five Met were substituted with Se-Met as determined by mass spectrometry.

Crystallization. Crystals of p58-cl42 were grown from 0.55 M $(NH_4)_2HPO_4$, 50 mM sodium citrate, pH 5.4, final pH 7.7. Hexagonal rods ($0.1 \times 0.1 \times 1.5\,mm^3$; space group $P6_1$; $a = b = 92.4$ Å, $c = 46.8$ Å; 1 molecule per asymmetric unit) grow two weeks after seeding. Se-met p58 crystallized under the same condition using the native crystals as seeds; the difference in cell dimensions was less than 0.5%. After the crystals were stabilized for at least 10 h in a harvesting solution (1.5 M $(NH_4)_2HPO_4$, 50 mM sodium citrate, pH 5.4, final pH 7.7), they were soaked for 2–5 min in a cryo-protecting solution (1.5 M $(NH_4)_2HPO_4$, 50 mM Na citrate, pH 5.4, 25% glycerol, final pH 7.7), and flash-cooled with liquid nitrogen.

Data collection. Multiwavelength anomalous dispersion (MAD)[26] data were collected to 2.2 Å with a 300-mm diameter MAR Research image-plate system at the X25 beamline of the National Synchrotron Light Source, Brookhaven National Laboratory. A high-resolution native data set was collected to 1.7 Å on the Princeton 2K CCD detector at F-1 beamline of the Cornell High Energy Synchrotron Source (CHESS). Data were processed (Table 1) using DENZO and SCALEPACK (HKL Research). Most of the subsequent processing used the CCP4 programs[19].

MAD phasing. MAD phasing was treated as a case of multiple isomorphous replacement[27]. Four selenium sites were identified from anomalous and dispersive difference Pattersons and were checked by difference Fouriers. The N-terminal methionine was disordered. Refinement of anomalous scatterer parameters and phase calculation were performed with MLPHARE[28]. Because of discrepancies between phasing statistics generated by MLPHARE and other programs[27], electron-density maps before and after model refinement are displayed instead of experimental phasing statistics (Fig. 4). The initial MAD map was improved by density modification using DM[19], assuming 40% solvent content. The correct space-group enantiomer $P6_1$ was identified by the presence of clear solvent boundary in the 2.2-Å electron-density maps.

Model refinement. The experimental MAD phases were used with the native data set to calculate the electron density for the native structure. Both density-modified and unmodified electron-density maps were used to build an 85% complete model with O (DATAONO AB). For refinement, data with $|F_{obs}| > 0$ were included. The model was initially refined at 10–2.2 Å using positional refinement and simulated annealing protocols in X-PLOR[29]. Several cycles of manual refitting and subsequent inclusion of lower-resolution data to 16 Å combined with bulk solvent correction allowed the missing loop regions to be traced. The resolution was then extended in one step to 1.7 Å. Refinement at this stage involved simulated annealing followed by *B*-factor refinement, with the extensive use of simulated annealing omit maps (Fig. 4b). The final model refined in X-PLOR contained residues 6–200 and 211 water molecules. This model was refined with REFMAC[19] (Table 1). The maximum-likelihood method in REFMAC lowered the *R*-values in the highest resolution shell (from 38.4 to 33.7% for R_{free} at 1.76–1.7 Å). All ϕ and ψ angles lie in the allowed regions of the Ramachandran plot, with 92% in the most favourable regions. Side-chain densities are well defined for all residues except 151–153 in a loop, which have *B*-factors >70 $Å^2$.

Figure preparation. Figures 1a, 2 and 3 were prepared using the program RIBBONS[30].

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erratum

Neurotactin, a membrane-anchored chemokine upregulated in brain inflammation

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The sequence of neurotactin reported in this Letter is identical to that of fractalkine, a CX_3C membrane-bound chemokine reported in a Letter by J. F. Bazan *et al.* in *Nature* **385,** 640–644 (1997), published while the paper by Pan *et al.* was under consideration. A note to this effect in the paper by Pan *et al.* was inadvertently omitted by *Nature*. □