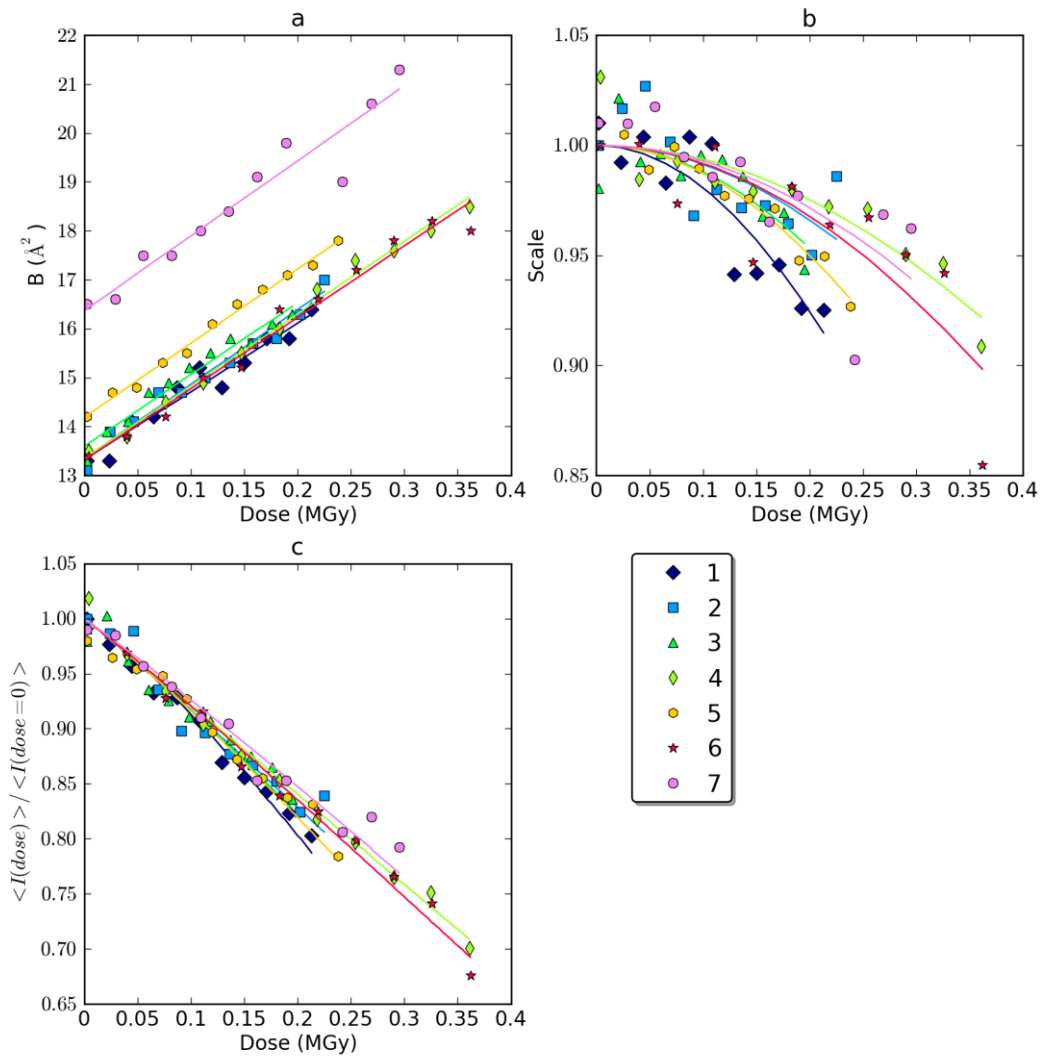


### Supplementary Figure

Variation in the scaling parameters and total scattering intensity with dose for fifteen different protein crystal types at room temperature. All sets of measurements are shown; each of the sets of symbols is a different series of wedge measurements. (a) B-factors: the solid line represents an approximation according to eq. 2 using the best fit of  $B_0$  and  $\beta$ . (b) *scale* factors divided by the *constant* (eq. 3), the solid line represents  $\exp(-\gamma^2 D^2)$  using the best fit value of  $\gamma$ . (c) Total scattered intensity, estimated by intensity summation (dots) and calculated according to Eq. (4) (solid lines), using the best fit  $B_0$ ,  $\beta$  and  $\gamma$  as in (a) and (b).

