Supporting Information Available.

SI Table 1. NMR resonance assignments of *frenolycin* ACP.

SI Figure 1. Structure of the 4′-phosphopantetheine prosthetic group labeled as assigned in SI Table 2.

SI Table 2. NMR resonance assignments of 4′-phosphopantetheine prosthetic group.

SI Table 3. Heteronuclear ^{15}N backbone relaxation and order parameters.

SI Table 1. NMR resonance assignments of *frenolycin* ACP.

Group	Atom	Nuc	Shift
A2	C	13C	47.565
A2	CA	13C	53.891
A2	CB	13C	20.395
A2	HA	1H	4.357
A2	QB	1H	1.405
A2	HN	1H	8.404
A2	N	15N	122.224
L3	C	13C	48.428
L3	CA	13C	56.088
L3	CB	13C	45.347
L3	CD1	13C	25.58
L3	CD2	13C	27.176
L3	CG	13C	28.72
L3	HA	1H	4.623
L3	HB2	1H	1.519
L3	HB3	1H	1.183
L3	HG	1H	1.504
L3	HN	1H	9.077
L3	N	15N	123.697
L3	QD1	1H	0.553
L3	QD2	1H	0.514
T4	C	13C	48.695
T4	CA	13C	61.136
T4	CB	13C	73.575
T4	CG2	13C	22.792
T4	HA	1H	4.718
T4	HB	1H	4.738
T4	HN	1H	9.12

T4	N	15N	116.582
T4	QG2	1H	1.296
V5	C	13C	47.297
V5	CA	13C	67.672
V5	CB	13C	32.657
V5	CG1	13C	22.215
V5	CG2	13C	24.569
V5	HA	1H	3.637
V5	HB	1H	2.121
V5	HN	1H	8.994
V5	N	15N	120.451
V5	QG1	1H	0.957
V5	QG2	1H	1.017
D6	C	13C	48.418
D6	CA	13C	58.776
D6	CB	13C	42.169
D6	HA	1H	4.451
D6	HB2	1H	2.587
D6	HB3	1H	2.994
D6	HN	1H	7.976
D6	N	15N	120.129
D7	C	13C	50.144
D7	CA	13C	58.541
D7	CB	13C	42.462
D7	HA	1H	4.425
D7	HB2	1H	2.98
D7	HB3	1H	2.59
D7	HN	1H	7.797
D7	N	15N	120.278
L8	C	13C	50.147

L8	CA	13C	58.936
L8	CB	13C	42.752
L8	CD1	13C	24.177
L8	CD2	13C	27.324
L8	CG	13C	28.193
L8	HA	1H	4.028
L8	HB2	1H	2.064
L8	HB3	1H	1.444
L8	HG	1H	1.677
L8	HN	1H	8.202
L8	N	15N	121.354
L8	QD1	1H	0.889
L8	QD2	1H	0.952
K9	C	13C	48.757
K9	CA	13C	61.316
K9	CB	13C	33.746
K9	CD	13C	31.168
K9	CE	13C	43.501
K9	CG	13C	26.389
K9	HA	1H	3.915
K9	HB2	1H	2.042
K9	HB3	1H	2.133
K9	HD2	1H	1.832
K9	HD3	1H	1.905
K9	HG2	1H	1.593
K9	HG3	1H	1.71
K9	HN	1H	8.691
K9	N	15N	119.867
K9	QE	1H	3.135
K10	C	13C	50.416

K10	CA	13C	60.693
K10	CB	13C	33.832
K10	CD	13C	30.707
K10	CE	13C	43.514
K10	CG	13C	26.764
K10	HA	1H	4.137
K10	HG2	1H	1.509
K10	HG3	1H	1.672
K10	HN	1H	7.621
K10	N	15N	118.897
K10	QB	1H	2.004
K10	QD	1H	1.756
K10	QE	1H	3.022
L11	C	13C	52.167
L11	CA	13C	59.152
L11	CB	13C	43.685
L11	CD1	13C	26.608
L11	CD2	13C	26.273
L11	CG	13C	28.158
L11	HA	1H	4.264
L11	HB2	1H	1.891
L11	HB3	1H	1.642
L11	HG	1H	1.881
L11	HN	1H	7.923
L11	N	15N	120.87
L11	QD1	1H	0.896
L11	QD2	1H	0.932
L12	C	13C	51.013
L12	CA	13C	58.828
L12	CB	13C	42.204

