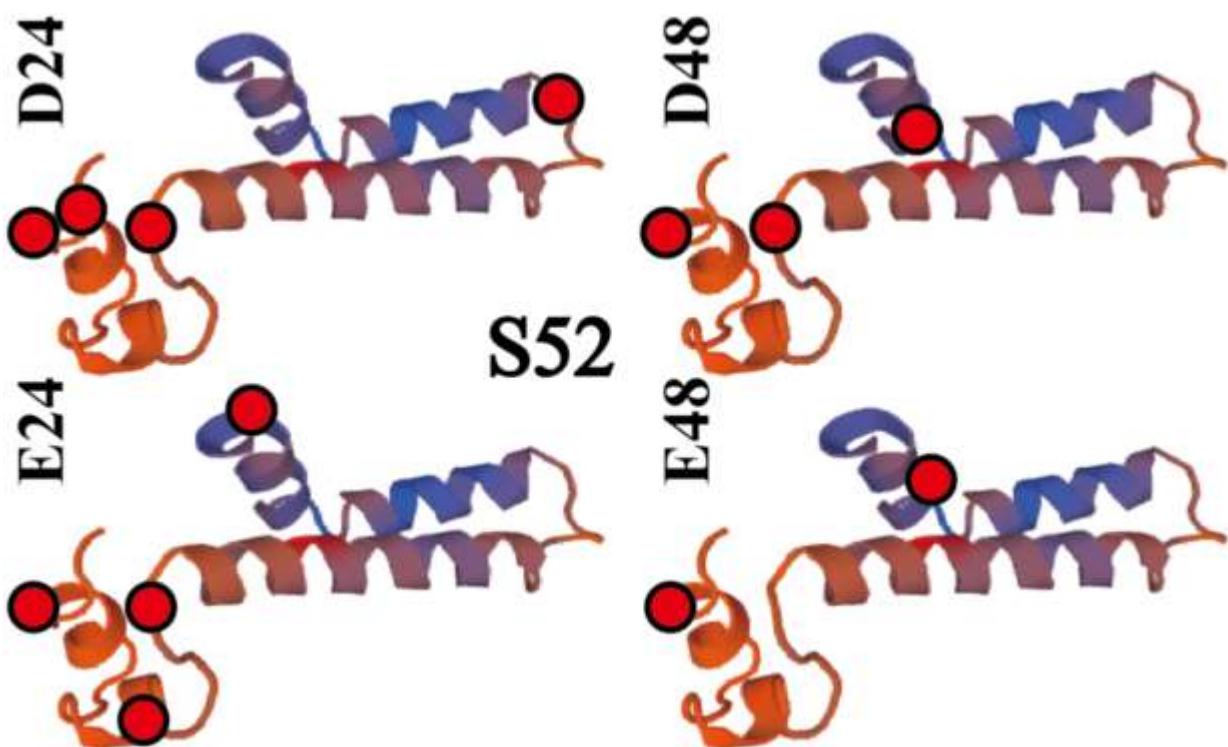
Changed pattern on DIGE gel:



Location in rubber genome: scaffold1222_136753.mRNA1

Protein name: Rubber elongation factor protein/REF138

Predicted 3-D structure and phosphorylated amino acids:



Detail information for phosphorylation of amino acid sites:

D24: MAEDEDNQQGQGEGLKYLGFVQDAATYAVTTFSNVYLFAKDKSGPLQPGVDIIEGPVKNAVPLYNRFSYIPNGA

E24: MAEDEDDNQQGQGEGLKYLGFVQDAATYAVTTFSNVYLFAKDKSGPLQPGVDIIEGPVKNAVPLYNRFSYIPNGA

D48: MAEDEDDNQQGQGEGLKYLGFVQDAATYAVTTFSNVYLFAKDKSGPLQPGVDIIEGPVKNAVPLYNRFSYIPNGA

E48: MAEDEDDNQQGQGEGLKYLGFVQDAATYAVTTFSNVYLFAKDKSGPLQPGVDIIEGPVKNAVPLYNRFSYIPNGA

D24: LKFVDSTVVASVTIIDRSLLPPIVKDASSIQVVSAIRAAPEAARSLASSLPGQTKILAKVFYGEN

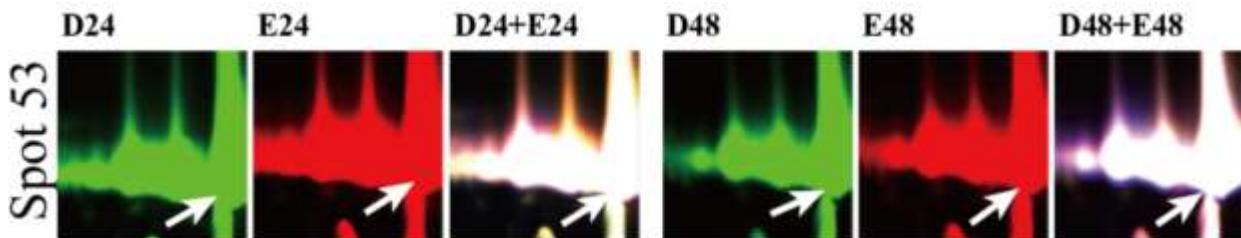
E24: LKFVDSTVVASVTIIDRSLLPPIVKDASIQVVSAIRAAPEAARSLASSLPGQTKILAKVFYGEN

D48: LKFVDSTVVASVTIIDRSLLPPIVKDASIQVVSAIRAAPEAARSLASSLPGQTTKILAKVFYGEN

E48: LKFVDSTVVASVTIIDRSLLPPIVKDASIQVVSAIRAAPEAARSLASSLPGQTKILAKVFYGEN

Spot No. 53

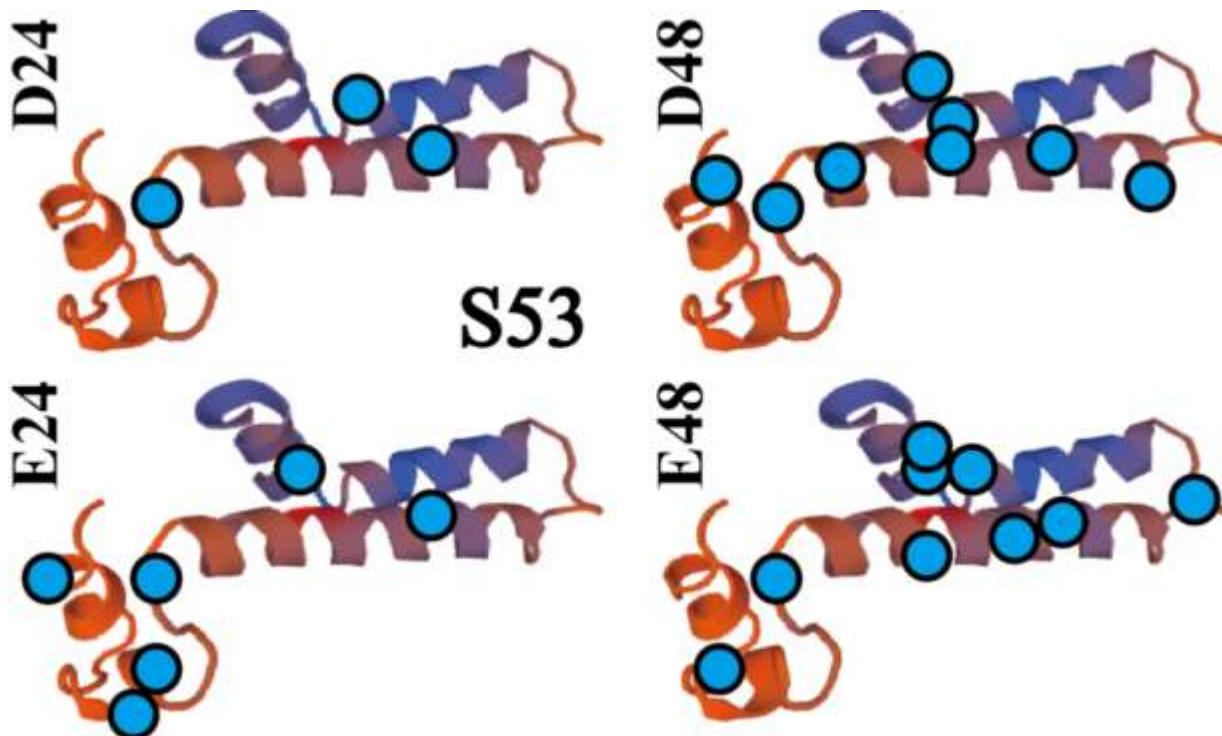
Changed pattern on DIGE gel:



Location in rubber genome: scaffold1222_136753.mRNA1

Protein name: Rubber elongation factor protein/REF138

Predicted 3-D structure and phosphorylated amino acids:



Detail information for phosphorylation of amino acid sites:

D24: MAEDEDNQQGQGEGLKYLGFVQDAATYAVTTFSNVYLFAKDKSSGPLQPGVDIIEGPVKNVAVPLYNRFSYIPNGA

E24: MAEDEDDNQQGQGEGLKYLGFVQDAATYAVTTFSNVYLFAKDKSSGPLQPGVDIIEGPVKNVAVPLYNRFSYIPNGA

D48: MAEDEDDNQQGQGEGLKYLGFVQDAATYAVTTFSNVYLFAKDKSSGPLQPGVDIIIEGPVKNVAVPLYNRFSYIPNGA

E48: MAEDEDNQQGQGEGLKYLGFVQDAATYAVTTFSNVYLFAKDKSSGPLQPGVDIIEGPVKNVAVPLYNRFSYIPNGA

D24: LKFVDSTVVASVTIIDRSLLPIVKDASIQVVSAIRAAPEAARSLASSSLPGQTKLAKVFYGEN

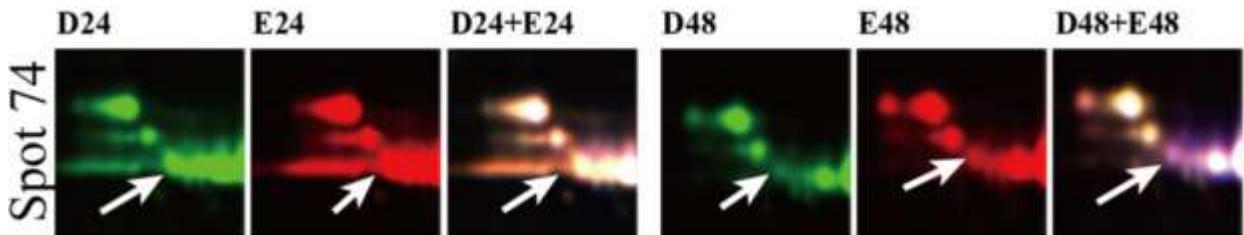
E24: LKFVDSTVVASVTIIDRSLLPIVKDASIQVVSAIRAAPEAARSLASSLPGQTTKILAKVFYGEN

D48: LKFVDSTVVASVTIIDRSSLLPIVKDASIQVVSAIRAAPEAARSLASSLPGQTKLAKVFYGEN

E48: LKFVDSTVVASVTIIDRSLLPIVKDASIQVVSAIRAAPEAARSLASSLPGQTTKLAKVFYGEN

Spot No. 74

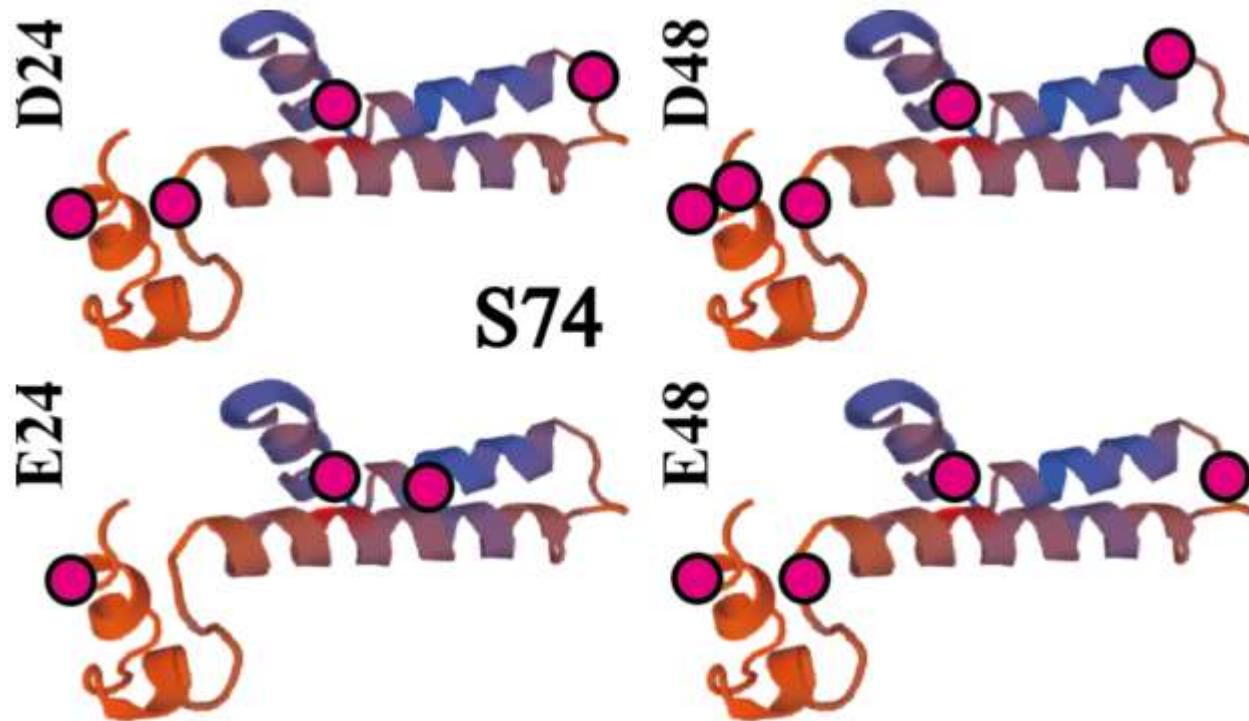
Changed pattern on DIGE gel:



Location in rubber genome: scaffold1222_136753.mRNA1

Protein name: Rubber elongation factor protein/REF138

Predicted 3-D structure and phosphorylated amino acids:



Detail information for phosphorylation of amino acid sites:

D24: MAEDEDDNQQGQGEGLKYLGFVQDAATYAVTTFSNVYLF~~A~~KDKSGPLQPGVDIIEGPVKNAVPLYNRFSYIPNGA

E24: MAEDEDDNQQGQGEGLKYLGFVQDAATYAVTTFSNVYLF~~A~~KDKSGPLQPGVDIIEGPVKNAVPLYNRFSYIPNGA

D48: MAEDEDDNQQGQGEGLKYLGFVQDAATYAVTTFSNVYLF~~A~~KDKSGPLQPGVDIIEGPVKNAVPLYNRFSYIPNGA

E48: MAEDEDDNQQGQGEGLKYLGFVQDAATYAVTTFSNVYLF~~A~~KDKSGPLQPGVDIIEGPVKNAVPLYNRFSYIPNGA

D24: LKFVDSTVVASVTIIDRSLLPPIVKDSIQVVS~~A~~IRAAPEAARS~~L~~ASSLPGTKILAKVFYGEN

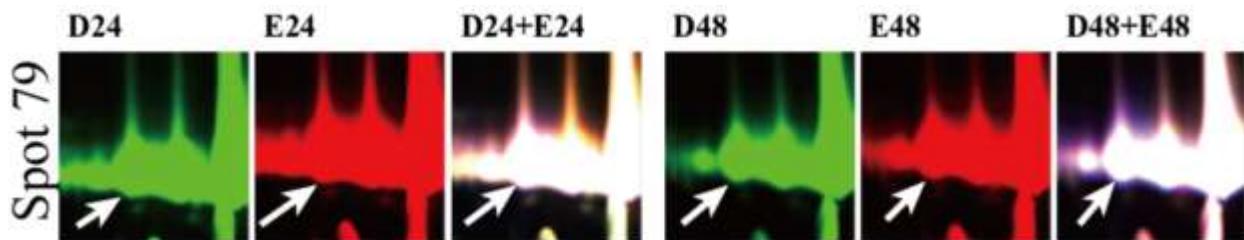
E24: LKFVDSTVVASVTIIDRSLLPPIVKDSIQVVS~~A~~IRAAPEAARS~~L~~ASSLPGTKILAKVFYGEN

D48: LKFVDSTVVASVTIIDRSLLPPIVKDSIQVVS~~A~~IRAAPEAARS~~L~~ASSLPGTKILAKVFYGEN

E48: LKFVDSTVVASVTIIDRSLLPPIVKDSIQVVS~~A~~IRAAPEAARS~~L~~ASSLPGTKILAKVFYGEN

Spot No. 79

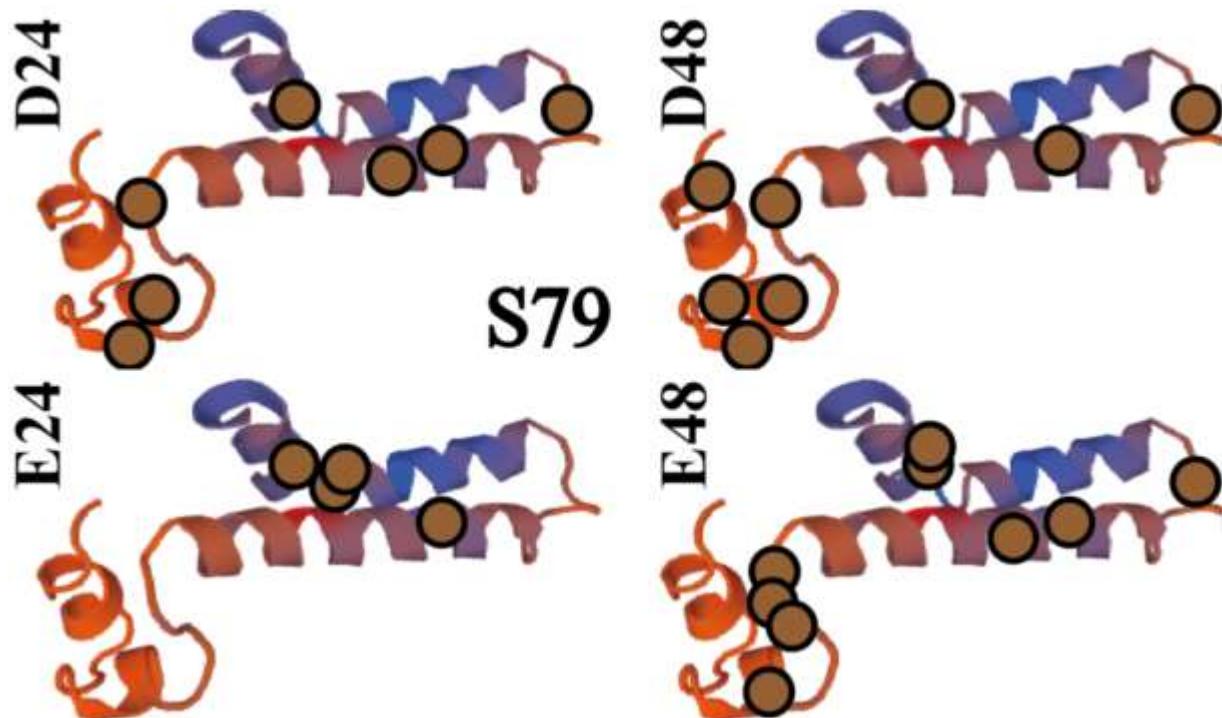
Changed pattern on DIGE gel:



Location in rubber genome: scaffold1222_136753.mRNA1

Protein name: Rubber elongation factor protein/REF138

Predicted 3-D structure and phosphorylated amino acids:



Detail information for phosphorylation of amino acid sites:

D24: MAEDEDNQQGQGEGLKYLGFVQDAATYAV**T**TFS**S**NVYLFAK**D**K**S**GPLQPGVDI IEGPVKNVAVPLYNRF**S**YIPNGA

E24: MAEDEDNQQGQGEGLKYLGFVQDAATYAV**T**TFS**S**NVYLFAK**D**K**S**GPLQPGVDI IEGPVKNVAVPLYNRF**S**YIPNGA

D48: MAE**D**EDNQQGQGEGLKYLGFVQDAATYAV**T**TYAV**T**TFS**S**NVYLFAK**D**K**S**GPLQPGVDI IEGPVKNVAVPLYNRF**S**YIPNGA

E48: MAEDEDNQQGQGEGLKYLGFVQDAATYAV**T**TFS**N**VYLFAK**D**K**S**GPLQPGVDI IEGPVKNVAVPLYNRF**S**YIPNGA

D24: LKFVDS**T**VVASVTI IDRSLPPIVK**D**ASIQVVSAIRAAPEAARS**L**ASSLPGQ**T**KILAKVFYGEN

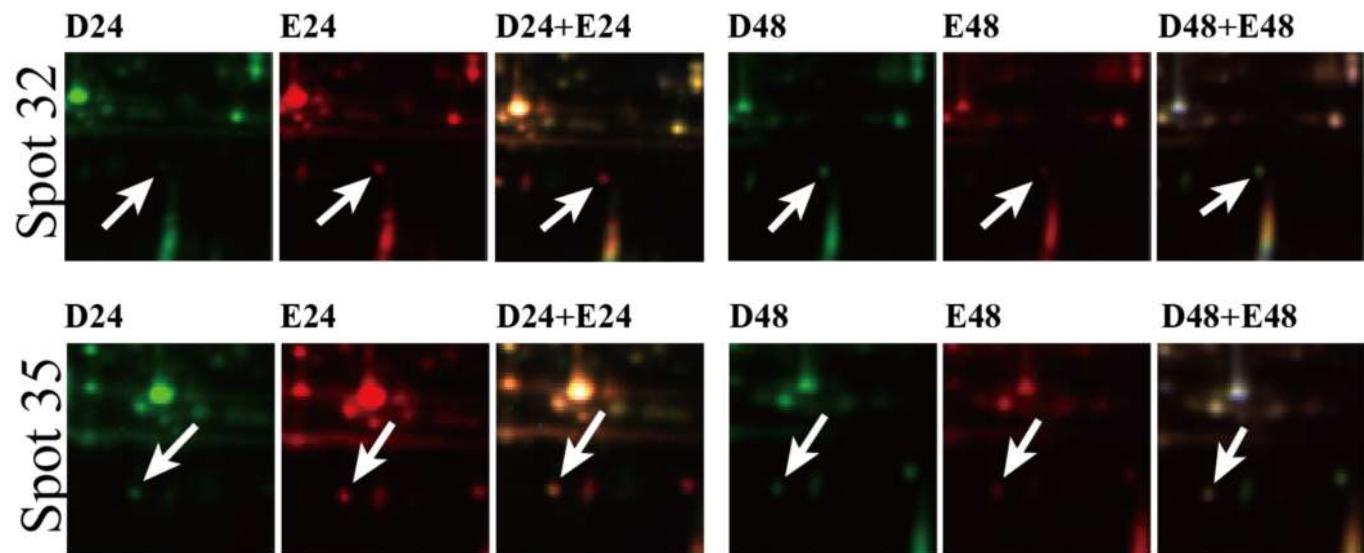
E24: LKFVDS**T**VVASVTI IDRSLPPIVK**D**ASIQVVSAIRAAPEAARSL**A**SSLPGQ**T**KILAKVFYGEN

D48: LKFVDS**T**VVASVTI IDRSLPPIVK**D**ASIQVVSAIRAAPEAARS**L**ASSLPGQ**T**KILAKVFYGEN

E48: LKFVDS**T**VVASVTI IDRSLPPIVK**D**ASIQVVSAIRAAPEAARSL**A**SSLPGQ**T**KILAKVFYGEN

Protein name: REF175

Location of the two spots identified as **REF175** by MS from 2-D DIGE gels:

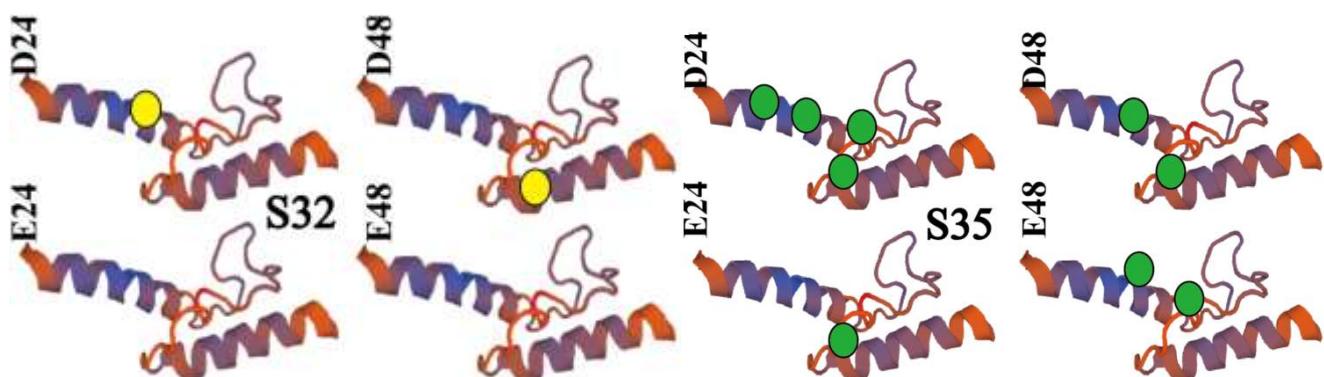


Detail information for phosphorylation of amino acid id sites in **REF175**:

