

Is it a “good” model?

X-ray structure of a voltage-dependent K⁺ channel

Youngh Jang*, Alice Lee, Jayun Chen, Vanessa Ruta, Marlene Cadene, Brian T. Chait & Roderick MacKinnon

Table 1 Data and refinement statistics

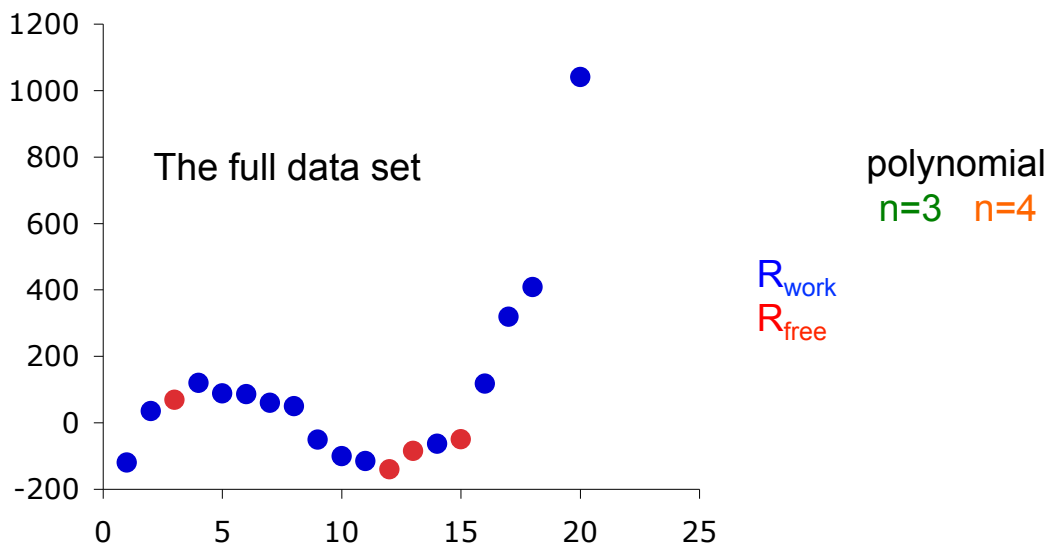
Protein	Fab 6E1-KvAP	Fab 33H1-isolated voltage sensor
Space group	I422	C2
Data source*	CHESS A1	CHESS A1
Resolution (Å)	30–3.2	30–1.9
Completeness (%)	98.8 (95.2)	97.1 (92.8)
Redundancy†	5.5	2.9
R _{sym} (%)‡	8.0 (42.4)	5.8 (17.7)
//σ	18 (2.2)	15.5 (5.8)
Unique reflections	22,476	56,778
Atoms refined	5,046 protein, 6 H ₂ O, 6 K ⁺ , 7 Cd	4,365 protein, 403 H ₂ O
R _{work} /R _{free} (%)§	25.6/29.9	23.1/25.1
r.m.s.d. of bond	1.44°/0.008 Å	1.48°/0.006 Å

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$$R = \frac{\sum ||F_{obs} - F_{calc}||}{\sum |F_{obs}|}$$

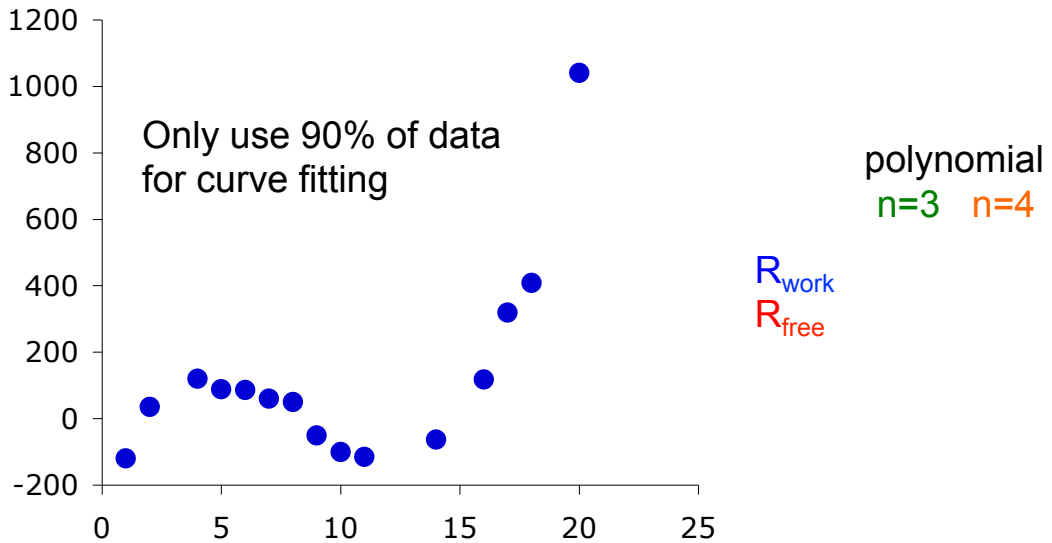
To Add Another Variable?

