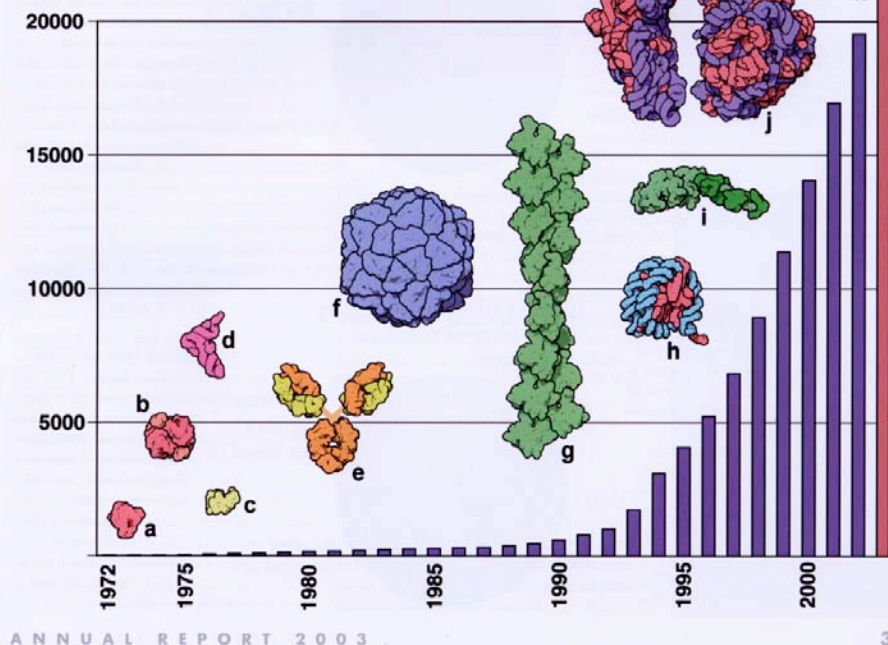


# J-PARCでの構造生物

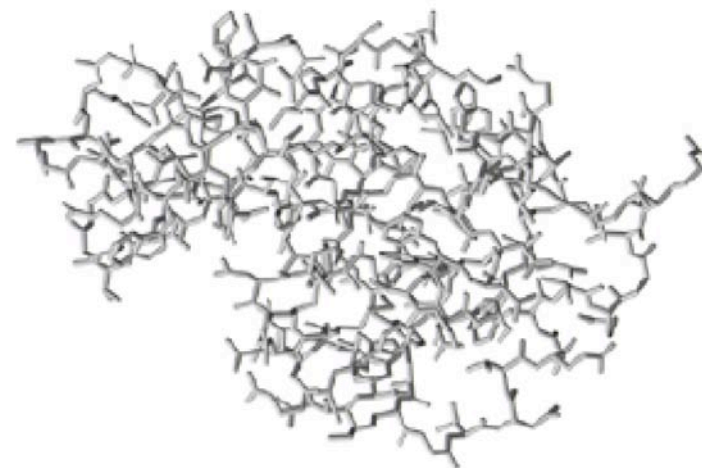
新村信雄  
茨城大学大学院応用粒子線科学専攻

This chart shows the increase in the total number of structures in the PDB per year, through July 1, 2003, as well as examples of the increasing complexity of these structures. In the 1970's, the first structures available to the scientific community included proteins such as a. myoglobin,<sup>3,4</sup> b. hemoglobin,<sup>5,6</sup> and c. lysozyme,<sup>7,8</sup> and other molecules such as d. transfer RNA.<sup>9,12</sup> In the 1980's, advances in experimental data collection methods allowed much larger structures to be solved, including e. antibodies,<sup>13,14</sup> and f. entire viruses.<sup>15</sup> By 2003, all aspects of structural science have advanced so that very complex and functionally significant structures could be made accessible to study, including g. actin,<sup>16</sup> the h. nucleosome,<sup>17</sup> i. myosin,<sup>18</sup> j. ribosomal subunits,<sup>19,21</sup> and the k. calcium pump.<sup>22</sup> Structures pictured here were taken from PDB entries 1mbn, 2dhh, 2lyz, 4tna + 6tna, 1fc1 + 1mcp, 2stv, 1ato, 1aol, 1dfk, 1ffk + 1fka + 1j5e, and 1iwo, respectively. Images were created by David S. Goodsell of The Scripps Research Institute, creator of the PDB Molecule of the Month series.