L12	CD1	13C	27.271
L12	CD2	13C	23.054
L12	CG	13C	28.242
L12	HA	1H	3.97
L12	HB2	1H	1.703
L12	HB3	1H	1.2
L12	HG	1H	1.522
L12	HN	1H	8.533
L12	N	15N	120.276
L12	QD1	1H	0.597
L12	QD2	1H	0.271
A13	C	13C	50.432
A13	CA	13C	55.805
A13	CB	13C	19.447
A13	HA	1H	4.288
A13	HB2	1H	1.478
A13	HN	1H	7.947
A13	N	15N	120.978
A13	QB	1H	1.552
E14	C	13C	51.566
E14	CA	13C	60.013
E14	CB	13C	30.916
E14	CG	13C	37.397
E14	HA	1H	4.155
E14	HB2	1H	2.295
E14	HB3	1H	2.236
E14	HG2	1H	2.567
E14	HG3	1H	2.309
E14	HN	1H	7.96
E14	N	15N	118.008

T15	C	13C	49.256
T15	CA	13C	65.302
T15	CG2	13C	23.471
T15	HA	1H	4.228
T15	HB	1H	4.248
T15	HN	1H	8.02
T15	N	15N	112.066
T15	QG2	1H	1.279
A16	C	13C	46.99
A16	CA	13C	53.925
A16	CB	13C	21.523
A16	HA	1H	4.542
A16	HN	1H	8.318
A16	N	15N	123.911
A16	QB	1H	1.587
G17	C	13C	49.566
G17	CA	13C	46.552
G17	HA1	1H	4.2
G17	HA2	1H	3.936
G17	HN	1H	7.978
G17	N	15N	108.18
E18	C	13C	45.343
E18	CA	13C	57.09
E18	CB	13C	32.286
E18	CG	13C	36.551
E18	HA	1H	4.401
E18	HB2	1H	1.969
E18	HB3	1H	2.116
E18	HN	1H	8.279
E18	N	15N	119.509

E18	QG	1H	2.296
D19	C	13C	46.497
D19	CA	13C	55.624
D19	CB	13C	42.56
D19	HA	1H	4.688
D19	HB2	1H	2.666
D19	HB3	1H	2.796
D19	HN	1H	8.585
D19	N	15N	122.054
D20	C	13C	47.566
D20	CA	13C	55.358
D20	CB	13C	42.181
D20	HA	1H	4.685
D20	HB2	1H	2.74
D20	HB3	1H	1.837
D20	HN	1H	8.524
D20	N	15N	122.34
S21	C	13C	47.853
S21	CA	13C	60.311
S21	CB	13C	65.068
S21	HA	1H	4.437
S21	HB2	1H	3.983
S21	HB3	1H	3.846
S21	HN	1H	8.555
S21	N	15N	115.89
S21	QB	1H	3.912
V22	C	13C	46.126
V22	CA	13C	63.329
V22	CB	13C	34.512
V22	CG1	13C	22.42

V22	CG2	13C	22.221
V22	HA	1H	4.07
V22	HB	1H	2.133
V22	HN	1H	7.964
V22	N	15N	122.618
V22	QG1	1H	0.955
V22	QG2	1H	0.931
D23	C	13C	46.994
D23	CA	13C	53.849
D23	CB	13C	41.381
D23	HA	1H	4.763
D23	HB2	1H	2.617
D23	HB3	1H	2.909
D23	HN	1H	8.821
D23	N	15N	126.625
L24	C	13C	48.177
L24	CA	13C	58.587
L24	CB	13C	44.166
L24	CD1	13C	26.435
L24	CD2	13C	25.889
L24	CG	13C	28.219
L24	HA	1H	3.856
L24	HB2	1H	1.561
L24	HB3	1H	1.476
L24	HG	1H	1.726
L24	HN	1H	8.193
L24	N	15N	126.747
L24	QD1	1H	0.88
L24	QD2	1H	0.927
A25	C	13C	49.28

A25	CA	13C	56.141
A25	CB	13C	19.4
A25	HA	1H	3.909
A25	HN	1H	8.322
A25	N	15N	117.981
A25	QB	1H	1.453
G26	C	13C	50.742
G26	CA	13C	46.378
G26	HA1	1H	4.317
G26	HA2	1H	3.855
G26	HN	1H	7.767
G26	N	15N	104.733
E27	C	13C	50.455
E27	CA	13C	55.585
E27	CB	13C	31.284
E27	CG	13C	34.649
E27	HA	1H	4.311
E27	HB2	1H	1.528
E27	HB3	1H	2.557
E27	HN	1H	7.671
E27	N	15N	120.601
E27	QG	1H	2.208
L28	C	13C	50.428
L28	CA	13C	59.307
L28	CB	13C	43.451
L28	CD1	13C	26.821
L28	CD2	13C	24.917
L28	CG	13C	28.149
L28	HA	1H	3.773
L28	HB2	1H	1.79

