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# PSM CBOR format documentation

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# 1 Introduction

PSM CBOR file is designed to record any PSM (peptide spectrum match) in a compact binary file, easy to manipulate, versatile, extendable. This file is used as a stream in any condition, allowing the users to use unix pipes, compression algorithms, network transparency.

This way, from a DDA identification engine search result converted in PSM CBOR, any process can be added :

- Feature computations
- Prediction process (retention times, ion mobility, MS2 prediction...)
- Rescoring
- Filtering

## 2 psm CBOR format

It could be something like that :

```
{
  "informations": {
    "executable": "mcql",
    "type": "psm",
    "pappsomspv_version": "0.9.46",
    "sysinfo_machine_hostname": "proteus1",
    "sysinfo_product_name": "Debian GNU/Linux 12 (bookworm)",
    "timestamp": "2025-06-25T10:33:51"
  },
  "log": [],
  "parameter_map": {
    "sage": {},
    "xtandem": {},
    "specoms": {}
  },
  "target_fasta_files": ["zea_mays.fasta", "contaminant.fasta"],
  "decoy_fasta_files": ["rev_zea_mays.fasta", "rev_contaminant.fasta"],
  "protein_map": {
    "GRMZM2G083841_P01": {
      "description": "",
      "sequence": "",
      "target": true,
      "contaminant": false,
      "props": {},
      "eval": {}
    },
    "GRMZM2G083841_P02": {}
  },
  "sample_list": [
    {
      "name": "tandem2017_nopatch_20120906_balliau_extract_1_A01_urnb-1",
      "identification_file_list": [
        {
          "name": "/home/langella/data1/tandem/
```

```

tandem2017_nopatch_20120906_balliau_extract_1_A01_urnb-1.xml"
  }
],
"peaklist_file": {
  "name": "tandem2017_nopatch_20120906_balliau_extract_1_A01_urnb-1.mzml"
},
"scan_list": [
  {
    "id": {
      "index": 1976
    },
    "precursor": {
      "z": 2,
      "mz": 1120.529471
    },
    "ms2": {
      "rt": 12648.87,
      "spectrum": {
        "mz": [1, 2, 3, 4],
        "intensity": [1, 2, 3, 4]
      }
    },
    "props": {},
    "psm_list": [
      {
        "proforma": "AQEEM[+15.99491]AQVAK",
        "protein_list": [
          {
            "accession": "GRMZM2G083841_P01",
            "positions": [15, 236]
          }
        ],
        "props": {
          "ion-series": {}
        },
        "eval": {
          "xtandem": {
            "evaluate": 0.0011
          },
          "specoms": {
            "evaluate": 0.0011
          }
        }
      }
    ]
  }
]
}
]
}
]
}
]
}

```

### 3 Root structure

root sections are required and the order must be respected.

**informations** (*object*) *Required*

**log** (*array*) *Required* contains an array that logs all the previous “informations” sections. It helps to keep trace of PSM treatments.

**parameter\_map** (*dictionary*) *Required* dictionary where each entry corresponds to a specific process (see [Process entries](#)). Each entry must contain the parameters used for this process.

**target\_fasta\_files** (*array*) *Required* List of file path to FASTA files (preferably absolute file path) used as reference target protein sequences for the identification engine.

**decoy\_fasta\_files** (*array*) *Optional* List of file path to FASTA files (preferably absolute file path) used as decoy protein sequences for the identification engine (if any and not generated on the fly).

**protein\_map** (*dictionary*) *Required* contains an entry for each protein, using the accession as a unique identifier.

**sample\_list** (*array*) *Required* an array of “sample” objects (see [Sample description](#))

### 4 Process entries

If a CBOR PSM process is intended to give new results in “eval” sections : it must have a unique key to define it. This key must corresponds to an entry (see [parameter\\_map in root](#)).

Currently, several entries are already defined, but anyone can create a new one:

**xtandem** psm and protein evaluations computed by the X!Tandem search engine

**sage** psm and protein evaluations computed by the Sage search engine

### 5 Protein description

The protein object is stored in the [protein\\_map in root](#). The protein accession is used as a dictionary key to reference each protein object. Protein accession is used in [PSM description](#) to link PSMs to proteins.

“protein” object is composed of (the order of the elements must be respected) :

**description** (*string*) *Required* Protein description, maybe empty

**sequence** (*string*) *Required* Protein amino acid sequence, maybe empty

**target** (*boolean*) *Required* Boolean (true by default), true if the protein belongs to the targeted sequences (target FASTA files). False otherwise.

**contaminant** (*boolean*) *Required* Boolean (false by default), true if the protein is tagged as a contaminant protein.

**props** (*object*) *Optional* Free structure designed to store any data (not related to a particular process) related to a protein as a propertie.

**eval** (*object*) *Required* Protein values computed by different algorithm or process (described in [Process entries](#)). Maybe empty.

## 6 Sample description

“sample” object is composed of :

**name** (*string*) *Required* Sample name

**identification\_\_file\_\_list** (*array*) *Optional* Identification engine search result files

**peaklist\_\_file** (*object*) *Required*

**scan\_\_list** (*array*) *Required* an array of “scan” objects (see [Scan description](#))

## 7 Scan description

“scan” object is composed of :

**id** (*object*) *Required* Scan identifier object [Scan identifier description](#)

**precursor** (*object*) *Required* Precursor description (MS1 related data)

**ms2** (*object*) *Required* MS2 related data

**props** (*object*) *Optional* Free structure designed to store any data (not related to a particular process) related to a scan as a propertie.

**psm\_\_list** (*array*) *Required* an array of “psm” objects (see [PSM description](#))

### 7.1 Scan identifier description

**index** (*integer*) *Optional* Index of the scan in the original peak list file. Strongly recommended, but sometimes not available at all.

**native\_\_id** (*string*) *Required* Unique identifier of the scan as defined in mzML file format.

**scan** (*integer*) *Optional* Scan number as written in the original peak list file.

## 8 PSM description

**proforma** (*string*) *Required* Peptide proforma notation

**protein\_\_list** (*array*) *Required* Related proteins, described in [Protein link description](#)

**props** (*object*) *Optional* Peptide properties

**eval** (*dictionary*) *Required* Peptide values computed by different algorithm or process (described in [Process entries](#)).

### 8.1 Protein link description

**accession** (*string*) *Required* Protein accession : must be described in [protein\\_map in root](#)

**positions** (*array*) *Required* Positions of this peptide (proforma in psm) in the protein sequence.  
Maybe empty if the position is not known.

**Important:** a position starts at 0 (first amino acid) to N-1 (N is the protein length) for the last amino acid.