

The screenshot shows the Phenix GUI with the 'Run' tab selected. The title bar reads 'Protocol Run: PhenixProtRunEMRinger'. The 'Protocol' is set to 'phenix - emringer'. The status is 'finished'. There are buttons for 'Cite' and 'Help'.

The 'Run' section has a red header. Below it, the 'Run name' is 'phenix - emringer refmac'. The 'Run mode' is set to 'Continue'. The 'Host' is 'localhost'. The 'Use queue?' option is set to 'No'. The 'Wait for' field is empty.


The 'Input' section has a red header. Below it, the 'Input Volume' is 'xmipp3 - extract unit cell sym C2.outputVolume'. The 'Input atomic structure' is 'ccp4 - refmac.outputPdb'.

The bottom section is labeled 'SUMMARY'. It contains the following text:

```
Optimal Threshold: 0.56 Rotamer-Ratio: 1.00
Max Zscore: 1.30 Model Length: 85
EMRinger Score: 1.41
```

Red arrows with numbers 1 through 6 point to specific elements in the GUI:

- 1: Points to the 'Run' tab header.
- 2: Points to the 'Input Volume' field.
- 3: Points to the 'Input atomic structure' field.
- 4: Points to the 'Execute' button.
- 5: Points to the 'SUMMARY' section header.
- 6: Points to the 'SUMMARY' section content.



A screenshot of the ChimeraX software interface. The 'Analyze Results' button in the bottom toolbar is highlighted with a red arrow and the number '5'. The background shows a 3D molecular model of a protein-ligand complex.