You have two spectra corresponding to the two chips of the Red Arm 580 setup of UVES-FLAMES (see slides about this instrument). The spectra are related to the same target, a giant star member of a globular cluster (the name of the cluster is in the spectrum names).

SLAB

(1) Plot the low and up spectra of your target, to identify the spectral regions where the counts are zero.

(2) Cut both the spectra excluding the edges where the pixels have zero counts.

(3) Normalize the spectra checking the three approaches, namely polynomial fit, smoothing and spline. For polynomial fit specify the degree of the polynomial and the number of standard deviations of the sigma-clipping (a number between 1 and 3, usually 2 is a good choice). For the spline specify the degree of the spline (usually 3 is a good choice but you can increase this value if the normalization is not correct). For the smoothing you need to specify only the size of the spectral windows use for the smoothing (of the order of 50-100 A, but feel free to check different values). Check the different normalization and select the approach that better normalize the spectra. If the normalizations are similar each other, ok, adopt that that you prefer.

(4) Calculate the RV with CCF against the synthetic spectrum provided as template. Check the quality of your RV by comparing the normalized, Doppler-corrected spectra with the synthetic spectrum (you can use the Python code check_rv.py in the data directory).

(5) Your target is member of a globular cluster. You can check the average radial velocity of the clusters here:
https://people.smp.uq.edu.au/HolgerBaumgardt/globular/orbits.html

(6) Adopting the normalized spectrum, you can estimate the SNR of your spectra using a wide spectral region without spectral lines.

(7) Using the command "fitline" perform the Gaussian fit for some of the spectral lines in the linelist file. Assume the average FWHM and calculate the corresponding spectral resolution. Assuming an intrinsic FWHM of 0.1 A, estimate the additional broadening.

SALVADOR

(1) In the input.autofit file set NORM=2 and INTER=n . In the list.stars file write the names of your spectra. In the linelist.txt file change the resolution according to the measured FWHM (provide here the resolution corresponding to the FWHM calculated obtained by subtracting in quadrature the measured FWHM and 0.1 A, intrinsic FWHM).

(2) Run SALVADOR on the normalized , Doppler-corrected spectra obtained with SLAB. Check the output pdf file.

(3) Check if the continuum windows are correct and modify the continuum file including additional spectral windows or removing other ones.

(4) If some lines are too weak to be detected or they appear damaged, exclude them from the linelist file.

(5) Run again SALVADOR and check the output pdf file.

(6) If some lines are not well fitted, you can run SALVADOR with the option INTER=y and modify interactively the fit.

(7) Check the mean average abundance ratios and compare the [Fe/H] with the values listed here https://physics.mcmaster.ca/~harris/mwgc.dat