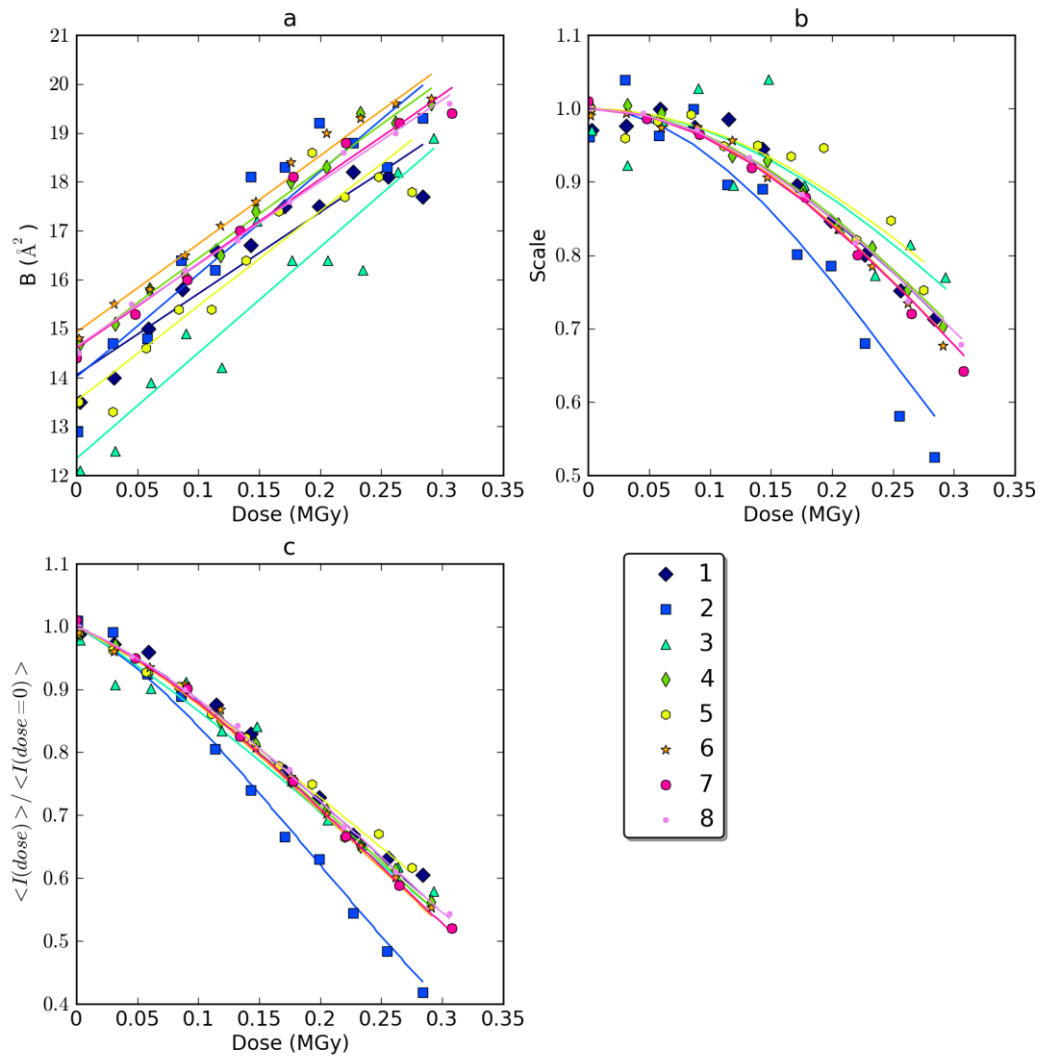
### Lysozyme monoclinic

LYZM



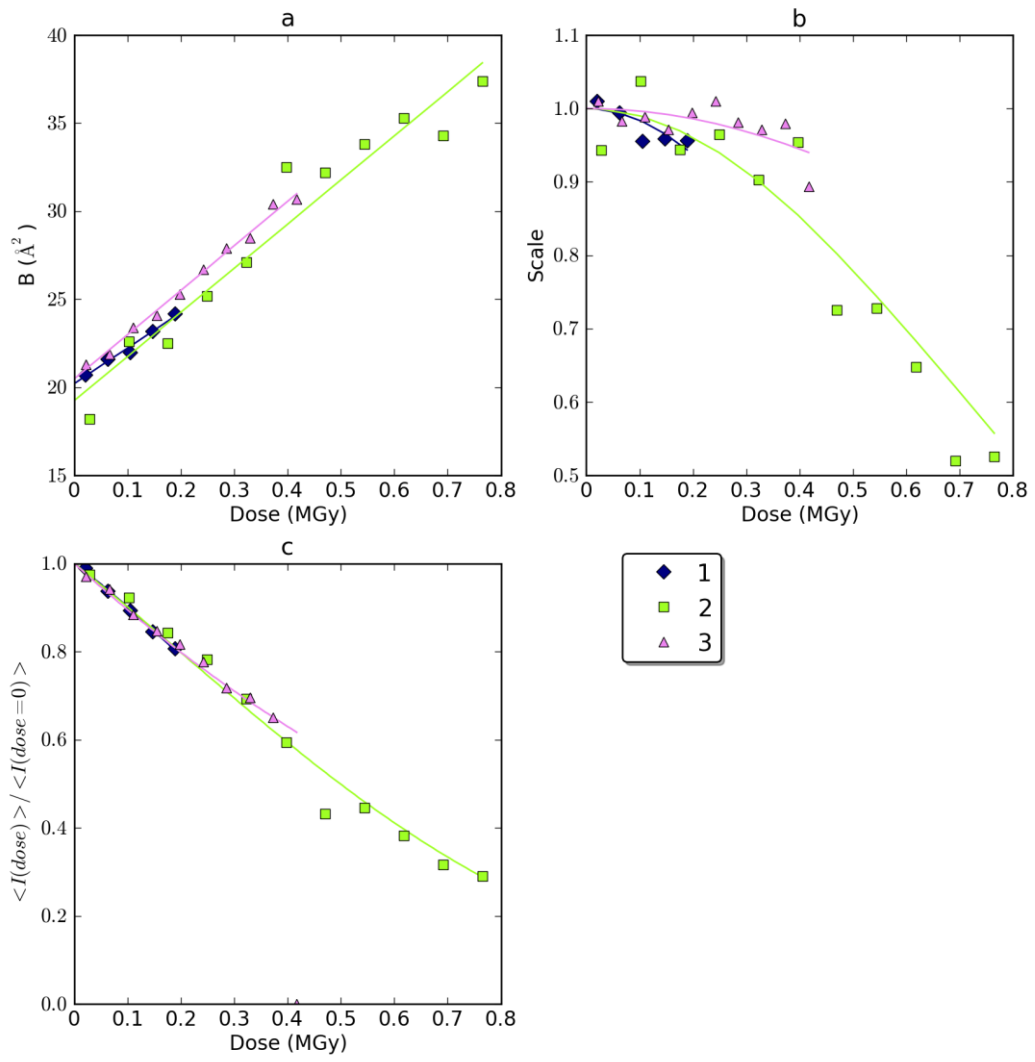
