Mutated C-terminus T270Y TREX

>query
ESRGYQGSSS SEGPWSPIQG GAAGPTGSAG HPDLGSSHTV WTIPGHTWGV GQEGKSDE

**Secondary Structure**

**PROFsec summary**

Protein can be classified as **mixed** given the following classes:

- 'all-alpha': %H > 45% AND %E < 5%
- 'all-beta': %H < 5% AND %E > 45%
- 'alpha-beta': %H > 30% AND %E > 20%
- 'mixed': all others

**Predicted secondary structure composition**

<table>
<thead>
<tr>
<th>sec str type</th>
<th>H</th>
<th>E</th>
<th>L</th>
</tr>
</thead>
<tbody>
<tr>
<td>% in protein</td>
<td>0</td>
<td>20.69</td>
<td>79.31</td>
</tr>
</tbody>
</table>

**Predicted solvent accessibility composition (core/surface ratio) for your protein:**

**Classes used:**

- e: residues exposed with more than 16% of their surface
- b: all other residues

<table>
<thead>
<tr>
<th>accessib type</th>
<th>b</th>
<th>e</th>
</tr>
</thead>
<tbody>
<tr>
<td>% in protein</td>
<td>15.52</td>
<td>84.48</td>
</tr>
</tbody>
</table>

**About your protein:**

<table>
<thead>
<tr>
<th>prot_id</th>
<th>query</th>
</tr>
</thead>
<tbody>
<tr>
<td>prot_nres</td>
<td>58</td>
</tr>
<tr>
<td>prot_nali</td>
<td>1</td>
</tr>
<tr>
<td>prot_nchn</td>
<td>1</td>
</tr>
<tr>
<td>prot_nfar</td>
<td>0</td>
</tr>
</tbody>
</table>

**Residue composition for your protein:**
**Residue composition for your protein:**

<table>
<thead>
<tr>
<th></th>
<th>%A: 5.2</th>
<th>%C: 0.0</th>
<th>%D: 3.5</th>
<th>%E: 6.9</th>
<th>%F: 0.0</th>
</tr>
</thead>
<tbody>
<tr>
<td>%G: 22.4</td>
<td>%H: 5.2</td>
<td>%I: 3.5</td>
<td>%K: 1.7</td>
<td>%L: 1.7</td>
<td></td>
</tr>
<tr>
<td>%M: 0.0</td>
<td>%N: 0.0</td>
<td>%P: 8.6</td>
<td>%Q: 5.2</td>
<td>%R: 1.7</td>
<td></td>
</tr>
<tr>
<td>%S: 17.2</td>
<td>%T: 6.9</td>
<td>%V: 3.5</td>
<td>%W: 5.2</td>
<td>%Y: 1.7</td>
<td></td>
</tr>
</tbody>
</table>

**PHD results (brief) (Show Landscape View)**

<table>
<thead>
<tr>
<th></th>
<th>....,...,....1,...,....2,...,....3,...,....4,...,....5,...,....6</th>
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<tbody>
<tr>
<td>AA</td>
<td>ESRGYQGSSSEGPWSPIQGGAAGPTGSAGHPDLGSSHTVWTIPGHTWGVQEGKSDE</td>
</tr>
<tr>
<td>Rel_sec</td>
<td>**********************************************************</td>
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<tr>
<td>PHD_h1m</td>
<td>PHD results (normal) (Show Landscape View)</td>
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</table>

<table>
<thead>
<tr>
<th></th>
<th>....,...,....1,...,....2,...,....3,...,....4,...,....5,...,....6</th>
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</thead>
<tbody>
<tr>
<td>AA</td>
<td>ESRGYQGSSSEGPWSPIQGGAAGPTGSAGHPDLGSSHTVWTIPGHTWGVQEGKSDE</td>
</tr>
<tr>
<td>Rel_sec</td>
<td>9999999999999999999999999999999999999999999999999999999999</td>
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<tr>
<td>SUB_sec</td>
<td>PHD_h1m</td>
</tr>
</tbody>
</table>
**Protein-Protein binding**

>query: stretc=5  crowd_predictions=7  gap=20  itr=0
ESRGYQGSSSEGSPWSPIQGGAAGPTGSDLGSSHTV
P-P------------P-PP-PP-PPPPPP-------

WTIPGHTWGVQEGKSDE
---PPPPPPP-------

**Prosite**

<table>
<thead>
<tr>
<th>Pattern-ID</th>
<th>PS00006</th>
<th>PDOC00006</th>
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</thead>
<tbody>
<tr>
<td>Pattern-DE</td>
<td>Casein kinase II phosphorylation site</td>
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</tr>
<tr>
<td>Pattern:</td>
<td>[ST].{2}[DE]</td>
<td></td>
</tr>
<tr>
<td>9</td>
<td>SSSE</td>
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</table>

<table>
<thead>
<tr>
<th>Pattern-ID</th>
<th>PS00008</th>
<th>PDOC00008</th>
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<tbody>
<tr>
<td>Pattern-DE</td>
<td>N-myristoylation site</td>
<td></td>
</tr>
<tr>
<td>Pattern:</td>
<td>G[^EDRKHPFYW].{2}[STAGCN][^P]</td>
<td></td>
</tr>
<tr>
<td>7</td>
<td>GSSSSE</td>
<td></td>
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<tr>
<td>35</td>
<td>GSSHTV</td>
<td></td>
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</tbody>
</table>

<table>
<thead>
<tr>
<th>Pattern-ID</th>
<th>PS00017</th>
<th>PDOC00017</th>
</tr>
</thead>
<tbody>
<tr>
<td>Pattern-DE</td>
<td>ATP/GTP-binding site motif A (P-loop)</td>
<td></td>
</tr>
<tr>
<td>Pattern:</td>
<td>[AG].{4}GK[ST]</td>
<td></td>
</tr>
<tr>
<td>49</td>
<td>GVGQEGKS</td>
<td></td>
</tr>
</tbody>
</table>

**References**


- Author: B Rost
- Contact: help@predictprotein.org
- URL: [PredictProtein Homepage](#)
- Description: PredictProtein is the acronym for all prediction programs run.