$y = ax^3 + bx^2 + cx + d$ or $y = zx^4 + ax^3 + bx^2 + cx + d$



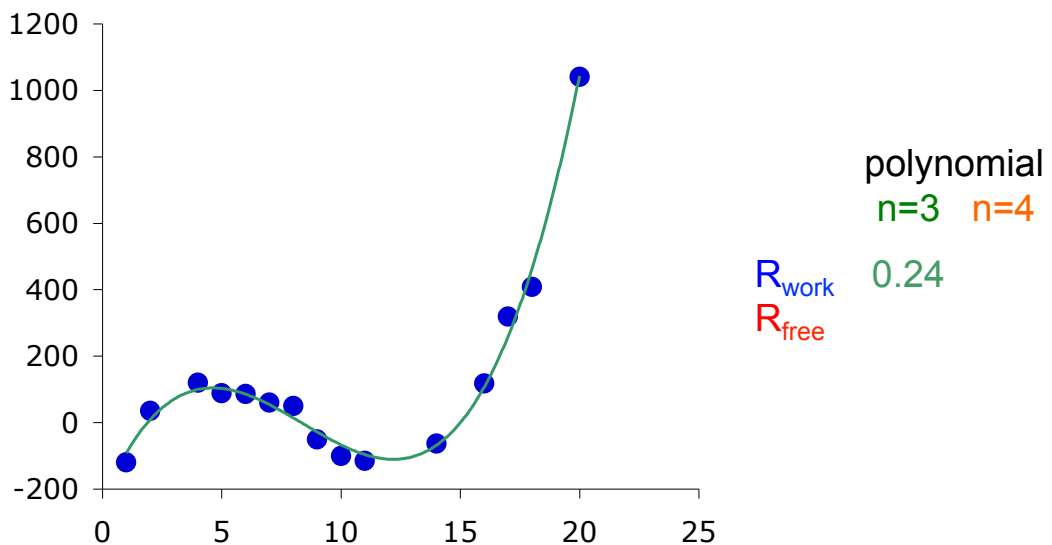
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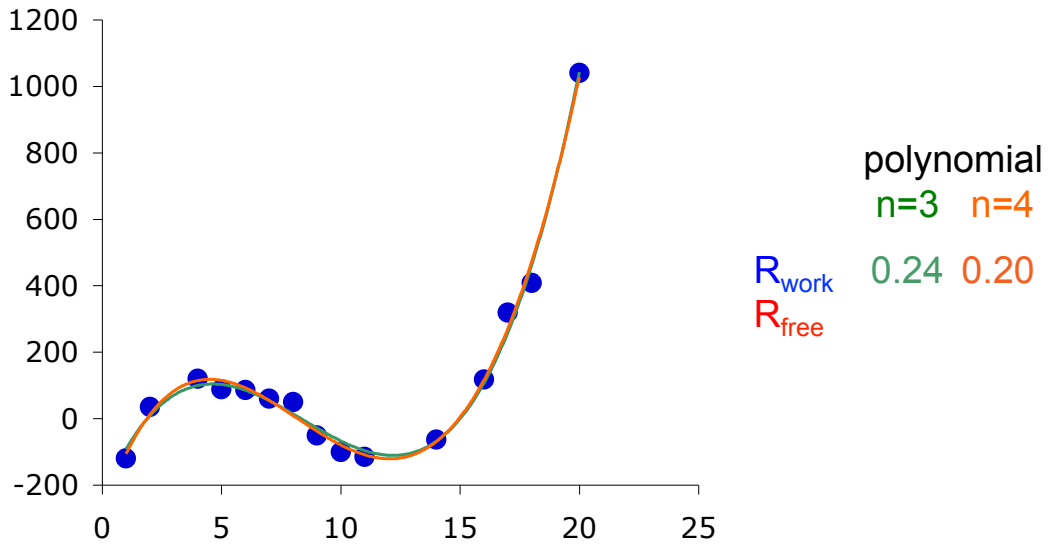
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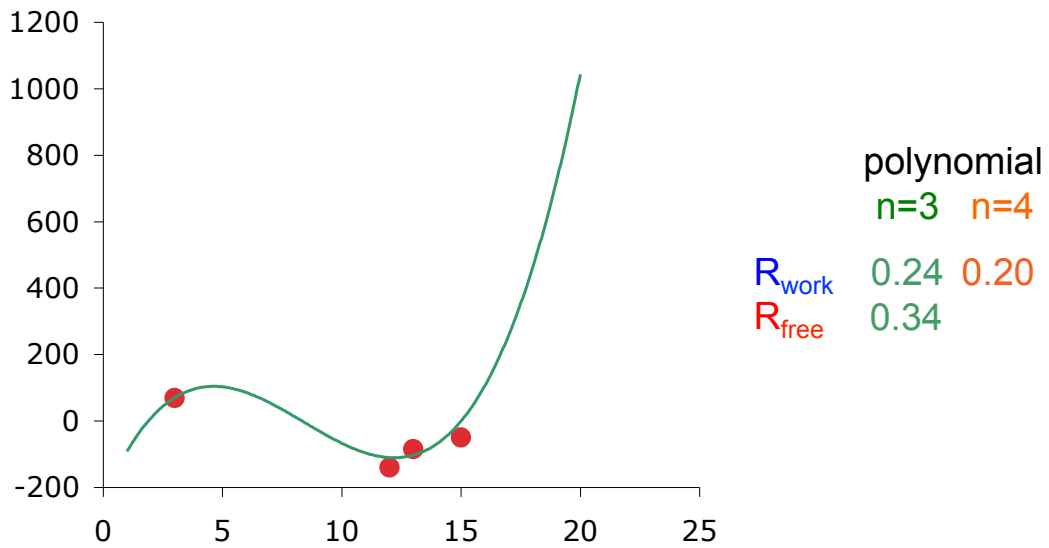
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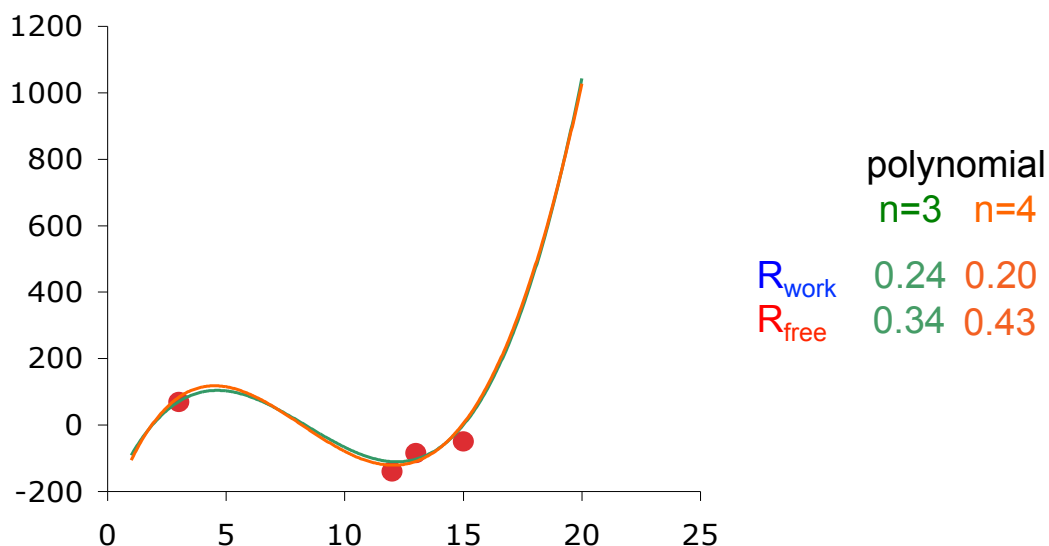
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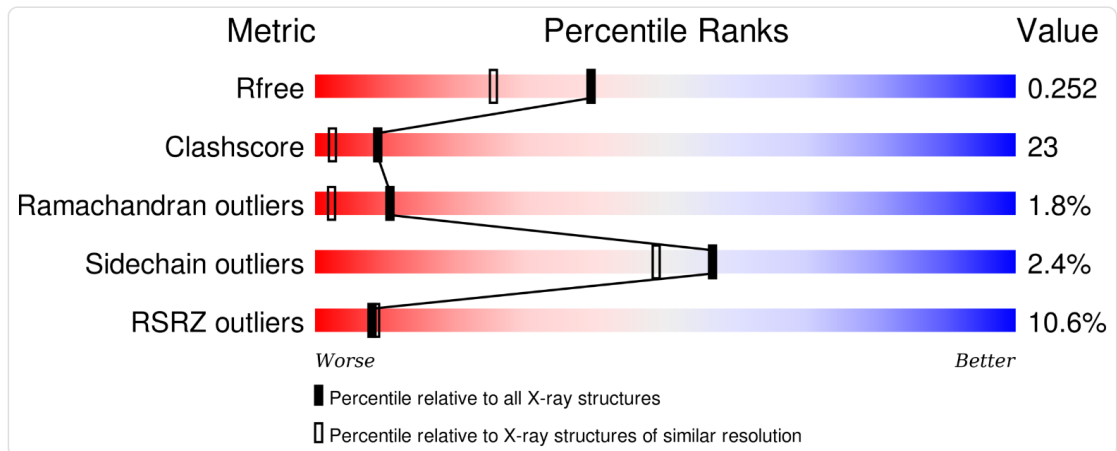
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Model Validation at PDB



Take Homes

- The R-factor measures the residual difference between the model and the experimental data. Lower values are better.
- R_{work} (or R_{cryst}) is calculated with the working data set, used in model building and refinement.
- R_{free} is calculated from the test data set, and tells you how well your model predicts the un-used data.
- Typically an R_{free} of **less than** 30% is considered satisfactory.