

BioPack Installation

Getting the files

- First download the BioPack.tgz and BioPack.README files from Varian website. The files are compressed using "gzip" to limit their sizes.
- for the installation you need to have or download the latest version of "extract". This is Contained in the loadbiopack.tgz file (from userlib/maclib).
- It is recommended that you also download the sample FIDS (fidlib). Use these to examine typical data. The fidlib has been updated to include AutoTripRes and AutoTripRes2D as well as 2H decoupling data.
- As vnmr1 (NMR root):
- place BioPack.README,BioPack.tgz, and BioPack_fidlib.tgz in /vnmr/userlib/psglib. Place loadbiopack.README and loadbiopack.tgz in /vnmr/userlib/maclib.

Single-User Mode

- Any user can type (in a UNIX shell):

```
cd /vnmr/userlib
```

```
extract maclib loadbiopack
```

- Then, in vnmr6.1C, enter "loadbiopack" on the command line.
- In vnmrj, select "Load Biopack" from drop-down Utilities/Tools Menu.
- The loadbiopack macro runs a script which automates the BioPack installation. It extracts the BioPack userlib/psglib file and puts the BioPack files into the user's vnmrsys directories (bin, maclib, manual, menulib, parlib, psg, psglib, shapelib, tablib, and templates).
- Follow directions to enter your probe's calibrations into the ghn_co.par parameter set followed by the "update" process (BPbiopack2 macro).
- AutoCalibration and AutoUpdate procedures update the probefile for the current user in the current user's vnmrsys, as well as create shaped pulses and *DEC files within the user's shapelib.

Multi-User Mode

- The system administrator (e.g., vnmr1) can type (in a UNIX shell):

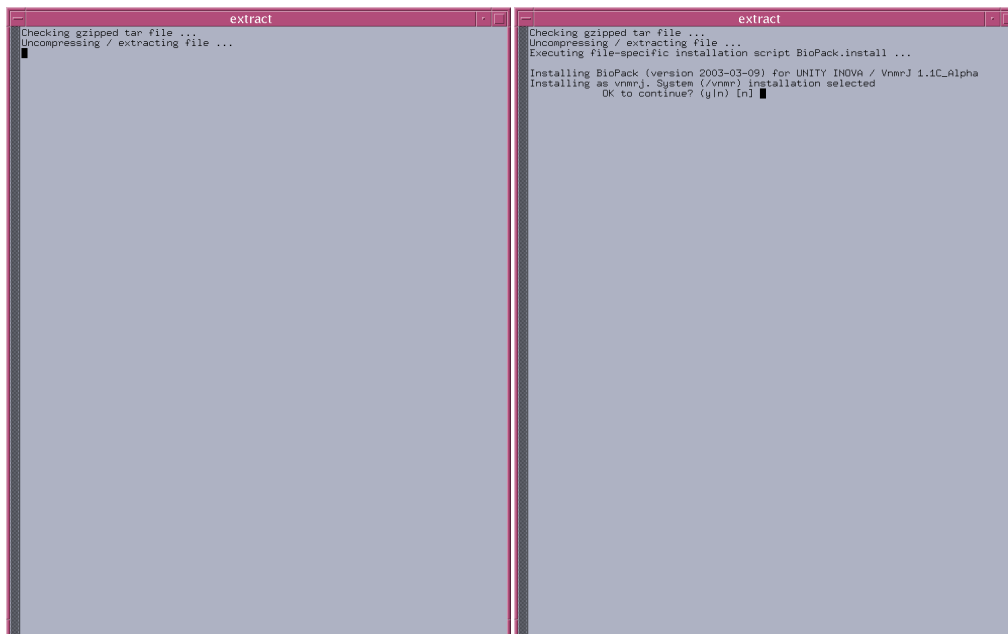
```
cd /vnmr/userlib
```

```
extract maclib loadbiopack /vnmr
```

```
extract psglib ProteinPack_fids /vnmr
```

- Then, in vnmr 6.1C, enter “loadbiopack” on the command line.