# Lysozyme tetragonal

LYZT



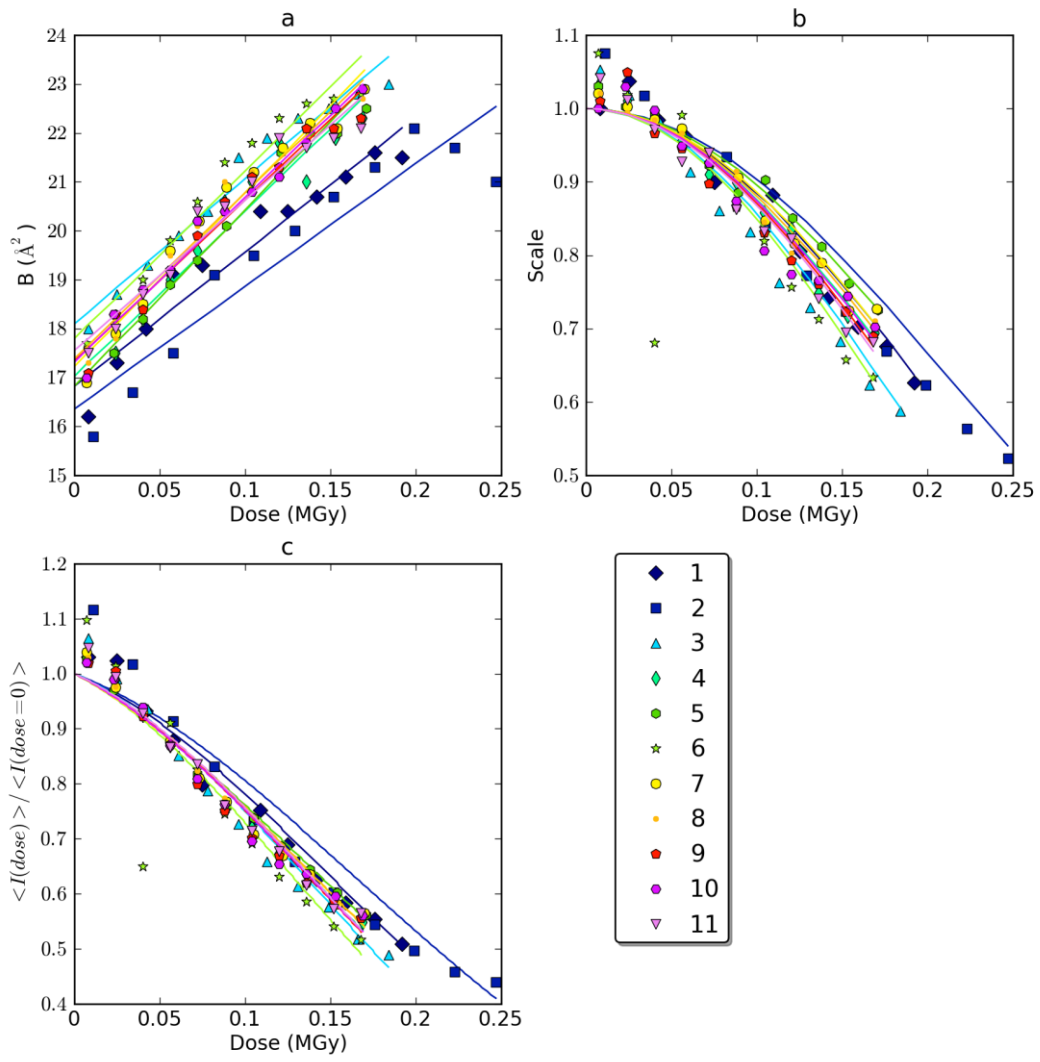