L28	HB3	1H	1.184
L28	HG	1H	1.895
L28	HN	1H	7.692
L28	N	15N	118.483
L28	QD1	1H	0.884
L28	QD2	1H	0.698
D29	C	13C	48.459
D29	CA	13C	54.615
D29	CB	13C	42.997
D29	HA	1H	5.037
D29	HB2	1H	2.378
D29	HB3	1H	3.044
D29	HN	1H	8.073
D29	N	15N	112.216
T30	C	13C	46.146
T30	CA	13C	61.206
T30	CB	13C	71.232
T30	CG2	13C	23.433
T30	HA	1H	4.474
T30	HB	1H	4.292
T30	HN	1H	7.76
T30	N	15N	123.793
T30	QG2	1H	1.368
P31	CA	13C	63.78
P31	CB	13C	34.1
P31	CD	13C	52.138
P31	CG	13C	29.693
P31	HA	1H	4.536
P31	HB2	1H	2.494
P31	HB3	1H	1.859

P31	HD2	1H	3.782
P31	HD3	1H	4.075
P31	HG2	1H	2.18
P31	HG3	1H	1.885
F32	CA	13C	64.351
F32	CB	13C	40.081
F32	CD1	13C	143.047
F32	CD2	13C	143.551
F32	HA	1H	4.342
F32	HB2	1H	3.033
F32	HB3	1H	3.514
F32	HD1	1H	7.228
F32	HD2	1H	6.969
F32	HN	1H	8.74
F32	N	15N	123.469
V33	C	13C	50.729
V33	CA	13C	66.232
V33	CB	13C	32.736
V33	CG1	13C	21.969
V33	HA	1H	4.106
V33	HB	1H	2.225
V33	HN	1H	8.583
V33	N	15N	114.828
V33	QQG	1H	1.089
D34	C	13C	50.138
D34	CA	13C	57.54
D34	CB	13C	41.561
D34	HA	1H	4.59
D34	HB2	1H	2.772
D34	HB3	1H	2.744

D34	HN	1H	7.39
D34	N	15N	123.124
L35	C	13C	49.001
L35	CA	13C	56.014
L35	CB	13C	44.477
L35	CD1	13C	23.647
L35	CD2	13C	27.073
L35	CG	13C	27.158
L35	HA	1H	4.34
L35	HB2	1H	1.769
L35	HB3	1H	2.243
L35	HG	1H	1.744
L35	HN	1H	7.675
L35	N	15N	119.675
L35	QD1	1H	0.88
L35	QD2	1H	0.9
G36	C	13C	47.593
G36	CA	13C	46.124
G36	HA1	1H	3.616
G36	HA2	1H	4.066
G36	HN	1H	7.513
G36	N	15N	104.489
Y37	CA	13C	58.223
Y37	CB	13C	40.529
Y37	CD2	13C	145.782
Y37	HA	1H	4.66
Y37	HB2	1H	2.709
Y37	HB3	1H	2.638
Y37	HD1	1H	7.306
Y37	HD2	1H	7.024

Y37	HE1	1H	6.875
Y37	HE2	1H	6.739
Y37	HN	1H	7.669
Y37	N	15N	120.491
D38	C	13C	45.547
D38	CA	13C	53.439
D38	CB	13C	43.026
D38	HA	1H	4.628
D38	HB2	1H	3.236
D38	HB3	1H	2.809
D38	HN	1H	8.332
D38	N	15N	123.013
S39	C	13C	47.224
S39	CA	13C	61.445
S39	CB	13C	66.844
S39	HA	1H	4.169
S39	HB2	1H	4.104
S39	HB3	1H	4.295
S39	HN	1H	8.741
S39	N	15N	113.214
L40	C	13C	47.571
L40	CA	13C	59.274
L40	CB	13C	42.113
L40	CD1	13C	25.459
L40	CD2	13C	25.762
L40	CG	13C	28.401
L40	HA	1H	4.195
L40	HB2	1H	1.831
L40	HB3	1H	1.721
L40	HG	1H	1.685

