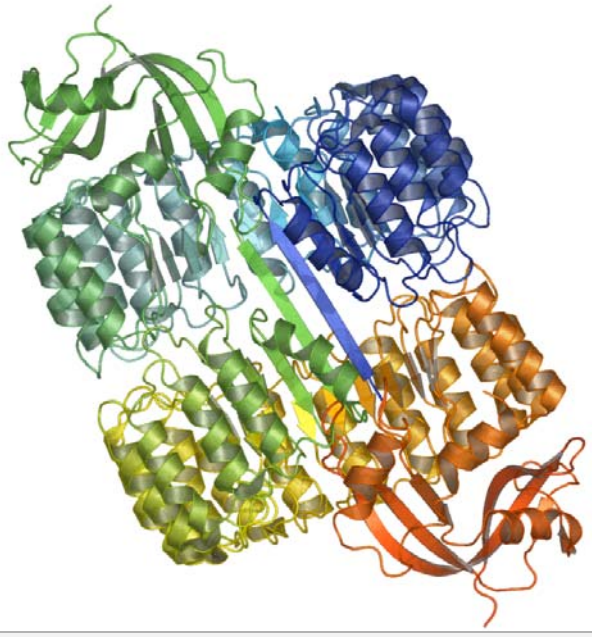
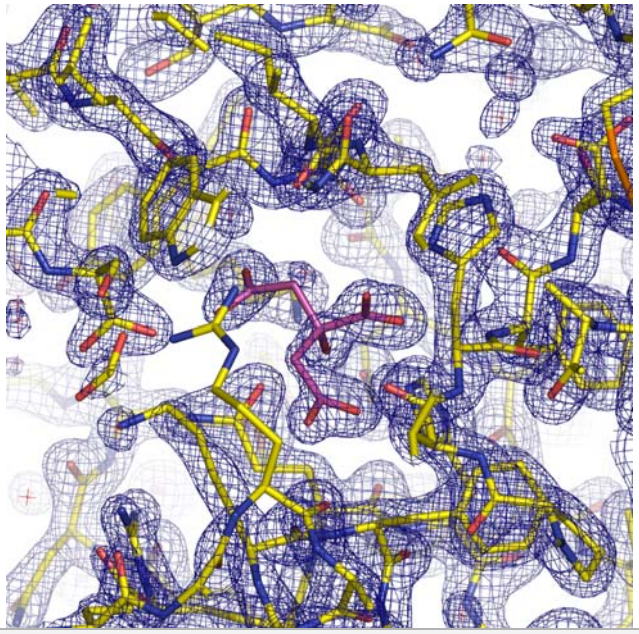
Center for Eukaryotic Structural Genomics

Protein Structure Initiative

Target ID	GO.78623 and GO.74631	
Source Organism	*Homo sapiens*	
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	*E. coli* 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.

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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