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Description	P31061
Date	Thu Jan 5 11:46:57 GMT 2012
Unique Job ID	59ff539b2f1b6acd

Protein structure analysis of RhoA (PDB ID: 1RHO). The image displays the full sequence (1-189) and a zoomed-in view of the GTP-binding domain (residues 1-29).

**Full Sequence (1-189):**

- Sequence:** MEVNKKQLADIFGASIRTIQNWQEQQGMPVLRGGGKGNEVL YD SAAVIRWYAERDAEIE NE
- Secondary structure:** Alpha-helices (green) and beta-sheets (blue) are shown.
- SS (Solvent Accessibility):** High accessibility (red) is observed in the N-terminal region and the C-terminal region.
- confidence:** Confidence scores are shown below the sequence.
- Disorder:** Disordered regions are indicated by question marks.
- Disorder confidence:** Confidence scores for disorder predictions are shown below the sequence.


**Zoomed-in View (Residues 1-29):**

- Sequence:** KLRREVEELRQASETDLQP GTIEYERHRLTRAQADAQELKNARDSAEVVETAFCTFVLSR
- Secondary structure:** Alpha-helices (green) and beta-sheets (blue) are shown.
- SS (Solvent Accessibility):** High accessibility (red) is observed in the N-terminal region and the C-terminal region.
- confidence:** Confidence scores are shown below the sequence.
- Disorder:** Disordered regions are indicated by question marks.
- Disorder confidence:** Confidence scores for disorder predictions are shown below the sequence.

**Residue 1-29 (GTP-binding domain):**


- Sequence:** RQYAGGSR
- Secondary structure:** Alpha-helices (green) and beta-sheets (blue) are shown.
- SS (Solvent Accessibility):** High accessibility (red) is observed in the N-terminal region and the C-terminal region.
- confidence:** Confidence scores are shown below the sequence.
- Disorder:** Disordered regions are indicated by question marks.
- Disorder confidence:** Confidence scores for disorder predictions are shown below the sequence.

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand