Insight into the role of dynamics in the conformational switch of the small GTP-binding protein Arf1

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Supplementary material

Figure S1. (A) HSQC ^{1}H-^{15}N spectra of Δ17Arf1-GTP (after 2 hours), T=298K. Peaks corresponding to Δ17Arf1-GDP are indicating by arrows. (B) HSQC ^{1}H-^{15}N spectra of Δ17Arf1-GTPγS (blue), T=298K. G24, T48, I49 and a side chain of tryptophan of the GTP form which have CSV> 0.2 are indicated by crosses.

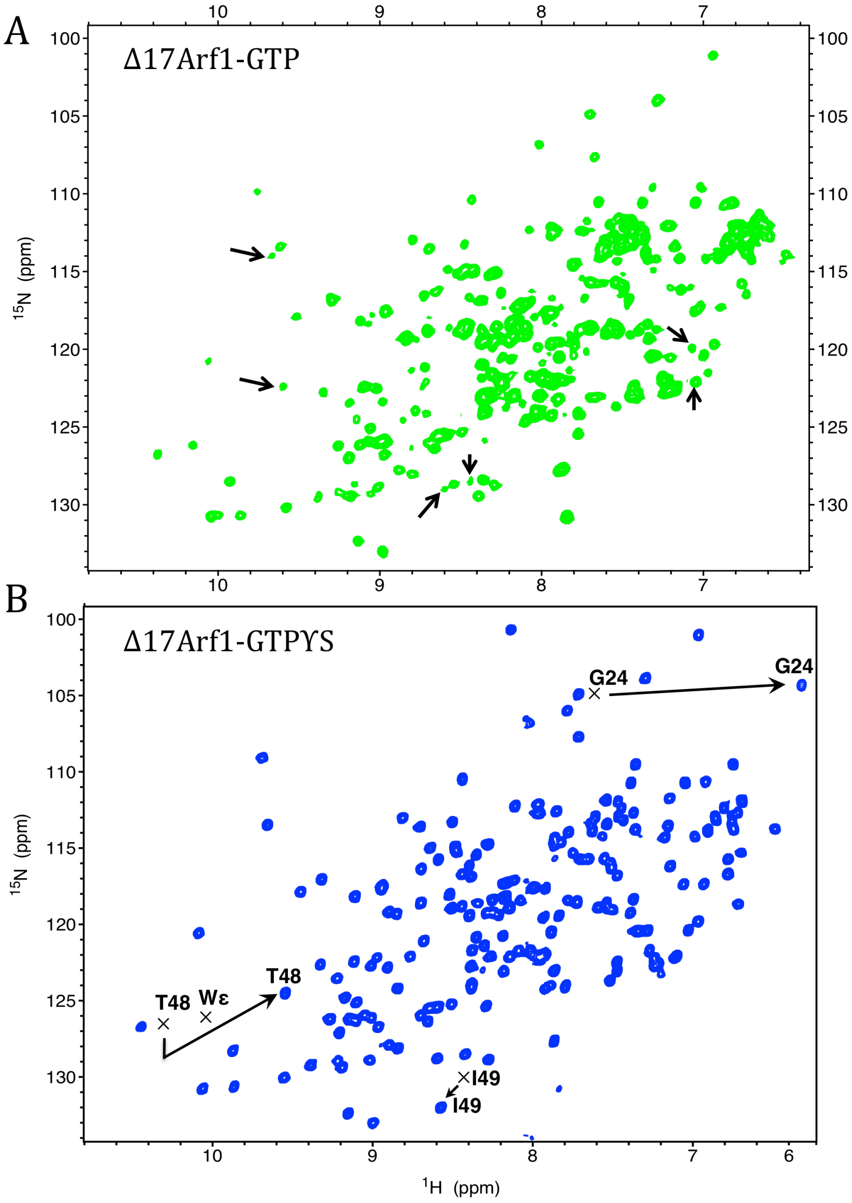

Figure S2. Normalized $^{1}H^{N}$ and ^{15}N Chemical Shifts Variation between (A) Arf1-GDP and Δ17Arf1-GDP and between (B) Δ17Arf1-GDP and Δ17Arf1-GTP. The secondary structures are represented as black and grey bars for strands and helices, respectively. Switch regions are indicated too.

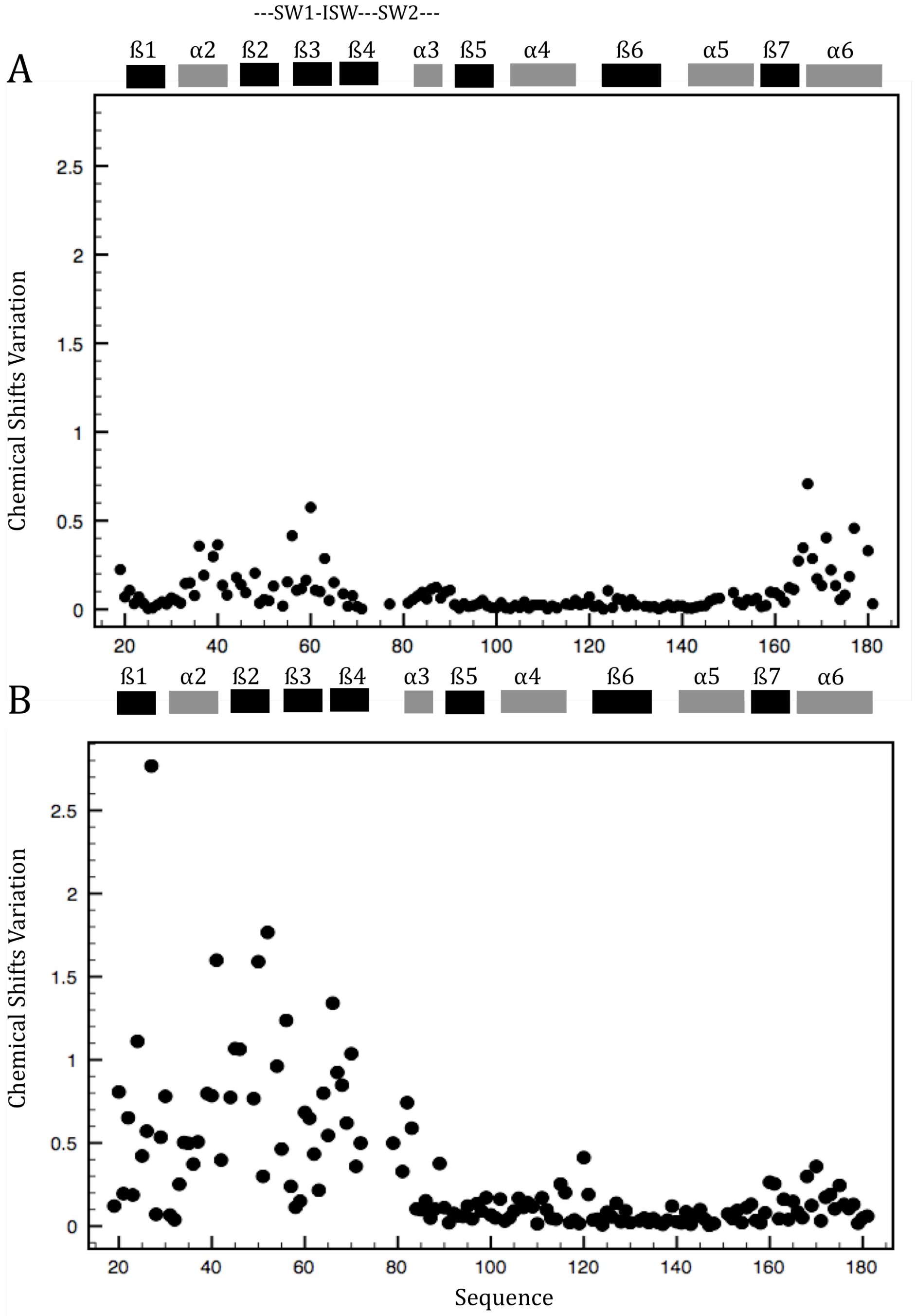

Figure S3. Back calculation of H^N in Δ17Arf1-GDP. ^{H}N Chemical Shift Variation calculated from experimental data (in blue) or predicted by SPARTA (x10, in red) between Arf1-GDP and Δ17Arf1-GDP.

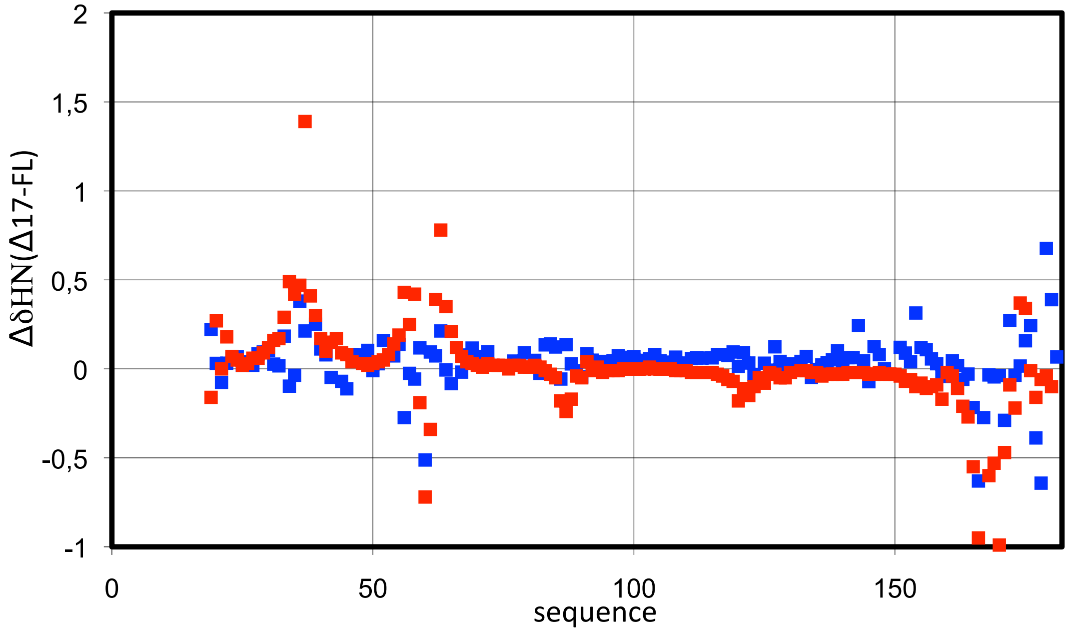

Figure S4. Half time conversion. The conformational exchange rates of GDP forms were obtained from the fit of the decreasing intensities of 29 peaks of GDP form.

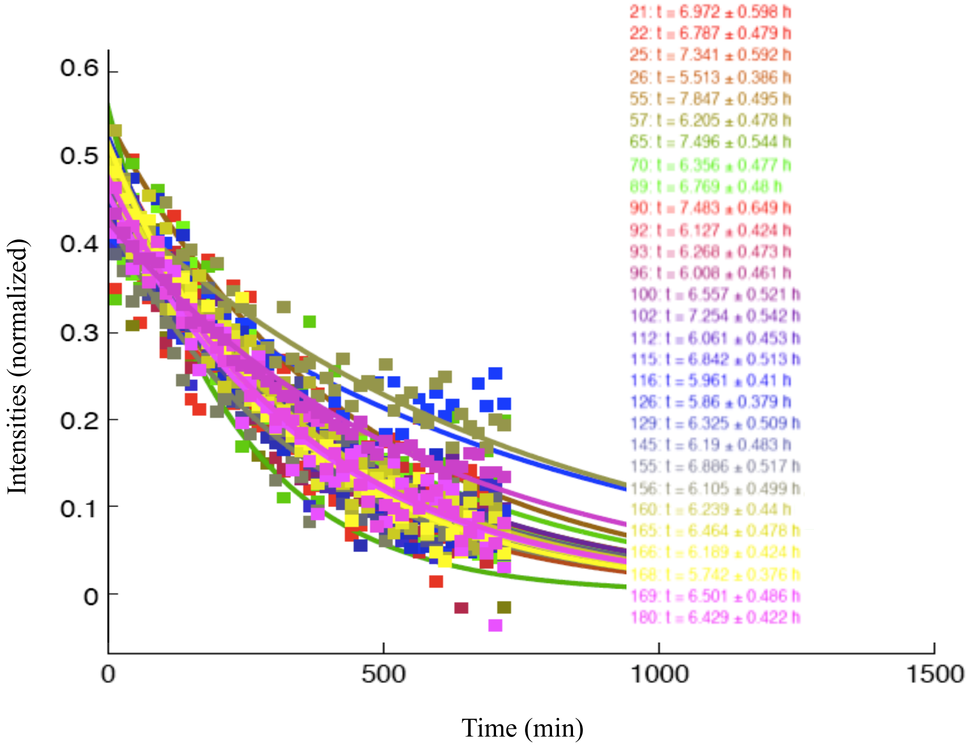

Figure S5. ^{15}N relaxation parameters (R1, R2 and nOe ^{1}H-^{15}N) measured on Arf1-GDP (black), Δ17Arf1-GDP (red) and Δ17Arf1-GTP (green) at 298K. The secondary structures are represented as black and grey bars for strands and helices, respectively. Switch regions are indicated too.

