

1 **Supplemental Table SI.** Data Collection and Refinement Statistics of Se-Met derivatized Cra protein, and
 2 same with its effector F1P

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Data collection	Se/Met Cra	Cra/F1P
Space group	P2 ₁	P2 ₁
Wavelength	0.97925 (peak)	0.933
Cell dimensions		
a, b, c (Å)	37.3, 118.5, 61.8	37.7, 120.2, 61.8
α , β , γ (°)	90, 107.1, 90	90, 107.4, 90
Resolution (Å)	59-2.0	60-2.3
Highest resolution bin	2.1-2.0	2.42-2.3
No. of unique reflections	34595 (5011)	23340 (3381)
Multiplicity	7.4 (7.4)	3.4 (3.4)
Completeness (%)	99.8 (99.8)	99.8 (100)
R _{sym} or R _{merge}	8.3 (40)	5.0 (35.8)
I / σ (I)	5.6 (1.7)	12.6 (2.2)
B-factor Wilson (Å ²)	28	42
Refinement statistics		
Resolution (Å)	15.0-2.0	15.0-2.3
R _{work} / R _{free}	18.4/21.8	18.4/22.1
Reflections (R _{free})	66122 (3320)	22057 (1130)
No. of atoms		
Protein	4193	4186
Ligand	12	32
Water	175	107
B-factors		
Protein A/B	41/40	50/51

Ligand C/D	37/58	30/34
Water	41	41
R.m.s deviations		
Bond lengths (Å)	0.003	0.003
Bond angles (°)	0.71	0.843
Ramachandran plot ^a	91.7/7.9/0/0.4	87.9/11.5/0.2/0.4

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2 * Highest-resolution shell is shown in parentheses.

3 ^a Percentage of residues in most favored regions, allowed regions, generously allowed regions and
4 disfavored regions, respectively.