

Supplementary Table 3

	GDP loaded KRas ^{G12D} MPB1	GTP loaded NRas ^{Q61R} MPB2	GTP loaded NRas ^{Q61R} MPB3	GMPPnP loaded KRas ^{G12D} KM12-AM
Data collection				
Space group	P2 ₁ 2 ₁ 2 ₁	H3	P2 ₁ 2 ₁ 2 ₁	C222 ₁
Cell dimensions				
<i>a</i> , <i>b</i> , <i>c</i> (Å)	41.4, 79.4, 128.5	112.2, 112.2, 58.6	83.9, 121.3, 124.9	84.1, 122.3, 105.6
<i>a</i> , <i>b</i> , <i>g</i> (°)	90, 90, 90	90, 90, 120	90, 90, 90	90, 90, 90
Resolution (Å)	1.9 (1.95-1.9)*	2.1 (2.15-2.10)*	1.85 (1.90-1.85)*	1.76 (1.88-1.76)*
<i>R</i> _{merge} (%)	8.7 (70.7)	9.1 (83.8)	8.9 (85.1)	7.8 (157.0)
<i>I</i> / <i>σ</i> <i>I</i>	13.6 (2.9)	10.0 (1.9)	15.9 (2.3)	14.3 (1.4)
Completeness (%)	99.8 (100)	99.7 (99.2)	100 (100)	94.1 (56.4)
Redundancy	6.5 (6.6)	4.9 (4.8)	13.7 (6.6)	10.1 (12.3)
Refinement				
Resolution (Å)	1.9	2.1	1.85	2.1
No. reflections	34233	16013	109131	31891
<i>R</i> _{work} / <i>R</i> _{free}	18.4 / 21.5	19.7 / 23.5	18.4 / 22.1	23.9 / 27.7
No. atoms				
Protein	2707	1351	8051	4189
Ligand/ion	292 / 2	178 / 1	1300 / 6	64 / 2
Water	370	123	1131	176
B-factors (Å ²)	30.8	42.5	26.5	43.2
R.m.s deviations				
Bond lengths (Å)	0.008	0.008	0.008	0.008
Bond angles (°)	1.0	0.95	0.98	0.93

Supplementary Table 4

Libraries creation	Forward Primers (%)	Reverse Primers
PCR I	RC1559 (20) + RC1560 (80)	RC1562
PCR II	RC1559 (20) + RC1560 (80)	RC1563
PCR III	RC1568 (100)	RC1562
PCR IV	RC1568 (100)	RC1563
VHH clone sequencing	CIR257	RC1089
PCR Primers	Primers sequence (5'-3')	
RC1559	ATTTTCTGTTATTGCTTCAGTGCTAGCACAGGTGCAGCTCGTGGAGTCTG	
RC1560	ATTTTCTGTTATTGCTTCAGTGCTAGCACAGGTGCAGCTGGTGGAGTCTG	
RC1562	CAGTTCCTGAGTCGACCCTCCGCCTCCTGAKGAGACRGTGACCAGGGTSCC	
RC1563	CAGTTCCTGAGTCGACCCTCCGCCTCCTGAGGAGACGGTGACCTGGGTCCC	
RC1568	ATTTTCTGTTATTGCTTCAGTGCTAGCATGAGGTGCAGCTGGTGGAGTCTG	
CIR257	GAAAAAACCCCGGATCGGACTACTAG	
RC1089	CGTTGGCCAAAATAGTAGTCG	