Table S1. Crystallographic data collection and refinement statistics

Data collection parameters	GMPPNP bound KRAS4B^{G12R} (1-169)
Wavelength	0.97918
Resolution range	49.36 - 1.5 (1.55 -1.5)
Space group	C 1 2 1
Unit cell	67.79 83.29 86.04 90 110.1 90
Total reflections	315524 (30381)
Unique reflections	70136 (6740)
Multiplicity	4.5 (4.5)
Completeness (%)	97.63 (94.33)
Mean I/sigma(I)	12.58 (1.16)
Wilson B-factor	26.11
R-merge	0.054 (0.87)
R-pim	0.028 (0.57)
CC1/2	0.998 (0.62)
CC*	0.999 (0.87)
Refinement parameters	
Resolution range (Å)	50.00 - 1.5 (1.54 - 1.50)
Reflections used in refinement	70087 (6740)
Reflections used for R-free	1854 (179)
R-work	0.202 (0.341)
R-free	0.229 (0.369)
CC (work)	0.961 (0.761)
CC (free)	0.949 (0.679)
Number of non-hydrogen atoms	4250
Macromolecules	3913
Ligands	105
Solvent	232
Protein residues	486
RMS(bonds)	0.007
RMS(angles)	1.2
Ramachandran favored (%)	97.88
Ramachandran allowed (%)	1.91
Ramachandran outliers (%)	0.21
Rotamer outliers (%)	0.70
Clash score	6.16
Average B-factor	40.78
Macromolecules	40.93
Ligands	33.54
Solvent	41.49

Statistics for the highest-resolution shell are shown in parentheses.