

## Table S1

Crystal diffraction and structural refinement statistics of atragin (after pH jump)

<b>Crystal data</b>	<b>Atragin (pH 7.4)</b>
Wavelength (Å)	1.00
Temperature (K)	110
Resolution Range (Å) (outermost shell)	30 - 3.23 (3.38-3.23)
Space group	<i>P</i> 4 <sub>3</sub> 2 <sub>1</sub> 2
Unique reflections	14,579
Completeness (%)	93.9 (99.8)
<i>I</i> / $\sigma$ <sub><i>I</i></sub>	18.1(6.0)
Average redundancy	6.8
<i>R</i> <sub>sym</sub> (%)	17.4 (36.0)
Mosaicity (°)	0.75
Unit-cell parameters (Å)	<i>a</i> = 91.12, <i>c</i> = 126.047
No. of protein molecules per A.U.	1
<b>Refinement results</b>	
Final refinement	<i>R</i> = 20.65 %, <i>R</i> <sub>free</sub> = 22.92%

$R_{\text{sym}} = \frac{\sum_h \sum_i [|I_i(h) - \langle I(h) \rangle|]}{\sum_h \sum_i I_i(h)}$ , where  $I_i$  is the *i*th measurement and  $\langle I(h) \rangle$  is the weighted mean of all measurements of  $I(h)$ .

Reflections of  $2\sigma_I$  cutoff were applied in generating the statistics.  $R = \frac{\sum_h |F_o - F_c|}{\sum_h F_o}$ , where  $F_o$  and  $F_c$  are the observed and calculated structure factor amplitudes of reflection.