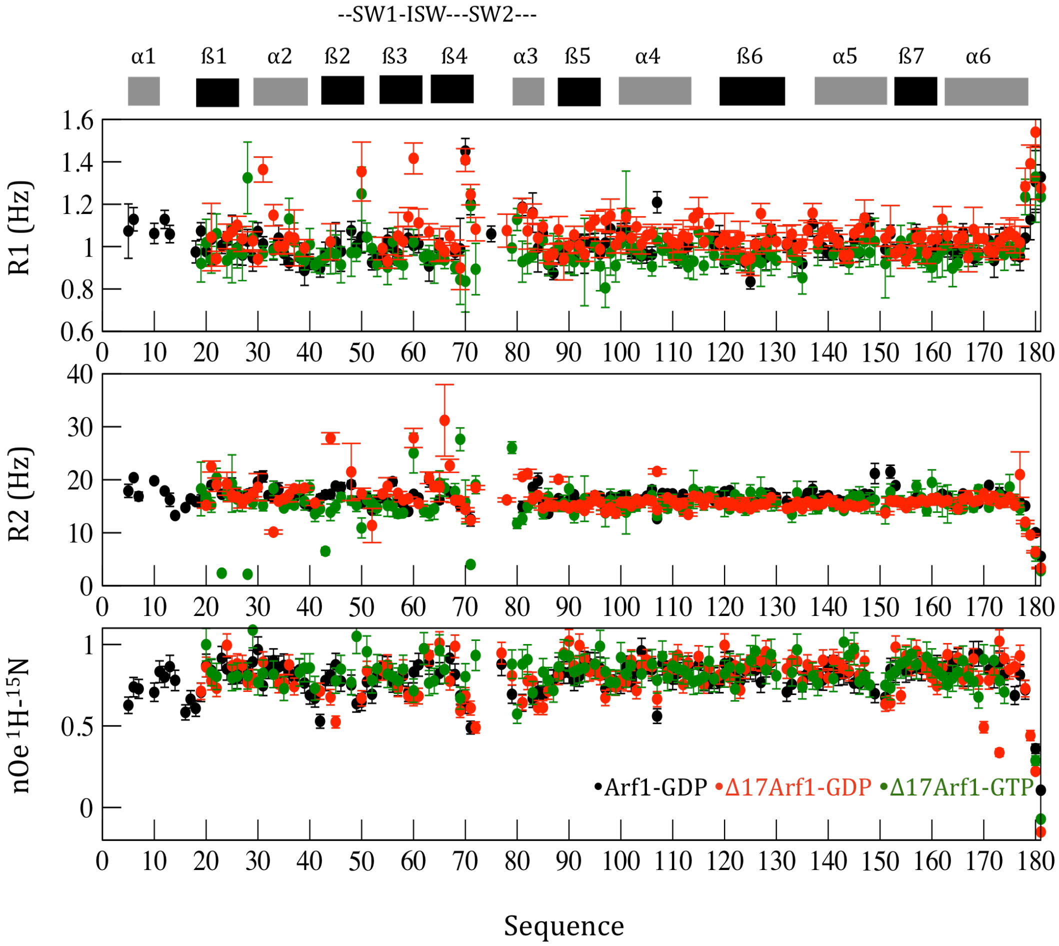

Figure S6. ^{31}P 1D spectra of 10mM GTPγS (500MHz, T=298K) used for the nucleotide exchange experiment. ^{31}P chemical shifts are referenced with respect to phosphoric acid 50%.

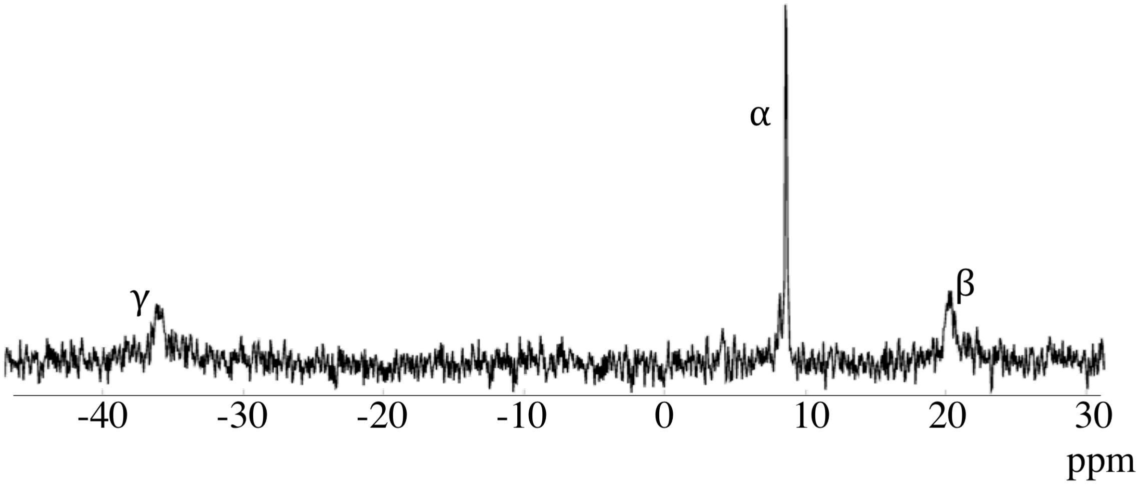

Table S1: ^{1}HN, ^{15}N, CA, CB, C chemicals shifts of Δ17Arf1-GDP (pH=7.3, T=298K).