L40	HN	1H	7.729
L40	N	15N	123.313
L40	QD1	1H	0.987
L40	QD2	1H	0.923
A41	C	13C	48.993
A41	CA	13C	56.35
A41	CB	13C	19.168
A41	HA	1H	4.232
A41	HN	1H	8.142
A41	N	15N	123.548
A41	QB	1H	1.635
L42	C	13C	53.265
L42	CA	13C	58.254
L42	CB	13C	41.905
L42	CD1	13C	25.434
L42	CD2	13C	22.482
L42	CG	13C	28.082
L42	HA	1H	3.768
L42	HB2	1H	1.246
L42	HB3	1H	1.665
L42	HG	1H	1.441
L42	HN	1H	8.028
L42	N	15N	120.906
L42	QD1	1H	-0.046
L42	QD2	1H	0.342
L43	C	13C	50.427
L43	CA	13C	59.675
L43	CB	13C	42.932
L43	CD1	13C	24.557
L43	CD2	13C	26.618

L43	CG	13C	28.437
L43	HA	1H	4.05
L43	HB2	1H	1.627
L43	HB3	1H	1.94
L43	HG	1H	1.76
L43	HN	1H	8.045
L43	N	15N	121.777
L43	QD1	1H	0.871
L43	QD2	1H	0.908
E44	C	13C	52.19
E44	CA	13C	60.353
E44	CB	13C	29.888
E44	CG	13C	36.496
E44	HA	1H	4.185
E44	HB2	1H	2.077
E44	HB3	1H	2.248
E44	HG2	1H	2.381
E44	HG3	1H	2.513
E44	HN	1H	8.399
E44	N	15N	121.156
T45	C	13C	50.993
T45	CA	13C	68.997
T45	CB	13C	68.98
T45	CG2	13C	21.571
T45	HA	1H	3.796
T45	HB	1H	4.208
T45	HN	1H	8.178
T45	N	15N	118.756
T45	QG2	1H	0.9
A46	C	13C	48.46

A46	CA	13C	56.616
A46	CB	13C	19.198
A46	HA	1H	3.962
A46	HN	1H	8.492
A46	N	15N	123.815
A46	QB	1H	1.522
A47	C	13C	51.212
A47	CA	13C	56.702
A47	CB	13C	18.879
A47	HA	1H	4.301
A47	HB2	1H	1.6
A47	HB3	1H	1.663
A47	HN	1H	7.898
A47	N	15N	122.999
V48	C	13C	47.29
V48	CA	13C	67.606
V48	CB	13C	32.689
V48	CG1	13C	23.386
V48	CG2	13C	23.916
V48	HA	1H	3.818
V48	HB	1H	2.231
V48	HN	1H	7.885
V48	N	15N	120.822
V48	QG1	1H	0.998
V48	QG2	1H	1.127
L49	C	13C	48.138
L49	CA	13C	60.049
L49	CB	13C	43.13
L49	CD1	13C	26.469
L49	CD2	13C	27.378

L49	CG	13C	28.25
L49	HA	1H	4.146
L49	HB2	1H	1.633
L49	HB3	1H	2.023
L49	HG	1H	1.872
L49	HN	1H	8.615
L49	N	15N	121.561
L49	QD1	1H	0.799
L49	QD2	1H	0.721
Q50	C	13C	45.828
Q50	CA	13C	61.114
Q50	CB	13C	29.69
Q50	CG	13C	35.379
Q50	HA	1H	4.058
Q50	HE21	1H	7.363
Q50	HE22	1H	6.86
Q50	HG2	1H	2.382
Q50	HG3	1H	2.315
Q50	HN	1H	8.13
Q50	N	15N	120.315
Q50	NE2	15N	111.039
Q50	QB	1H	2.319
Q51	C	13C	50.42
Q51	CA	13C	60.017
Q51	CB	13C	30.243
Q51	CG	13C	34.941
Q51	HA	1H	4.022
Q51	HE21	1H	6.905
Q51	HE22	1H	7.532
Q51	HG2	1H	2.58

Q51	HG3	1H	2.437
Q51	HN	1H	7.941
Q51	N	15N	119.455
Q51	NE2	15N	111.918
Q51	QB	1H	2.226
R52	C	13C	48.731
R52	CA	13C	59.523
R52	CB	13C	32.926
R52	CD	13C	44.784
R52	CG	13C	28.428
R52	HA	1H	4.1
R52	HB2	1H	1.687
R52	HB3	1H	1.349
R52	HD2	1H	2.8
R52	HD3	1H	3.109
R52	HE	1H	7.258
R52	HG2	1H	1.592
R52	HG3	1H	1.24
R52	HN	1H	8.901
R52	N	15N	116.295
R52	NE	15N	84.005
Y53	CA	13C	59.312
Y53	CB	13C	41.273
Y53	CE1	13C	112.425
Y53	CE2	13C	112.988
Y53	HA	1H	4.758
Y53	HB2	1H	2.965
Y53	HB3	1H	3.336
Y53	HD1	1H	7.16
Y53	HD2	1H	7.261

Y53	HE1	1H	6.817
Y53	HE2	1H	6.74
Y53	HN	1H	7.997
Y53	N	15N	113.481
G54	C	13C	47.869
G54	CA	13C	47.748
G54	HN	1H	7.806
G54	N	15N	109.725
G54	QA	1H	4.068
I55	C	13C	45.318
I55	CA	13C	61.338
I55	CB	13C	41.421
I55	CD1	13C	15.239
I55	CG1	13C	28.213
I55	CG2	13C	18.477
I55	HA	1H	4.221
I55	HB	1H	1.564
I55	HD1	1H	0.782
I55	HD2	1H	0.917
I55	HG12	1H	1.488
I55	HG13	1H	1.087
I55	HN	1H	6.936
I55	N	15N	119.325
I55	QG2	1H	0.863
A56	C	13C	45.263
A56	CA	13C	52.391
A56	CB	13C	20.665
A56	HA	1H	4.531
A56	HN	1H	8.645
A56	N	15N	130.355

A56	QB	1H	1.287
L57	C	13C	48.139
L57	CA	13C	54.676
L57	CB	13C	45.09
L57	CD1	13C	27.016
L57	CD2	13C	25.099
L57	HA	1H	4.724
L57	HB2	1H	1.252
L57	HB3	1H	1.599
L57	HG	1H	1.211
L57	HN	1H	8.511
L57	N	15N	124.828
L57	QD1	1H	0.696
L57	QD2	1H	0.791
T58	C	13C	48.665
T58	CA	13C	62.264
T58	CB	13C	72.163
T58	CG2	13C	23.142
T58	HA	1H	4.379
T58	HB	1H	4.685
T58	HN	1H	8.539
T58	N	15N	114.464
T58	QG2	1H	1.346
D59	C	13C	46.429
D59	CA	13C	58.348
D59	CB	13C	40.729
D59	HA	1H	4.157
D59	HN	1H	8.853
D59	N	15N	122.1
D59	QB	1H	2.648

E60	C	13C	50.265
E60	CA	13C	60.484
E60	CB	13C	30.536
E60	CG	13C	37.606
E60	HA	1H	4.011
E60	HB2	1H	1.959
E60	HB3	1H	2.052
E60	HN	1H	8.607
E60	N	15N	119.589
E60	QG	1H	2.282
T61	C	13C	50.128
T61	CA	13C	67.445
T61	CB	13C	69.456
T61	CG2	13C	23.497
T61	HA	1H	3.864
T61	HB	1H	4.295
T61	HN	1H	7.774
T61	N	15N	117.892
T61	QG2	1H	1.162
V62	C	13C	47.828
V62	CA	13C	63.571
V62	CB	13C	32.642
V62	CG1	13C	23.102
V62	CG2	13C	22.282
V62	HA	1H	3.934
V62	HB	1H	2.08
V62	HN	1H	8.328
V62	N	15N	121.119
V62	QG1	1H	0.782
V62	QG2	1H	0.953

V62	QQG	1H	0.901
G63	C	13C	49.29
G63	CA	13C	46.371
G63	HN	1H	7.849
G63	N	15N	104.598
G63	QA	1H	3.948
R64	C	13C	45.889
R64	CA	13C	57.325
R64	CB	13C	31.97
R64	CD	13C	44.808
R64	CG	13C	28.763
R64	HA	1H	4.582
R64	HB2	1H	1.924
R64	HB3	1H	1.982
R64	HD2	1H	2.75
R64	HD3	1H	3.207
R64	HE	1H	7.438
R64	HG2	1H	1.724
R64	HG3	1H	1.807
R64	HN	1H	7.647
R64	N	15N	117.198
R64	NE	15N	85.099
R64	QB	1H	1.781
L65	C	13C	47.567
L65	CA	13C	55.299
L65	CB	13C	41.944
L65	CD1	13C	23.703
L65	CG	13C	28.194
L65	HA	1H	4.537
L65	HB2	1H	2.181

L65	HB3	1H	1.17
L65	HG	1H	0.84
L65	HN	1H	8.59
L65	N	15N	121.998
L65	QD1	1H	0.765
L65	QD2	1H	0.873
G66	C	13C	47.678
G66	CA	13C	47.885
G66	HA1	1H	4.378
G66	HA2	1H	4.106
G66	HN	1H	8.659
G66	N	15N	110.106
G66	QA	1H	4.039
T67	C	13C	45.878
T67	CA	13C	58.976
T67	CB	13C	71.213
T67	CG2	13C	22.615
T67	HA	1H	4.452
T67	HB	1H	4.374
T67	HN	1H	7.418
T67	N	15N	110.457
T67	QG2	1H	0.866
P68	CA	13C	67.303
P68	CB	13C	33.349
P68	CD	13C	52.491
P68	CG	13C	28.539
P68	HA	1H	4.016
P68	HD2	1H	2.907
P68	HD3	1H	3.775
P68	HG2	1H	2.039

P68	HG3	1H	1.292
P68	QB	1H	1.956
R69	C	13C	48.728
R69	CA	13C	61.322
R69	CB	13C	31.988
R69	CD	13C	44.108
R69	CG	13C	28.305
R69	HA	1H	3.621
R69	HB2	1H	1.514
R69	HB3	1H	1.785
R69	HD2	1H	3.003
R69	HD3	1H	3.426
R69	HE	1H	9.116
R69	HN	1H	9.003
R69	N	15N	116.629
R69	NE	15N	83.799
R69	QG	1H	1.56
E70	C	13C	49.567
E70	CA	13C	60.223
E70	CB	13C	31.162
E70	CG	13C	37.983
E70	HA	1H	4.116
E70	HG2	1H	2.408
E70	HG3	1H	2.469
E70	HN	1H	7.701
E70	N	15N	116.165
E70	QB	1H	2.198
L71	C	13C	51.315
L71	CA	13C	60.36
L71	CB	13C	43.29

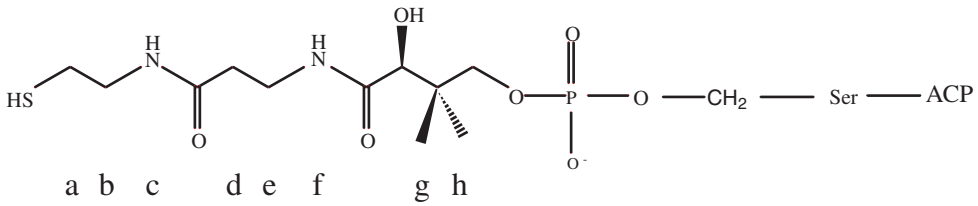
L71	CD1	13C	26.329
L71	CD2	13C	27.4
L71	CG	13C	29.219
L71	HA	1H	4.204
L71	HB2	1H	2.167
L71	HB3	1H	1.731
L71	HG	1H	1.573
L71	HN	1H	7.935
L71	N	15N	120.516
L71	QD1	1H	0.812
L71	QD2	1H	0.837
L72	C	13C	48.994
L72	CA	13C	59.641
L72	CB	13C	42.893
L72	CD1	13C	25.142
L72	CD2	13C	26.743
L72	CG	13C	28.142
L72	HA	1H	3.752
L72	HB2	1H	1.549
L72	HB3	1H	1.801
L72	HG	1H	1.635
L72	HN	1H	8.653
L72	N	15N	120.329
L72	QD1	1H	0.643
L72	QD2	1H	0.709
D73	C	13C	49.835
D73	CA	13C	58.398
D73	CB	13C	40.993
D73	HA	1H	4.394
D73	HB2	1H	2.625

D73	HB3	1H	2.718
D73	HN	1H	8.699
D73	N	15N	118.086
E74	C	13C	45.775
E74	CA	13C	60.182
E74	CB	13C	30.684
E74	CG	13C	36.073
E74	HA	1H	4.019
E74	HB2	1H	2.047
E74	HB3	1H	2.274
E74	HG2	1H	2.149
E74	HG3	1H	2.21
E74	HN	1H	7.897
E74	N	15N	120.769
V75	C	13C	50.716
V75	CA	13C	66.56
V75	CB	13C	32.878
V75	CG1	13C	23.463
V75	CG2	13C	23.782
V75	HA	1H	3.713
V75	HB	1H	2.108
V75	HN	1H	8.24
V75	N	15N	116.683
V75	QG1	1H	0.804
V75	QG2	1H	0.967
N76	C	13C	48.712
N76	CA	13C	55.305
N76	CB	13C	39.81
N76	HA	1H	4.918
N76	HB3	1H	2.767