# Insulin rhombohedral

INSR



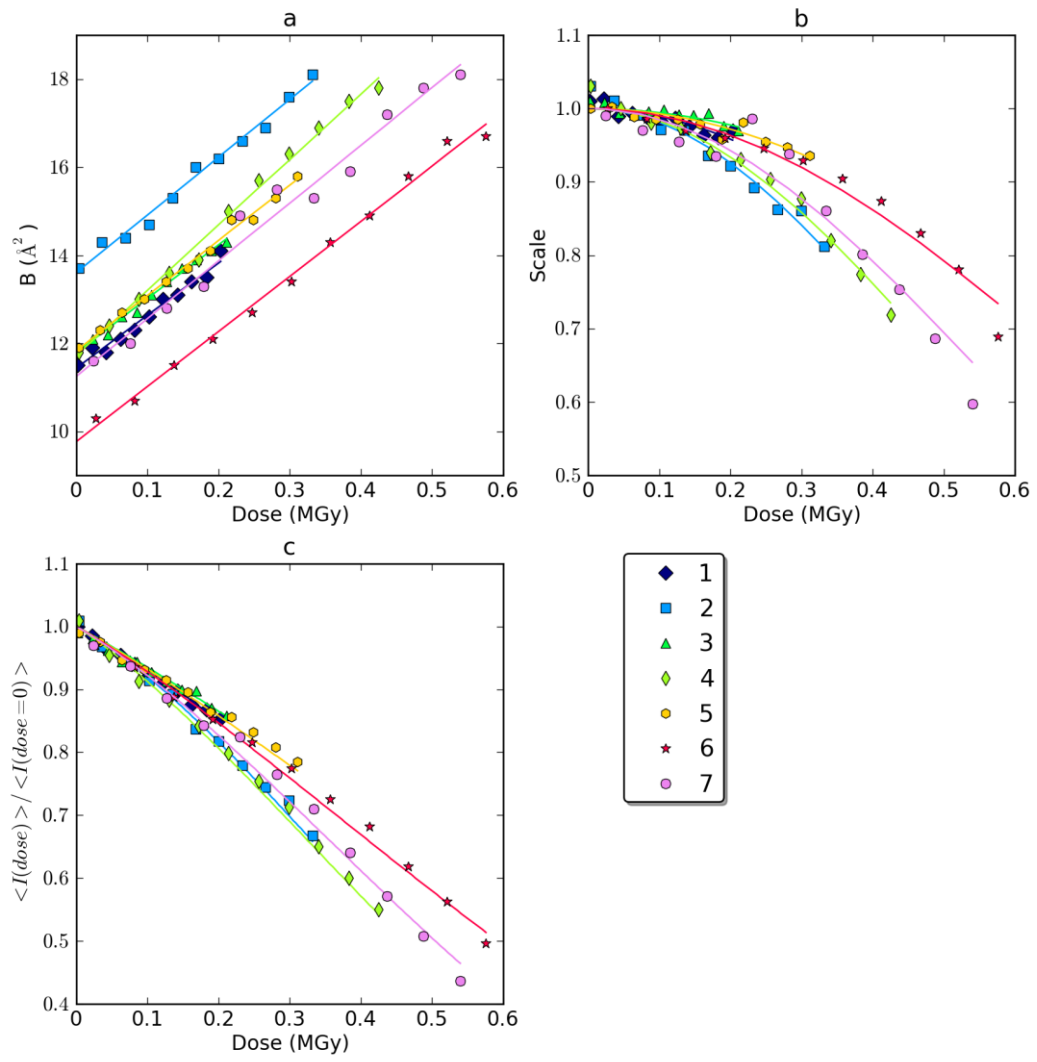
# Insulin cubic

INSC



