2.3 Å resolution. The crystal belongs to space group $P2_1$, with cell dimensions of $a = 57.3$ Å, $b = 66.4$ Å, $c = 90.0$ Å and $\beta = 103.1°$. For the β_4 core crystal, a 3.0 Å resolution data set was collected. The crystal also belongs to space group $P2_1$, but is non-isomorphous with that of β_3 core, with cell dimensions of $a = 60.3$ Å, $b = 83.2$ Å, $c = 72.3$ Å and $\beta = 94.9°$. The data set for the β_3 core–AID crystal was collected to 2.6 Å resolution. It belongs to space group $C2$, with cell dimensions of $a = 252.3$ Å, $b = 69.0$ Å, $c = 60.7$ Å and $\beta = 96.7°$. There are two molecules in the asymmetric unit for all three crystals, giving a V_m (Matthew's coefficient) of 2.0 Å^3 Da^{-1}, 2.3 Å^3 Da^{-1} and 2.9 Å^3 Da^{-1}, respectively. All diffraction data were collected at the X4A beamline of the Brookhaven National Laboratory. The diffraction images were processed and scaled with the HKL package[22]. The data processing statistics are summarized in Supplementary Table 1.

Structure determination and refinement

The locations of Se atoms in the β_3 core crystal were determined with the program SOLVE[23]. Reflection phases to 2.3 Å resolution were calculated and improved with the same program, which also automatically located 50% of the residues in the molecule. The full atomic model was built into the electron density with the program O[24]. Structure refinement was carried out with the program CNS[25]. The structures of the β_3 core–AID complex and β_4 core were determined by the molecular replacement method with the program COMO[26] using the β_3 core structure as the model, and were refined as described above. The statistics on structural refinement are summarized in Supplementary Table 1. The current models fit the electron density map well and all main-chain dihedral angles are located in favourable regions on the Ramachandran plot (Supplementary Fig. 2).

Oocyte expression and electrophysiology

All constructs for oocyte expression were subcloned into variants of pGEMHE. cRNAs were synthesized *in intro* and injected in various combinations into *Xenopus* oocytes, which were obtained and maintained as described[27]. Two-electrode voltage-clamp recordings were performed as described[27]. Data are presented as mean ± s.d. (number of observations).

Received 5 March; accepted 10 May 2004; doi:10.1038/nature02641.
Published online 30 May 2004.