N76	HD21	1H	7.601
N76	HD22	1H	7.705
N76	HN	1H	8.189
N76	N	15N	116.019
N76	ND2	15N	111.868
N76	QB	1H	2.957
T77	C	13C	47.578
T77	CA	13C	63.749
T77	CB	13C	70.965
T77	CG2	13C	22.498
T77	HA	1H	4.419
T77	HB	1H	4.348
T77	HN	1H	7.608
T77	N	15N	113.771
T77	QG2	1H	1.264
T78	C	13C	45.877
T78	CA	13C	61.72
T78	CB	13C	71.006
T78	CG2	13C	22.32
T78	HA	1H	4.636
T78	HB	1H	4.171
T78	HN	1H	8.063
T78	N	15N	121.845
T78	QG2	1H	1.303
P79	CA	13C	64.28
P79	CB	13C	33.507
P79	CD	13C	52.504
P79	CG	13C	28.716
P79	HA	1H	4.433
P79	HB2	1H	1.94

P79	HB3	1H	2.353
P79	HD2	1H	3.774
P79	HD3	1H	2.905
P79	HG2	1H	1.988
P79	HG3	1H	2.091
A80	C	13C	41.568
A80	CA	13C	53.795
A80	CB	13C	20.505
A80	HA	1H	4.411
A80	HB2	1H	1.322
A80	HB3	1H	1.471
A80	HN	1H	8.589
A80	N	15N	125.294
T81	C	13C	49.59
T81	CA	13C	62.957
T81	CB	13C	70.671
T81	CG2	13C	23.174
T81	HA	1H	4.33
T81	HB	1H	4.261
T81	HN	1H	8.346
T81	N	15N	114.394
T81	QG2	1H	1.248
A82	C	13C	45.002
A82	CA	13C	55.167
A82	CB	13C	21.371
A82	HA	1H	4.175
A82	HN	1H	8.062
A82	N	15N	132.439
A82	QB	1H	1.367

SI Figure 1. Structure of the 4′-phosphopantetheine prosthetic group labeled as assigned in SI Table 2.



SI Table 2. NMR resonance assignments of 4′-phosphopantetheine prosthetic group.

Position [a]	^{1}H (ppm)	^{13}C (ppm)	^{15}N (ppm)
a	2.65	27.3	
b	3.35	46.5	
c	8.27		124.7
d	2.55	39.4	
e	3.50	39.4	
f	8.10		120.1
g, h	0.76, 0.84	22.0, 24.7	

[a] As indicated in SI Figure 1.

SI Table 3. Heteronuclear ^{15}N backbone relaxation and order parameters.

Residue	T_1 (s)	StDev	T_2 (s)	StDev	NOE	StDev	S^2	StDev	Note
S1									a
A2	0.567	0.029	0.358	0.037			0.127	98.729	b
L3	0.547	0.008	0.158	0.003	0.565	0.057	0.692	0.004	
T4	0.499	0.012	0.127	0.001	0.731	0.073	0.848	0.002	
V5	0.487	0.007	0.136	0.004	0.705	0.071	0.802	0.005	
D6	0.486	0.007	0.135	0.003	0.671	0.067	0.804	0.004	
D7	0.475	0.014	0.126	0.003	0.744	0.074	0.858	0.006	
L8	0.470	0.014	0.121	0.003	0.741	0.074	0.890	0.006	
K9	0.478	0.007	0.126	0.001	0.734	0.073	0.855	0.001	
K10	0.469	0.020	0.126	0.002	0.729	0.073	0.858	0.004	
L11	0.486	0.010	0.125	0.001	0.726	0.073	0.866	0.001	
L12	0.470	0.002	0.120	0.003	0.737	0.074	0.879	0.003	
A13	0.486	0.007	0.125	0.002	0.742	0.074	0.864	0.003	
E14	0.507	0.013	0.125	0.002	0.701	0.070	0.863	0.003	
T15	0.474	0.011	0.134	0.003	0.640	0.064	0.811	0.005	
A16	0.508	0.006	0.142	0.003	0.641	0.064	0.768	0.004	
G17	0.545	0.006	0.175	0.002	0.545	0.054			c
E18	0.558	0.009	0.182	0.003	0.519	0.052	0.530	0.019	
D19	0.554	0.010	0.196	0.003	0.445	0.044	0.463	0.017	
D20	0.560	0.020	0.193	0.004	0.441	0.044	0.480	0.030	
S21	0.530	0.006	0.186	0.002	0.503	0.050	0.465	0.016	
V22	0.508	0.010	0.190	0.002	0.498	0.050	0.427	0.023	
D23	0.524	0.014	0.166	0.003	0.494	0.049	0.589	0.027	
L24	0.504	0.012	0.150	0.001	0.641	0.064			c
A25	0.508	0.009	0.104	0.003	0.648	0.065	1.000	0.005	
G26	0.488	0.017	0.127	0.003	0.700	0.070	0.850	0.005	
E27									a
L28	0.474	0.012	0.106	0.004	0.710	0.071	0.862	0.022	
D29	0.493	0.008	0.098	0.001	0.725	0.073	0.828	0.013	

