Electronic Supplementary Information

A Lyotropic Inverse Ribbon Phase in a Branched-chain Polyoxyethylene Surfactant: Pressure Effects

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Wide-angle X-Ray Scattering (WAXS) Methodology

WAXS studies were performed using a Philips PW1140 fixed tube, line source X-ray generator system, which was fitted with a nickel filter and a quartz crystal monochromator in order to isolate Cu-K_{a1} radiation (λ = 1.5405 Å). All samples were prepared using the same method as for the small-angle X-ray scattering studies and then introduced into 1.5 mm thin-walled glass capillaries, which were both flame-sealed and sealed with silicone sealant to ensure that no dehydration occurred during examination. WAXS diffraction patterns were recorded onto Kodak Biomax MS autoradiography film using a Guinier camera. The temperature of the sample was controlled and maintained by a Thermo Haake DC50 heating circulator head combined with a Thermo Haake K20 refrigerator bath vessel and Haake based heat transfer fluid (SIL180), which was circulated about the sample holder via a heat exchanger block in order to achieve an accessible temperature range of -20 – 135 °C, with a sample temperature variation after stabilisation of approximately 0.1 °C. X-ray films were scanned at high resolution using an Epson Perfection 4990 Photo scanner, and subsequently processed and analysed using 'AXcess', a software program developed in-house by Dr. A. Heron. The calibrant used for the WAXS measurements was silver behenate (with d₀₀₁ = 58.38 Å).

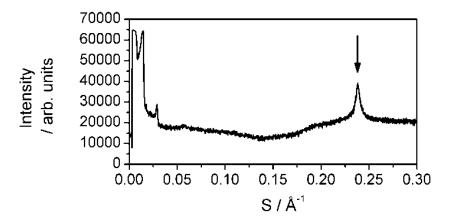


Fig. S1 The WAXS diffraction pattern produced by $C_{14}C_{16}EO_4$ / 66 wt% water held at 5°C, showing a single sharp peak at 4.20 Å signifying an L_β lamellar gel phase.

Determination of the unit cell parameters for the inverse ribbon phase

The cell parameters of the inverse ribbon phase (*a* and *b*) were determined from the Bragg peaks observed by using an iterative procedure written for usage in the IDL computing environment (ITT Visual Information Solutions). The main program 'cr_powell' calls the function 'powcr', in which the values of all observed peaks must be input.

pro cr_powell, event

; defining the fractional tolerance ftol = 1.0e-8 ; define the starting point ; here these correspond to initial a and initial c values P = [71, 83] ;Define the starting directional vectors in column format: xi = TRANSPOSE([[1.0,0.0],[0.0,1.0]]) ; minimise the function: POWELL, P, xi, ftol, fmin, 'powcr' ; print the solution point: print, 'a and b are: ', P ; print the value at the solution point - this is a least squares fit so should be as near 0 as possible print, 'value at the solution point: ', fmin end ; this is what you'll want to edit, notably changing the hkl if necessary (this shouldn't really be the

case)

; and change ep - the observed values that you obtained for each hkl

; note. if you don't have the exp value, then put 0 in. The program will then ignore it.

function powcr, X

; define a few Miller indices for 2d centred rectangular hkl=intarr(2,5) hkl=[[1,1],[0,2],[2,0],[2,2],[1,3]] ; define experimentally obtained lattice spacings exp=[54.20,43.13,34.81,27.09,26.65] ; calculate the calculated values of the interplanar spacings d=fltarr(5) n=n_elements(d) for i=0,n-1 do begin
if exp[i] eq 0 then d[i]=0 else \$
d[i]=1/(SQRT(((hkl[0,i]^2)/(X[0]^2)) + ((hkl[1,i]^2)/(X[1]^2))))
endfor
diffs=fltarr(5)
sumdiffs=0.0
; calculate the sum of the differences between the calculated and observed values
n=n_elements(exp)
for i=0, n-1 do begin
diffs[i]=(d[i]-exp[i])^2
sumdiffs=sumdiffs+diffs[i]
endfor
return, sumdiffs
end