1. Catterall, W. A. Structure and regulation of voltage-gated Ca^{2+} channels. *Annu. Rev. Cell Dev. Biol.* **16,** 521–555 (2000).
2. Birnbaumer, L. *et al.* Structures and functions of calcium channel beta subunits. *J. Bioenerg. Biomembr.* **30,** 357–375 (1998).
3. Arikkath, J. & Campbell, K. P. Auxiliary subunits: essential components of the voltage-gated calcium channel complex. *Curr. Opin. Neurobiol.* **13,** 298–307 (2003).
4. Dolphin, A. C. β subunits of voltage-gated calcium channels. *J. Bioenerg. Biomembr.* **55,** 607–627 (2003).
5. De Waard, M., Pragnell, M. & Campbell, K. P. Ca^{2+} channel regulation by a conserved beta subunit domain. *Neuron* **13,** 495–503 (1994).
6. De Waard, M., Scott, V. E., Pragnell, M. & Campbell, K. P. Identification of critical amino acids involved in α1-β interaction in voltage-dependent Ca^{2+} channels. *FEBS Lett.* **380,** 272–276 (1996).
7. Pragnell, M. *et al.* Calcium channel β-subunit binds to a conserved motif in the I–II cytoplasmic linker of the α_1-subunit. *Nature* **368,** 67–70 (1994).
8. Canti, C. *et al.* Evidence for two concentration-dependent processes for β-subunit effects on α1B calcium channels. *Biophys. J.* **81,** 1439–1451 (2001).
9. Opatowsky, Y., Chomsky-Hecht, O., Kang, M. G., Campbell, K. P. & Hirsch, J. A. The voltage-dependent calcium channel beta subunit contains two stable interacting domains. *J. Biol. Chem.* **278,** 52323–52332 (2003).
10. Hanlon, M. R., Berrow, N. S., Dolphin, A. C. & Wallace, B. A. Modelling of a voltage-dependent Ca^{2+} channel beta subunit as a basis for understanding its functional properties. *FEBS Lett.* **445,** 366–370 (1999).
11. Hendrickson, W. A. Determination of macromolecular structures from anomalous diffraction of synchrotron radiation. *Science* **254,** 51–58 (1991).
12. Tavares, G. A., Panepucci, E. H. & Brunger, A. T. Structural characterization of the intramolecular interaction between the SH3 and guanylate kinase domains of PSD-95. *Mol. Cell* **8,** 1313–1325 (2001).
13. Zarrinpar, A., Bhattacharyya, R. P. & Lim, W. A. The structure and function of proline recognition domains. *Sci. STKE* **2003,** RE8 (2003).
14. Larson, S. M. & Davidson, A. R. The identification of conserved interactions within the SH3 domain by alignment of sequences and structures. *Protein Sci.* **9,** 2170–2180 (2000).
15. Blaszcyk, J., Li, Y., Yan, H. & Ji, X. Crystal structure of unligated guanylate kinase from yeast reveals GMP-induced conformational changes. *J. Mol. Biol.* **307,** 247–257 (2001).
16. Sheng, M. & Pak, D. T. Ligand-gated ion channel interactions with cytoskeletal and signaling proteins. *Annu. Rev. Physiol.* **62,** 755–778 (2000).
17. Beguin, P. *et al.* Regulation of Ca^{2+} channel expression at the cell surface by the small G-protein kir/Gem. *Nature* **411,** 701–706 (2001).
18. Finlin, B. S., Crump, S. M., Satin, J. & Andres, D. A. Regulation of voltage-gated calcium channel activity by the Rem and Rad GTPases. *Proc. Natl Acad. Sci. USA* **100,** 14469–14474 (2003).
19. McGee, A. W. *et al.* Structure of the SH3-guanylate kinase module from PSD-95 suggests a mechanism for regulated assembly of MAGUK scaffolding proteins. *Mol. Cell* **8,** 1291–1301 (2001).
20. Garcia, E. P. *et al.* SAP90 binds and clusters kainate receptors causing incomplete desensitization. *Neuron* **21,** 727–739 (1998).
21. Maximov, A., Sudhof, T. C. & Bezprozvanny, I. Association of neuronal calcium channels with modular adaptor proteins. *J. Biol. Chem.* **274,** 24453–24456 (1999).
22. Otwinowski, Z. & Minor, W. Processing of X-ray diffraction data collected in oscillation mode. *Methods Enzymol.* **276,** 307–326 (1997).
23. Terwilliger, T. C. & Berendzen, J. Automated MAD and MIR structure solution. *Acta Crystallogr. D* **55,** 849–861 (1999).
24. Jones, T. A., Zou, J. Y.,, Cowan, S. W. & Kjeldgaard, M. Improved methods for building protein models in electron density maps and the location of errors in these models. *Acta Crystallogr. A* **47,** 110–119 (1991).
25. Brunger, A. T. *et al.* Crystallography & NMR system: A new software suite for macromolecular structure determination. *Acta Crystallogr. D* **54,** 905–921 (1998).
26. Jogl, G., Tao, X., Xu, Y. & Tong, L. COMO: a program for combined molecular replacement. *Acta Crystallogr. D* **57,** 1127–1134 (2001).
27. Wu, L., Bauer, C. S., Zhen, X. G., Xie, C. & Yang, J. Dual regulation of voltage-gated calcium channels by PtdIns(4,5)P2. *Nature* **419,** 947–952 (2002).
28. Carson, M. Ribbon models of macromolecules. *J. Mol. Graph.* **5,** 103–106 (1987).
29. Nicholls, A., Sharp, K. & Honig, B. H. Protein folding and association: insights from the interfacial and thermodynamic properties of hydrocarbons. *Proteins Struct. Funct. Genet.* **11,** 281–296 (1991).
30. Kraulis, P. MOLSCRIPT: a program to produce both detailed and schematic plots of protein structures. *J. Appl. Crystallogr.* **24,** 946–950 (1991).

Supplementary Information accompanies the paper on **www.nature.com/nature**.

Acknowledgements We thank Y. Mori for $Ca_V2.1$ complementary DNA; E. Perez-Reyes for all β-subunit cDNAs; T. Tanabe for $\alpha_2\delta$ cDNA; and the staff at X4A of NSLS, Brookhaven National Laboratory, for synchrotron support. This work was supported by grants to L.T. and J.Y. from the National Institutes of Health. J.Y. is a recipient of the McKnight Scholar Award, the Scholar Research Programme of the EJLB Foundation and the Established Investigator Award of the American Heart Association.

Competing interests statement The authors declare that they have no competing financial interests.

Correspondence and requests for materials should be addressed to J.Y. (jy160@columbia.edu).
Coordinates have been deposited in the Protein Data Bank under accession codes 1VYU, 1VYT and 1VYV.

corrigendum

Photonic structures in biology

Pete Vukusic & J. Roy Sambles

Nature **424,** 852–855 (2003).

In this Insight Review Article, a reference to earlier work was inadvertently deleted on proof. The omitted citation is Parker, A. R. *Proc. R. Soc. B* **265**, 967–972 (1998). □