



	<b>Experiment title:</b> <b>A number of Proteins from Bacteria to Eukarya and from Antarctic to Volcanic Areas</b>	<b>Experiment number:</b> LS-1824
<b>Beamline:</b> <b>ID14-3</b>	<b>Date of experiment:</b> from: 9 Feb. 2001 to: 12 Feb. 2001	<b>Date of report:</b> 28/02/01
<b>Shifts:</b> <b>9</b>	<b>Local contact(s):</b> <b>Dr. Hassan Belrhali</b>	<i>Received at ESRF:</i>
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## Report:

The crystals of retinol dehydratase (iRD) in complex with the cofactor PAPS diffracted up to 2.0Å. However, these crystals suffer from apparently high anisotropic mosaicity, possibly due to their bidimensional character. All crystals tested at the ID14-3 beamline showed this marked anisotropic behaviour, and did not seem to provide an improvement from already existing data, despite the higher resolution to which they diffracted.

Four different data set were collected on the Retinol Binding Protein (RBP) at three different pHs of 3, 5, and 7.

The table below summarizes the data processing for data set at pH=7 (max. Resolution 1.27 Å).

N	1/d <sup>2</sup>	Dmin(A)	Rfac	Rfull	Rcum	Ranom	Nanom	Av_I	SIGMA	I/sigma	sd	Mn(I)/sd	Nmeas	Nref
1	0.0616	4.03	0.055	0.045	0.055	0.000	0	56244.	5831.3	9.6	3621.	30.8	5688	1227
2	0.1233	2.85	0.051	0.043	0.052	0.000	0	52877.	4926.7	10.7	3640.	29.1	10752	2370
3	0.1849	2.33	0.055	0.041	0.053	0.000	0	18777.	1972.6	9.5	1562.	22.3	10243	3116
4	0.2466	2.01	0.054	0.037	0.053	0.000	0	13773.	1372.2	10.0	1207.	20.6	12022	3696
5	0.3082	1.80	0.059	0.043	0.053	0.000	0	7139.	779.9	9.2	659.	18.1	13501	4171
6	0.3699	1.64	0.063	0.049	0.054	0.000	0	3452.	365.5	9.4	356.	15.6	14900	4641
7	0.4315	1.52	0.079	0.061	0.054	0.000	0	2122.	269.4	7.9	275.	12.5	15906	4965
8	0.4931	1.42	0.106	0.085	0.055	0.000	0	1340.	213.4	6.3	254.	9.0	17068	5368
9	0.5548	1.34	0.161	0.127	0.056	0.000	0	812.	405.6	2.0	232.	6.4	17616	5548
10	0.6164	1.27	0.237	0.194	0.057	0.000	0	576.	290.0	2.0	242.	4.0	10362	3502
Overall:			0.057	0.045	0.057	0.000	0	11488.	2039.7	5.6	935.	14.4	128058	38604

N	1/resol <sup>2</sup>	Dmin	Nmeas	Nref	Ncent	%poss	Cm%poss	Mlplcty	AnomCmpl	AnomFrc	Rmeas	Rmeas0	(Rsym)
1	0.062	4.03	5841	1380	337	89.5	89.5	4.2	0.0	0.0	0.063	0.063	0.055
2	0.123	2.85	10916	2534	359	95.4	93.3	4.3	0.0	0.0	0.058	0.058	0.051
3	0.185	2.33	10464	3337	389	98.4	95.7	3.1	0.0	0.0	0.066	0.066	0.055
4	0.247	2.01	12315	3989	432	99.8	97.1	3.1	0.0	0.0	0.065	0.065	0.054
5	0.308	1.80	13831	4501	448	99.7	97.9	3.1	0.0	0.0	0.072	0.072	0.059
6	0.370	1.64	15238	4979	451	100.3	98.4	3.1	0.0	0.0	0.077	0.077	0.063
7	0.432	1.52	16289	5348	451	99.4	98.6	3.0	0.0	0.0	0.096	0.096	0.079
8	0.493	1.42	17484	5784	454	100.4	98.9	3.0	0.0	0.0	0.129	0.129	0.106
9	0.555	1.34	18133	6065	437	99.2	99.0	3.0	0.0	0.0	0.194	0.194	0.161
10	0.616	1.27	11178	4318	275	67.1	94.3	2.6	0.0	0.0	0.291	0.291	0.237
Overall			131689	42235	4033	94.3	94.3	3.1	0.0	0.0	0.067	0.067	0.057

At the moment (28/02/01), further shifts are requested on ID14-3 beamline to complete this study as pH function.