

**Table 1: Crystallographic data, phasing, and refinement****A. Data collection statistics**

	No. of unique refl.	Redundancy	Completeness (%)	I/ $\sigma$	R <sub>sym</sub> <sup>1</sup> (%)
SeMet $\lambda_1$ (1.06883 Å)	24057	5.44 (2.03)	93.6 (68.3)	25.3 (2.8)	5.6 (20.2)
97984 Å)	25278	5.82 (3.07)	98.4 (88.2)	20.5 (2.2)	7.1 (40.0)
SeMet $\lambda_3$ (0.97961 Å)	25300	5.89 (3.05)	98.4 (89.0)	20.8 (2.3)	7.2 (40.5)
SeMet $\lambda_4$ (0.92526 Å)	25598	6.01 (3.83)	99.6 (97.1)	17. (1.9)	8.3 (57.2)

**B. Phasing statistics**Overall isomorphous and dispersive differences<sup>2</sup>Phasing power as defined in CNS<sup>3</sup>

Wavelength	$\lambda_1$	$\lambda_2$	$\lambda_3$	$\lambda_4$	<b>F</b> <sup>+</sup> Friedel mate (reference)	<b>F</b> <sup>-</sup> Friedel mate
$\lambda_1$ (remote)	0.0427	0.0766	0.0916	0.0569		0.51
$\lambda_2$ (inflection)		0.0570	0.0484	0.0859	2.67	2.79
$\lambda_3$ (peak)			0.0707	0.0967	3.80	3.31
$\lambda_4$ (remote)				0.0843	0.69	1.06

**C. Figure-of-merit<sup>3</sup>**

Bragg Spacing Limits (Å)	Overall (43.14-1.79)	3.58	2.84	2.48	2.26	2.09	1.97	1.87	1.79
Figure of Merit (FOM)	0.72	0.92	0.91	0.85	0.77	0.69	0.58	0.46	0.33

**D. Refinement**

	Overall											
Resolution range	Overall											
Resolution (Å)	500-1.8 Å	500-3.88	3.08	2.69	2.44	2.27	2.13	2.03	1.94	1.86	1.80	
R-value <sup>4</sup>	20.6	20.8	20.4	21.3	18.1	20.7	20.1	20.2	20.5	23.6	25.2	
R <sub>free</sub> <sup>5</sup>	22.5	22.5	22.0	22.3	19.0	22.8	23.4	23.0	24.2	27.4	24.6	
Luzzati coordinate error	0.21 Å											
Cross-validated Luzzati coord. error	0.23 Å											
Bond-length deviation	0.005 Å											
Bond-angle deviation	1.12°											
Improper-angle deviation	0.68°											
Dihedrals	18.0°											
Average B-factor	20.9 Å <sup>2</sup>											
RMSD for bonded main chain atoms	1.87 Å <sup>2</sup>											
RMSD for bonded side chain atoms	3.32 Å <sup>2</sup>											
Minimum B-factor	7.46 Å <sup>2</sup>											
Maximum B-factor	62.3 Å <sup>2</sup>											
% Residues in core $\phi$ - $\psi$ region	91.1%											
% Residues in disallowed regions	0.0 %											

## Captions for Table 1

Values in parentheses are for the high-resolution bin (SPECIFY BIN???).

<sup>1</sup> $R_{\text{sym}} = \sum_{\mathbf{h}} \sum_i |I_i(\mathbf{h}) - \langle I(\mathbf{h}) \rangle| / \sum_{\mathbf{h}} \sum_i I_i(\mathbf{h})$  where  $I_i(\mathbf{h})$  is the  $i$ -th measurement and  $\langle I(\mathbf{h}) \rangle$  is the mean of all measurements of  $I(\mathbf{h})$  for Miller indices  $\mathbf{h}$ .

<sup>2</sup>Values are  $\langle (\Delta|\mathbf{F}|)^2 \rangle^{1/2} / \langle |\mathbf{F}|^2 \rangle^{1/2}$ , where  $\Delta|\mathbf{F}|$  is the dispersive (off-diagonal element), or Bijvoet difference (diagonal elements), computed between 500 and 1.8 Å resolution.

<sup>3</sup>MAD phasing power is defined as  $[\langle (|\mathbf{F}_{\lambda_1}^+| - |\mathbf{F}_{\lambda_i}^{(+/)}|)^2 \rangle / \int_{\phi} P(\phi) (|\mathbf{F}_{\lambda_1}^+| e^{i\phi} + \Delta\mathbf{F} - |\mathbf{F}_{\lambda_i}^{(+/)}|)^2 d\phi]^{1/2}$  where  $P(\phi)$  is the experimental phase probability distribution,  $i$  is any wavelength.  $\mathbf{F}^+$  and  $\mathbf{F}^-$  correspond to a Bijvoet pair of structure factors.  $\Delta\mathbf{F}$  is the anomalous scatterer structure factor difference for a particular lack of closure expression.

$$^4R = \sum (|\mathbf{F}_{\text{obs}}| - k|\mathbf{F}_{\text{calc}}|) / \sum |\mathbf{F}_{\text{obs}}|.$$

<sup>5</sup>Free  $R$  value is the  $R$  value obtained for a test set of reflections, consisting of a randomly selected 10 % subset of the diffraction data, not used during refinement.