# **File naming convention:**

## 0. The Tutorial Descriptions

The tutorial texts are provided as pdf files with the following naming convention:

## exp\$ protein experiment tutorial.pdf

The place holders for protein and experiment are explained in Table 1.

### 1. Data Collection

The diffraction images are named according to the following scheme:

# exp\$\_protein\_experiment\_qualifier\_###.img

The place holders for protein, experiment and qualifier are explained in Table 1.

## 2. Data Processing

The input file for the data processing program XDS (Kabsch, 1993, 2010a,b) is simply called XDS.INP and is supplied as such. All other files are named as they were named by the processing procedure.

#### 3. Structure Solution

All files created during the structure solution process are archived in a tar file, which was downloaded from the respective Auto-Rickshaw run:

## exp\$\_protein\_experiment\_autorickshaw.tar

The files in the archive can be retrieved using the command tar xvf file.tar

## 4. Structure Refinement

For the structure refinement part, the following three files are supplied:

exp\$\_protein\_experiment\_refine.def
exp\$\_protein\_experiment\_refine.log
exp\$\_protein\_experiment\_refine.pdb
exp\$\_protein\_experiment\_refine.mtz
command file for running REFMAC5
log file from REFMAC5-run
final refined coordinate file
final refined structure factor file

**Table 1.** File naming convention.

Experiment No.	Protein	<b>Experiment type</b>	Qualifier
exp1	ins	ssad	-
exp2	thau	mad	peak
			infl
			hrem
			lrem
exp3	lyso	molrep	-
exp4	lyso	ions	-
exp5	lyso	ligands	-
exp6	lyso	siras	native
			deriv
exp7	thau	rip	before
			after

# **Directory Structure of the Tutorial**

The whole tutorial is organized according to the following directory structure, which consists of either three or four levels.

## **Level**

# 1 2 3 4

**exp\$** contains the tutorial itself exp\$\_protein\_experiment\_tutorial.pdf

data contains all images, unless more than one data set is present

xds contains all processing files

In the cases an experiment consists of more than one data set, an additional layer is inserted in between data and xds:

qualifier2 xds

. . .

**struct\_sol** contains the archive file provided for the structure solution path

**struct\_ref** contains all files provided for structure refinement

alternative representation:

Level 1	Level 2	Level 3	Level 4			
exp\$	contains the	tutorial file itself exp\$_protein_experiment_tutorial.pdf				
	data	contains all images, unless more than one data set is present				
		xds	contains all processing files			
In the cas	ses an experim	ent consists of	more than or	ne data set, an additional layer is inserted in		
between o	data and xds:					
		qualifier1	image directory			
			xds	processing directory		
		qualifier2				
			xds			
		•••				
	struct_sol	contains the Auto-Rickshaw archive file with all files provided for the structure solution path				
	struct_ref	contains all files provided for structure refinement				