

Appendix for **Helix-7 in Argonaute2 shapes the microRNA seed region for rapid target recognition**

Shannon M. Klum, Stanley D. Chandradoss, Nicole T. Schirle, Chirlmin Joo* and Ian J. MacRae*

*Correspondence: c.joo@tudelft.nl or macrae@scripps.edu

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Appendix Table S1.

Crystallographic statistics for 5WEA.

Space group	P 1 2 ₁ 1
Unit cell dimensions	
a, b, c (Å)	63.3, 107.9, 68.7
α, β, γ (°)	90.0, 107.5, 90.0
Ago2 molecules per asymmetric unit	1
Data collection	
Wavelength (Å)	0.97918
Resolution	66-3.1 (3.2-3.1)
Number of reflections	
Total	47817
Unique	14855
Completeness (%)	94.5 (96.8)
Redundancy	3.2 (3.2)
I/sigma	9.0 (2.4)
R _{merge}	0.11 (0.40)
Refinement	
Resolution (Å)	3.12
R-free	0.289
R-work	0.264
RMS deviation Z-scores	
Bond distances	0.28
Bond angles	0.46
Number of atoms	
Non-hydrogen, protein	764
Non-hydrogen, RNA	8
Water	23
Ramachandran plot	
Total analyzed: 744/764	
Preferred (%)	94.1
Allowed (%)	5.5
Outliers (%)	0.4

$R_{\text{merge}} = \frac{\sum_h \sum_i |I_h - I_{hi}|}{\sum_h \sum_i I_{hi}}$, where I_h is the mean of I_{hi} observations of reflection h . Numbers in parentheses represent data for the highest-resolution shell.

R_{work} and $R_{\text{free}} = \frac{\sum |F_{\text{obs}}| - |F_{\text{calc}}|}{\sum |F_{\text{obs}}|} \times 100$ for 95% of the recorded data (R_{work}) or 5% of the data (R_{free}).