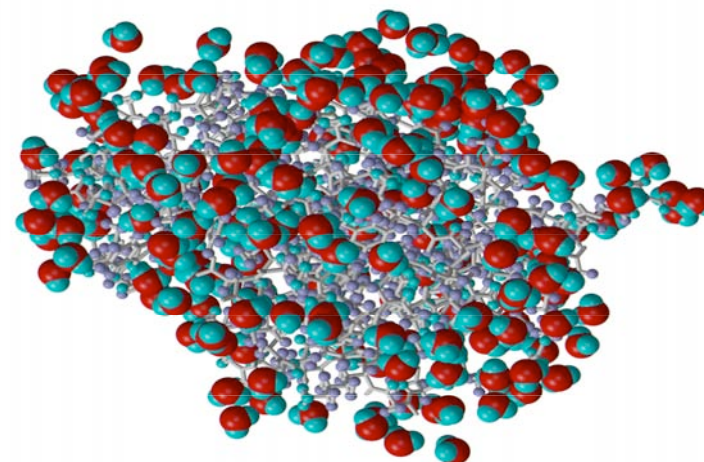


ドラッグデザインなど創薬への応用

## タンパク質の水素・水和分子

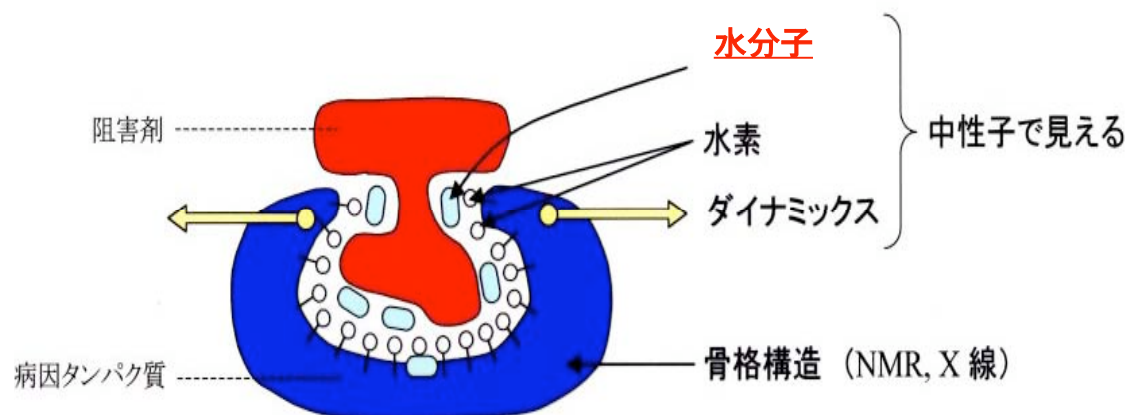


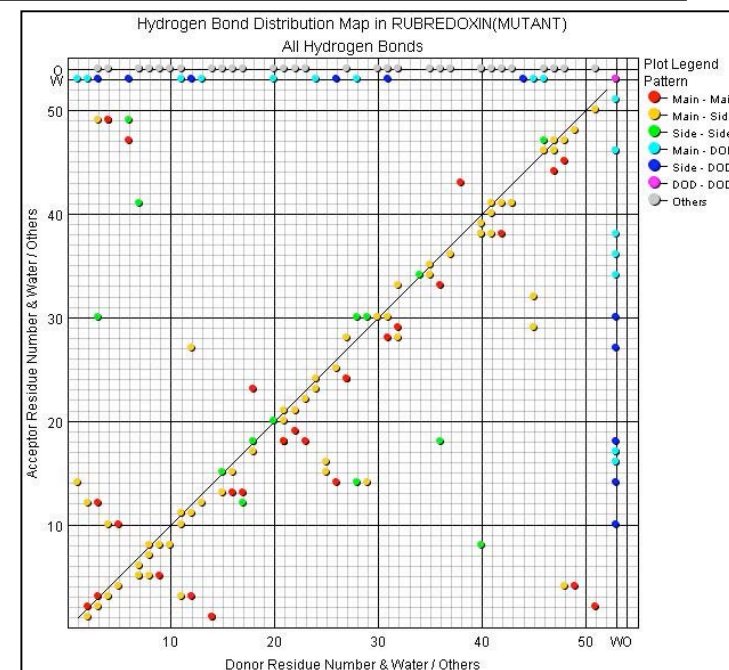