	Δ17Arf1-GDP				
	C	CA	CB	HN	N
R19	174.8	56.41	31.02	8.949	125.2
I20	174.8	58.40	39.05	8.650	125.6
L21	174.7	-	52.32	8.103	128.3
M22	172.8	53.96	-	9.065	126.3
V23	174.2	57.56	36.59	8.450	115.1
G24	173.1	43.50	-	6.461	102.6
L25	178.3	55.74	40.81	10.14	124.8
D26	175.3	55.80	40.32	8.727	119.7
A27	175.5	53.38	16.56	10.69	122.8
A28	176.2	55.55	19.62	7.454	123.2
G29	174.0	45.66	-	8.588	102.8
K30	177.3	59.84	31.59	9.669	122.7
T31	175.8	-	-	9.070	121.8
T32	176.7	67.13	71.99	8.824	119.4
I33	176.3	-	36.74	7.922	122.2
L34	179.6	58.12	41.50	7.829	117.8
Y35	179.3	61.57	38.03	8.097	116.3
K36	178.2	56.41	31.10	8.227	121.7
L37	-	56.23	41.42	7.626	116.5
K38	175.9	56.92	29.87	7.416	114.3
L39	-	55.17	41.72	8.132	119.1
G40	172.6	44.45	-	7.061	103.2
E41	-	56.33	-	8.291	120.7
I42	-	-	-	8.227	124.5
V43	176.0	62.10	32.78	-	-
T44	-	61.84	69.67	8.716	124.6
T45	172.4	60.77	71.13	9.169	121.7
I46	-	58.07	38.03	8.382	123.2
P47	-	-	-	-	-
T48	171.8	60.42	69.78	7.339	109.8
I49	177.0	63.38	36.86	7.840	124.0
G50	173.4	44.87	-	8.732	114.2
F51	171.0	54.77	39.84	8.234	123.2
N52	-	52.55	39.98	7.778	121.9
V53	175.7	61.43	33.75	-	-
E54	175.7	54.48	32.36	8.763	126.4
T55	173.5	59.66	72.20	8.910	113.9
V56	172.8	61.21	35.02	8.214	119.3
E57	174.8	55.09	31.32	8.390	125.9
Y58	173.3	56.72	41.06	9.005	125.6
K59	175.8	58.18	29.33	8.729	124.1
N60	173.7	53.85	37.62	8.351	117.1
I61	174.5	61.13	39.27	8.631	122.4
S62	173.6	56.90	64.47	8.318	121.0
F63	176.1	57.45	42.07	9.279	125.8
T64	173.2	63.46	70.38	8.255	119.8
V65	176.1	60.44	34.63	9.360	127.0
W66	172.6	57.48	30.72	7.629	122.8
D67	176.7	53.37	41.41	8.769	117.0
V68	175.3	59.52	31.78	7.805	114.2
G69	174.4	45.13	-	8.213	107.4
G70	174.8	45.70	-	8.706	110.3
Q71	176.7	56.20	28.98	8.496	119.4
D72	-	56.22	40.56	8.480	121.0
K73	-	-	-	-	-
I74	-	-	-	-	-
R75	-	-	-	-	-
P76	-	-	-	-	-
L77	178.1	56.67	41.10	7.529	116.2
W78	-	55.34	35.77	7.352	117.1
R79	-	-	-	7.014	115.7
H80	176.5	58.28	29.20	-	-
Y81	176.8	59.18	38.41	7.379	115.9
F82	177.4	56.25	38.13	7.652	115.8
Q83	176.0	57.59	28.32	7.554	118.3
N84	174.6	54.09	37.47	8.862	118.1
T85	174.7	64.92	69.26	7.978	116.7
Q86	175.7	57.33	31.09	8.473	124.1
G87	168.4	44.63	-	7.635	104.7
L88	173.4	53.16	45.86	9.224	126.1
I89	174.3	58.91	-	9.536	125.1
F90	174.4	55.91	43.52	9.120	129.3
V91	173.6	61.60	-	8.369	128.5
V92	173.5	59.33	35.70	8.748	123.2
D93	177.5	53.42	40.65	9.092	124.0
S94	172.8	61.25	63.43	8.420	123.6
N95	174.0	53.07	41.86	9.090	117.8
D96	176.6	51.73	39.15	6.901	119.4
R97	178.5	58.95	29.28	8.056	124.2
E98	178.6	58.87	29.47	8.398	118.6
R99	177.1	56.44	30.75	7.334	114.3
V100	175.7	65.67	31.02	7.008	121.5
N101	177.3	56.45	37.55	8.305	119.6
E102	178.5	59.21	28.84	7.676	123.0
A103	178.3	55.87	17.38	8.024	121.9
R104	177.5	60.17	28.97	8.099	116.9
E105	180.1	59.55	28.82	8.048	117.8
E106	177.4	58.51	24.75	8.262	117.3
L107	178.2	58.59	39.49	8.360	123.0
M108	179.8	57.32	30.44	8.452	115.3
R109	179.8	59.63	30.13	7.929	119.4
M110	177.7	58.62	31.70	7.630	118.7
L111	177.0	55.93	40.12	7.975	114.1
A112	178.3	52.18	18.74	7.102	119.9
E113	178.8	56.26	28.03	7.326	118.7
D114	179.2	58.20	40.94	9.214	129.3
E115	177.2	58.84	29.76	9.564	116.5
L116	178.1	53.35	41.14	7.346	114.9
R117	175.9	59.99	29.86	7.441	123.0
D118	176.2	53.99	41.51	8.437	115.1
A119	178.1	52.77	17.60	7.195	122.4
V120	173.5	62.72	32.09	7.501	122.8
L121	172.7	53.60	45.84	8.505	127.0
L122	174.1	55.34	34.06	9.200	128.9
V123	175.9	56.36	31.65	8.992	125.7
F124	174.5	52.77	39.36	8.654	125.5
A125	174.6	50.09	16.55	8.641	129.1
N126	176.7	52.83	41.11	8.674	121.7
K127	176.3	57.07	-	7.602	116.9
Q128	174.8	56.96	28.47	7.973	112.8
D129	174.6	54.33	40.54	9.713	114.0
L130	-	54.84	38.98	7.222	122.5
P131	177.5	64.61	31.57	-	-
N132	175.2	52.30	38.41	8.522	115.1
A133	178.5	53.36	18.22	7.293	121.9
M134	175.1	56.47	35.43	8.191	122.7
N135	175.3	51.41	38.65	8.700	118.9
A136	180.0	55.84	17.69	8.844	119.3