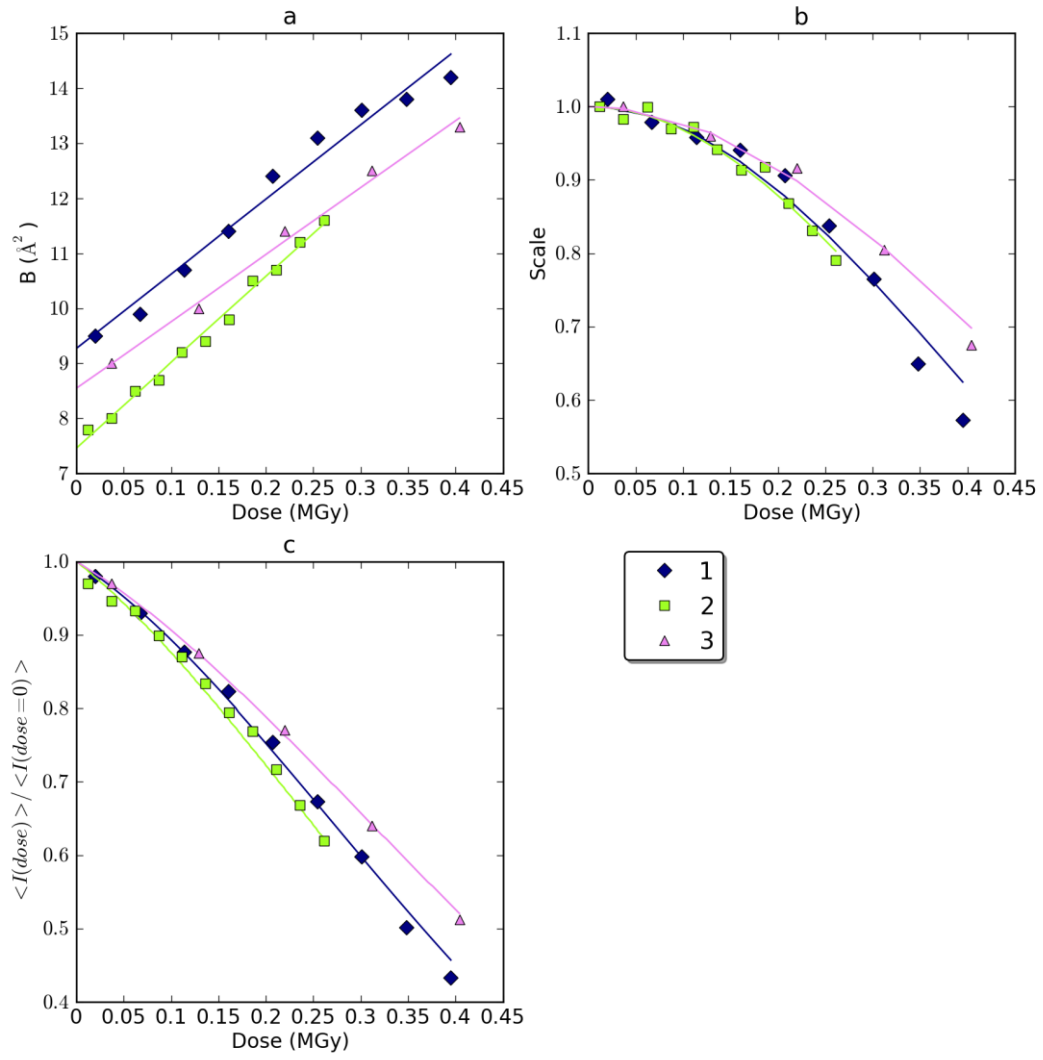
# Bovine pancreatic trypsin, trigonal

BPTRR



