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ERRATUM

# Erratum to "Structure and Function of an Archaeal Homolog of Survival Protein E (SurEα): An Acid Phosphatase with Purine Nucleotide Specificity"☆

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It is regretted that there is an error in Table 1 and the corrected version follows:

**Table 1.** Crystallographic statistics for *Pae* SurEα

| | Data collection and MAD phasing | | | Model refinement | |
|---|---|---|---|---|---|
| Data set | Inflection | Peak | High-energy remote | Resolution range (Å) | 20.0–2.0 |
| Wavelength (Å) | 0.97870 | 0.97860 | 0.96485 | No. reflections (working/test set) | 38,377/2033 |
| Resolution range (Å) | 100.0–2.40 | 100.0–2.00 | 100.0–2.85 | No. protein residues (A/B)[a] | 276/278 |
| No. reflections (total/unique) | 242,223/ 47,599 | 297,069/ 42,129 | 206,830/ 28,846 | $\langle B \rangle$ (protein atoms, Å$^2$) | 35.73 |
| Completeness (%)[b] | 100.0 [100.0] | 99.9 [100.0] | 99.9 [100.0] | $\langle B \rangle$ (Wilson plot, Å$^2$) | 28.79 |
| $I/\sigma(I)$ | 15.9 [2.3] | 17.4 [2.5] | 14.0 [3.3] | *No. solvent molecules* ($\langle B \rangle$, Å$^2$) | |
| $R_{merge}$ (%)[c] | 9.8 [77.8] | 9.9 [78.1] | 14.7 [94.1] | Water | 287 (44.8) |
| Anomalous signal ($\langle \chi^2 \rangle$)[d] | – | 4.3 [1.9] | – | Glycerol | 7 (73.9) |
| No. Se sites per a.u. (used/expected)[e] | – | 8/12 | – | Acetate | 2 (59.8) |
| Phasing resolution range (Å) | 38.0–2.85 | 38.0–2.85 | 38.0–2.85 | No. Ramachandran violations | 2/560 residues |
| $R_{cullis}$[f] Acentric | – | 0.94/0.65 | 0.96/0.95 | RMSDs (bonds (Å)/angles (deg.)) | 0.014/1.79 |
| Centric | – | 0.90 | 0.93 | $R_{cryst}/R_{free}$ (%)[g] | 18.5/22.3 |
| Figure of merit[h] | 0.43/0.59 | – | – | PDB submission code | 1L5X |

[a] Number of SurEα residues built in monomers A and B, out of 280 residues per monomer of recombinant protein (the His-tag and linker add 14 residues to the wild-type sequence).
[b] Statistics for the highest-resolution shell are given in square brackets.
[c] $R_{merge}(I) = \Sigma_{hkl}((\Sigma_i|I_{hkl,i} - \langle I_{hkl} \rangle|)/\Sigma_i I_{hkl,i})$.
[d] Anomalous signal as measured by the normalized $\chi^2$ for merging Bijvoet pairs $I^+$, $I^-$. That is, $\chi^2 = \Sigma_{I+,I-}((I - \langle I \rangle)^2/\sigma^2(n/n-1))$. Values >2 suggest a usefully strong anomalous signal.
[e] Number of Se sites calculated by SHELXD and used for phasing (out of 12 sites expected per a.u.).
[f] $R_{cullis} = (\Sigma_{hkl}||F_{PH} \pm |F_P| - F_{H,calc}||)/\Sigma_{hkl}|F_{PH} \pm F_P|$. Statistics for acentric reflections are given as isomorphous/anomalous.
[g] $R_{cryst} = \Sigma_{hkl}||F_{obs}| - |F_{calc}||/\Sigma_{hkl}|F_{obs}|$. $R_{free}$ was computed identically, except that 4.6% of the reflections were omitted as a test set.
[h] Values are given before/after density modification and phase extension to 2.0 Å.

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