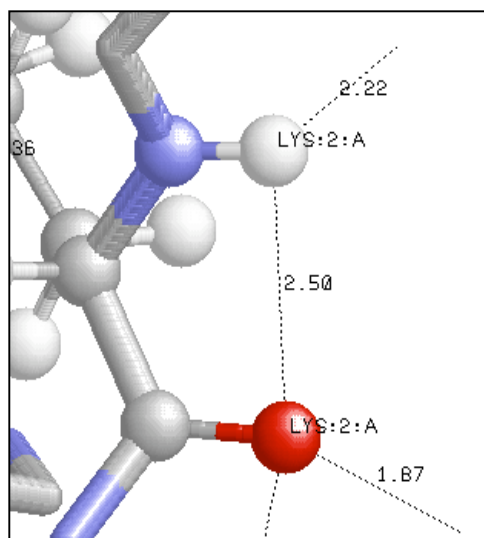
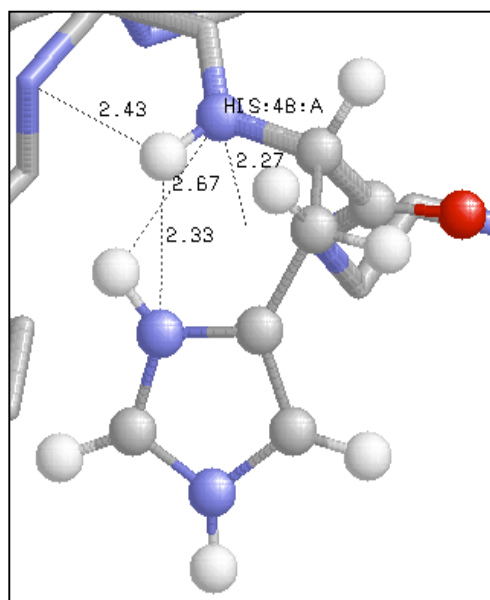
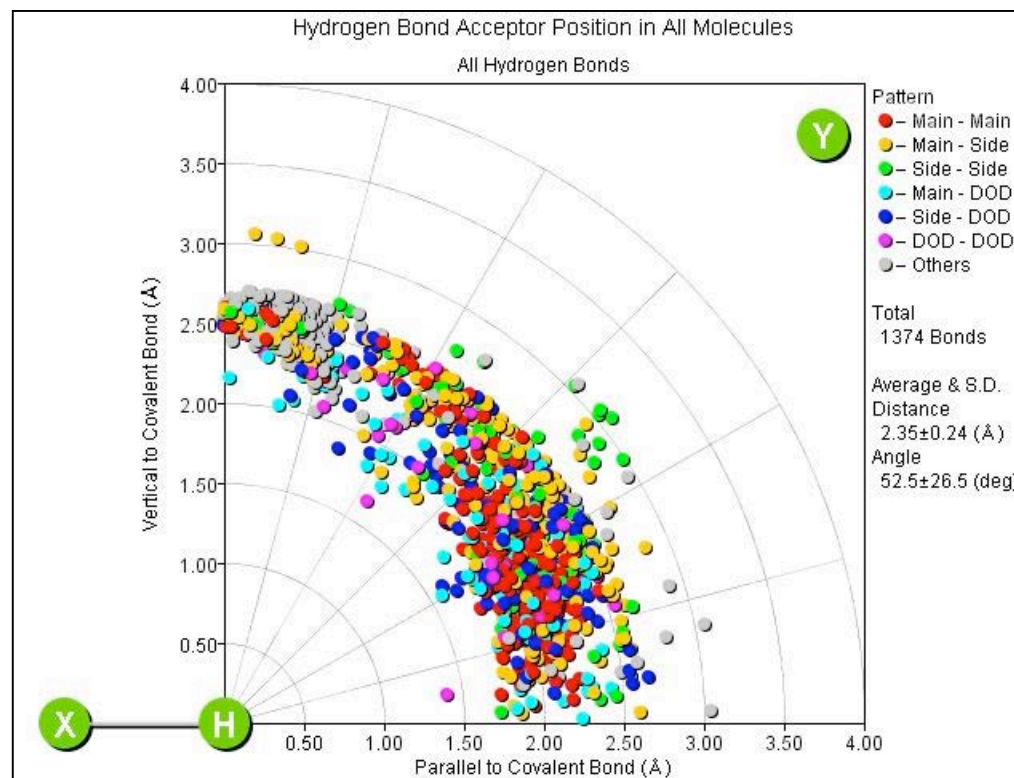
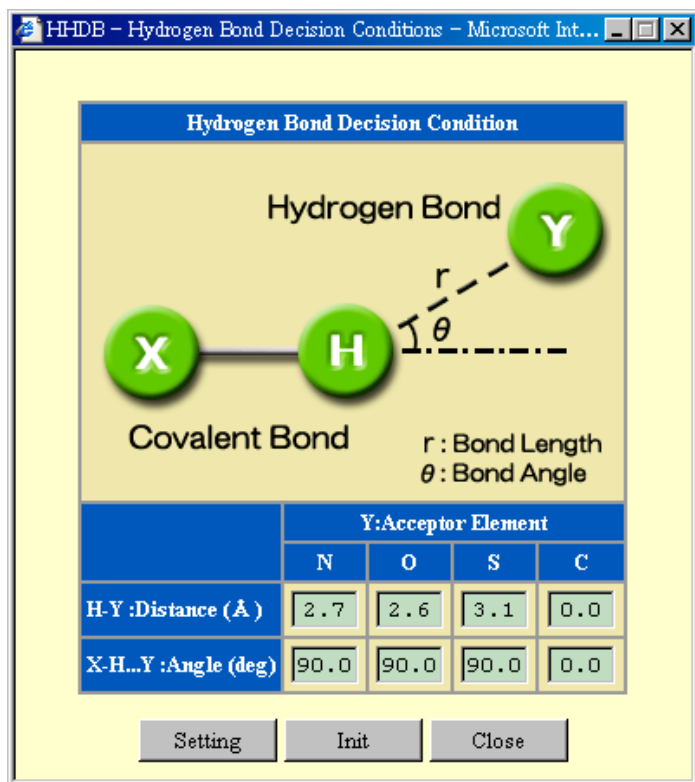
X線構造解析



