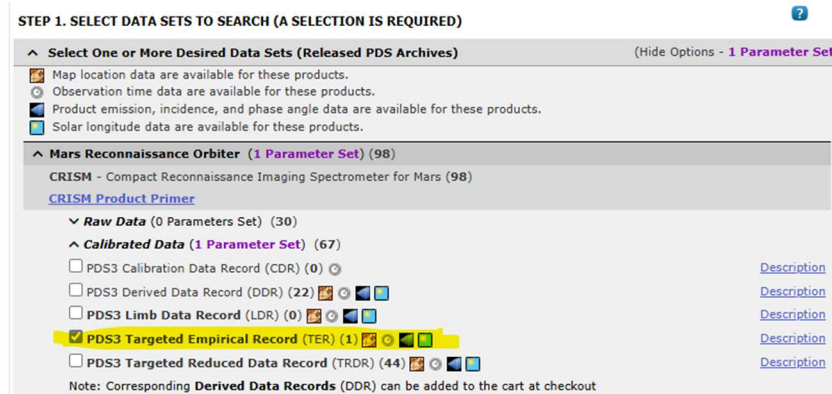


## Step 1 – Import and Process CRISM MRO Spectral Library Data

Navigate to the folder MRO\_Spectra\_Library\_Conversion and run the script CRISM\_Replication\_Library.py to process the spectral library data.

## Step 2 – Download CRISM TER3 Data for a Target Region

1. Go to <https://ode.rsl.wustl.edu/mars/productsearch>.
2. In Step 1, select TER3 as the product type.



STEP 1. SELECT DATA SETS TO SEARCH (A SELECTION IS REQUIRED)

^ Select One or More Desired Data Sets (Released PDS Archives) (Hide Options - 1 Parameter Set)

Map location data are available for these products.  
Observation time data are available for these products.  
Product emission, incidence, and phase angle data are available for these products.  
Solar longitude data are available for these products.

^ Mars Reconnaissance Orbiter (1 Parameter Set) (98)

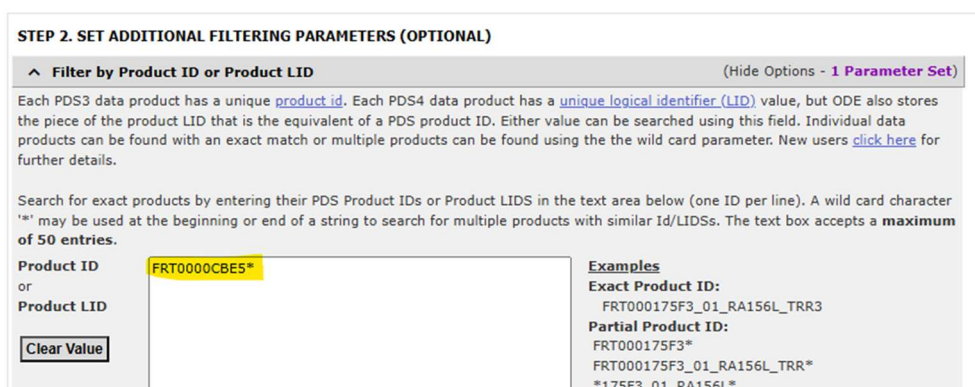
CRISM - Compact Reconnaissance Imaging Spectrometer for Mars (98)  
[CRISM Product Primer](#)

Raw Data (0 Parameters Set) (30)  
^ Calibrated Data (1 Parameter Set) (67)

☐ PDS3 Calibration Data Record (CDR) (0) [Description](#)  
☐ PDS3 Derived Data Record (DDR) (22) [Description](#)  
☐ PDS3 Limb Data Record (LDR) (0) [Description](#)  
☒ PDS3 Targeted Empirical Record (TER) (1) [Description](#)  
☐ PDS3 Targeted Reduced Data Record (TRDR) (44) [Description](#)

Note: Corresponding Derived Data Records (DDR) can be added to the cart at checkout

3. In Step 2, define your target region by entering the appropriate location ID.



STEP 2. SET ADDITIONAL FILTERING PARAMETERS (OPTIONAL)

^ Filter by Product ID or Product LID (Hide Options - 1 Parameter Set)

Each PDS3 data product has a unique [product id](#). Each PDS4 data product has a [unique logical identifier \(LID\)](#) value, but ODE also stores the piece of the product LID that is the equivalent of a PDS product ID. Either value can be searched using this field. Individual data products can be found with an exact match or multiple products can be found using the the wild card parameter. New users [click here](#) for further details.

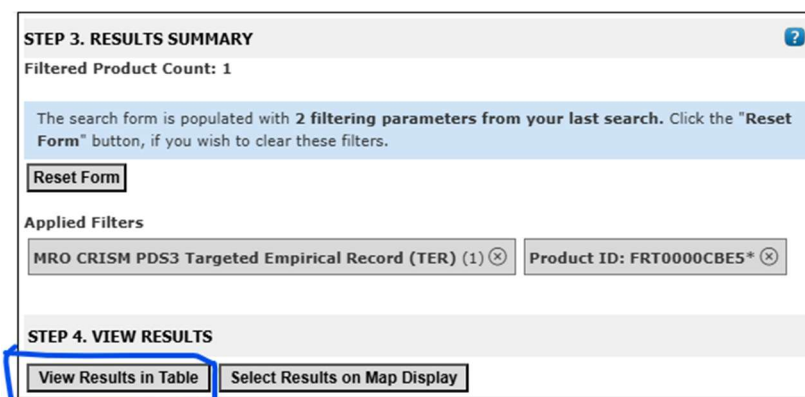
Search for exact products by entering their PDS Product IDs or Product LIDS in the text area below (one ID per line). A wild card character '\*' may be used at the beginning or end of a string to search for multiple products with similar Id/LIDSs. The text box accepts a **maximum of 50 entries**.

