

peptides. However, it contradicts the fact that one side of a protein knows what has happened on the other side – a property which is needed for there to be communication across a protein.

When dynamical effects such as collective long-range modes are included in the description of proteins, it is clear that the docking of a peptide at a specific site will have a global influence on the wring mode – the standing collective mode of the folded protein (type II for the inequality above). Long-range wring modes can thereby form the foundation for communication. The importance of wring modes for protein–protein communication and peptide–protein chemistry will therefore need to be considered.

The existence of proteins with many sub-conformations has been suggested [13]. We note that switching between different wring states provides a means to switch between the different states of a protein.

#### *Enzymatic and electromagnetic activities*

The mechanism whereby some proteins exhibit enzymatic activity is not fully understood. Standing wring modes in proteins can provide an attractive energy basin as well as mechanical action in this regard. Finally, there appears to be evidence that the interaction of non-ionizing electromagnetic radiation with biological systems is not completely understood, as is suggested by recent epidemiological studies [14]. Collective modes in proteins and other chain molecules will couple to electromagnetic radiation and therefore form the basis for an additional interaction between electromagnetic radiation and biological systems.

#### References

- [1] Griko Y.V., *et al.*, *J. Mol. Biol.* **202** (1988) 127.
- [2] Wolynes P.G., Onuchic J.N. & Thirumalai D., *Science* **276** (1995) 1619.
- [3] Dill K.A., *et al.*, *Protein Sci.* **4** (1995) 561.
- [4] Branden C. & Tooze J., *Introduction to Protein Structure* (Garland, NY) 1991.
- [5] Zwanzig R., *Proc. Nat. Acad. Sci. USA* **92** (1995) 9801.
- [6] Iori G., *Int. J. Neural Systems* **3** (1992) 201.
- [7] White J.H., *Amer. J. Math.* **91** (1969) 693.
- [8] Bohr J., Bohr H. & Brunak S., in: *Protein Folds: A Distance-Based Approach*; Eds. H. Bohr & S. Brunak (CRC Press, New York) 1995.
- [9] Eyles S.J., *et al.*, *Biochem.* **33** (1994) 13038.
- [10] Sosnick T.R., *et al.*, *Biophys. J.* **70** (1996) A378.
- [11] Berman A., *et al.*, *Proc. Nat. Acad. Sci. USA* **91** (1994) 4044.
- [12] Miura N., *et al.*, *Biopolymers* **34** (1994) 357.
- [13] Frauenfelder H., Sidlar S.G. & Wolynes P.G., *Science* **254** (1991) 1598.
- [14] Infante-Rivard C., *The Lancet* **346** (1995) 177.

## Highlights

### Element 112 Discovered

An international team based at the Gesellschaft für Schwerionenforschung (GSI), Darmstadt, and led for more than 20 years by P. Armbruster discovered on 9 February 1996 its sixth element, which has an atomic number of 112 and is the heaviest ever produced [S. Hofmann, *et al.*, submitted to *Z. Physik A*, 21 February 1996]. Two decay chains of the isotope  $^{277}112$  were observed in irradiations of  $^{208}\text{Pb}$  targets with  $^{70}\text{Zn}$  projectiles having a kinetic energy of 344 MeV. The isotope decayed by the emission of  $\alpha$ -particles with a half-life of  $240^{+430}_{-90}$  ms. Two different  $\alpha$ -energies were measured for the two observed decays.

Previous work [see *EN* **26** (1995) 103] using  $^{208}\text{Pb}$  and  $^{204}\text{Bi}$  had led to the discovery of  $^{269}111$ ,  $^{271}110$  and  $^{273}111$  nuclei produced by fusion reactions with the emission of one neutron. The measured cross-sections gave an estimated cross-section of 1–3 pb for the production of the isotope  $^{277}112$  by the  $^{70}\text{Zn} + ^{208}\text{Pb}$  reaction (the measured value turned out to be  $1.0^{+1.2}_{-0.4}$  pb).

