Chapter 9.11

R-TENSOR

Sean Parkin, Biochemistry Department, Box 3711, Duke University Medical Center Durham NC, USA email : <u>mailto:sparkin@pop.uky.edu</u> The program R-tensor calculates the anisotropic R tensor as described by Parkin (*Acta Cryst* (2000), **A56**, 157-162), an agreement index which is dependent on the reciprocal space directions.

The results are printed in CIF format (file *RT.CIF*) for each reflection, and a short summary file is printed to the TextServer. The only required input is a *name.FCF* file, which must be in the LIST 4 format output from SHELXL.

A sample output is :

Rcryst	=	0.0248						
Average Reff	=	0.0248						
Highest Reff	=	0.0294	for	-1	2	-1		
Lowest Reff	=	0.0219	for	1	7	7		
Axial R(h00)	=	0.0261						
Axial R(OkO)	=	0.0261						
Axial R(001)	=	0.0252						
No. of data	=	3881						
R-tensor in m	natrix	form :		1.0510	C	-0.0871	0.2020	
			-	-0.0873	1	1.0524	-0.1431	
				0.2020	0	-0.1431	1.0144	
Eigenvalues d	of R−te	ensor :		1.3303	1	0.9705	0.8172	
Results written to file RT.CIF								

When using this program please quote : S. Parkin (2000), Acta Cryst, A56, 157-162 $\,$