- In vnmrj, select “Loadbiopack” in drop-down Utilities Menu.
- This will place the BioPack files in /vnmr (bin, maclib, manual, menulib, parlib, psg, psglib,shapelib, tablib, and user_templates).
- BioPack files are stored in /vnmr. At installation, the pulse sequences are compiled in vnmr1’s psglib and then source and compiled codes are moved to /vnmr/psglib and /vnmr/seqlib.
- For the system administrator, AutoCalibration/Update procedures will update the probefile and re-create the shaped pulses in /vnmr/shapelib.
- Any other user can then run BioPack using these calibrations from /vnmr; if (s)he runs AutoCalibration/Update, probefile calibrations and updated pulse shapes and *.DEC patterns will be stored in the current user's vnmrsys.

While the installation is in progress, the pop window will show the current status and the screen will update as given from left to right and top to bottom.



```

extract
Checking gzipped tar file ...
Uncompressing / extracting file ...
Executing file-specific installation script BioPack.install ...
Installing BioPack (version 2003-03-09) for UNITY INOVA / Vnmrj 1.1C_Alpha
Installing as vnmrj_System /vnmrj installation selected
OK to continue? [y]n [n] y
Removing files not required for Vnmrj 1.1C_Alpha
Starting BioPack installation in /export/home/vnmrj_1.1C_Alpha_2003-03-17

Now starting file transfer to target directories; existing
files that are altered by BioPack will be backed out first.
This will take a few minutes ...
  Checking directory "bin" ... OK
    installing data ... done.
  Checking directory "BioPack_dir/BP_doc" ... OK
    installing data ... done.
  Checking directory "jpsg/lib" ... 1 file backed out
    installing data ... done.
  Checking directory "maclib" ... 7 files backed out
    installing data ... done.
  Checking directory "menulib" ... 23 files backed out
    installing data ... done.
  Checking directory "parlib" ... 5 files backed out
    installing data ... done.
  Checking directory "psg" ... 1 file backed out
    installing data ... done.
  Checking directory "psglib" ... 2 files backed out
    installing data ... done.
  Checking directory "shapelib" ... 1 file backed out
    installing data ... done.
  Checking directory "spincad/psglib" ... OK
    installing data ... done.
  Checking directory "tablib" ... OK
    installing data ... done.
  Checking directory "vnmrj" ... 14 files backed out
    installing data ... done.

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extract
installing data ... done.
Checking directory "templates/layout" ... 37 files backed out
installing data ... done.
Checking directory "templates/vnmrj" ... 1 file backed out
installing data ... done.
"maclib/footout" modified for aplab packages
the original version was backed out
BioPack backup directory:
/export/home/vnmrj_1.1C_Alpha_2003-03-17/adm/BioPack.bkups/2003-03-17_14:04
Total number of files backed out: 95

Looking for local BioPack files that are identical to those in /vnmrj:
bin: none found.
maclib: none found.
manual: none found.
menulib: none found.
parlib: none found.
psg: none found.
psglib: none found.
shapelib: none found.
spincad/psglib: none found.
tablib: none found.
templates/dg: none found.
templates/layout: none found.
templates/vnmrj: none found.

Backing out local BioPack files that differ from those in /vnmrj:
No local files were backed out.

Compiling 176 pulse sequences ...