A137	180.2	55.74	17.58	8.356	123.9
E138	179.3	59.23	29.29	8.302	121.7
I139	177.1	63.62	35.69	8.410	119.3
T140	176.2	67.94	-	8.158	117.1
D141	179.1	57.53	41.49	7.333	120.4
K142	178.7	58.70	32.77	8.538	118.9
L143	175.4	54.93	41.41	8.316	115.0
G144	177.3	46.35	-	7.316	104.1
L145	-	56.80	37.42	7.229	116.1
H146	176.6	58.81	29.42	7.963	112.3
S147	176.7	59.18	63.84	7.533	113.3
L148	174.4	54.82	40.14	7.215	122.5
R149	176.7	58.6	-	8.34	123.01
H150	176.9	56.11	28.26	122.2	7.94
R151	174.0	53.46	31.66	7.769	118.7
N152	173.6	52.75	38.23	9.225	127.3
W153	173.9	53.98	34.64	7.862	121.4
Y154	172.7	56.99	39.90	8.096	121.7
I155	170.4	57.76	40.67	7.078	123.3
Q156	174.8	52.33	32.50	8.841	126.4
A157	178.0	52.31	18.75	8.987	133.2
T158	173.8	60.85	72.96	8.662	116.1
C159	174.6	57.85	28.75	8.270	120.5
A160	177.0	55.28	19.92	9.404	132.5
T161	176.7	63.61	66.97	7.055	103.3
S162	176.1	58.17	64.55	7.522	115.2
G163	173.4	45.10	-	8.246	112.5
D164	176.7	56.33	41.12	7.825	124.0
G165	174.5	47.03	-	8.603	113.4
L166	178.7	57.92	41.37	7.098	117.7
Y167	178.4	61.84	36.39	8.430	117.1
E168	180.7	61.03	27.93	9.595	122.3
G169	174.5	47.72	-	8.139	106.8
L170	179.2	58.07	40.66	8.268	121.9
D171	178.4	57.57	40.96	8.839	121.6
W172	178.8	62.94	27.46	7.511	120.8
L173	178.0	58.27	42.39	8.035	119.9
S174	173.8	61.75	62.81	8.729	113.6
N175	177.5	56.11	38.06	7.765	118.6
Q176	178.1	56.71	27.85	7.501	117.3
L177	177.8	55.30	41.12	7.374	117.1
R178	176.4	57.53	29.82	7.395	118.8
N179	174.8	53.42	38.71	7.928	117.3
Q180	174.9	55.83	29.09	7.815	120.4
K181	-	57.73	32.86	7.913	127.8

Table S2: ^{1}HN, ^{15}N, CA, CB, C chemicals shifts of Δ17Arf1-GTPγS and ^{1}HN, ^{15}N chemicals shifts of Δ17Arf1-GTP (pH=7.3, T=298K).

	GTPγS					GTP	
	C	CA	CB	HN	N	HN	N
M18	174.5	55.40	33.80	-	-	-	-
R19	174.8	57.22	30.46	9.137	126.4	-	-
I20	173.8	56.61	38.52	9.415	129.3	129.488	9.398
L21	172.9	53.49	45.35	8.302	128.9	128.849	8.308
M22	172.6	54.58	35.84	9.573	130.0	130.195	9.605
V23	173.8	57.28	34.91	8.304	114.7	115.064	8.315
G24	173.2	43.51	-	5.990	105.7	104.712	7.586
L25	175.9	55.73	39.99	10.10	120.7	120.793	10.08
D26	176.2	54.02	40.92	8.397	116.2	116.345	8.314
A27	175.5	53.71	16.90	8.001	117.6	117.770	8.005
A28	176.0	56.17	19.70	7.495	122.6	122.547	7.493
G29	173.0	45.45	-	8.153	100.7	100.597	8.139
K30	179.6	58.52	38.39	8.990	122.3	122.179	9.105
T31	176.7	59.87	63.38	9.130	122.4	122.486	9.124
T32	176.9	65.61	67.97	8.916	119.2	119.373	8.877
I33	176.7	66.61	37.33	8.159	122.2	121.640	8.201
L34	178.1	58.24	41.42	8.310	119.3	119.484	8.315
Y35	177.9	63.30	37.93	7.872	112.6	112.518	7.816
K36	180.4	58.12	30.88	8.308	125.4	125.540	8.306
L37	178.6	57.16	41.92	8.085	118.4	118.517	8.133
K38	176.9	58.16	33.57	8.404	116.9	116.862	8.398
L39	178.6	54.60	43.66	8.721	113.6	113.515	8.726
G40	173.8	46.05	-	7.728	107.8	107.694	7.720
E41	174.3	53.98	33.68	6.805	116.7	116.616	6.781
I42	176.2	59.40	36.48	8.370	120.9	120.932	8.384
V43	175.4	59.47	33.17	7.883	123.1	123.158	7.917
T44	174.7	62.68	68.63	8.269	118.4	118.490	8.286
T45	173.9	59.72	70.87	8.200	118.3	118.205	8.201
I46	-	58.71	38.50	7.884	114.5	114.432	7.830
P47	177.6	64.61	31.76	-	-	-	-
T48	173.9	63.02	69.03	9.561	124.5	126.630	10.38
I49	175.5	59.39	34.61	8.584	131.9	129.592	8.410
G50	174.6	45.21	-	7.165	111.7	111.892	7.212
F51	173.5	55.49	42.08	7.958	122.0	121.966	7.952
N52	173.2	52.17	42.28	9.470	117.9	117.905	9.541
V53	171.3	59.53	33.35	8.704	121.2	121.135	8.715
E54	174.8	53.38	33.30	7.977	122.1	122.717	7.987
T55	174.1	61.72	69.64	9.131	118.2	118.205	9.133
V56	173.9	60.36	34.65	9.281	126.2	126.202	9.286
E57	176.0	55.04	30.47	8.677	126.3	126.311	8.669
Y58	173.6	57.98	40.96	8.998	126.7	126.747	8.985
K59	175.5	57.78	29.59	8.672	125.6	125.566	8.676
N60	173.9	54.60	37.56	8.460	110.5	110.539	8.453
I61	174.0	59.87	39.26	8.031	121.8	121.876	8.030
S62	173.3	56.95	63.33	7.951	119.5	119.534	7.946
F63	175.2	56.43	40.19	9.130	125.1	125.114	9.101
T64	172.5	63.27	68.97	9.030	122.6	122.701	9.044
V65	173.7	61.23	32.09	8.868	128.1	128.224	8.854
W66	173.4	57.29	29.28	8.934	127.9	127.875	8.912
D67	175.3	52.57	44.19	9.087	125.9	126.125	9.080
V68	175.5	59.87	32.84	7.302	120.5	120.710	7.262
G69	174.5	47.23	-	7.795	106.0	105.808	7.674
G70	176.0	45.11	-	9.727	109.2	109.056	9.714
Q71	177.0	57.98	28.92	8.393	122.8	122.903	8.386
D72	178.5	58.75	40.17	8.941	122.9	123.149	8.961
K73	176.8	58.10	31.93	8.612	115.9	116.201	8.677
I74	176.5	59.89	36.79	7.883	114.7	114.737	7.833
R75	-	-	27.04	7.141	122.3	122.296	7.115
P76	177.6	65.62	30.92	-	-	-	-
L77	177.3	55.30	40.32	7.791	114.0	114.563	7.827
W78	176.9	59.18	29.55	8.293	122.1	122.344	8.282
R79	177.7	56.26	28.88	6.943	110.7	110.866	6.932
H80	175.6	56.90	29.01	7.514	119.1	118.985	7.499
Y81	175.7	57.21	39.17	7.685	115.8	115.652	7.655
F82	177.3	56.44	37.47	6.953	117.5	117.295	6.938
Q83	176.1	57.92	28.01	8.173	118.9	119.131	8.183