■ Spot 32 ■ Spot 35

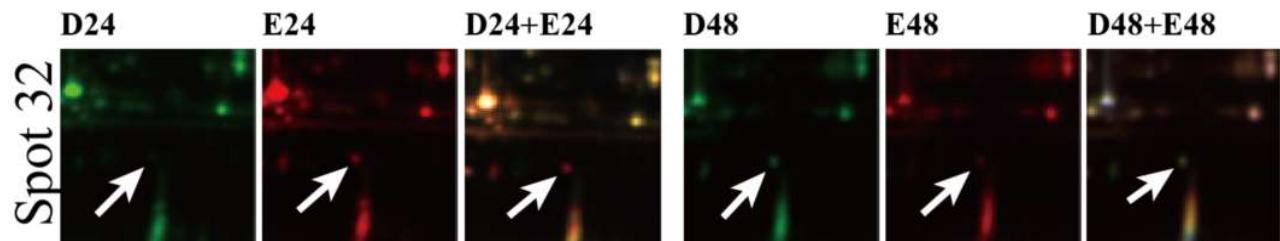
D24h	MAEGEEEVNIQEEANKGEENPQEEANIQEEETNKGEENIQEEANKEEESLKYLD LDFVQAATVYARA S FSKLYLF A KDKS
E24h	MAEGEEEVNIQEEANKGEENPQEEANIQEEETNKGEENIQEEANKEEESLKYLDFVQAATVYARASFSKLYLFAKDKS
D48h	MAEGEEEVNIQEEANKGEENPQEEANIQEEETNKGEENIQEEANKEEESLKYLD FVQAATVYARA S FSKLYLF A KDKS
E48h	MAEGEEEVNIQEEANKGEENPQEEANIQEEETNKGEENIQEEANKEEESLKYLD FVQAATVYARA S FSKLYLF A KDKS
D24h	GPFKPGVNTVESRFKSVRPVPYV NKFQPV PVNKVL KFADRRV DAY VTVL DRIVPPIV KRAS IQAYSVAPGAARAVASYLPLHTKRL SKVLYGDG
E24h	GPFKPGVNTVESRFKSVRPVPYVNKFQPVPVNKVLKFADRRVDAYVTVLDRIVPPIVKRASIQAYSVAPGAARAVASYLPLHTKRL SKVLYGDG
D48h	GPFKPGVNTVESRFKSVRPVPYV NKFQPV PVNKVL KFADRRV DAY VTVL DRIVPPIV KRAS IQAYSVAPGAARAVASYLPLHTKRL SKVLYGDG
E48h	GPFKPGVNTVESRFKSVRPVPYVNKFQPVPVNKVLKFADRRVDAYVTVLDRIVPPIVKRASIQAYSVAPGAARAVASYLPLHTKRL SKVLYGDG

Predicted 3-D structure and phosphorylated amino acids in different **REF175** isoforms:



Spot No. 32

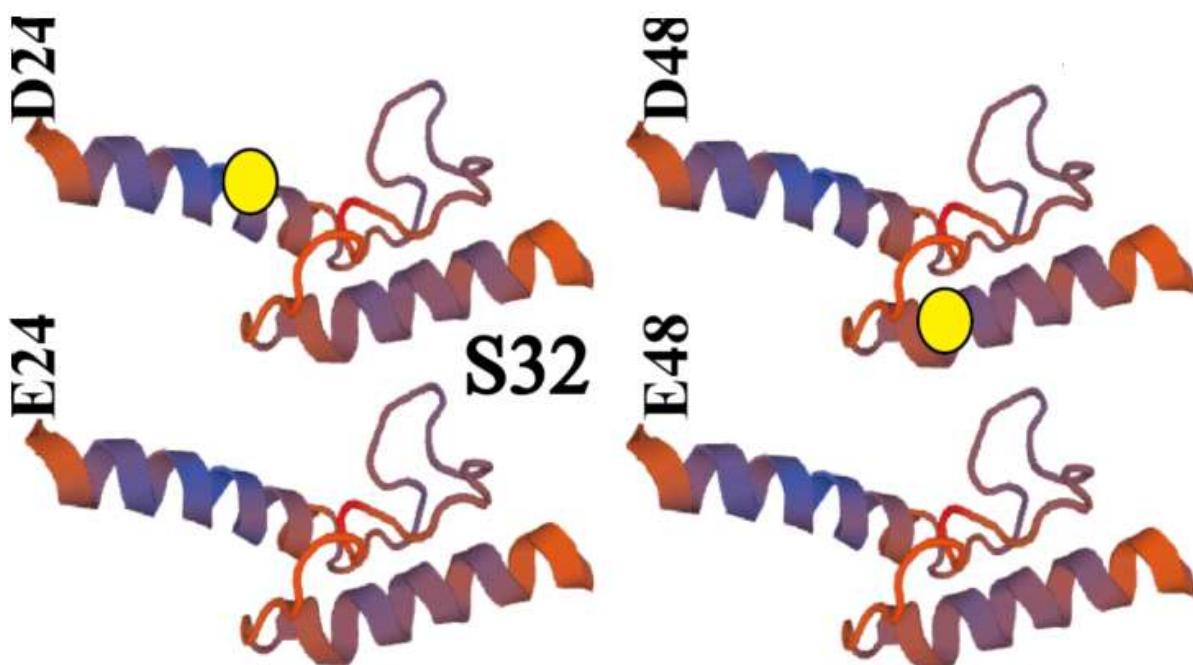
Changed pattern on DIGE gel:



Location in rubber genome: scaffold1222_100110.mRNA1

Protein name: Rubber elongation factor protein/REF175

Predicted 3-D structure and phosphorylated amino acids:



Detail information for phosphorylation of amino acid sites:

D24: MAEGEEEVNIQEEANKGEENPQEEANIQEETNKGEENIQEEANIQEANKEESLKYLDFVQAATVYARA**S**FSKL

E24: MAEGEEEVNIQEEANKGEENPQEEANIQEETNKGEENIQEEANIQEANKEESLKYLDFVQAATVYARASFSKL

D48: MAEGEEEVNIQEEANKGEENPQEEANIQEETNKGEENIQEEANIQEANKEESLKYLDFVQAATVYARASFSKL

E48: MAEGEEEVNIQEEANKGEENPQEEANIQEETNKGEENIQEEANIQEANKEESLKYLDFVQAATVYARASFSKL

D24: YLFAKDKSGPFKPGVNTVESRFKSVVRPVYNKFQPVPNVLKFADRRVDAYTVLDRIVPPIVKRASI**Q**AYSVAP

E24: YLFAKDKSGPFKPGVNTVESRFKSVVRPVYNKFQPVPNVLKFADRRVDAYTVLDRIVPPIVKRASI**Q**AYSVAP

D48: YLFAKDKSGPFKPGVNTVESRFKSVVRPVYNKFQPVPNVLKFADRRVDAYTVLDRIVPPIVKRASI**Q**AYS**V**AP

E48: YLFAKDKSGPFKPGVNTVESRFKSVVRPVYNKFQPVPNVLKFADRRVDAYTVLDRIVPPIVKRASI**Q**AYSVAP

D24: GAARAVASYLPLHTKRLSKVLYGDG

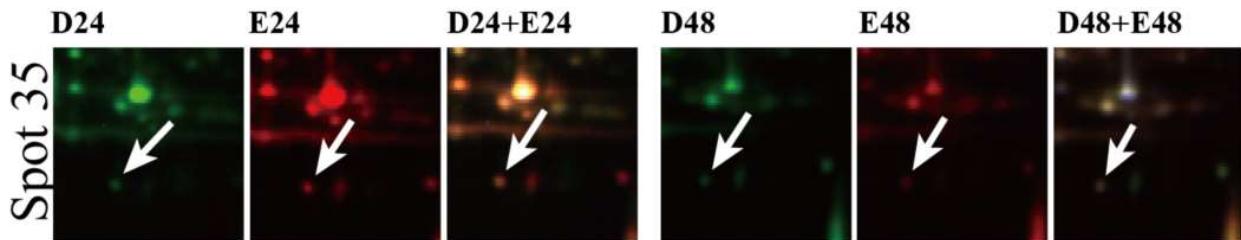
E24: GAARAVASYLPLHTKRLSKVLYGDG

D48: GAARAVASYLPLHTKRLSKVLYGDG

E48: GAARAVASYLPLHTKRLSKVLYGDG

Spot No. 35

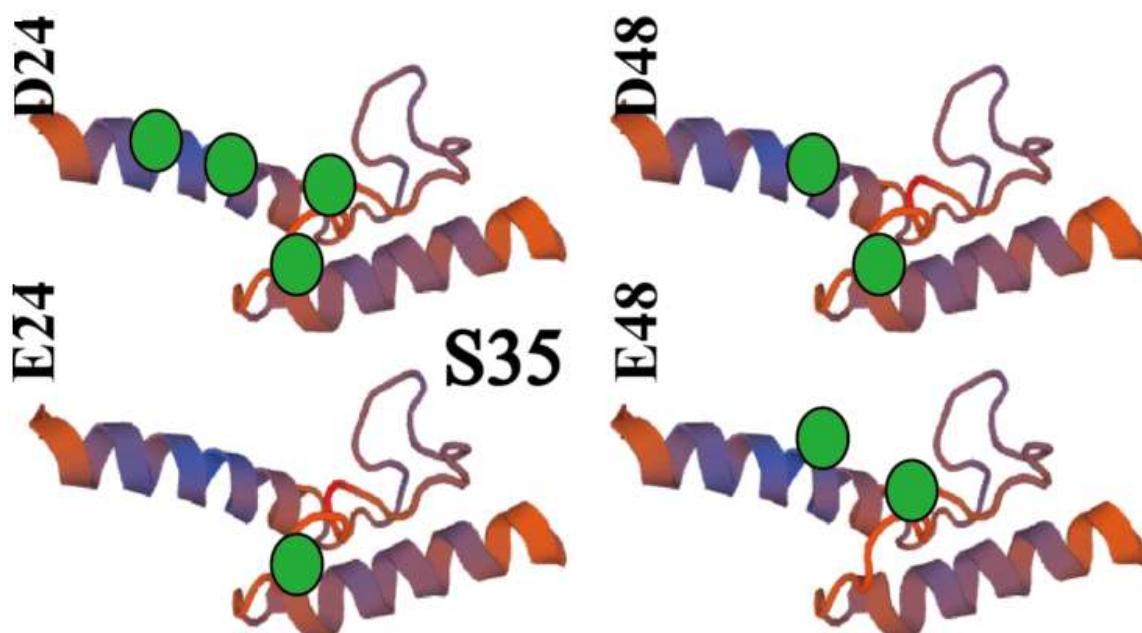
Changed pattern on DIGE gel:



Location in rubber genome: scaffold1222_100110.mRNA1

Protein name: Rubber elongation factor protein/REF175

Predicted 3-D structure and phosphorylated amino acids:



Detail information for phosphorylation of amino acid sites:

D24: MAEGEEEVNIQEEANKGEENPQEEANIQEETNKGEENIQEEANIQEANKEEESLKYLDFVQAATVYARASFSKL

E24: MAEGEEEVNIQEEANKGEENPQEEANIQEETNKGEENIQEEANIQEANKEEESLKYLDFVQAATVYARASFSKL

D48: MAEGEEEVNIQEEANKGEENPQEEANIQEETNKGEENIQEEANIQEANKEEESLKYLDFVQAATVYARASFSKL

E48: MAEGEEEVNIQEEANKGEENPQEEANIQEETNKGEENIQEEANIQEANKEEESLKYLDFVQAATVYARASFSKL

D24: YLFAKDKSGPFKPGVNTVESRFKSVRPVYNKFQPVPKVLKFADRRVDAYVTLDRIVPPIVKRASSIQAYSVAP

E24: YLFAKDKSGPFKPGVNTVESRFKSVRPVYNKFQPVPKVLKFADRRVDAYVTLDRIVPPIVKRASSIQAYSVAP

D48: YLFAKDKSGPFKPGVNTVESRFKSVRPVYNKFQPVPKVLKFADRRVDAYVTLDRIVPPIVKRASSIQAYSVAP

E48: YLFAKDKSGPFKPGVNTVESRFKSVRPVYNKFQPVPKVLKFADRRVDAYVTLDRIVPPIVKRASIQAYSVAP

D24: GAARAVASYLPLHTKRLSKVLYGDG

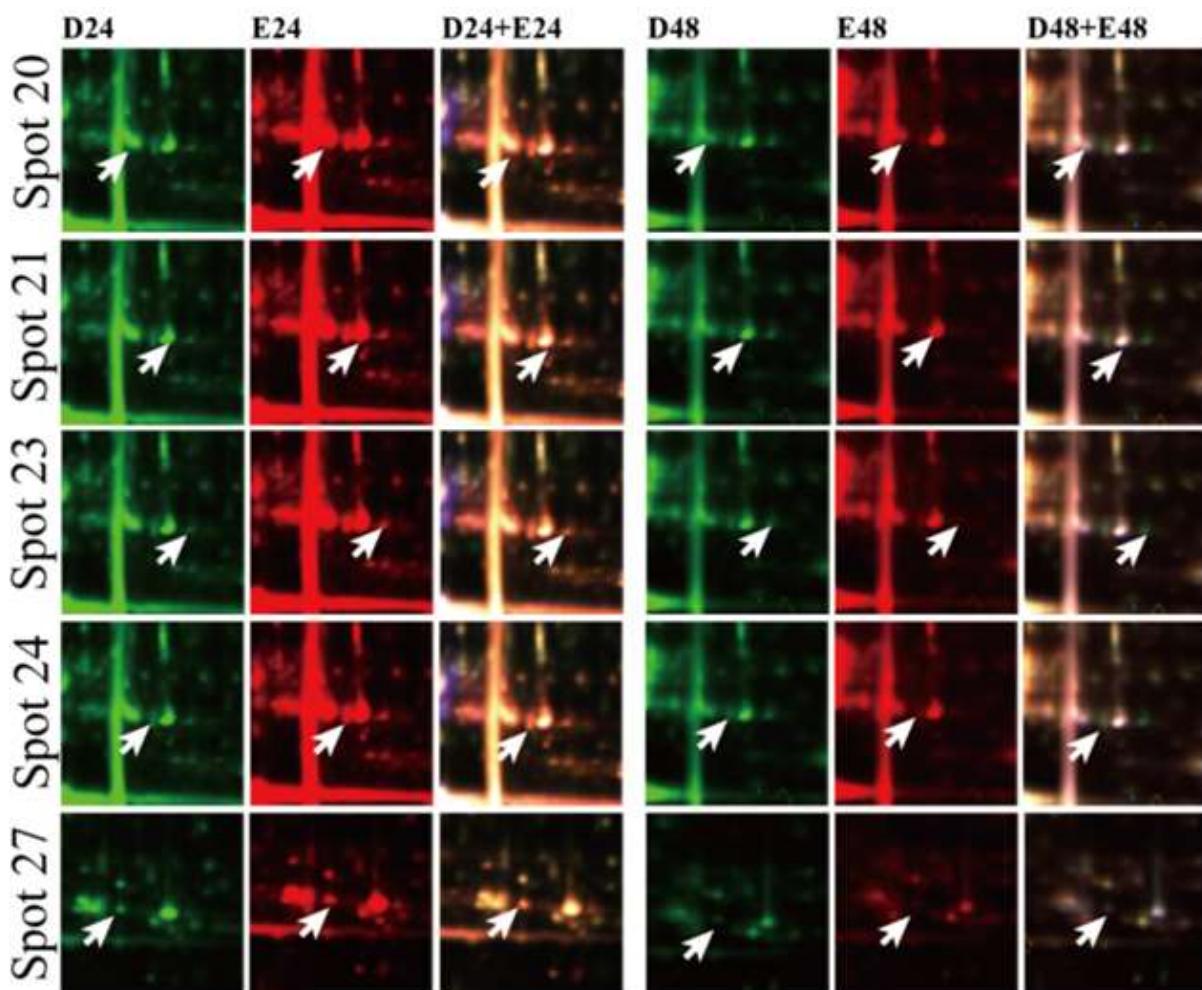
E24: GAARAVASYLPLHTKRLSKVLYGDG

D48: GAARAVASYLPLHTKRLSKVLYGDG

E48: GAARAVASYLPLHTKRLSKVLYGDG

Protein name: REF258

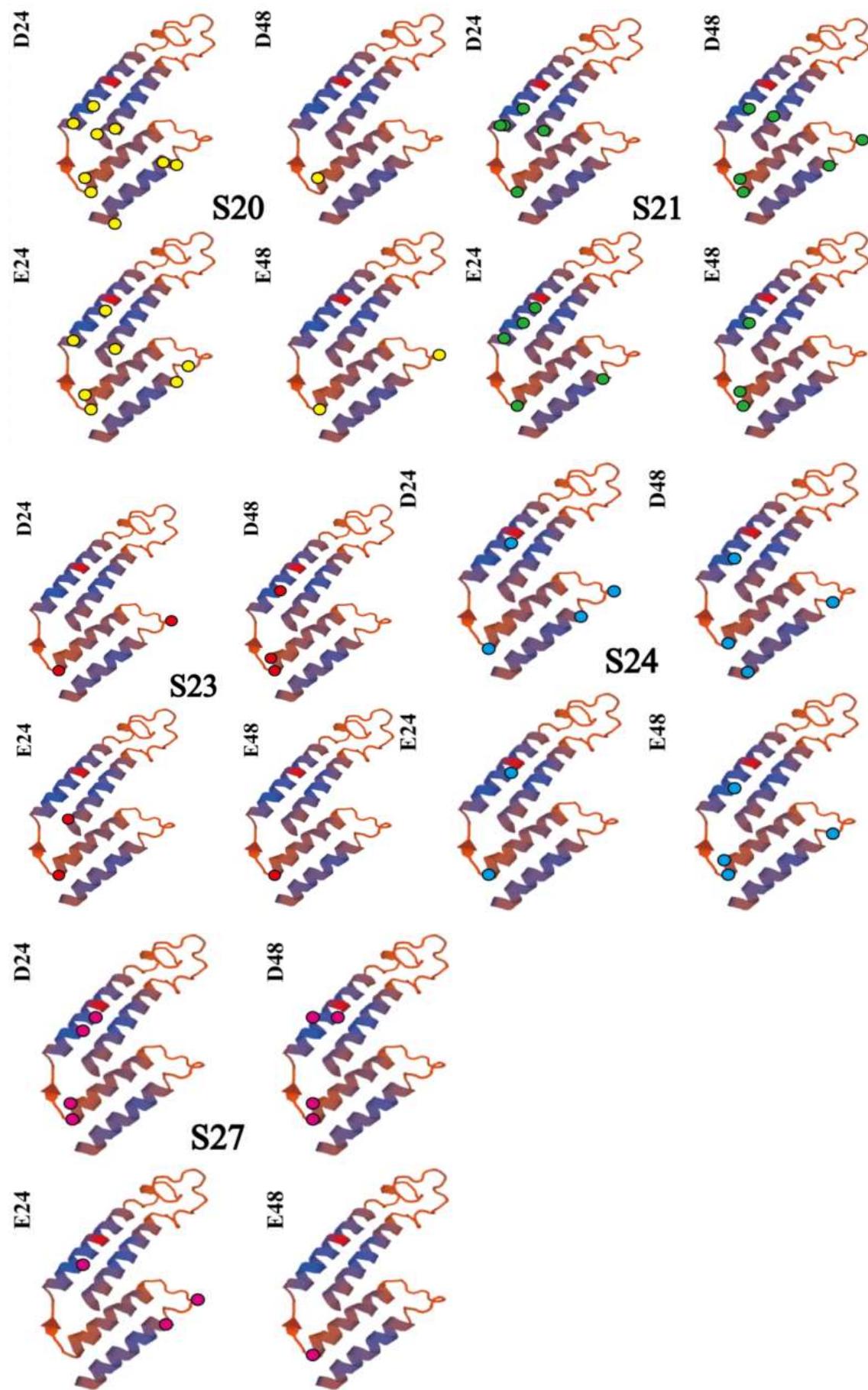
Location of the **five** spots identified as **REF258** by MS from 2-D DIGE gels:



Detail information for phosphorylation of amino acid id sites in **REF258**:

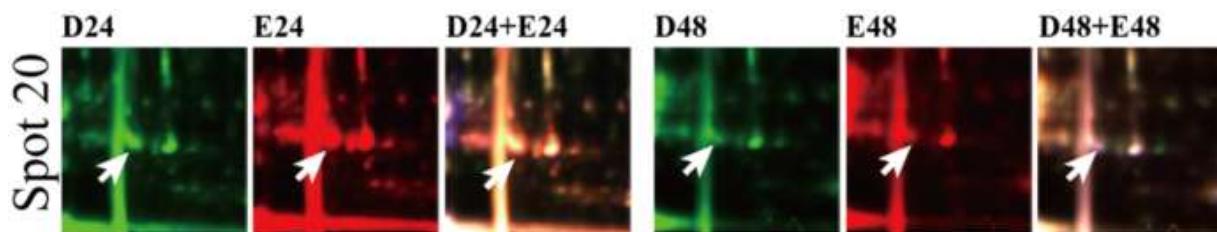
	Spot 20	Spot 21	Spot 23	Spot 24	Spot 27	Share
D24h	MASLLGAASVINAASNVVEEAVKGVENAQQEVARANAVSNP S NIVKDVASAA D IVEEEAKGVENVQKEVARANAVNSSSNIVKDVASAA D IVEEEAKVVDNVQQGVV S A A NVVEEAAKGVGNQEKVDDDEED					
E24h	MASLLGAASVINAASNVVEEAVKGVENAQQEVARANAVSNP S NIVKDVASAA D IVEEEAKGVENVQKEVARANAVNSSSNIVKDVASAA D IVEEEAKVVDNVQQGVV S A A NVVEEAAKGVGNQEKVDDDEED					
D48h	MASLLGAASVINAASNVVEEAVKGVENAQQEVARANAVSNP S NIVKDVASAA D IVEEEAKGVENVQKEVARANAVNSSSNIVKDVASAA D IVEEEAKVVDNVQQGVV S A A NVVEEAAKGVGNQEKVDDDEED					
E48h	MASLLGAASVINAASNVVEEAVKGVENAQQEVARANAVSNPSNIVKDVA S A T DIVEEEAKGVENVQKEVARANAVNSSSNIVKDVASAA D IVEEEAKVVDNVQQGVV S A A NVVEEAAKGVGNQEKVDDDEED					
D24h	DEEI TLKYLDIVQAALVLALVSS K L I LYLFVKD N GPLPGV D EAEVTIKSVVRPFYYRFHD V PKVLKFADNQVDA S T T VLRYAPPV V KQVSTRAYSVARNAPRAALALVSYLPLPT N R L C K LLSED K					
E24h	DEEI TLKYLDIVQAALVLALVSS K L I LYLFVKD N GPLPGV D EAEVTIKSVVRPFYYRFHD V PKVLKFADNQVDA S T T VLRYAPPV V KQVSTRAYSVARNAPRAALALVSYLPLPT N R L C K LLSED K					
D48h	DEEI TLKYLDIVQAALVLALVSS K L I LYLFVKD N GPLPGV D EAEVTIKSVVRPFYYRFHD V PKVLKFADNQVDA S T T VLRYAPPV V KQVSTRAYSVARNAPRAALALV V Y L PLPT N R L C K LLSED K					
E48h	DEEI TLKYLDIVQAALVLALVSS K L I LYLFVKD N GPLPGV D EAEVTIKSVVRPFYYRFHD V PKVLKFADNQVDA S T T VLRYAPPV V KQVSTRAYSVARNAPRAALALV V Y L PLPT N R L C K LLSED K					

Predicted 3-D structure and phosphorylated amino acids in different REF258 isoforms:



Spot No. 20

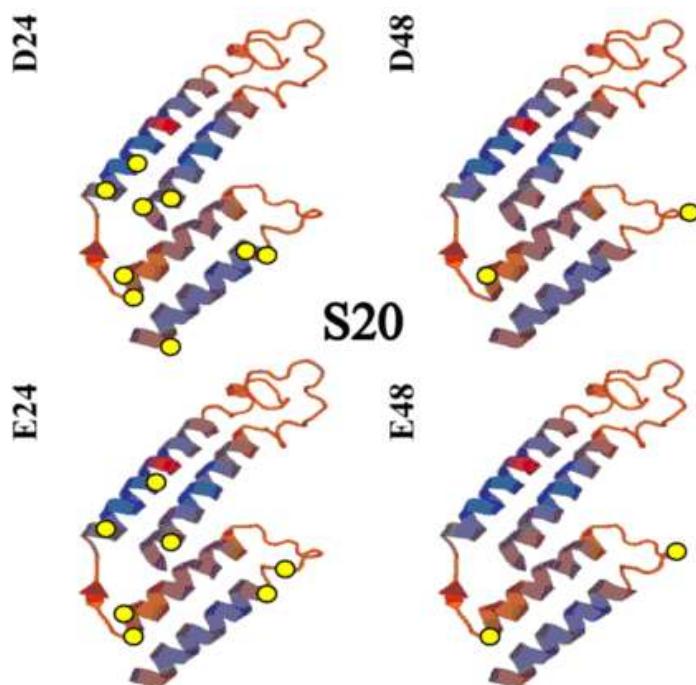
Changed pattern on DIGE gel:



Location in rubber genome: scaffold1222_175215.mRNA1

Protein name: Rubber elongation factor protein/REF258

Predicted 3-D structure and phosphorylated amino acids:



Detail information for phosphorylation of amino acid sites:

D24: MASLLGAASNVINAASNVVEEAVKGVENAQEVANAVSNPSSNIVKDVASAATDIVEEAAKGVENVQKEVANAVSN

E24: MASLLGAASNVINAASNVVEEAVKGVENAQEVANAVSNPSSNIVKDVASAATDIVEEAAKGVENVQKEVANAVSN

D48: MASLLGAASNVINAASNVVEEAVKGVENAQEVANAVSNPSNIVKDVASAATDIVEEAAKGVENVQKEVANAVSN

E48: MASLLGAASNVINAASNVVEEAVKGVENAQEVANAVSNPSNIVKDVASAATDIVEEAAKGVENVQKEVANAVSN

D24: SSNIVKDVASAATDIVEEAAKVVDNVQQGVVSASNVVEEAAKGVGNIQEKVDEEEEDTLKYLDIVQAALVLALV

E24: SSNIVKDVASAATDIVEEAAKVVDNVQQGVVSASNVVEEAAKGVGNIQEKVDEEEEDTLKYLDIVQAALVLALV

D48: SSNIVKDVASAATDIVEEAAKVVDNVQQGVVSASNVVEEAAKGVGNIQEKVDEEEEDTLKYLDIVQAALVLALV

E48: SSNIVKDVASAATDIVEEAAKVVDNVQQGVVSASNVVEEAAKGVGNIQEKVDEEEEDTLKYLDIVQAALVLALV

D24: SSSSKL^YL^FV^KDKSGPLKPGVDTAEVTIKSVVRPFYYRFHDVPNKVLKFADNQVDASVTLVLRYAPPVVKQVSTRA

E24: SSSSKL^YL^FV^KDKSGPLKPGVDTAEVTIKSVVRPFYYRFHDVPNKVLKFADNQVDASVTLVLRYAPPVVKQVSTRA

D48: SSSSKL^YL^FV^KDKSGPLKPGVDTAEVTIKSVVRPFYYRFHDVPNKVLKFADNQVDASVTLVLRYAPPVVKQVSTRA

E48: SSSSKL^YL^FV^KDKSGPLKPGVDTAEVTIKSVVRPFYYRFHDVPNKVLKFADNQVDASVTLVLRYAPPVVKQVSTRA

D24: YSVARNAPRAALALVSYLPLPTTNRLCKLLSEDK

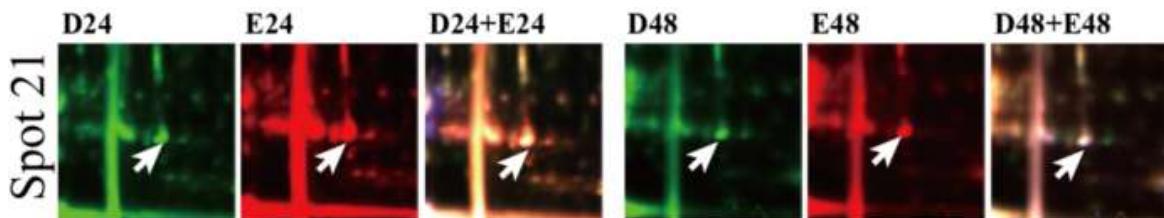
E24: YSVARNAPRAALALVSYLPLPTTNRLCKLLSEDK

D48: YSVARNAPRAALALVSYLPLPTNRLCKLLSEDK

E48: YSVARNAPRAALALVSYLPLPTNRLCKLLSEDK

Spot No. 21

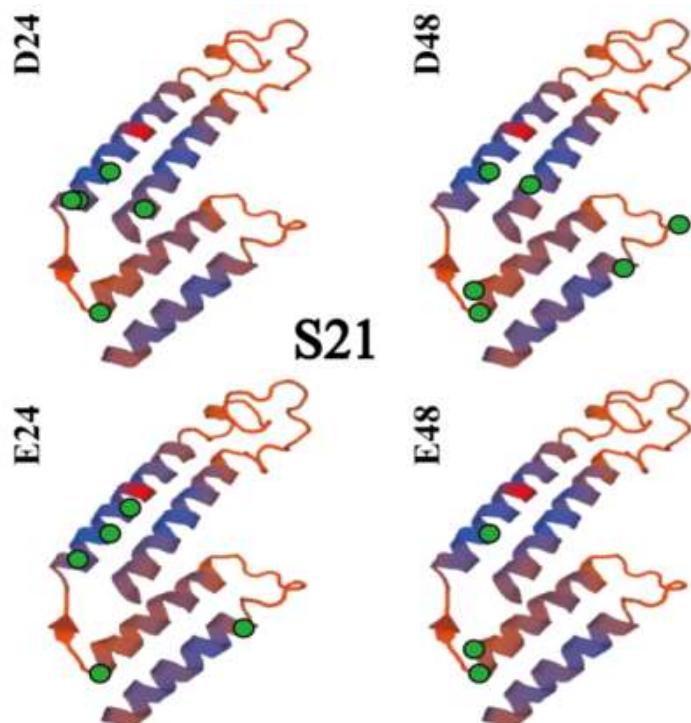
Changed pattern on DIGE gel:



Location in rubber genome: scaffold1222_175215.mRNA1

Protein name: Rubber elongation factor protein/REF258

Predicted 3-D structure and phosphorylated amino acids:



Detail information for phosphorylation of amino acid sites:

D24: MASLLGAASNVINAASNVVEEAVKGVENAQEVANAVSNPSNIVKDVASAATDIVEAAKGVENVQKEVANAVSN

E24: MASLLGAASNVINAASNVVEEAVKGVENAQEVANAVSNPSSNIVKDVASAATDIVEAAKGVENVQKEVANAVSN

D48: MASLLGAASNVINAASNVVEEAVKGVENAQEVANAVSNPSSNIVKDVASAATTDIVEAAKGVENVQKEVANAVSN

E48: MASLLGAASNVINAASNVVEEAVKGVENAQEVANAVSNPSNIVKDVASAATDIVEAAKGVENVQKEVANAVSN

D24: SSNIVKDVASAATDIVEAAKVVDNVQQGVVSAASSNVVEEAAKGVGNIQEKFADNQVDASVTLVRYAPPVVKQVSTRA

E24: SSNIVKDVASAATDIVEAAKVVDNVQQGVVSAASSNVVEEAAKGVGNIQEKFADNQVDASVTLVRYAPPVVKQVSTRA

D48: SSNIVKDVASAATDIVEAAKVVDNVQQGVVSAASSNVVEEAAKGVGNIQEKFADNQVDASVTLVRYAPPVVKQVSTRA

E48: SSNIVKDVASAATDIVEAAKVVDNVQQGVVSAASSNVVEEAAKGVGNIQEKFADNQVDASVTLVRYAPPVVKQVSTRA

D24: SSSKLYLFVKDKSGPLKPGVDTAEVTIKSVVRPFYYRFHDVPNKVLKFADNQVDASVTLVRYAPPVVKQVSTRA

E24: SSSKLYLFVKDKSGPLKPGVDTAEVTIKSVVRPFYYRFHDVPNKVLKFADNQVDASVTLVRYAPPVVKQVSTRA

D48: SSSKLYLFVKDKSGPLKPGVDTAEVTIKSVVRPFYYRFHDVPNKVLKFADNQVDASVTLVRYAPPVVKQVSTRA

E48: SSSKLYLFVKDKSGPLKPGVDTAEVTIKSVVRPFYYRFHDVPNKVLKFADNQVDASVTLVRYAPPVVKQVSTRA

D24: YSVARNAPRAALALVSYLPLPTTNRLCKLLSEDK

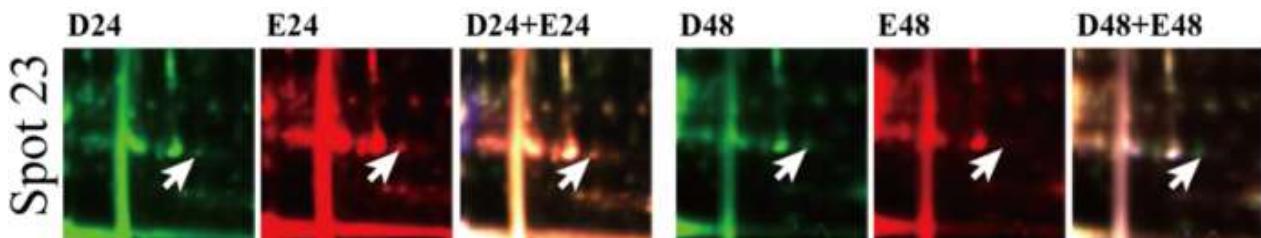
E24: YSVARNAPRAALALVSYLPLPTNRLCKLLSEDK

D48: YSVARNAPRAALALVSYLPLPTNRLCKLLSEDK

E48: YSVARNAPRAALALVSYLPLPTNRLCKLLSEDK

Spot No. 23

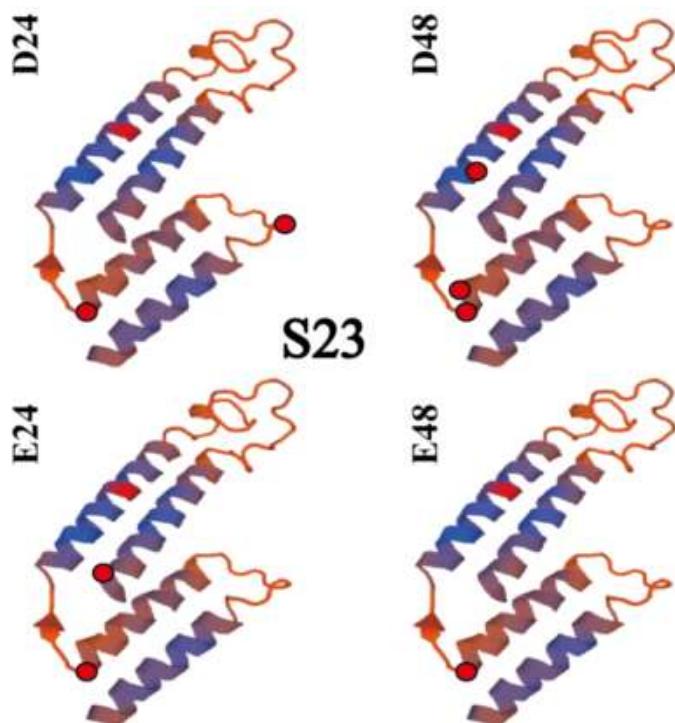
Changed pattern on DIGE gel:



Location in rubber genome: scaffold1222_175215.mRNA1

Protein name: Rubber elongation factor protein/REF258

Predicted 3-D structure and phosphorylated amino acids:



Detail information for phosphorylation of amino acid sites:

D24: MASLLGAASNVINAASNVVEEAVKGVENAQEVANAVSNPSNIVKDVASAATDIVEAAKGVENVQKEVANAVSN

E24: MASLLGAASNVINAASNVVEEAVKGVENAQEVANAVSNPSNIVKDVASAATDIVEAAKGVENVQKEVANAVSN

D48: MASLLGAASNVINAASNVVEEAVKGVENAQEVANAVSNPSNIVKDVASAATDIVEAAKGVENVQKEVANAVSN

E48: MASLLGAASNVINAASNVVEEAVKGVENAQEVANAVSNPSNIVKDVASAATDIVEAAKGVENVQKEVANAVSN

D24: SSNIVKDVAATDIVEAAKVVDNVQQGVVSAASNNVVEEAAKGVGNIQEKFADNQVDASVTLVRYAPPVVKQVSTRA

E24: SSNIVKDVAATDIVEAAKVVDNVQQGVVSAASNNVVEEAAKGVGNIQEKFADNQVDASVTLVRYAPPVVKQVSTRA

D48: SSNIVKDVAATDIVEAAKVVDNVQQGVVSAASNNVVEEAAKGVGNIQEKFADNQVDASVTLVRYAPPVVKQVSTRA

E48: SSNIVKDVAATDIVEAAKVVDNVQQGVVSAASNNVVEEAAKGVGNIQEKFADNQVDASVTLVRYAPPVVKQVSTRA

D24: SSSKLYLFVKDKSGPLKPGVDTAEVTIKSVVRPFYRFHDVPNKVLKFADNQVDASVTLVRYAPPVVKQVSTRA

E24: SSSKLYLFVKDKSGPLKPGVDTAEVTIKSVVRPFYRFHDVPNKVLKFADNQVDASVTLVRYAPPVVKQVSTRA

D48: SSSKLYLFVKDKSGPLKPGVDTAEVTIKSVVRPFYRFHDVPNKVLKFADNQVDASVTLVRYAPPVVKQVSTRA

E48: SSSKLYLFVKDKSGPLKPGVDTAEVTIKSVVRPFYRFHDVPNKVLKFADNQVDASVTLVRYAPPVVKQVSTRA

D24: YSVARNAPRAALALVSYLPLPTNRLCKLLSEDK

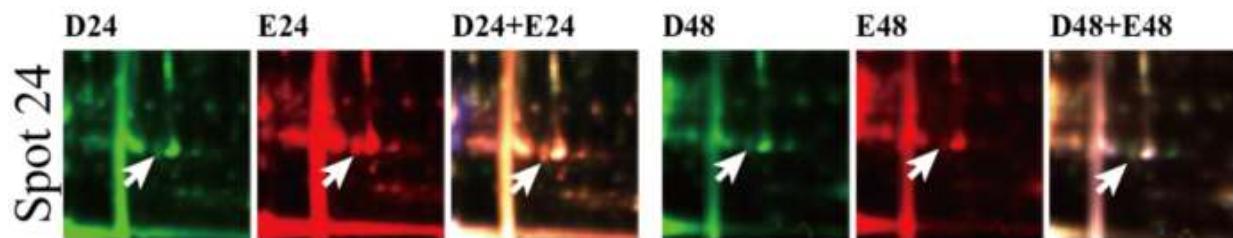
E24: YSVARNAPRAALALVSYLPLPTNRLCKLLSEDK

D48: YSVARNAPRAALALVSYLPLPTNRLCKLLSEDK

E48: YSVARNAPRAALALVSYLPLPTNRLCKLLSEDK

Spot No. 24

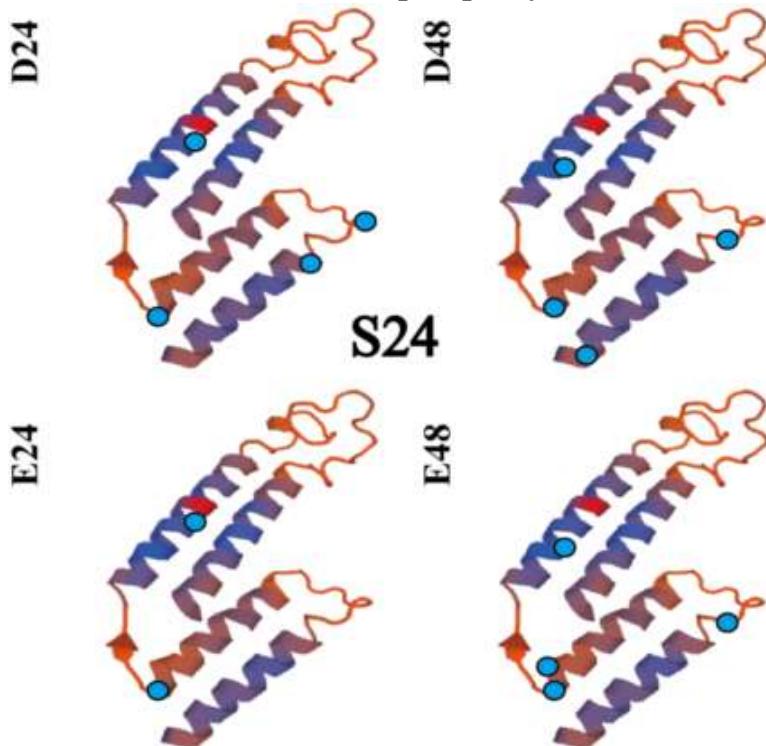
Changed pattern on DIGE gel:



Location in rubber genome: scaffold1222_175215.mRNA1

Protein name: Rubber elongation factor protein/REF258

Predicted 3-D structure and phosphorylated amino acids:



Detail information for phosphorylation of amino acid sites:

D24: MASLLGAASNVINAASNVVEEAVKGVENAQEVANAVSNPS**S**NIVKDVASAA**T**DIVEEEAKGVENVQKEVANAVSN

E24: MASLLGAASNVINAASNVVEEAVKGVENAQEVANAVSNPSNIVKDVASATDIVEEEAKGVENVQKEVANAVSN

D48: MASLLGAA**S**NVINAASNVVEEAVKGVENAQEVANAVSNPSNIVKDVA**S**AATDIVEEEAKGVENVQKEVANAVSN

E48: MASLLGAASNVINAASNVVEEAVKGVENAQEVANAVSNPSNIVKDVA**S**AATDIVEEEAKGVENVQKEVANAVSN

D24: SSNIVKDVASAATDIVEEEAKVVDNVQQGVVSAAS**S**NNVVEEAAKGVGNIQEKVDEEEDTLKYLDIVQAALVLALV

E24: SSNIVKDVASAATDIVEEEAKVVDNVQQGVVSAAS**S**NNVVEEAAKGVGNIQEKVDEEEDTLKYLDIVQAALVLALV

D48: SSNIVKDVASAATDIVEEEAKVVDNVQQGVVSAAS**S**NNVVEEAAKGVGNIQEKVDEEEDTLKYLDIVQAALVLALV

E48: SSNIVKDVASAATDIVEEEAKVVDNVQQGVV**S**AASNNVVEEAAKGVGNIQEKVDEEEDTLKYLDIVQAALVLALV

D24: SSSKLYLFVKDKSGPLKPGVDT**A**EVTIKSVVRPFYYRFHDVPNKVLKFADNQVDASVTLVRYAPPVVKQVSTRA

E24: SSSKLYLFVKDKSGPLKPGVDT**A**EVTIKSVVRPFYYRFHDVPNKVLKFADNQVDASVTLVRYAPPVVKQVSTRA

D48: SSSKLYLFVKDK**S**GPLKPGVDTAEVTIKSVVRPFYYRFHDVPNKVLKFADNQVDASVTLVRYAPPVVKQVSTRA

E48: SSSKLYLFVKDK**S**GPLKPGVDTAEVTIKSVVRPFYYRFHDVPNKVLKFADNQVDASVTLVRYAPPVVKQVSTRA

D24: YSVARNAPRAALALVSYLPLPTNRLCKLLSEDK

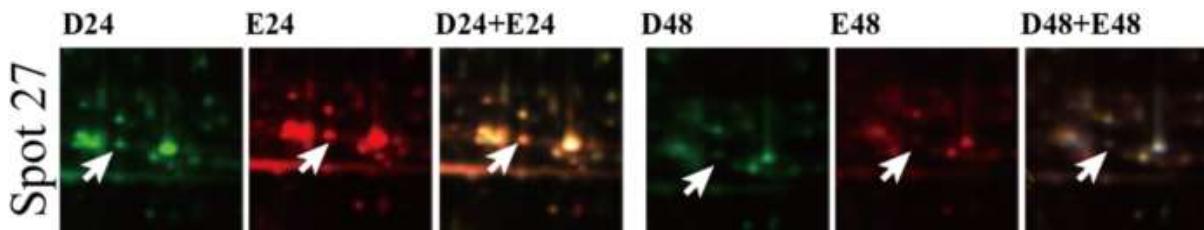
E24: YSVARNAPRAALALVSYLPLPTNRLCKLLSEDK

D48: YSVARNAPRAALALVSYLPLPTNRLCKLLSEDK

E48: YSVARNAPRAALALVSYLPLPTNRLCKLLSEDK

Spot No. 27

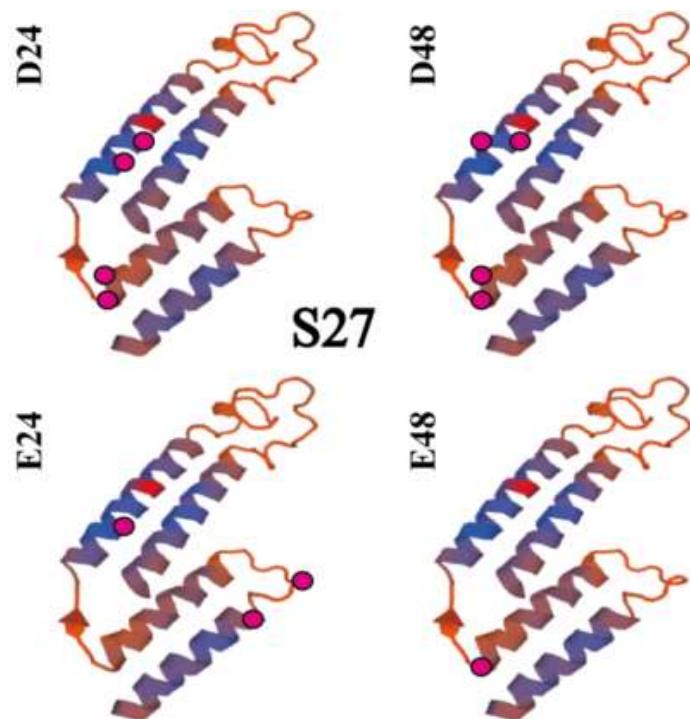
Changed pattern on DIGE gel:



Location in rubber genome: scaffold1222_175215.mRNA1

Protein name: Rubber elongation factor protein/REF258

Predicted 3-D structure and phosphorylated amino acids:



Detail information for phosphorylation of amino acid sites:

D24: MASLLGAASNVINAASNVVEEAVKGVENAQQEVARAVSNPSNIVKDVASAATDIVEEAAGVENVQKEVANAVSN

E24: MASLLGAASNVINAASNVVEEAVKGVENAQQEVARAVSNPS**S**NIVKDVASAAT**T**DIVEEAAGVENVQKEVANAVSN

D48: MASLLGAASNVINAASNVVEEAVKGVENAQQEVARAVSNPSNIVKDVASAATDIVEEAAGVENVQKEVANAVSN

E48: MASLLGAASNVINAASNVVEEAVKGVENAQQEVARAVSNPSNIVKDVASAATDIVEEAAGVENVQKEVANAVSN

D24: SSNIVKDVAATDIVEEAAKVVDNVQQGVV**S****A****S**NVVEEAAKGVGNIQEKVDDDEEDTLKYLDIVQAALVLALV

E24: SSNIVKDVAATDIVEEAAKVVDNVQQGVV**S****A****S**NVVEEAAKGVGNIQEKVDDDEEDTLKYLDIVQAALVLALV

D48: SSNIVKDVAATDIVEEAAKVVDNVQQGVV**S****A****S**NVVEEAAKGVGNIQEKVDDDEEDTLKYLDIVQAALVLALV

E48: SSNIVKDVAATDIVEEAAKVVDNVQQGVV**S****A****S**NVVEEAAKGVGNIQEKVDDDEEDTLKYLDIVQAALVLALV

D24: SSSKLYLFVKDK**S**GPLKPGVDTAEVTIKSVVRPFYYRFHDVPNKVLKFADNQVDASVTLVRYAPPVVKQVSTRA

E24: SSSKLYLFVKDK**S**GPLKPGVDTAEVTIKSVVRPFYYRFHDVPNKVLKFADNQVDASVTLVRYAPPVVKQVSTRA

D48: SSSKLYLFVKDK**S**GPLKPGVDTAEVTIKSVVRPFYYRFHDVPNKVLKFADNQVDASVTLVRYAPPVVKQVSTRA

E48: SSSKLYLFVKDK**S**GPLKPGVDTAEVTIKSVVRPFYYRFHDVPNKVLKFADNQVDASVTLVRYAPPVVKQVSTRA

D24: YSVARNAPRAALALVSYLPLPTNRLCKLLSEDK

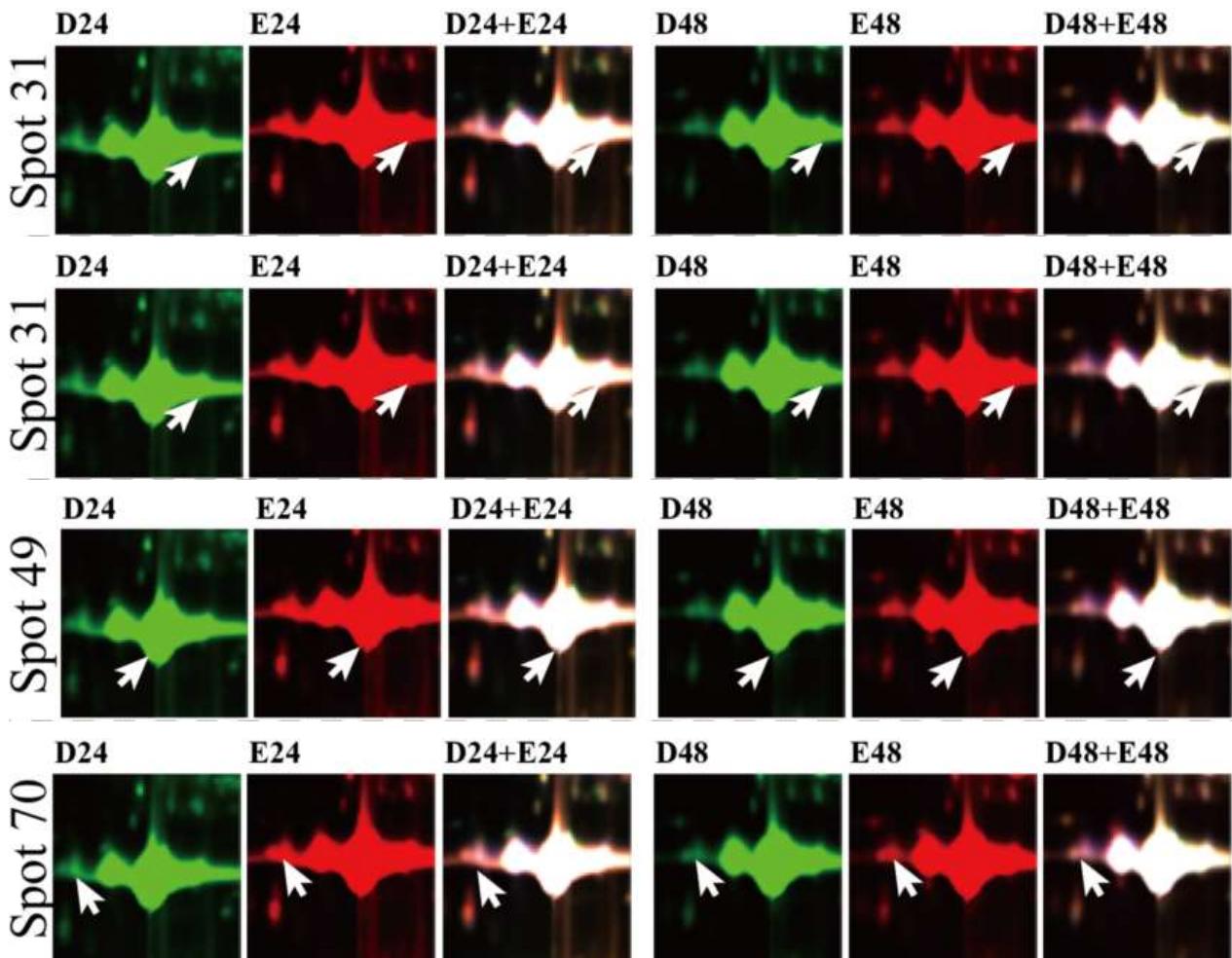
E24: YSVARNAPRAALALVSYLPLPTNRLCKLLSEDK

D48: YSVARNAPRAALALVSYLPLPTNRLCKLLSEDK

E48: YSVARNAPRAALALVSYLPLPTNRLCKLLSEDK

Protein name: SRPP204

Location of the three spots identified as **SRPP204** by MS from 2-D DIGE gels:

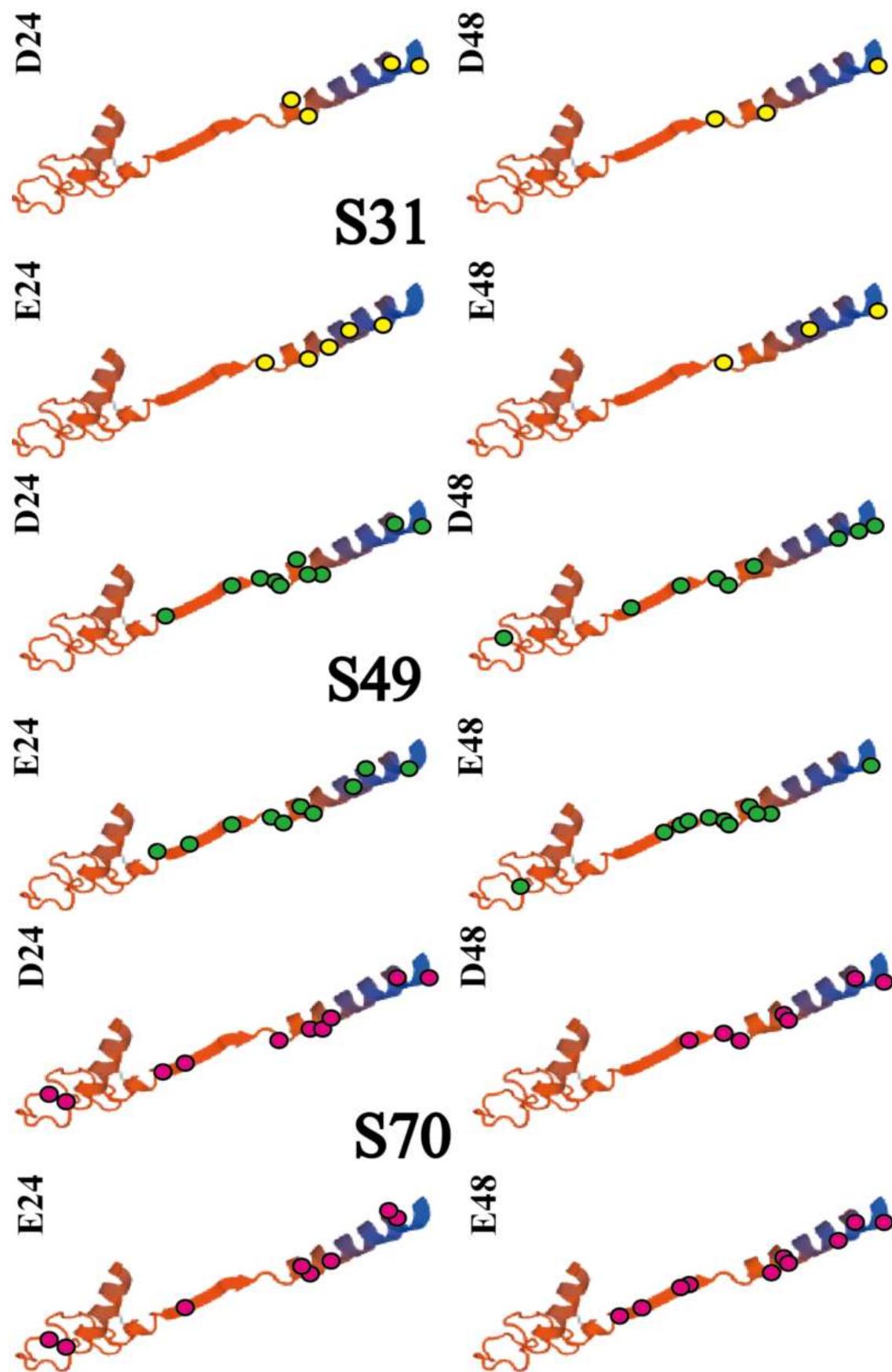


Detail information for phosphorylation of amino acid id sites in **SRPP204**:

█ Spot 31 █ Spot 49 █ Spot 70 █ █ █ Share

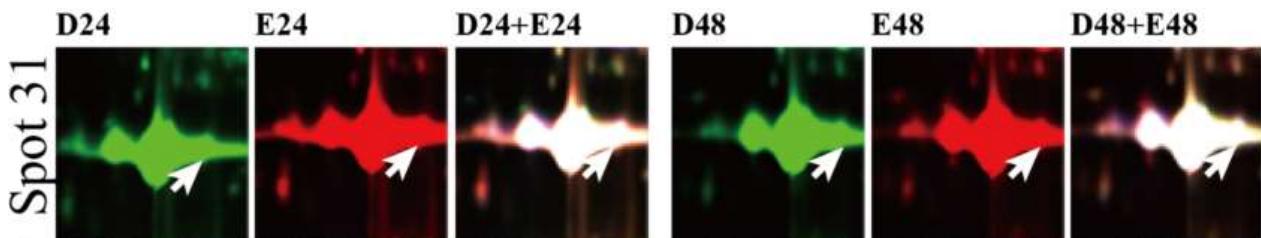
D24h	MAEEVEEERLKYLD F VRAAGVYAVD S F TLYLYAKDISGPLKPGVD I EENVVKTVV I PVYYIPL A VFV D K V D S V SLDGVVPPVI K Q V SA Q T Y VAQDAP
E24h	MAEEVEEERLKYLD F VRAAGVYAVD S F TLYLYAKDISGPLKPGVD I EENVVKTVV I PVYYIPL A VFV D K V D S V TSLDGVVVPPVI K Q V SA Q T Y VAQDAP
D48h	MAEEVEEERLKYLD F VRAAGVYAVD S F TLYLYAKDISGPLKPGVD I EENVVKTVV I VTPVYYIPL A VFV D K V D S V TSLDGVVVPPVI K Q V SA Q T Y VAQDAP
E48h	MAEEVEEERLKYLD F VRAAGVYAVD S F TLYLYAKDISGPLKPGVD I EENVVKTVV I PVYYIPL A VFV D K V D S V TSLDGVVVPPVI K Q V SA Q T Y VAQDAP
D24h	RIVLD V A S V F NTGV Q EGAKALYANLEP K AE Q Y A VTW R ALNKLPL V P Q VANVV V PTAV Y F S E K YND V VRG T TE Q GY R V S T YLPL L P E K I T KVFG D EA S
E24h	RIVLD V A S V F NTGV Q EGAKALYANLEP K AE Q Y A VTW R ALNKLPL V P Q VANVV V PTAV Y F S E K YND V VRG T TE Q GY R V S T YLPL L P E K I T KVFG D EA S
D48h	RIVLD V A S V F NTGV Q EGAKALYANLEP K AE Q Y A VTW R ALNKLPL V P Q VANVV V PTAV Y F S E K YND V VRG T TE Q GY R V S T YLPL L P E K I T KVFG D EA S
E48h	RIVLD V A S V F NTGV Q EGAKALYANLEP K AE Q Y A VTW R ALNKLPL V P Q VANVV V PTAV Y F S E K YND V VRG T TE Q GY R V S T YLPL L P E K I T KVFG D EA S

Predicted 3-D structure and phosphorylated amino acids in different SRPP204 isoforms:



Spot No. 31

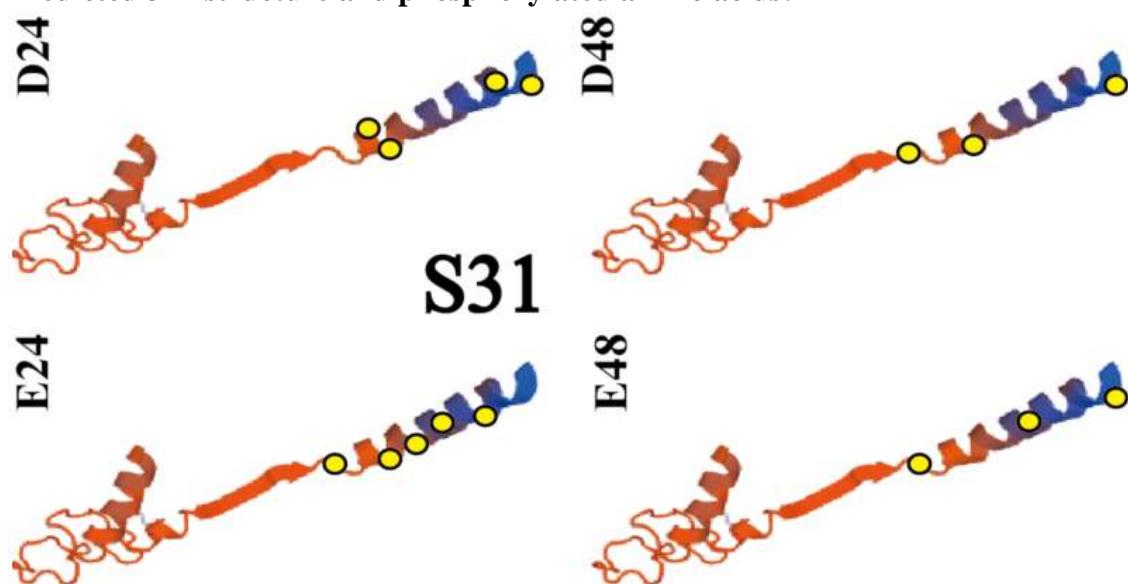
Changed pattern on DIGE gel:



Location in rubber genome: scaffold1222_60641.mRNA1

Protein name: Small rubber particle protein/SRPP204

Predicted 3-D structure and phosphorylated amino acids:



Detail information for phosphorylation of amino acid sites:

D24: MAEEVEEERLKYLDFVRAAGVYAVDSFSTLYAKDISGPLKPGVDTIENVVKTVVTPVYYIPLEAVKFVDKTVD

E24: MAEEVEEERLKYLDFVRAAGVYAVDSFSTLYAKDISGPLKPGVDTIENVVKTVVTPVYYIPLEAVKFVDKTVD

D48: MAEEVEEERLKYLDFVRAAGVYAVDSFSTLYAKDISGPLKPGVDTIENVVKTVVTPVYYIPLEAVKFVDKTVD

E48: MAEEVEEERLKYLDFVRAAGVYAVDSFSTLYAKDISGPLKPGVDTIENVVKTVVTPVYYIPLEAVKFVDKTVD

D24: VSVTSLDGVVPPVIKQVSSAQTYSVAQDAPRIVLDVASSVFNTGVQEGAKALYANLEPKAEQYAVITWRALNKLPL

E24: VSVTSLDGVVPPVIKQVSSAQTYSVAQDAPRIVLDVASSSVFNTGVQEGAKALYANLEPKAEQYAVITWRALNKLPL

D48: VSVTSLDGVVPPVIKQVSSAQTYSVAQDAPRIVLDVASSVFNTGVQEGAKALYANLEPKAEQYAVITWRALNKLPL

E48: VSVTSLDGVVPPVIKQVSSAQTYSVAQDAPRIVLDVASSSVFNTGVQEGAKALYANLEPKAEQYAVITWRALNKLPL

D24: VPQVANVVVPTAVYFSEKYNDVVRGTTEQGYRVSYLPPLLPEKITKVFGDEAS

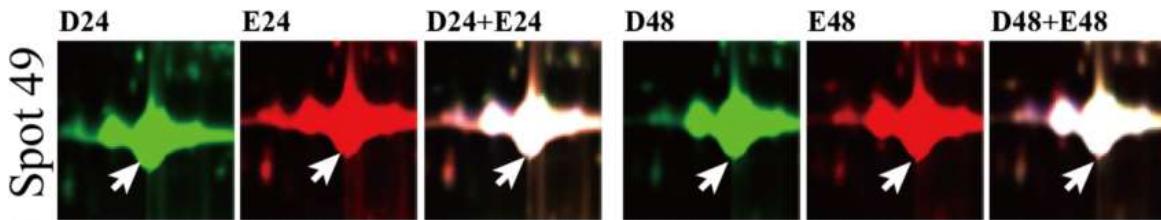
E24: VPQVANVVVPTAVYFSEKYNDVVRGTTEQGYRVSSYLPPLLPEKITKVFGDEAS

D48: VPQVANVVVPTAVYFSEKYNDVVRGTTEQGYRVSSYLPPLLPEKITKVFGDEAS

E48: VPQVANVVVPTAVYFSEKYNDVVRGTTEQGYRVSSYLPPLLPEKITKVFGDEAS

Spot No. 49

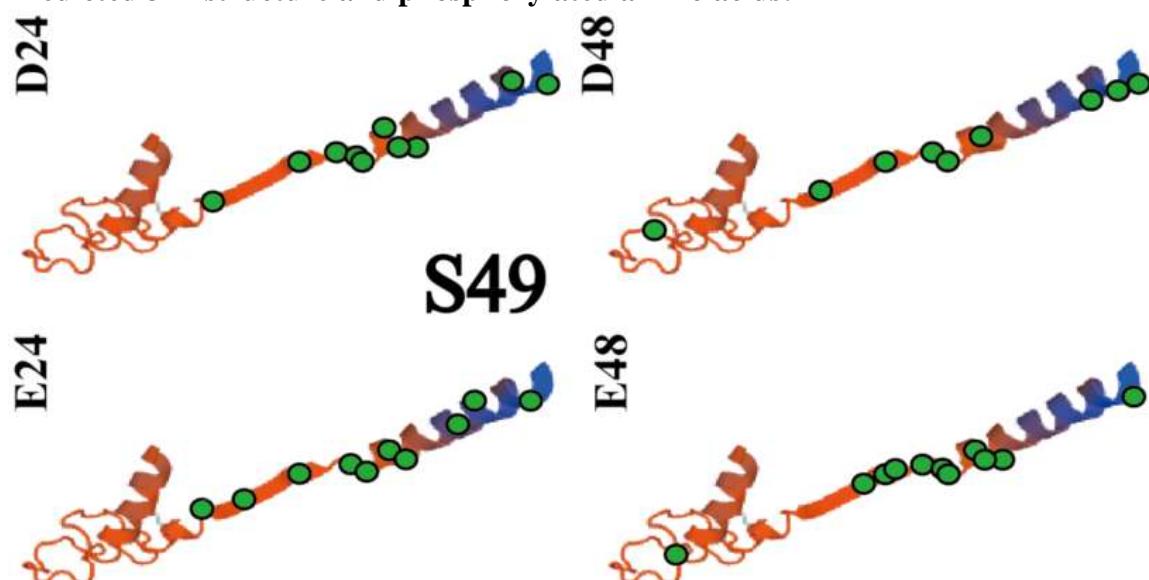
Changed pattern on DIGE gel:



Location in rubber genome: scaffold1222_60641.mRNA1

Protein name: Small rubber particle protein/SRPP204

Predicted 3-D structure and phosphorylated amino acids:



Detail information for phosphorylation of amino acid sites:

D24: MAEEVEEERLKYLDFVRAAGVYAVDSFSTLYLYAKDISGPLKPGVD**T**IENVVKTVVTPVYYIPLEAVKFVD**K**TV

E24: MAEEVEEERLKYLDFVRAAGVYAVDSFSTLYLYAKDISGPLKPGVD**D**TIENVVKTVV**T**PVYYIPLEAVKFVD**K**TV

D48: MAEEVEEERLKYLDFVRAAGVYAVDSF**S**TLYLYAKDISGPLKPGVDTIENVV**K**TVVTPVYYIPLEAVKFVD**K**TV

E48: MAEEVEEERLKYLDFVRAAGVYAVD**S**FSTLYLYAKDISGPLKPGVDTIENVVKTVVTPVYYIPLEAV**K**FVD**K**TV

D24: V**S****T****S**LDGVVPPV**K**QVSA**Q****T****S**VADAPRIVLDVASSVFNTGVQEGAKALYANLEPKAEQYAVITWRALNKLPL

E24: V**S****T****S**LDGVVPPV**K**QV**S**A**Q****T****S**VADAPRIVLDV**A****S**SVFNTGVQEGAKALYANLEPKAEQYAVITWRALNKLPL

D48: V**S****T****S**LDGVVPPV**K**QVSA**Q****T****S**VADAPRIVLDV**A****S**SVFNTGVQEGAKALYANLEPKAEQYAVITWRALNKLPL

E48: V**S****T****S**LDGVVPPV**K**QV**S**A**Q****T****S**VADAPRIVLDV**A****S**SVFNTGVQEGAKALYANLEPKAEQYAVITWRALNKLPL

D24: VPQVANVVPTAVYFSEKYNDVVRGTTEQGYRV**S**YLPLLPTEK**I****T**KVFGDEAS

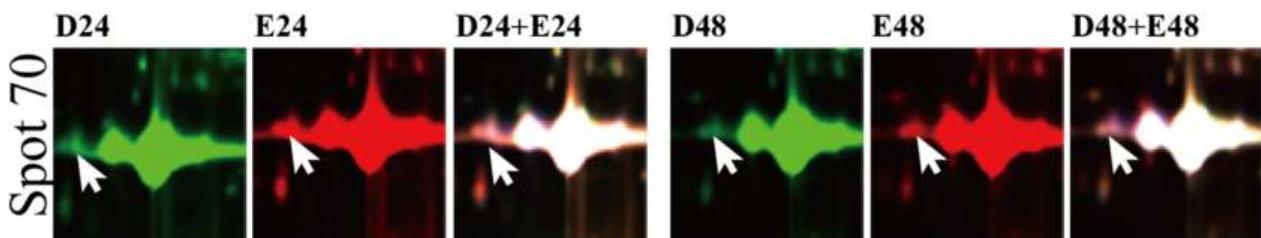
E24: VPQVANVVPTAVYFSEKYNDVVRGTTEQGYRV**S**YLPLLPTEK**I****T**KVFGDEAS

D48: VPQVANVVPTAVYFSEKYNDVVRGT**T**EQGYRV**S**YLPLLPTEK**I****T**KVFGDEAS

E48: VPQVANVVPTAVYFSEKYNDVVRGTTEQGYRV**S**YLPLLPTEK**I****T**KVFGDEAS

Spot No. 70

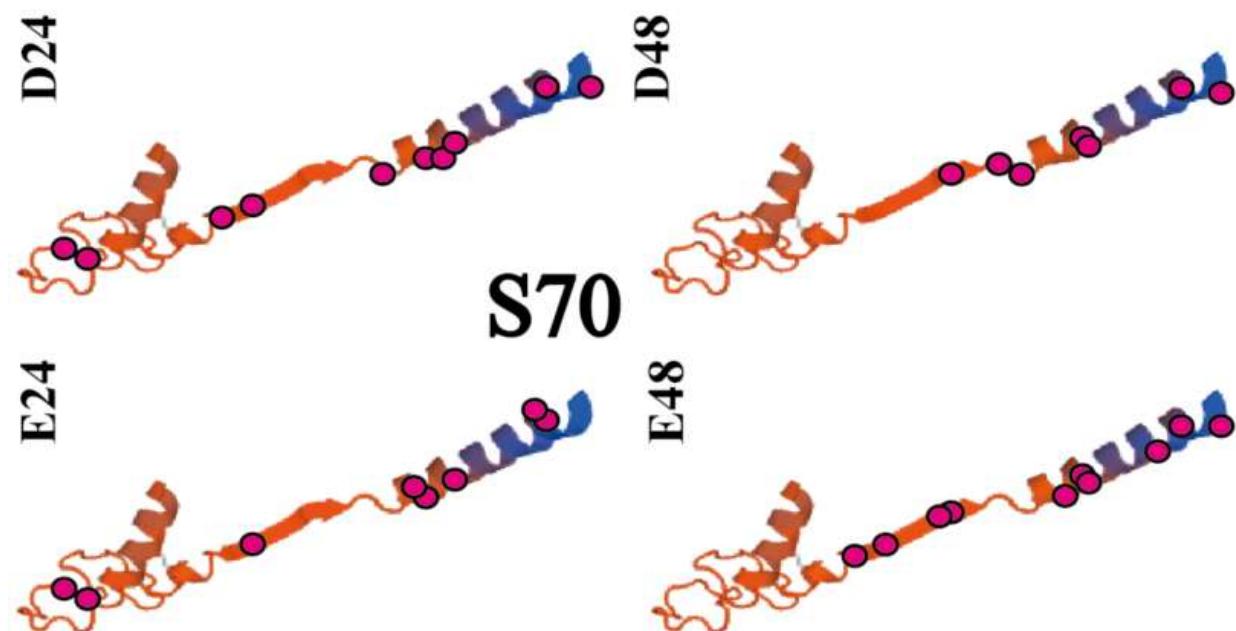
Changed pattern on DIGE gel:



Location in rubber genome: scaffold1222_60641.mRNA1

Protein name: Small rubber particle protein/SRPP204

Predicted 3-D structure and phosphorylated amino acids:



Detail information for phosphorylation of amino acid sites:

D24: MAEEVEEERLKYLDFVRAAGVYAVD**S****S**TLYLYAKDISGPLKPGVDT**T**IENVVKTVV**T**PVYYIPLEAVKFVDKTVD

E24: MAEEVEEERLKYLDFVRAAGVYAVD**S****S**TLYLYAKDISGPLKPGVDTIENVVKTVV**T**PVYYIPLEAVKFVDKTVD

D48: MAEEVEEERLKYLDFVRAAGVYAVDS**F**STLYLYAKDISGPLKPGVDTIENVVKTVV**T**PVYYIPLEAVKFVD**K**TVD

E48: MAEEVEEERLKYLDFVRAAGVYAVDS**F**STLYLYAKDISGPLKPGVDT**T**IENVVKTVV**T**PVYYIPLEAVKFVD**K**TVD

D24: VSVT**S**LDGVVPPVIKQVSA**Q****T****S**VADAPRIVLDVA**S****S**VFNTGVQEGAKALYANLEPKAEQYAVITWRALNKLPL

E24: VSVTSLDGVVPPVIKQV**S****A****Q****T****S**VADAPRIVLDVA**S****S**VFNTGVQEGAKALYANLEPKAEQYAVITWRALNKLPL

D48: V**S****V**T**S**LDGVVPPVIKQVSA**Q****T****S**VADAPRIVLDVA**S****S**VFNTGVQEGAKALYANLEPKAEQYAVITWRALNKLPL

E48: VSVTSLDGVVPPVIKQVSA**Q****T****S**VADAPRIVLDVA**S****S**VFNTGVQEGAKALYANLEPKAEQYAVIT**T**WRALNKLPL

D24: VPQVANVVVPTAVYFSEKYNDVVRGTTEQGYRV**S****S**YLPLLPTEK**I****T**KVFGDEAS

E24: VPQVANVVVPTAVYFSEKYNDVVRGTTEQGYRV**SS**YLPLLPTEK**I****T**KVFGDEAS

D48: VPQVANVVVPTAVYFSEKYNDVVRGTTEQGYRV**S****S**YLPLLPTEK**I****T**KVFGDEAS

E48: VPQVANVVVPTAVYFSEKYNDVVRGTTEQGYRV**S****S**YLPLLPTEK**I****T**KVFGDEAS