this will take ca. 15 minutes
1/176: CPMgHnqc.c compiled OK
4/176: CPMgnoesy.c compiled OK
3/176: CtGhncq.c compiled OK
4/176: SShnoesy.c compiled OK
5/176: WgHnqc.c compiled OK
6/176: ddec_pwcal.c compiled OK
7/176: ddec_sgcal.c compiled OK
8/176: flpback_cal.c compiled OK
9/176: gLlNHnqc.c compiled OK
10/176: gLlNHnqa.c compiled OK
11/176: gLHnqc.c compiled OK
12/176: gLHnqa.c compiled OK
13/176: gHnqc.c compiled OK
14/176: gChmqnoesyHnqa.c compiled OK
15/176: gChmqnoesyHnqa.c compiled OK
16/176: gHnqc.c compiled OK
17/176: gChqa.c compiled OK
18/176: gChqaP.c compiled OK
19/176: gChqnoesy.c compiled OK
20/176: gChqnoesyA.c compiled OK
21/176: gChqnoesyA.c compiled OK
22/176: gChqctocsyA.c compiled OK
23/176: gLRCC.c compiled OK
24/176: gLRCH.c compiled OK
25/176: gNNOE.c compiled OK
26/176: gNT1.c compiled OK
27/176: gNT2.c compiled OK
28/176: gNHnqc.c compiled OK
29/176: gNHnqa.c compiled OK

```

```

extract
***** VARIAN NMR USER GROUP LIBRARY *****
***** SUBMISSION FORM *****

Your name: George A. Gray
Company/University: Varian
Address: Palo Alto
Phone: (650)-424-5423
FAX: (650)-494-2186
email: george.gray@varianinc.com

Date submitted: 2002-08-16 - first implementation from ProteinPack and RnaPack
followed by various updates, see below.
2003-02-11 - improved installation, many updates, see below.
2003-02-13 - several updates, see below.
2003-03-09 - various updates and corrections, see below.

File name: BioPack
Directory: psglib
Description: "user-friendly" water suppression, double and triple resonance
2D/3D/4D pulse sequences, includes TROSY options and BioNMR
PSG programming; featuring automatic calibration and
expeted execution. Includes experiments for non-labeled
and labeled biomolecules such as peptides, proteins, RNA's
and DNA's

BioPack is the result of the merging of ProteinPack and RnaPack.
ProteinPack: originally contributed by Robin Bendall (Melbourne)
RnaPack: originally contributed by Peter Lukavsky (Stanford)
Automated Shape Creation: contributed by Eriks Kupce (Varian)
SpinCAD pulse sequences for proteins contributed by Robin Bendall.

BioPack also incorporates the use of "probe files" as is customary in
Vnmrj/Vnmrj Cnpack. This means that calibrations are stored in probe
files rather than in parameter sets. Experiment setup macros (e.g.
"ghn_co") and the "BPrtpar" macro includes retrievals from the active
probe file for calibrations of all types.

The pulse sequences comprising BioPack are:
-----
COMMON NAME SEQUENCE NAME(S)
PRESAT - includes PRESAT, MET,
shaped-pulse PRESAT_jump-return,
watergate (soft, 3919, w5) water
watergate NOESY wnoesy
watergate ROESY wroesy
watergate TOCSY wgtocsy
wet NOESY wnoesy
wet ROESY wroesy
CPMG-NOESY qnoesy, qnoesyA NEW
SS-NOESY SNoesy
magic-angle DQFQDSY gnoesy
z-filtered DIPSI-TOCSY zdipitocsy
CLEARNEX N15-HSQC gLlNHnqa NEW
Fast N15-HSQC gHnqc, gHnqa NEW
Fast N15-HSQC with Homodecoupling gHnqcHD, gNHnqcHD NEW
Fast N15-IPAP-HSQC with Homodec. gHnqcIPAPHD, gNHnqcIPAPHD NEW
N15-HMQC gHnmc
--More-- (133)

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extract
(references are given in manual files and psglib codes)

Many sequences have a TROSY option, with gradient selection.