N84	174.7	54.60	37.17	8.958	117.4	117.481	8.966
T85	174.6	65.37	68.58	7.945	117.7	117.610	7.955
Q86	176.1	57.45	30.98	8.609	125.5	125.472	8.624
G87	168.5	44.57	-	7.749	105.0	104.856	7.716
L88	174.6	52.81	46.41	9.164	126.2	126.146	9.149
I89	174.1	59.82	-	9.233	123.5	123.474	9.225
F90	174.5	55.83	42.38	9.034	128.9	128.906	9.051
V91	173.8	61.62	32.39	8.445	128.5	128.434	8.398
V92	174.0	59.40	35.53	8.863	124.1	123.981	8.825
D93	180.0	53.30	40.69	9.190	124.7	124.615	9.164
S94	172.9	61.15	63.10	8.405	124.1	124.033	8.394
N95	174.1	53.05	41.86	8.971	117.7	117.752	9.003
D96	176.8	51.43	38.75	6.986	119.9	119.787	6.975
R97	178.8	59.23	29.64	7.944	124.1	124.241	7.956
E98	178.5	58.74	29.32	8.532	118.1	118.368	8.505
R99	177.0	56.27	30.74	7.182	113.6	113.482	7.221
V100	176.0	65.72	31.06	7.113	122.1	122.088	7.098
N101	177.1	56.34	37.49	8.403	119.4	119.486	8.386
E102	178.4	59.11	28.88	7.539	123.7	123.725	7.560
A103	178.4	55.87	17.45	8.017	121.9	121.847	8.035
R104	177.5	60.38	29.53	8.181	117.3	117.240	8.167
E105	180.1	59.79	29.18	8.188	118.1	118.031	8.184
E106	179.9	58.08	28.75	8.130	117.2	117.073	8.132
L107	178.1	58.41	40.54	8.398	121.8	121.833	8.404
M108	179.8	57.05	30.54	8.655	115.0	114.945	8.614
R109	179.7	59.57	30.12	7.851	119.4	119.425	7.842
M110	177.3	59.19	32.80	7.615	118.9	118.932	7.644
L111	177.1	55.76	39.59	7.843	114.6	114.608	7.845
A112	178.4	52.18	18.75	7.049	120.4	120.377	7.039
E113	178.7	56.36	28.00	7.391	118.4	118.415	7.387
D114	179.1	57.95	40.75	9.253	128.9	128.922	9.194
E115	177.2	58.85	30.46	9.326	117.0	117.166	9.354
L116	178.2	53.02	41.85	7.196	114.3	114.284	7.191
R117	176.0	60.19	29.96	7.492	123.1	123.079	7.483
D118	176.3	54.17	41.59	8.505	114.9	114.913	8.476
A119	178.4	52.81	17.88	7.239	122.6	122.577	7.226
V120	173.6	61.63	32.07	7.415	119.3	119.332	7.373
L121	172.0	54.02	45.88	8.514	125.3	125.308	8.515
L122	173.9	52.24	45.25	9.212	129.4	129.431	9.213
V123	175.9	57.92	41.16	9.031	126.2	126.149	9.031
F124	174.7	52.28	39.36	8.645	125.5	125.517	8.639
A125	174.9	49.91	17.05	8.615	128.8	128.798	8.614
N126	-	52.86	41.71	8.784	122.1	122.087	8.785
K127	176.3	57.02	28.77	7.537	116.0	116.000	7.545
Q128	174.8	56.95	28.75	7.981	112.7	112.696	7.980
D129	176.7	54.34	40.44	9.669	113.5	113.419	9.674
L130	-	54.83	40.53	7.260	122.5	122.125	7.265
P131	177.5	64.58	31.73	-	-	-	-
N132	175.3	52.32	38.41	8.487	115.3	115.318	8.526
A133	178.6	53.25	18.14	7.296	121.8	121.750	7.301
M134	175.1	56.32	35.42	8.196	123.0	122.967	8.208
N135	175.4	51.36	38.69	8.717	118.6	118.659	8.719
A136	177.5	55.71	17.89	8.870	119.3	119.334	8.841
A137	180.2	55.74	17.51	8.403	124.1	123.902	8.398
E138	179.3	59.21	29.36	8.323	121.5	121.474	8.332
I139	177.0	64.11	35.93	8.284	119.2	119.183	8.283
T140	176.3	67.91	-	8.191	117.4	117.362	8.203
D141	179.1	57.48	41.38	7.353	120.5	120.491	7.351
K142	178.8	58.69	32.87	8.468	118.8	118.782	8.467
L143	175.5	55.05	41.80	8.366	115.4	115.393	8.374
G144	177.3	46.30	-	7.314	103.9	103.908	7.321
L145	177.3	56.86	37.66	7.166	116.3	116.202	7.170
H146	176.9	58.71	29.76	7.976	112.2	112.174	7.946
S147	174.7	59.18	63.85	7.554	113.5	113.411	7.552
L148	177.4	54.74	41.21	7.267	122.7	122.803	7.271
R149	176.0	58.67	28.54	8.335	123.0	123.034	8.339
H150	174.1	56.25	28.45	8.536	119.0	118.994	8.536
R151	174.1	53.35	31.98	7.737	118.6	118.653	7.730
N152	173.7	52.93	38.08	9.229	127.0	127.000	9.206
W153	173.7	55.17	34.59	7.983	122.1	121.936	7.993
Y154	172.6	56.87	39.97	8.108	121.7	121.770	8.102
I155	170.3	57.50	41.36	6.983	123.2	123.197	6.996
Q156	174.9	52.29	32.00	8.708	126.0	126.096	8.735
A157	177.8	52.20	18.60	9.010	132.9	133.034	9.001
T158	173.7	60.56	72.77	8.714	116.3	116.313	8.708
C159	174.5	58.12	28.73	8.212	120.8	120.730	8.224
A160	176.8	55.62	20.82	9.171	132.4	132.373	9.177
T161	176.4	63.36	66.79	6.981	101.1	101.184	6.986
S162	176.2	58.15	64.50	7.571	115.7	115.704	7.577
G163	173.5	45.05	-	8.131	112.3	112.334	8.118
D164	176.7	56.22	40.98	7.820	124.1	124.062	7.823
G165	174.5	47.02	-	8.520	113.3	113.332	8.492
L166	179.2	57.84	41.24	7.079	117.4	117.393	7.066
Y167	177.8	61.77	35.79	8.466	116.7	116.698	8.458
E168	181.1	61.10	27.76	9.346	122.6	122.716	9.337
G169	176.9	47.57	-	8.035	106.7	106.786	8.049
L170	-	55.72	39.44	7.942	122.0	121.934	7.942
D171	178.5	58.04	40.92	7.948	122.0	122.007	7.956
W172	178.9	62.87	27.59	7.379	120.5	120.413	7.387
L173	178.5	58.17	42.63	8.232	119.4	119.383	8.243
S174	175.7	61.91	62.90	8.827	113.0	113.040	8.835
N175	177.3	55.76	38.08	7.555	118.9	118.947	7.565
Q176	178.0	56.26	27.85	7.525	116.4	116.210	7.528
L177	177.6	55.54	41.58	7.493	116.9	116.840	7.500
R178	-	57.45	29.98	7.565	118.6	118.532	7.563
N179	174.9	53.40	38.64	7.997	117.6	117.689	7.978
Q180	174.9	55.83	29.21	7.909	120.6	120.499	7.898
K181	-	57.65	33.20	7.889	127.7	127.682	7.888