Product ID or Product LID:

[Clear Value](#)

**Examples**  
**Exact Product ID:**  
FRT000175F3\_01\_RA156L\_TRR3  
**Partial Product ID:**  
FRT000175F3\*  
FRT000175F3\_01\_RA156L\_TRR\*  
\*175F3\_01\_RA156L\*

4. Review the search results.



STEP 3. RESULTS SUMMARY

Filtered Product Count: 1

The search form is populated with 2 filtering parameters from your last search. Click the "Reset Form" button, if you wish to clear these filters.

[Reset Form](#)

Applied Filters

MRO CRISM PDS3 Targeted Empirical Record (TER) (1) X Product ID: FRT0000CBES\* X

STEP 4. VIEW RESULTS

[View Results in Table](#) [Select Results on Map Display](#)

**SEARCH RESULTS** [Output Results](#) [View on Map](#) [Back To Search](#) ?

Products Found: 1 [Add All Results to Cart](#)

Sort Order:    ☐

	MRO CRISM PDS3 Targeted Empirical Record (TER) (Calibrated Data) 	<input type="checkbox"/>
<a href="#">FRT0000CBE5_07_IF166J_TER3</a>	Obs Time: 2008-09-29T18:16:29	

- Download all files containing "if".

[Download All Product & Derived Files with Aspera](#) [Aspera Download Help](#)

**PDS Product Files** **Derived Files**

Product Files & Labels	KB
<a href="#">frt0000cbe5_07_if166j_ter3.hdr</a> Product Data File	18
<a href="#">frt0000cbe5_07_if166j_ter3.img</a> Product Data File	669,697
<a href="#">frt0000cbe5_07_if166j_ter3.lbl</a> Product Label File	5
<a href="#">frt0000cbe5_07_in166j_ter3.hdr</a> Data Processing Info ENVI Header	1
<a href="#">frt0000cbe5_07_in166j_ter3.img</a> Data Processing Info File	11,060

### Step 3 – Convert TER3 Data into Summary Products

- Place all downloaded TER3 files in a single folder.
- Open the script CRISM\_Spectral\_Conversion.py located in the CRISM\_Spectral\_Conversion folder.
- Specify the path to the TER3 .img files and set the desired output directory in the script.

```
#SPECIFY INPUTS AND OUTPUT LOCATIONS
#-----
TER3_Location = "D:/CRISM Data/FRT0000CBE5/TER3 Data/frt0000cbe5_07_if166j_ter3.img"
Output_Location = "D:/CRISM Data/FRT0000CBE5/Python_Converted"
h5_file_path = os.path.join(Output_Location, "stacked_frames.h5")
```

- Run the script. *Note: This process may take several hours.*

### Step 4 – Train the SOM

- Open som\_training.py in the SOM\_Training folder.
- Set the path to the .h5 file generated in Step 3.
- Configure the SOM training parameters as needed.

#### 4. Run the script to train the Self-Organizing Map.

```
# -----  
# Import Processed TER3 Data (H5 File)  
# -----  
file_path = "D:/CRISM Data/FRT0000634B/TER_Data/Python_Converted/stacked_frames.h5"  
with h5py.File(file_path, mode="r") as f:  
    combined_data = f['stacked_frames'][:] # Load all data at once  
  
# -----  
# Minimum Group Size  
# -----  
#Kmeans is used to segregate data into groups until the size of the smallest group contains less than the number of  
#instances specified here, instances are then sampled equally from each of these groups to ensure smaller groups, which  
#are more likely to contain interesting features obtain more representation in the SOM training.  
  
min_instance = 2000 # Number of instances for smallest group  
  
# -----  
# SOM Training Parameters  
# -----  
X = 10 # SOM Size (X)  
Y = 10 # SOM Size (Y)  
samples_iter = 5000 # Number of instances per iteration  
l_rate = 0.5 # Initial learning rate  
burn_iter = 50 # Burn-in iterations  
num_iter = 1000 # Learning iterations
```

### Step 5 – Visualise Mineral Locations

1. Open the script Layer\_Visuals.py located in the SOM\_Analysis folder.
2. Many data sources need to be specified, all of which should be familiar from steps 1-4.
3. There are many choices under the section “Identify Spatial Distribution of a Specific Mineral” to specify.
4. The output is a false or bespoke image view of the Martian surface showing the identified spatial distribution of the nominated mineral.

### Step 6 – SOM Hierarchical Analysis

1. Open the script SOM\_analysis located in the SOM\_Analysis folder.
2. Specify the output locations from Step 4.
3. Run the code to obtain comprehensive topological analysis of the SOM model.

### **Step 7 – KMeans Comparison**

1. The SOM model must be trained first to run this code as the inputs `reshapped_data_loc` and `reshapped_locations_loc` are generated during this process.
2. Open the script `kmeans.py` located in the KMeans folder, specify data locations and mineral information before running the script.