SPINCAD experiments for proteins:
-----
COMMON NAME SEQUENCE NAME(S)
N15-HSQC gHnqcSP NEW
C(CO)NH (or C(CC-TOCSY-CO)NH) gc_co_nhSP NEW
L(CO)NH gcba_co_nhSP NEW
C(CO)NH gcba_nhSP NEW
H(CO)NH (or H(CC-TOCSY-CO)NH) ghcc_co_nhSP NEW
DE-H(C)CH-TOCSY ghcc_tocsySP NEW
HCCHTOCSY hchh_tocsy NEW
HNA gna NEW
HN(CA)CO ghn_ca_coSP NEW
HN(CB)CO ghn_cb_coSP NEW
HNCO ghn_coSP NEW
HN(CO)CA ghn_co_caSP NEW
(these have been written to provide the same features as
the above equivalents)

EXPERIMENTS optimized for polynucleotides
-----
COMMON NAME SEQUENCE NAME(S)
1H PRESAT, MET, jump-return, rna_water
1H PRESAT-NOESY rna_trnoesy
1H PRESAT-DQFQDSY rna_trdqdsy
1H MET-ROESY rna_wroesy
1H WATERGATE-ROESY rna_wroesy
1H WATERGATE-NOESY rna_wnoesy
1H MET-NOESY rna_wetnoesy
1H MET-TOCSY rna_wettrtoesy
1H SS-NOESY rna_SNoesy
13C HSQC rna_gHnqc, rna_gChqa NEW
13C TROSY rna_gTrnoesy, rna_gTrnoesyA NEW
15N HSQC rna_gHnqc, rna_gHnqa NEW
15N TROSY rna_gHntrnoesy
13C HMQC rna_gHnqc
13C HMQC-TOCSY rna_hmqc_tocsy
13C CT-HMQC rna_CtHmqc, rna_CtGhmqcA NEW
15N HMQC rna_gHnqc
15N Wg-HSQC rna_WgHnqc
15N HSQC (long-range) rna_WgHnqa
15N CPMG-HSQC rna_CPMgHnqc
13C NOESY-HSQC rna_gnoesyHnqc, rna_gnoesyHnqa NEW
15N NOESY-HSQC rna_gnoesyHnqc, rna_gnoesyHnqa NEW
gd-HCCH-TOCSY rna_gchch_tocsy
DE-H(C)CH-TOCSY rna_hcch_tocsy, rna_hcch_tocsyA NEW
HCCH-ROESY rna_hcch_roesy, rna_hcch_roesyA NEW
HCCH-RELAY rna_hcch_relay, rna_hcch_relayA NEW
CPMG-NOESY rna_CPMg_noesy
HCH rna_HCH NEW
HCP rna_HCP NEW
HF-COSY rna_HFcosyHCP NEW
C-HNCCCH rna_CHNccch NEW
U-HNCCCH rna_UHNccch NEW
A-HNCC-TOCSY-CH rna_AHnccch
--More-- (403)

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Once the installation is complete, strike the Enter key in the key board and follow the instruction displayed on the graphics area of VNMJR/VNMR. The experiment ghn_co is used as a basis template and is loaded first. Set known pw/power parameters here and update the probe file.

The following are the experiments in BioPack with their common name and BioPack pulse sequence names.

Homonuclear 1D and 2D BioPack Sequences

COMMON NAME	SEQUENCE NAME(S)
PRESAT(includes presat, multi-frequency presat, wet, swet, purge shaped-pulse presat, jump-return watergate (soft, 3919, W5)	water
Saturation Transfer Diff. 1D	satxfer1D
watergate COSY	wgcosy
watergate DQFCOSY	wgdqfcosy
watergate NOESY	wgnoesy
watergate ROESY	wgroesy
watergate TOCSY	wgtocsy
wet NOESY	wnoesy
wet ROESY	wroesy
"quiet" NOESY	qwnoesy, qwnoesyA
CPMG-NOESY	CPMGnoesy