Table S3. Results of the fits of the ^{15}N CPMG relaxation dispersion curves of Δ17Arf1-GDP at two magnetic fields (700MHz and 950MHz) at 298K to a global two state fast exchange. The optimized value of the global τ_{ex} was found equal to 0.65±0.05 ms. Since the exchange regime is fast, it is not possible to extract both population and chemical shift differences. The fitted parameter is then $p_B(1-p_B)(\Delta\delta)^2$ for each residue. The values of Δδ given in the table correspond to the minimal differences of chemical shifts between the two states in exchange, i.e. with p_B=0.5.

#res	Δδ(ppm)	R$_2$_1(s^{-1}) (a)	R$_{ex}$_1(s^{-1})	R$_2$_2(s^{-1})	R$_{ex}$_2(s^{-1})	R$_{ex}$_1/R$_{ex}$_2
21	0.505 (0.269)	30.75 (1.81) (b)	14.73 (4.06)	17.79 (1.22)	8.00 (2.20)	1,84
22	0.349 (0.194)	26.71 (1.10)	7.01 (2.10)	20.12 (0.70)	3.81 (1.14)	1,84
26	0.419 (0.171)	22.44 (0.74)	10.13 (1.54)	17.41 (0.55)	5.50 (0.84)	1,84
37	0.501 (0.232)	29.34 (1.49)	14.49 (2.99)	18.88 (0.85)	7.87 (1.62)	1,84
41	0.347 (0.140)	20.32 (0.46)	6.97 (1.03)	8.74 (1.23)	3.79 (0.56)	1,84
54	0.523 (0.224)	26.20 (1.45)	15.80 (2.69)	17.21 (0.74)	8.58 (1.46)	1,84
58	0.429 (0.162)	24.50 (0.70)	10.65 (1.30)	16.41 (0.39)	5.78 (0.71)	1,84
59	0.408 (0.160)	23.19 (0.67)	9.61 (1.36)	17.70 (0.43)	5.22 (0.74)	1,84
61	0.379 (0.165)	22.24 (0.73)	8.31 (1.47)	16.18 (0.54)	4.51 (0.80)	1,84
63	0.681 (0.248)	26.33 (1.28)	26.81 (3.08)	20.74 (0.90)	14.56 (1.67)	1,84
64	0.317 (0.150)	26.01 (0.67)	5.79 (1.22)	13.57 (0.39)	3.15 (0.66)	1,84
70	0.509 (0.154)	17.28 (0.49)	14.95 (0.90)	14.20 (0.32)	8.12 (0.49)	1,84
71	0.222 (0.112)	14.37 (0.33)	2.85 (0.69)	11.80 (0.28)	1.55 (0.38)	1,84
81	0.226 (0.145)	30.49 (1.02)	2.95 (1.21)	6.00 (0.34)	1.58 (0.68)	1,87
86	0.215 (0.156)	18.28 (0.83)	2.66 (1.38)	15.22 (0.56)	1.32 (0.85)	2,02
88	0.628 (0.216)	28.52 (0.96)	22.80 (2.27)	21.58 (0.72)	12.38 (1.23)	1,84
102	0.231 (0.104)	18.79 (0.29)	3.07 (0.57)	15.46 (0.26)	1.67 (0.31)	1,84
109	0.245 (0.122)	21.89 (0.43)	3.47 (0.83)	14.25 (0.31)	1.88 (0.45)	1,85
120	0.350 (0.131)	22.10 (0.41)	7.09 (0.85)	17.14 (0.39)	3.85 (0.46)	1,84
121	0.295 (0.135)	20.83 (0.48)	5.03 (1.00)	16.38 (0.52)	2.73 (0.54)	1,84
124	0.228 (0.140)	20.73 (0.57)	3.00 (1.14)	16.09 (0.44)	1.62 (0.63)	1,85
127	0.245 (0.140)	20.50 (0.54)	3.47 (1.10)	15.85 (0.48)	1.88 (0.60)	1,85
156	0.208 (0.124)	20.07 (0.43)	2.49 (0.87)	17.56 (0.40)	1.34 (0.48)	1,86
159	0.286 (0.117)	20.52 (0.38)	4.71 (0.71)	17.55 (0.25)	2.56 (0.39)	1,84
161	0.284 (0.125)	18.23 (0.43)	4.66 (0.84)	16.54 (0.33)	2.53 (0.46)	1,84
167	0.266 (0.168)	22.36 (0.85)	4.08 (1.61)	18.04 (0.64)	2.17 (0.93)	1,88
168	0.398 (0.143)	20.49 (0.50)	9.14 (0.99)	19.95 (0.44)	4.96 (0.54)	1,84
171	0.277 (0.145)	23.70 (0.62)	4.42 (1.18)	18.45 (0.44)	2.40 (0.65)	1,84
172	0.340 (0.146)	21.48 (0.52)	6.68 (1.10)	18.17 (0.43)	3.63 (0.60)	1,84
175	0.270 (0.106)	22.98 (0.29)	4.21 (0.57)	16.60 (0.21)	2.29 (0.31)	1,84
176	0.287 (0.118)	21.20 (0.36)	4.76 (0.74)	16.22 (0.30)	2.58 (0.40)	1,84
179	0.174 (0.117)	10.63 (0.43)	1.75 (0.78)	9.30 (0.30)	0.92 (0.45)	1,90