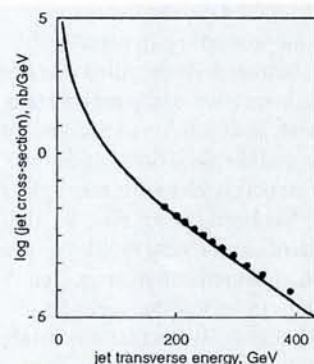
The energy of the  $\alpha$ -particles allows a very important theoretical prediction to be verified. Atomic nuclei with 162 neutrons should be more strongly bound than their neighbours because of their inner structure. Such structure phenomena led to the prediction some 30 years ago that super-heavy nuclei with a neutron number near 184 could exist; the same structure explains the existence of the six heaviest elements, all of which have been discovered at GSI. The decay chain of element 112, which demonstrates the stabilization at 162 neutrons, confirms the predictive power of the model for nuclear structure and must be regarded as a major success for nuclear physics.

The team had looked for the isotope  $^{290}116$  late last year, but since systematics in this range of atomic numbers are less well established than for 112, identifying the optimum beam energy was difficult. Nonetheless, the successful production of the element 112 confirms that it should be possible to continue to penetrate further into the region of super-heavy atoms.

### Data Question Quark Structure

The 450-member Collider Detector at Fermilab (CDF) collaboration has reported data [F. Abe, *et al.*, FERMILAB-PUB-96/020-E; submitted to *Phys. Rev. Lett.* (24 January 1996)] from experiments carried out over the past two years at the Fermi National Accelerator Laboratory's Tevatron Collider showing that the probability of particle scattering in high-energy proton–antiproton collisions is significantly larger than that predicted by current theoretical models. Collaborators believe that more studies of both experimental data and theoretical analyses will show whether relatively small adjustments to theory can reconcile the discrepancy, or whether the data are the first hint that quarks are made up of something smaller and may not be fundamental after all.

One prosaic explanation for the observed discrepancy is that the quark–gluon mixture



A comparison of the inclusive jet cross-section (points) for pp collisions observed at CDF with the cross-section predicted by perturbative quantum chromodynamics for jet transverse energies of 15–440 GeV. The CDF cross-section is larger than the QCD prediction above 200 GeV. From F. Abe, *et al.*, FERMILAB-PUB-96/020-E.

which makes up the proton shares the momentum of the proton in such a way that one piece carries a larger fraction of the momentum than previously believed. This interpretation needs to be reconciled with a large body of data from many other experiments.

### A Dry, Windy, Rocky Jupiter

Preliminary analyses of data from the Galileo atmospheric probe that plunged into Jupiter last December gave an estimated ratio of helium to hydrogen by mass – a key parameter for theories of planetary evolution – of only 14% for Jupiter. A more comprehensive analysis has raised this estimate to 24%, so the ratio of the two elements making up 99% of the Jovian atmosphere closely matches that found in the Sun. This suggests that Jupiter's bulk composition has not changed since the planet formed from the primitive solar nebula which spawned the planets. The revised helium abundance also indicates that gravitational settling of helium toward the interior of Jupiter has not occurred nearly as fast as it apparently has on Saturn, where the approximate helium-to-hydrogen ratio is 6%. This may force a revision of projections for the size of the rocky core believed to exist deep in the centre of Jupiter.

Estimated amounts of key heavy elements such as carbon and sulphur (probably from the influx of meteorites and other small bodies) have increased, but minimal organic compounds were detected. The detection of minimal amounts of organic compounds indicate that such complex combinations of carbon and hydrogen are rare on Jupiter, and that the chances of finding biological activity are extremely remote. Measurements also suggest much less water than the amounts found on the Sun and predicted from data sent by the Voyager spacecraft that flew by Jupiter in 1979.

Preliminary estimates of wind speeds have grown from 530 km/h to more than 640 km/h. The winds persisted far below the one cloud layer detected, strongly suggesting that the winds – a feature of all the giant outer planets – are driven by heat escaping from deep in the planet's interior rather than by solar heating.