SS-NOESY	SSnoesy
NOESY-C_chirp_purge_lek_v3a	noesyCA
C and/or N filtered NOESY	CNfilnoesy
magic-angle DQFCOSY	gmacosy
z-filtered DIPSI-TOCSY	zdipsitocsy
Multi-Frequency Presat NOESY, TOCSY, ROESY	tnnoesy, tntocsy, tnroesy

Heteronuclear N15 Indirect Detection 2D Sequences in BioPack

COMMON NAME	SEQUENCE NAME(S)
CLEANEX N15-HSQC	gCLNfhsqc, gCLNfhsqcA
Fast N15-HSQC	gNfhsqc, gNfhsqcA
Fast N15-HSQC with Homodecoupling	gNfhsqcHD, gNfhsqcHDA
Fast N15-IPAP-HSQC with Homodec.	gNfhsqc_IPAPHD, gNfhsqc_IPAPHDA
N15-HMQC	gNhmqc
N15-HSQC	gNhsqc, gNhsqcA
N15-HSQC with Homodecoupling	gNhsqcHD, gNhsqcHDA
N15-HSQC(IPAP)	gNhsqc_IPAP, gNhsqc_IPAPA

CPMG-N15-HSQC	CPMGgNhsqc
watrgate N15-HSQC	WGgNhsqc
N15-T1 (TROSY)	gNT1
N15-T2 (TROSY)	gNT2
N15-NOE (TROSY)	gNNOE
N15-NOE	gNnoe
N15-CPMG for exchange	gNcpmgex
N15-ultra fast HMQC	sofastNhmqc, sofastNhmqcA

BioPack 3D and 4D N15 HSQC and/or HMQC Experiments

COMMON NAME	SEQUENCE NAME(S)
N15-NOESYHSQC	gnoesyNhsqc, gnoesyNhsqcA
N15-HSQCNOESY	gNhsqcnoesy, gNhsqcnoesyA
N15-HSQC-NOESY-N15-HSQC(3D)	gNhsqcnoesyNhsqc3D N15, C13-NOESYHSQC
C13,15 edited NOESY	gnoesyCNhsqc, gnoesyCNhsqcA
N15-TOCSYHSQC	gtocsyNhsqc, gtocsyNhsqcA
N15-HSQCTOCSY	gNhsqctocsy, gNhsqctocsyA
C13-HMQCNOESY-N15-HSQC(4D)	gChmqcnoesyNhsqc, gChmqcnoesyNhsqcA
N15-HMQCNOESY-N15-HSQC(4D)	gNhmqcnoesyNhsqc
N15-HSQCNOESY-N15-HSQC(4D)	gNhsqcnoesyNhsqc, gNhsqcnoesyNhsqcA
N15-HSQCTOCSYNOESY-N15-HSQC(4D)	gNhsqctocsynoesyNhsqc,
13C,15N edited NOESY with TROSY(4D)	CN4Dnoesy_troSYA
4D 15N,15N edited NOESY with TROSY(4D)	NN4Dnoesy_troSYA

BioPack Sequences Involving 13C HSQC and/or HMQC indirect Detection

COMMON NAME	SEQUENCE NAME(S)
C13-HMQCNOESYHSQC(4D)	gChmqcnoesyNhsqc, gChmqcnoesyNhsqcA
C13-NOESYHSQC	gnoesyChsqc, gnoesyChsqcA
C13-NOESYHMQC	gnoesyChmqc
C13NOESYHSQC-SE	gnoesyChsqcSE
C13-HSQCNOESY	gChsqcnoesy, gChsqcnoesyA
C13-TOCSYHSQC	gtocsyChsqc, gtocsyChsqcA, gtocsyChsqcSE
C13-HSQCTOCSY	gChsqctocsy, gChsqctocsyA

C13,N15-NOESYHSQC	gnoesyCNhsqc, gnoesyCNhsqcA
C13-HMQC	gChmqc
C13-HMBC	gChmbc
CT-C13-HMQC	CTgChmqc
Fast 13C-HSQC	gCfhsqc, gCfhsqcA
C13-HSQC	gChsqc, gChsqcP, gChsqcA

3D C(methyl-CT)-noesy-C(methyl-CT)-H(methyl) methylnoesy4D 13C,15N edited NOESY with TROSY	CN4Dnoesy_trosyA
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Triple-Resonance Assignment Experiments in BioPack

COMMON NAME	SEQUENCE NAME(S)
C(CO)NH (or C(CC-TOCSY-CO)N-NH)	gc_co_nh, gc_co_nhP, gc_co_nhA
H(CCO)NH (or H(CC-TOCSY-CO)N-NH)	ghc_co_nh, ghc_co_nhP, ghc_co_nhA
CBCA(CO)NH	gcbca_co_nh, gcbca_co_nhP, gcbca_co_nhA
