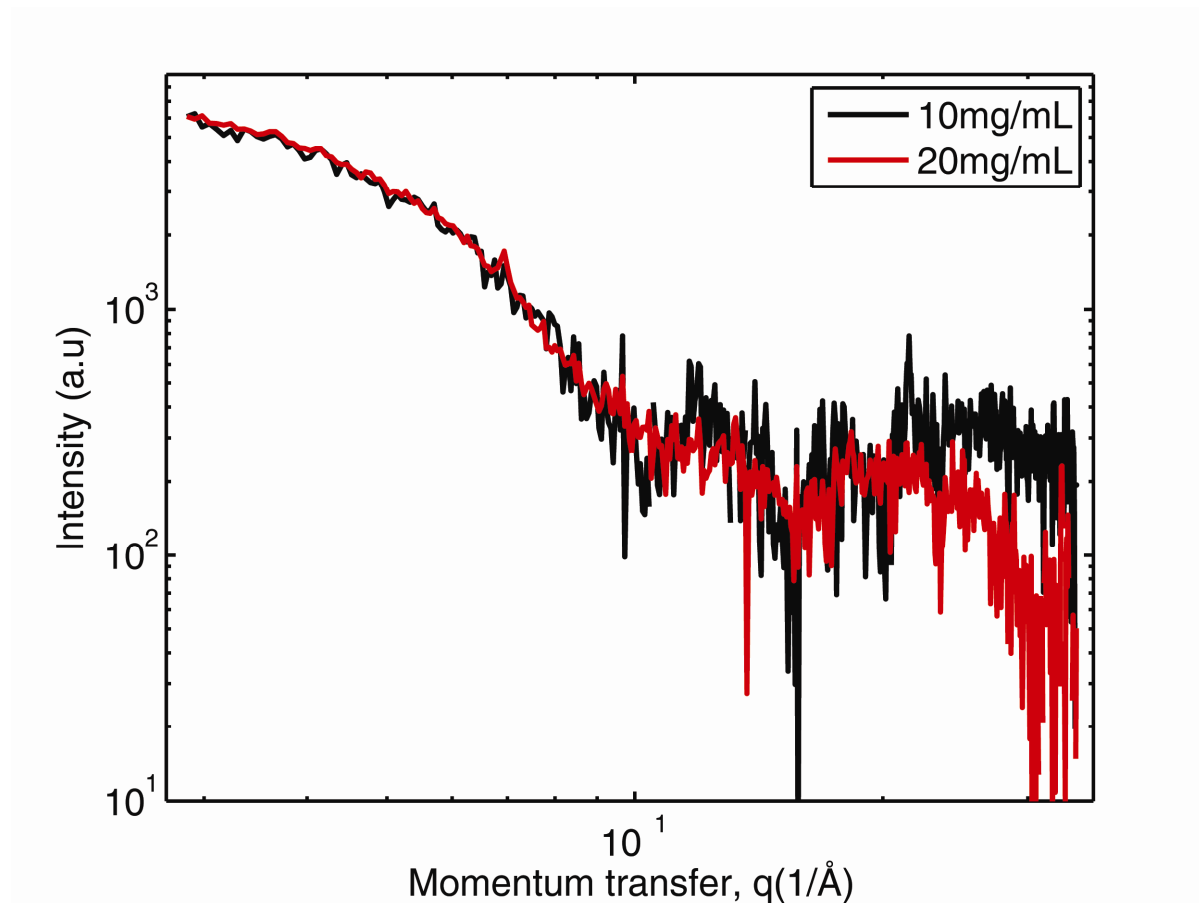


Supplementary Material

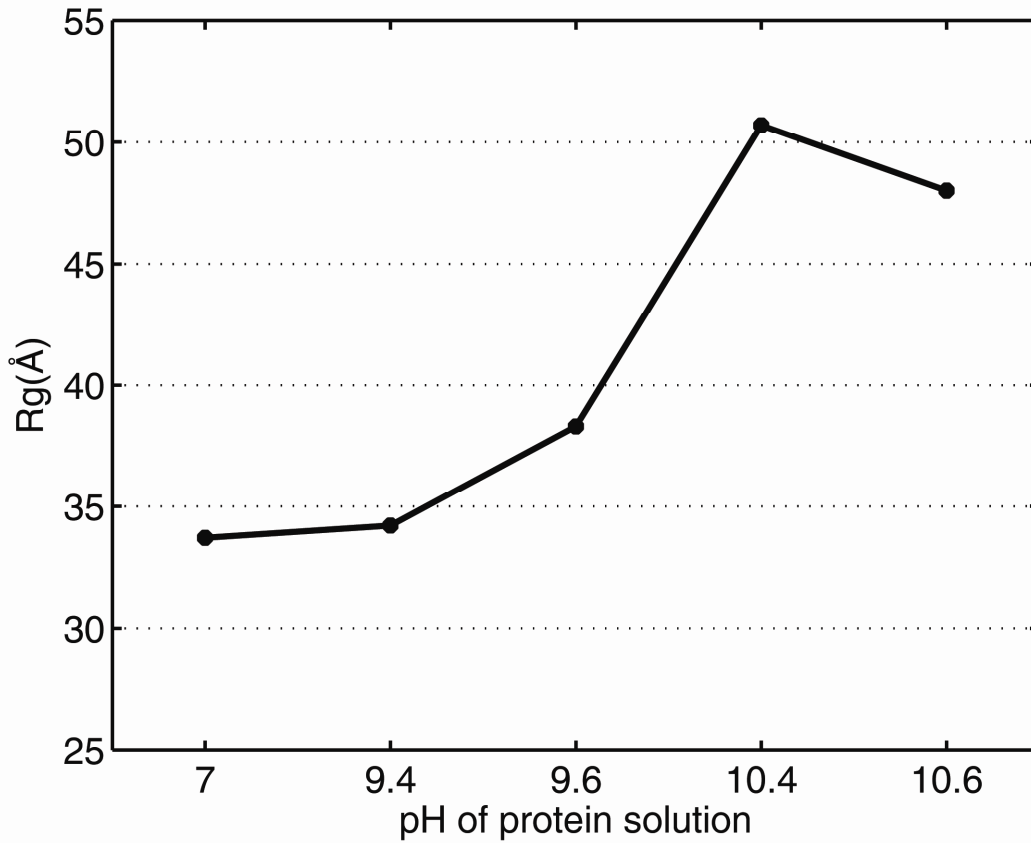
Supplementary Figure S1

Superposition of scattering intensity profiles collected for pH 7.0 sISDH solution at two different concentrations.



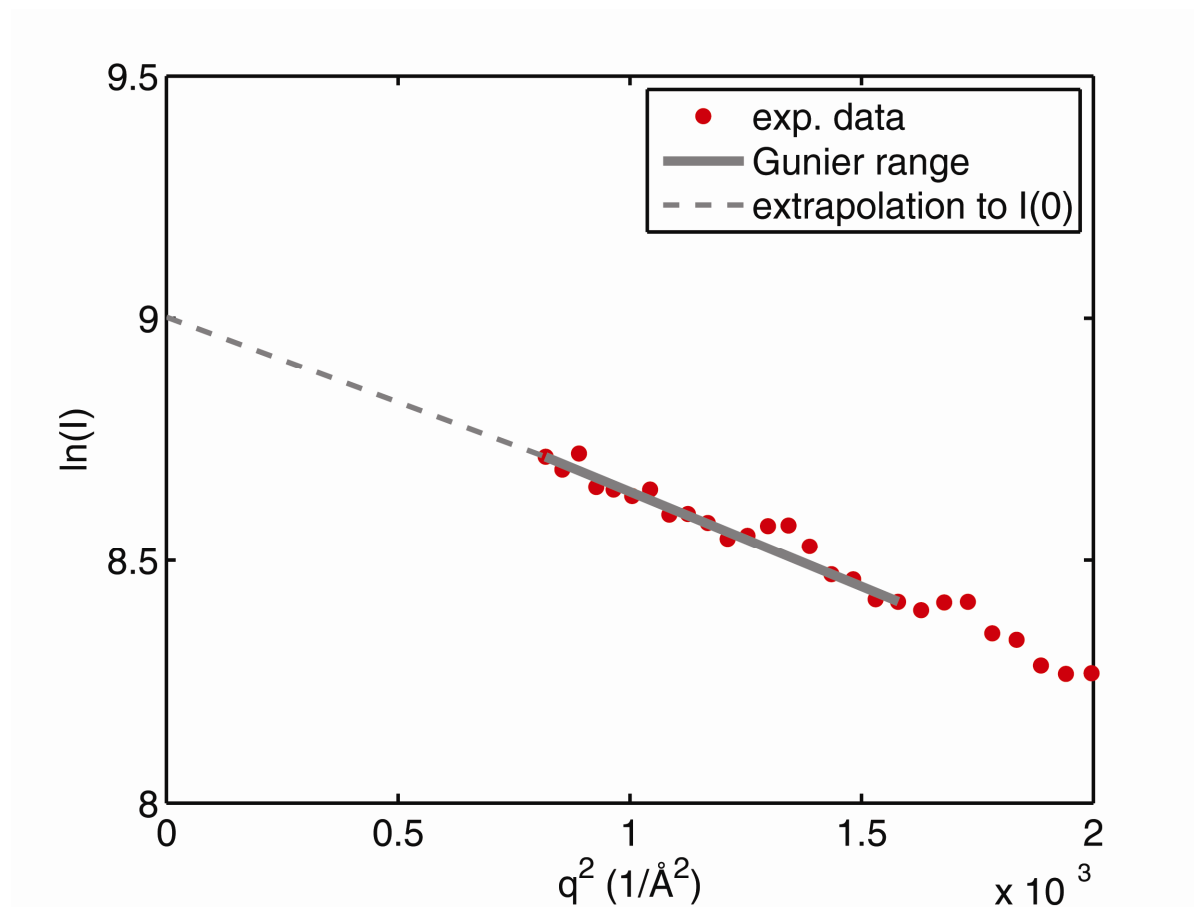
Supplementary Figure S2

Radius of Gyration of sLSDH as a function of pH. Sheep liver sorbitol dehydrogenase has a radius of gyration consistent with a tetrameric state when the pH is close to 7.0. A sharp transition to larger radius occurs near pH 10.0.



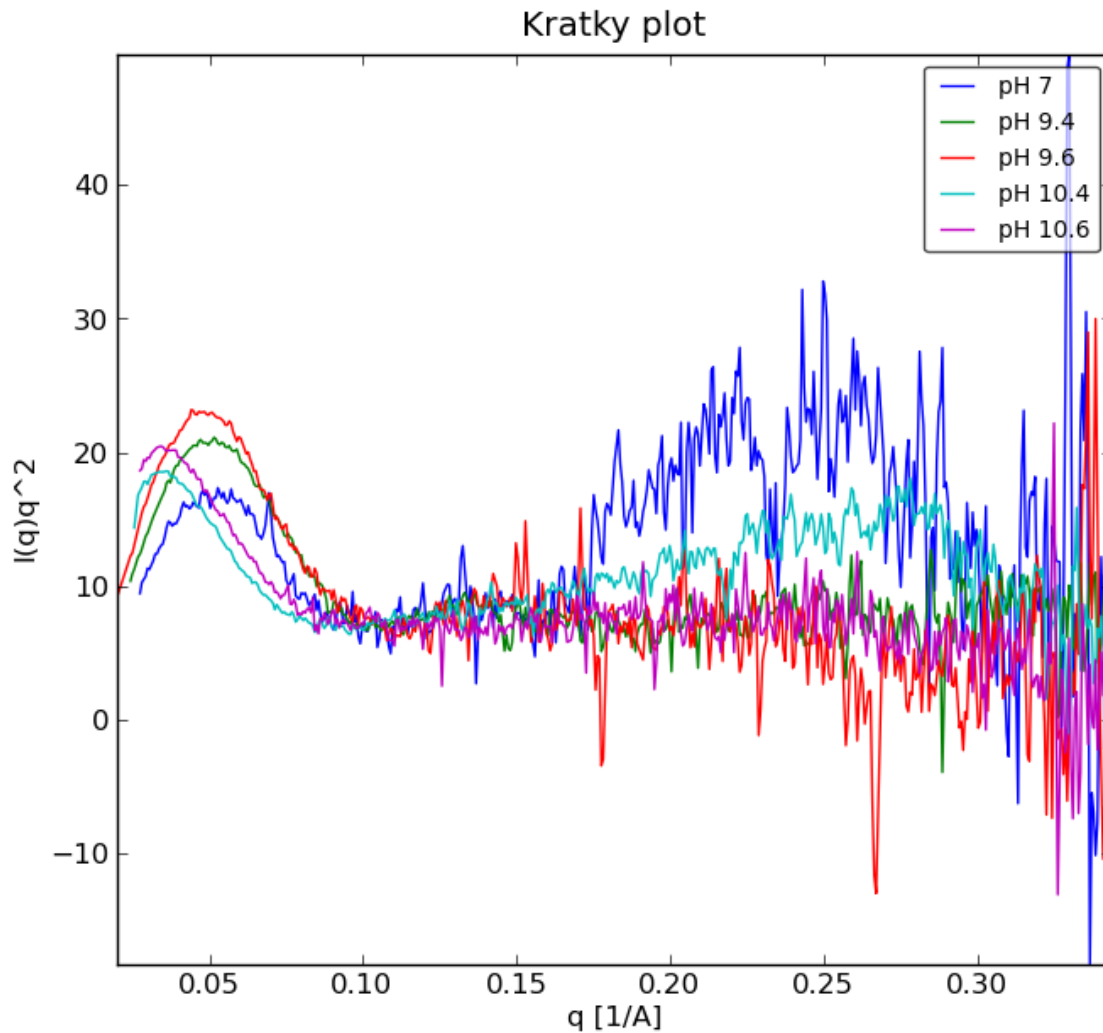
Supplementary Figure S3

Guinier plot for estimation of Radius of gyration (R_g) of sISDH at 20mg/ml and pH 7.0. The solid line indicates the range of data used in the fitting for which $qR_g < 1.3$



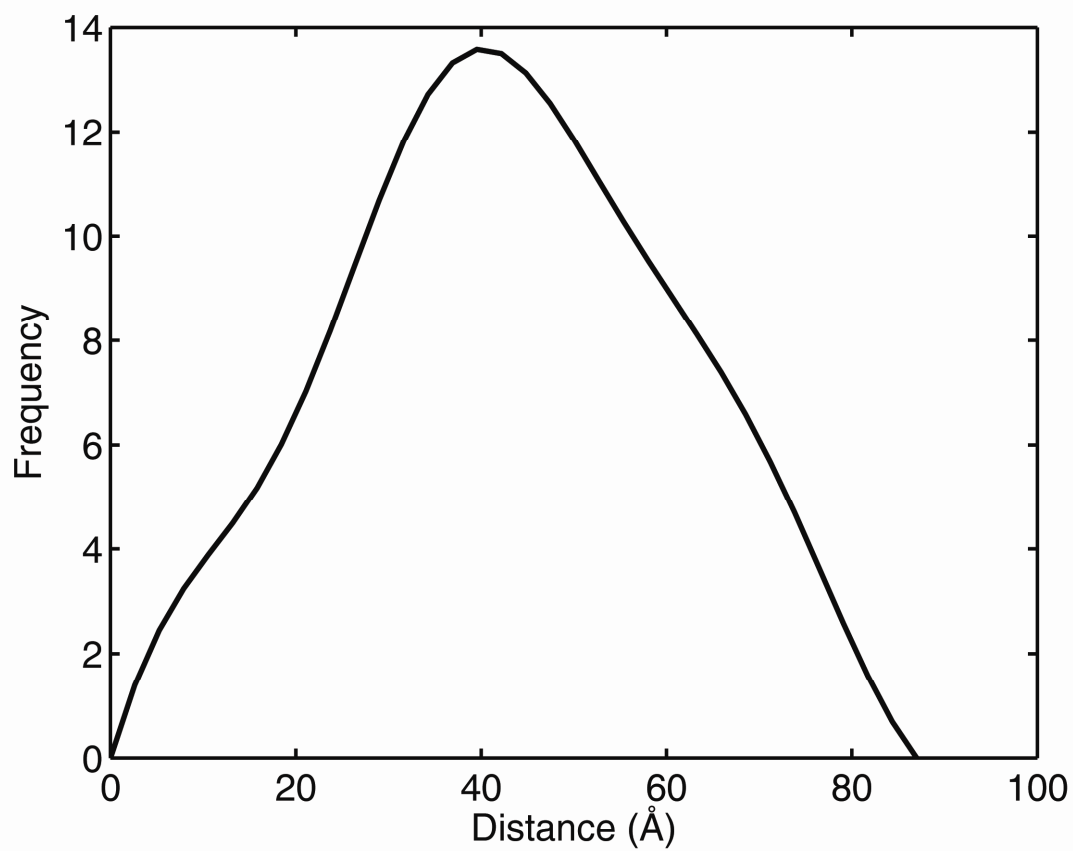
Supplementary Figure S4

Kratky plots of sISDH over a range of pH values. Kratky plots for all measured pH values display the bell-shaped profile that is characteristic of folded protein. While some rise in the pH 7 and pH 10.4 curves is evident at wide angles, data beyond that resolution range ($q > 0.2 \text{ \AA}^{-1}$) have not been used in the analysis.



Supplementary Figure S5

Indirect fourier transform (IFT) curve for pH 7.0 sLSDH solution **at 20 mg/ml**.



Supplementary Table S1 Volume fractions of components derived from hypothetical model combinations using the program OLIGOMER. Tetramer 1 is universally favored, except when it is omitted from the test combination.

pH 7 SAXS data	Volume fractions		
Pdb files given	Dimer	Tetramer 1	Tetramer 2
Dimer + Tetramer 1	0.028	0.963	
Dimer + Tetramer 2	0.294		0.706
Dimer + Tetramer 1 + Tetramer 2	0.073	0.709	0.210
Tetramer 1 + Tetramer 2		0.815	0.176