1. Name of the scanner manufacturer:

[ ]  GE [ ]  Siemens [ ]  Philips [ ]  Toshiba [ ]  Other, specify:

1. Name of the scanner software and its version number:

Name:

Version Number:

1. Magnetic Field Strength of Scanner Used:

[ ]  1.5 T [ ]  3.0 T [ ]  4.0 T [ ]  7.0 T [ ]  Other: T

1. Body part scanned:

[ ]  Brain

[ ]  Cervical spine

[ ]  Thoracic spine

[ ]  Lumbar spine

[ ]  Calf

[ ]  Thigh

[ ]  Other

Table for RF Coil(s)

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Intentionally left blank | Name of Coil | Type of CoilSurface | Type of CoilVolume | Transmit (Tx) | Receive (Rx) | Tx/Rx | #of Channels |
|  | Data to be entered by site | **[ ]**  | **[ ]**  | **[ ]**  | **[ ]**  | **[ ]**  | Data to be entered by site |
|  | Data to be entered by site | **[ ]**  | **[ ]**  | **[ ]**  | **[ ]**  | **[ ]**  | Data to be entered by site |
|  | Data to be entered by site | **[ ]**  | **[ ]**  | ***[ ]***  | **[ ]**  | **[ ]**  | Data to be entered by site |
|  | Data to be entered by site | **[ ]**  | **[ ]**  | **[ ]**  | **[ ]**  | **[ ]**  | Data to be entered by site |

1. Nuclei: [ ]  H [ ]  13C [ ]  31P [ ]  23Na [ ]  Other
2. Anatomical Reference Image

Sequence (e.g., GE)

TR ms

TE ms

Orientation

FOV X mm2

1. Spectroscopy
	1. Sequence(s) used: (check all that apply)

[ ]  Unlocalized

[ ]  Spectroscopic Imaging (SI)-2D

[ ]  PRESS

[ ]  Single voxel (SVS)

[ ]  SI-3D

[ ]  STEAM

[ ]  Multivoxel voxel

[ ]  ISIS

[ ]  Spin-echo

[ ]  Other, specify:

* 1. Spectroscopy sequence parameters

Repetition time (TR): ms

TE: ms; For STEAM, TM= ms

Number of averages:;

Acquisition time: minutes

Bandwidth: Hz/Pixel

Spectral points (data size): Points

For PRESS, is it symmetric (TE = TE1 + TE2; TE1 = TE2) or asymmetric (TE1 ≠ TE2)?

**[ ]**  Symmetric **[ ]**  Asymmetric, TE1 = ms; TE2 = ms

* 1. Geometry
		1. Anatomical location of voxel or slice: [ ]  N/A
		2. Voxel or slice size: left-right: mm; anterior-posterior: mm; inferior-superior: mm
		3. Voxel volume: mm3
		4. or matrix size: In-plane: x ; z-direction (3D):
	2. Water suppression:[ ]  Yes [ ]  No

If yes, [ ]  CHESS [ ]  Other

Water signal suppression bandwidth: Hz [ ]  N/A

* 1. Water reference data acquisition performed in addition to water suppression acquisition

[ ]  Yes [ ]  No

If yes, number of averages: ;

Note any differences in sequence parameters from water suppressed (e.g., TR):

1. Post processing
	1. B0-shift correction: [ ]  Yes [ ]  No
	2. Eddy-current-induced spectral distortion correction? [ ]  Yes [ ]  No
	3. Residual water signal removed? [ ]  Yes [ ]  No

If yes, water signal removal filter used:

* 1. Raw Data Saved [ ]  Yes [ ]  No

## General Instructions

This CRF includes data typically recorded for Magnetic Resonance Spectroscopy. This technique is used to study metabolic changes in diseases affecting the brain. Biochemical information can be obtained in a non-invasive way, as opposed to an MRI which provides information about the structure of the body.

## Specific Instructions

Please see the Data Dictionary for definitions for each of the data elements included in this CRF Module.

* Field of view - Answer should be recorded as a dimension (AAxAA) and in millimeters squared (mm2).
* Repetition time – Answer should be recorded in milliseconds (ms)
* Echo time – Answer should be recorded in milliseconds (ms)
* Acquisition time – Answer should be recorded in minutes
* Bandwidth – Answer should be recorded in Hz/Pixel
* Points count **–** Answer should be recorded in points