CBCANH	gcbca_nh, gcbca_nhP, gcbca_nhA
HCACO	ghca_co, ghca_coA
HCACON	ghca_co_n, ghca_co_nA
HCACOCANH	ghca_co_canh, ghca_co_canhA
HNCO	ghn_co, ghn_coP, ghn_coA
HNCOCO	ghn_coco, ghn_cocoA
HNN	ghnn, ghnnA
HNCN	ghcn, ghcnA
HN(CO)HB	ghn_co_hb, ghn_co_hbA
HNCA	ghn_ca, ghn_caP, ghn_caA
HNCA (intra-residue-only)	ghnca_intraA
CT-HNCA	ghn_ca_CT, ghn_ca_CTA
HCAN	ghca_n
HNCACB	ghn_cacb, ghn_cacbP, ghn_cacbA
HNCACB (intra-residue-only)	ghncacb_intraA
CT-HNCACB	ghn_cacbCTP
HN(CO)CA	ghn_co_ca, ghn_co_caP, ghn_co_caA
HN(CA)CO	ghn_ca_co, ghn_ca_coP, ghn_ca_coA
HN(COCA)CB	ghn_coca_cb, ghn_coca_cbA
HBHA(CO)NH	hacahbA
C(b),C(a)-CO-H(a)	hbcbcacocahaA

Most sequences have a TROSY option, with gradient selection.

Triple-Resonance TROSY Experiments for Fully-Deuterated Proteins

COMMON NAME	SEQUENCE NAME(S)
HNCO 3D	ghnco_trosy_3DA
HNCA 3D	ghnca_trosy_3DA
HNCACB 3D	ghncacb_trosy_3DA
HNCOACB 3D	ghncocacb_trosy_3DA
HN(CO)CA 3D (sequential)	ghncoca_seq_trosy_3DA
HN(CO)CA 4D (sequential)	ghncoca_seq_trosy_4DA
HN(CO)CA 4D (same aa)	ghncoca_sim_trosy_3DA
HN(CA)CO 3D	ghncaco_trosy_3DA
HN(CA)CO 4D	ghncaco_trosy_4DA

(contributed by Lewis Kay, U. Toronto and Eriks Kupce, Varian)

Triple-Resonance Experiments in BioPack

COMMON NAME	SEQUENCE NAME(S)
<u>Aromatics:</u>	
aromatic proton-beta carbon correlation	hbcbcgdcceheA, hbcbcgcdhdA
<u>Relaxation:</u>	
HNCO_NOE	ghn_co_noe, ghn_co_noeA
<u>Side-Chain Assignments:</u>	
C-CH-TOCSY	cch_tocsyA
HCCH-TOCSY	hcch_tocsy, hcch_tocsyP, hcch_tocsyA
HCCH-COSY	hcch_cosy, hcch_cosyA
DE-H(C)CH-TOCSY	ghcch_tocsy
CACB-TOCSY-C(methyl)H(methyl)	gcacb_tocsy_cmhmA
CACB-TOCSY-C(methyl)H(methyl)-SQ	gcacb_tocsy_cmhm_sqA

Many sequences have a TROSY option, with gradient selection.

Coupling Measurement Experiments in BioPack

COMMON NAME	SEQUENCE NAME(S)
LR-JCH	gLRCH
LR-JCC	gLRCC
HNCO_JNH	ghn_co_JNH, ghn_co
HNHA	ghnha
HNHB	ghnhb
N15-HMQCJ	gNhmqcJ
gNhsqcS3 S3 a,b-filtering for J(NH)	gNtroSy
S3 for J(N-CO)/(HN-CO) doublets	ghn_Jnco_2DS3
S3 J(NCa) in 1H-15N correlation	ghn_Jnca_2DS3
3D 1J(HaCa) and 2J(N(i)H(i))	ghnca_Jnha_3D
S3 2D J(CoCa) in a 1H-15N correlation	ghn_Jcoca_2DS3
S3 3D J(N-CO) in 1H-15N-13CO correlation	ghnco_Jnco_3DS3
S3 3D 1J(NCa), 2J(NCa), 2J(HNCa) & 3J(HNCa)	ghnco_Jnca_3DS3
S3 3D 1J(COCa) & 3J(HNCa)	ghnco_Jcoca_3DS3

3D experiments : gbcba_co_nh.c, gbcba_nh.c, ghc_co_nh.c, ghn_ca.c,ghn_ca_co.c, ghn_cacb.c, ghn_co.c, ghn_co_ca.c, gnoesyNhsqc.c, gtocsyNhsqc.c, gnoesyChsqcSE.c and their autocal (*A.c) versions.

