

### Question

What is the age of the patient with the lowest APP-Z score?

### Main Agent Request

I need to find what 'APP-Z score' refers to in the context of the UCEC CPTAC3 dataset. The provided metadata file does not contain a column with this name. I need to know if this score is known by another name in the dataset or if it is derived from other columns. Please search for information on 'APP-Z score' and its relation to the CPTAC UCEC study.

### Search Agent Response

Based on the search results, 'APP-Z score' in the context of the CPTAC UCEC dataset does not refer to a specific column name but is a derived value. Here is a breakdown of the findings:

1. **'APP'** stands for Acute Phase Protein: The initial search results strongly indicated that 'APP' is an acronym for Acute Phase Protein. These are proteins whose plasma concentrations change in response to inflammation.

2. **'Z-score'** refers to a normalization method: The analysis of CPTAC data, particularly through portals like UALCAN, commonly uses z-score normalization. A z-score represents the number of standard deviations a data point is from the mean or median of a reference set (e.g., normal tissue or the entire cohort). This is a standard procedure in proteomics to compare protein expression levels across different samples.

3. **Specific APPs in the CPTAC UCEC Dataset:** The search identified specific Acute Phase Proteins that have been analyzed within the CPTAC UCEC dataset:

- SAAL1 (Serum Amyloid A-like 1):** One study (aging-us.com) explicitly identifies SAAL1 as a major Acute Phase Protein and confirms that its protein levels were found to be significantly upregulated in UCEC tumors within the CPTAC database.
- Bikunin (from the AMBP gene):** Another study (PMC9889512) identifies Bikunin as a positive Acute Phase Protein and analyzes its expression in the CPTAC UCEC dataset, noting a significant reduction in protein expression in tumors compared to normal tissue.

**Conclusion:** The 'APP-Z score' is the z-score normalized expression value for a specific Acute Phase Protein. It is not a pre-existing column in the metadata but a calculated score. To find the source of this score, you should look for columns in your dataset corresponding to the gene or protein names of known Acute Phase Proteins, such as **SAAL1** or **AMBP** (the precursor gene for Bikunin). The z-score would then be calculated from the expression values in that column.