T30	0.464	0.009	0.108	0.004	0.779	0.078	0.881	0.018	
P31									a
F32	0.505	0.011	0.108	0.003	0.751	0.075	0.809	0.017	
V33	0.487	0.004	0.088	0.003	0.784	0.078	0.839	0.007	
D34	0.507	0.008	0.119	0.001	0.794	0.079	0.805	0.013	
L35	0.515	0.023	0.112	0.004	0.736	0.074	0.793	0.035	
G36	0.475	0.014	0.121	0.002	0.712	0.071	0.894	0.004	
Y37	0.489	0.015	0.138	0.005	0.715	0.072	0.788	0.008	
D38	0.528	0.012	0.182	0.002	0.666	0.067			c
S39	0.514	0.008	0.096	0.001	0.712	0.071	0.795	0.012	
L40	0.482	0.017	0.126	0.001	0.671	0.067	0.854	0.003	
A41	0.503	0.008	0.129	0.002	0.711	0.071	0.832	0.003	
L42	0.495	0.005	0.117	0.003	0.693	0.069	0.893	0.004	
L43	0.530	0.009	0.186	0.005					b
E44	0.494	0.014	0.119	0.003	0.707	0.071	0.898	0.006	
T45	0.488	0.010	0.117	0.001	0.738	0.074	0.836	0.017	
A46	0.496	0.015	0.118	0.004	0.727	0.073	0.824	0.025	
A47	0.472	0.022	0.117	0.000	0.716	0.072	0.921	0.001	
V48	0.486	0.012	0.125	0.002	0.742	0.074	0.865	0.003	
L49	0.492	0.004	0.120	0.001	0.777	0.078	0.830	0.007	
Q50	0.506	0.005	0.141	0.005	0.827	0.083			c
Q51	0.497	0.004	0.122	0.002	0.718	0.072	0.822	0.007	
R52	0.493	0.004	0.108	0.002	0.722	0.072	0.829	0.008	
Y53	0.512	0.018	0.111	0.003	0.716	0.072	0.798	0.029	
G54	0.476	0.017	0.128	0.002	0.698	0.070	0.842	0.004	
I55	0.528	0.032	0.101	0.004	0.702	0.070	0.774	0.047	
A56	0.543	0.014	0.109	0.002	0.640	0.064	0.984	0.003	
L57	0.588	0.010	0.161	0.008	0.562	0.056	0.677	0.007	
T58	0.526	0.017	0.127	0.003	0.718	0.072	0.848	0.005	
D59	0.492	0.004	0.128	0.001	0.648	0.065	0.843	0.003	
E60	0.484	0.005	0.114	0.002	0.687	0.069	0.845	0.009	
T61	0.473	0.008	0.086	0.003	0.714	0.071	0.863	0.014	

V62	0.494	0.009	0.119	0.006			0.875	0.009	b
G63	0.490	0.022	0.251	0.005	0.728	0.073			c
R64	0.488	0.026	0.103	0.003	0.731	0.073	0.837	0.044	
L65	0.554	0.012	0.196	0.002					b
G66	0.529	0.016	0.131	0.005	0.629	0.063	0.815	0.008	
T67	0.493	0.028	0.103	0.002	0.727	0.073	0.829	0.048	
P68									a
R69	0.470	0.005	0.106	0.003	0.774	0.077	0.869	0.008	
E70	0.481	0.018	0.103	0.001	0.781	0.078	0.849	0.031	
L71	0.486	0.004	0.125	0.001	0.797	0.080	0.865	0.001	
L72	0.484	0.007	0.115	0.002	0.764	0.076	0.843	0.012	
D73	0.493	0.012	0.119	0.003	0.741	0.074	0.897	0.006	
E74									a
V75	0.504	0.008	0.104	0.002	0.774	0.077	0.810	0.013	
N76	0.508	0.009	0.109	0.002	0.714	0.071	0.803	0.014	
T77	0.484	0.019	0.142	0.003	0.640	0.064	0.761	0.004	
T78	0.530	0.009	0.186	0.003					b
P79									a
A80	0.612	0.008	0.287	0.014	-0.051	0.005	0.247	0.014	
T81	0.695	0.012	0.343	0.008	-0.442	0.044	0.200	0.010	
A82	0.956	0.020	0.734	0.021	-1.254	0.125	0.033	0.007	

[a] No relaxation data.

[b] Partial relaxation data.

[c] No appropriate model for order parameter determination.