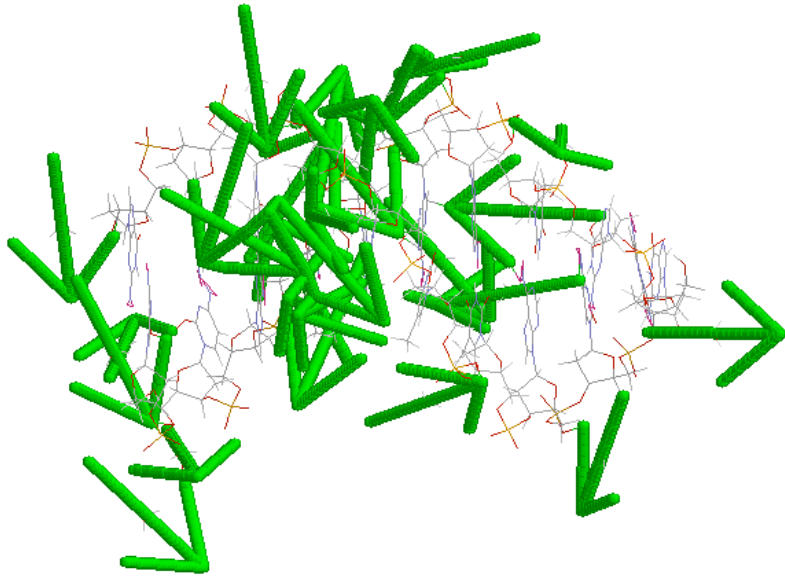
中性子構造解析

5-10 Proteins /year

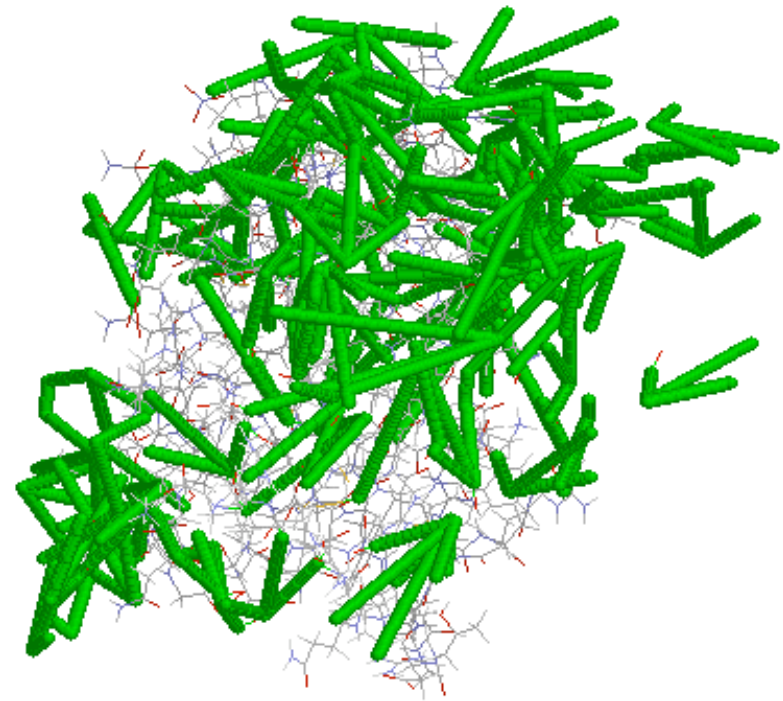




## Dipole Moment of Hydration Water molecules



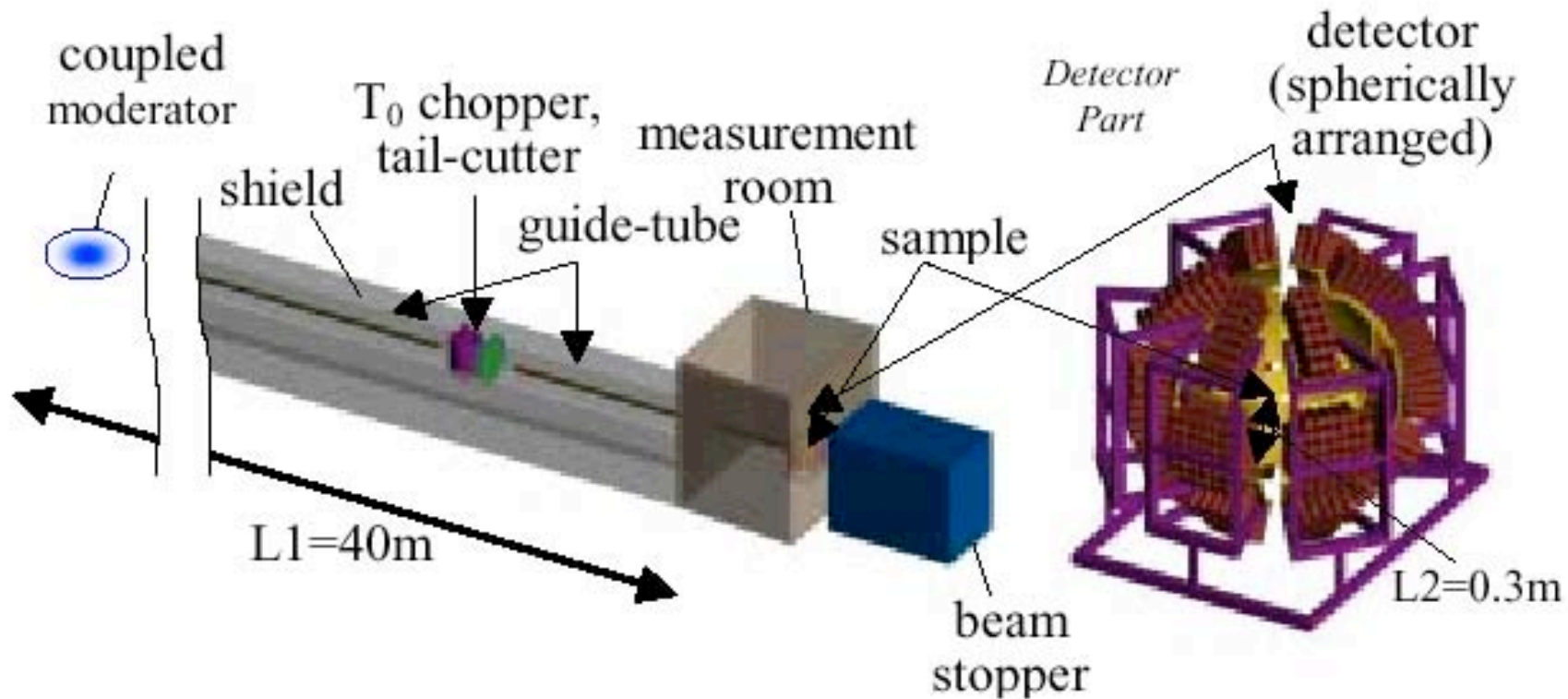
B-DNA(CCATTAATGG)<sub>2</sub>



Hen Egg White  
Lysozyme



# Diffractionmeter for Bio-Macromolecule at J-PARC



*Figure 8: Three-dimensional image of BIX-P1.*

100 - 150 times detection Efficiency

200 - 500 proteins / year of 1 mm<sup>3</sup> crystal

50 - 100 proteins /year of 0.5mm x 0.5mm x 0.5mm crystal