Nine new experiments submitted by Eriks Kupce and Lewis Kay. Each have the "autocal" option that makes the sequence BioPack-compatible and uses Pbox to create shaped pulses and assign parameter values to local variables.

These are backbone assignment experiments for large FULLY-DEUTERATED proteins using TROSY. The recent Nietlsbach method (J.BioMol.NMR,31,161(2005) method for suppression of the non-trosy peak is implemented:

ghnca_trosy_3DA.c ghncacb_trosy_3DA.c, ghncaco_trosy_3DA.c,
ghncaco_trosy_4DA.c ghncoc_trosy_3DA.c, ghncoca_seq_trosy_3DA.c,
ghncoca_seq_trosy_4DA.c ghncoca_sim_trosy_4DA.c ghncocacb_trosy_3DA.c.

Do not use these on protonated or partially-deuterated proteins since proton decoupling is not used in these sequences. Only the ghnco_trosy_3DA.c sequence will show signals for a non-

deuterated protein. All experiments are fully supported with macros, manuals, parameter sets, pulse sequences and templates/layout files for the VnmrJ interface.

BioPack 1D and 2D Experiments optimized for polynucleotides

COMMON NAME	SEQUENCE NAME(S)
PRESAT, WET, jump-return, watergate	rna_water
PRESAT-NOESY	rna_tnnoesy
PRESAT-DQCOSY	rna_tndqcosy
WET-ROESY	rna_wroesy
WATERGATE-ROESY	rna_wroesy
WATERGATE-NOESY	rna_WGnoesy
WET-NOESY	rna_wetnoesy
WET-TOCSY	rna_wettntocsy
SS-NOESY	rna_SSnoesy
1-1 echo NOESY	rna_11noesy
13C HSQC	rna_gChsqc, rna_gChsqcA
13C TROSY	rna_gCtrocy, rna_gCtrocyA
15N HSQC	rna_gNhsqc, rna_gNhsqcA
15N TROSY	rna_WGgNtrocy
13C HMQC	rna_gChmqc
13C HMQC-TOCSY	rna_hmqc_tocsy
13C CT-HMQC	rna_CTgChmqc, rna_CTgChmqcA
15N HMQC	rna_gNhmqc
15N WG-HSQC	rna_WGgNhsqc
15N HSQC(long-range)	rna_WGgNhsqc
15N CPMG-HSQC	rna_CPMGgNhsqc

BioPack 3D Experiments optimized for polynucleotides

COMMON NAME	SEQUENCE NAME(S)
13C NOESY-HSQC	rna_gnoesyChsqc, rna_gnoesyChsqcA
15N NOESY-HSQC	rna_gnoesyNhsqc, rna_gnoesyNhsqcA
HCCH-TOCSY	rna_hcch_tocsy
DE-H(C)CH-TOCSY	rna_ghcch_tocsy
HCCH-COSY	rna_hcch_cosy, rna_hcch_cosyA
HCCH-RELAY	rna_hcch_cosy, rna_hcch_cosyA

CPMG-NOESY

HCN

HCP

HP-COSY

C-HNCCCH

U-HNCCCH

A-HNC-TOCSY-CH

A-HCCH-TOCSY

G-HNC-TOCSY-CH

HNN-COSY

rna_CPMG_noesy

rna_HCN

rna_HCP

rna_HPcosyHCP

rna_CUhnccch

rna_CUhnccch

rna_Ahnccch

rna_hcch_tocsy

rna_Ghnccch

rna_HNNcosy, rna_HNNcosyA, rna_fHNNcosyA