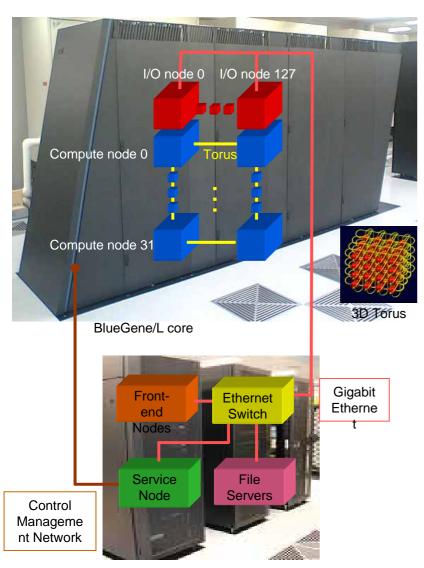
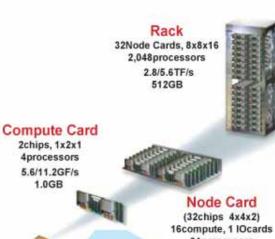
BlueGene/L System



Front End Node, Service Node, File System

| Processor | 8,192 processors (Dual PowerPC 440 700MHz; per node) |
|----------------------|--|
| Memory | 2 TeraBytes (512 MB SDRAM-DDR per node) |
| Networks | 3D Torus - 175MB/sec in each direction Collective Network — 350MB/sec; 1.5 µ sec latency Global Barrier/Interrupt Gigabit Ethernet (machine control and outside connectivity) |
| Compute Nodes | Dual processor; 4096 nodes (1024 nodes per rack) |
| I/O Nodes | Dual processor; 128 nodes (32 nodes per rack) |
| Operating Systems | Compute Node – Lightweight proprietary kernel I/O Node – Embedded Linux Front End Nodes – SuSE SLES 9 Linux Service Nodes – SuSE SLES 8 Linux |
| Performance | 22.9 teraflops peak (virtual node mode) 11.4 teraflops peak (coprocessor mode) 18.2 teraflops Linpack |
| Size | Width:4517mm / Depth:915mm / Height:1958mm Weight:2740kg |
| Power | 124kVA (31kVA/rack) |
| | |
| File System | General Parallel File System for Linux 8 File Servers (xSeries 345), 20TeraByte Disk System |
| Front End Node | 2way Power5 1.65GHz (p520), C++, Fortran |
| Service Node | 4way Power4+ 1.5GHz (p650), DB2 UDB |





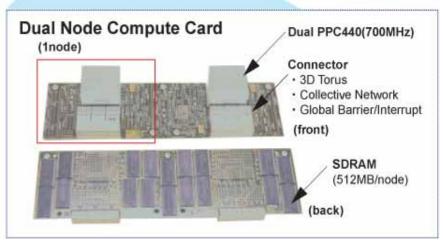
Chip

2processors

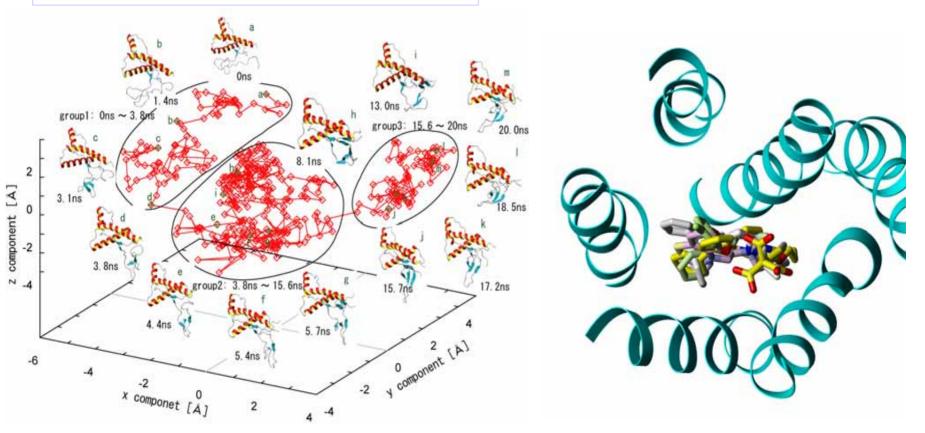
2.8/5.6GF/s







Possible applications at CBRC



A trajectory of a disease-related mutant of human prion protein (P102L) projected along its first three principal components (by Sekijima et al.).

Molecular dynamics simulations

Analysis of the molecular dynamics of diseaserelated proteins, or target proteins of drug design. Complex model of histamine H1 receptor (light blue) and its antagonist (by Hirokawa).

Protein-ligand docking simulations

Protein-ligand binding prediction,

estimation of binding free energy, etc.