(a) R$_2$ and exchange contribution R$_{ex}$ underscored 1 and 2 correspond to those at 950MHz and 700MHz, respectively. (b) Uncertainties (in brackets) are the standart deviations obtained from 1000 Monte Carlo simulations.

Table S4: $^{1}H/^{2}H$ exchange rates of amide protons for Δ17Arf1-GDP and Arf1-GDP. Data are shown only for assigned residues with no overlapping. "<min" means that the amide proton has disappeared in the first (^{1}H,^{15}N) HSQC.

Arf1-GDP			Δ17Arf1-GDP		
Residue	T (h)	dT (h)	**Residue**	T (h)	dT (h)
6	<min				
7	<min				
9	<min				
10	<min				
12-13	<min				
17-19	<min		**19**	<min	
20	>120		**20**		
21	>120		**21**	>120	
22	>120		**22**	>120	
24	<min		**24**	3.885	1.013
25	3.255	0.537	**25**	6.876	0.652
26	<min		**26**	<min	
27	4.819	3.526	**27**	3.299	0.613
29	>120		**29**	25.504	2.012
30	<min		**30**	<min	
31	>120		**31**	27.908	4.089
32	>120		**32**		
33	>120		**33**		
34	>120		**34**	>120	
35	>120		**35**	>120	
36	7.568	0.677	**36**	<min	
37	0.65	0.166	**37**	3.515	0.308
38-54	<min		**38-42,44-52, 54**	<min <min	
55	0.514	0.284	**55-72**	<min	
56	1.479	0.342			
57	<min				
58	21.212	3.848			
59-60	<min				
61	2.134	0.201			
62	14.91	1.452			
63	18.292	1.956			
65	>120				
67	0.331	0.251			
68	1.946	0.425			
69-71	<min				
77,79	<min		**77-79**	<min	
81-86	<min		**81-86**	<min	
87	0.63	0.291	**87**	0.587	0.524
88-92	>120		**88-92**	>120	
93	3.602	0.611	**93**	4.793	0.331
94	>120		**94**		
95	>120		**95**	>120	
96	1.663	0.401	**96**	4.502	0.324
97-98	<min		**97-102**	<min	
99	>120				
100,102	<min		**103**	46.595	3.259
104	14.209	1.401	**104**	39.286	2.338
105	2.476	0.266	**105**	6.943	0.374
106			**106**	>120	
107	>120		**107-108**	>120	
108					
109	1.165	0.155	**109**	3.811	0.22
110			**110**	>120	
111	>120		**111**	>120	
112-113, 115	<min		**112**	0.656	0.836
			113-115	<min	
116	<min		**116**	0.899	0.972
118			**118**	>120	
119	<min				
120	1.422	0.177	**120**	8.049	0.642
			121	>120	
122	>120		**122**	>120	
123	>120		**123**	>120	
124	>120		**124**		
125	>120		**125**	>120	
126	>120		**126**	>120	
127	>120		**127**	26.14	9.409
128	>120		**128**		
129	1.939	0.287	**129**	4.957	0.305
132-133	<min		**132-133**	<min	
134	14.062	1.376	**134**		
135	<min		**135**	<min	
137	<min		**137**	<min	
138	<min		**138**	<min	
139	19.489	1.164	**139**	79.012	7.723
140	0.572	0.294	**140**	<min	
141-142	<min		**141-142**	<min	
143	13.168	0.71	**143**	49.772	2.807
144-147	<min		**144-147**	<min	
149	<min		**149**		
151-153	<min		**151-153**	<min	
154	>120		**154**	>120	
155	0.568	0.158	**155**	0.843	0.146
156	>120		**156**	>120	
157	<min		**157**	<min	
158	>120		**158**	>120	

159			**159**	<min	
160	7.186	0.624	**160**	6.363	0.344
161-165	<min		**161-168**	<min	
166	0.282	0.262			
167	<min				
169	58.727	14.367	**169**	5.458	0.353
170			**170**	12.741	0.605

171	>120		**171**	1.841	0.328
172	5.841	0.602	**172**	3.713	0.315
173	>120		**173**	>120	
174	>120		**174**	1.646	0.129
176-177	<min		**175-181**	<min	
180-181	<min				