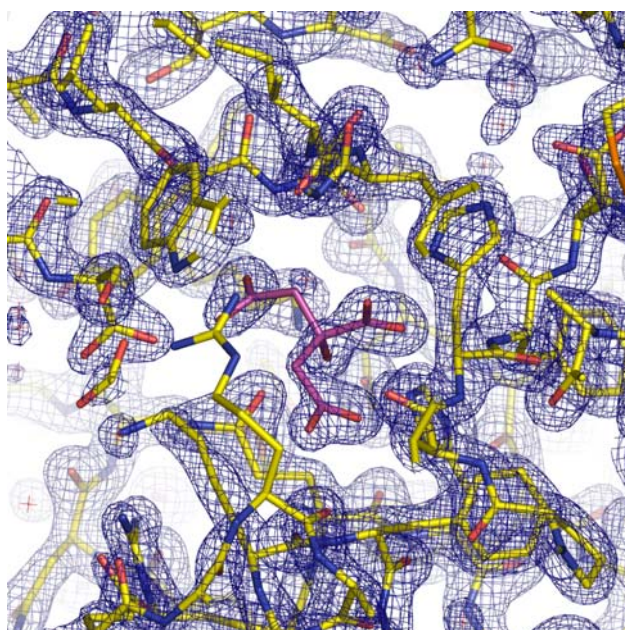
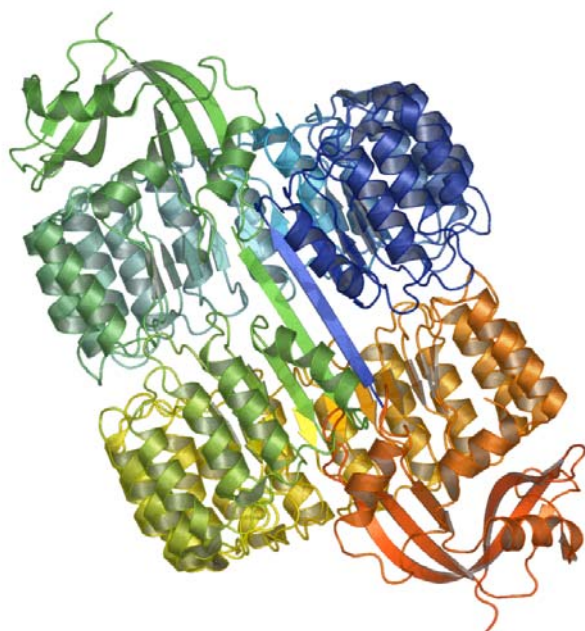




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|---------------------------|--|---------------------------------|
| Target ID | GO.78623 and GO.74631 | |
| Source Organism | <i>Homo sapiens</i> | |
| Target Name | RNase/hRI Complex | |
| PDB Entry | 1Z7X | Deposition: 21-Jun-2005 |
| Function | pancreatic ribonuclease A complexed with inhibitor (EC 3.1.27.5) (FF/Refine: 2Q4G) | |
| Produced From | <i>E. coli</i> BL21(DE3) pET-22B | |
| Structure by X-ray | Resolution: 1.95 Å | R-value (R-free): 17.8% (23.6%) |
| | No. of Residues/ASU: 1175 | Complexes/ASU: 2 |
| Data Collected At | Advanced Photon Source SBC 22-ID 12-Mar-2005 | |
| Authors | J.G. McCoy, G.N. Phillips, Jr., E. Bitto, G.E. Wesenberg, C.A. Bingman | |



Structural Features

The x-ray crystal structure of human ribonuclease inhibitor (hRI) in complex with human pancreatic ribonuclease (RNase 1), solved in collaboration with the Ronald Raines lab (also at UW-Madison Biochemistry), gives a molecular picture of how the cell regulates the potentially damaging activity of RNase 1. It is the third structure of hRI in complex with a member of the ribonuclease A (RNase A) superfamily. By comparison to the other three structures, the hRI/RNase 1 complex shows the plasticity and generality of the leucine-rich repeat structure of hRI for accommodating, but still tightly inhibiting different members of the RNase A superfamily. Ribonucleases show promise as possible cancer therapeutics. Ribonucleases can be transformed into cancer therapeutics by blocking the inhibitory interaction of hRI. Creating variants of RNase 1 that evade hRI has been difficult, but this crystal structure may provide the important link to create cancer therapeutics using RNase 1.

References: (1) Johnson, R.J., McCoy, J.G., Bingman, C.A., Phillips, G.N., Jr., Raines, R.T. (2007) Inhibition of human pancreatic ribonuclease by the human ribonuclease inhibitor protein. *J Mol Biol* 368(2):434-49.

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|---|------------------------|
| Percent Identity with Nearest PDB Structure at Time Solved | 91% over 127 aa (1E21) |
| | 95% over 460 aa (2BEX) |
| Pfam Cluster | RNase_A, |
| Sequence Cluster Size : Structures in PDB | 449 and 883 |

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