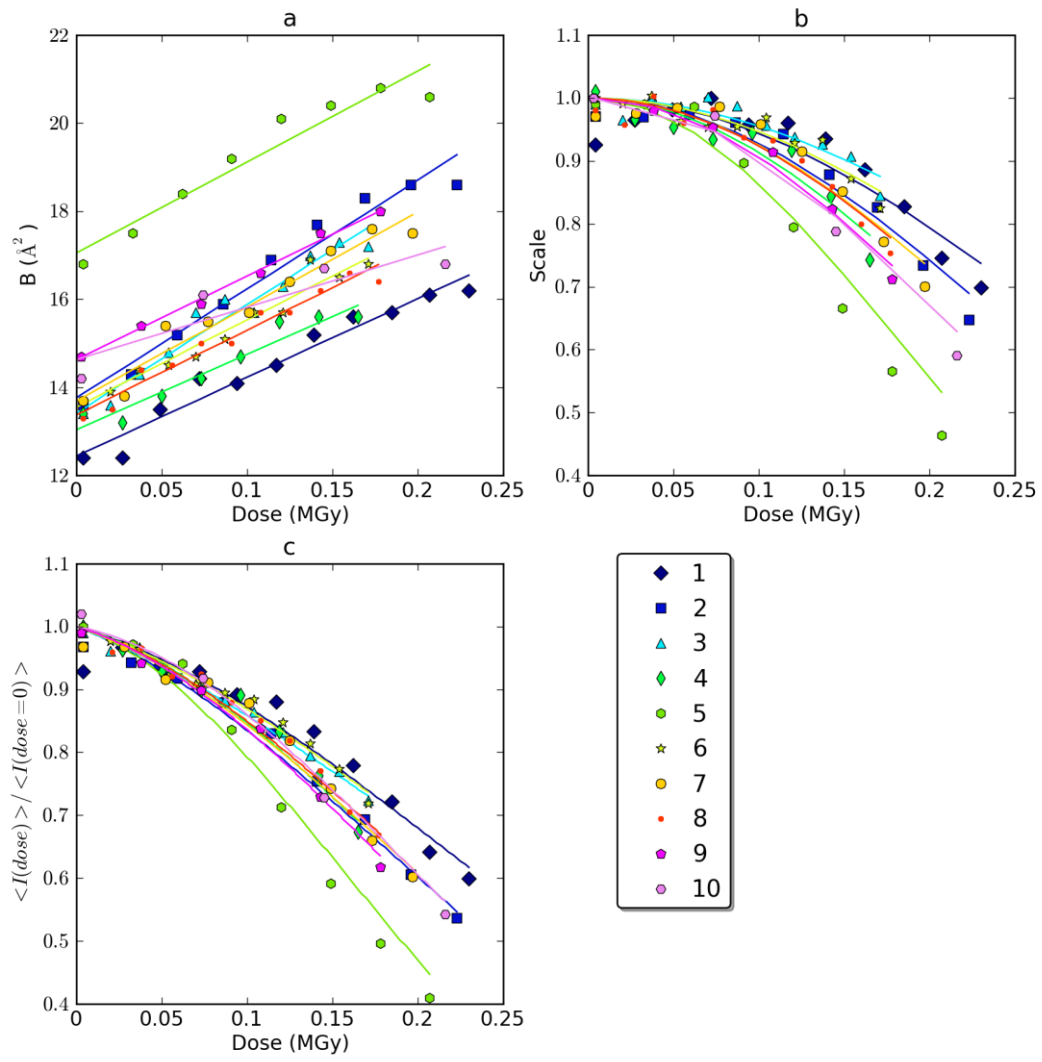
Bovine pancreatic trypsin, orthorhombic, high density form

BPTOH



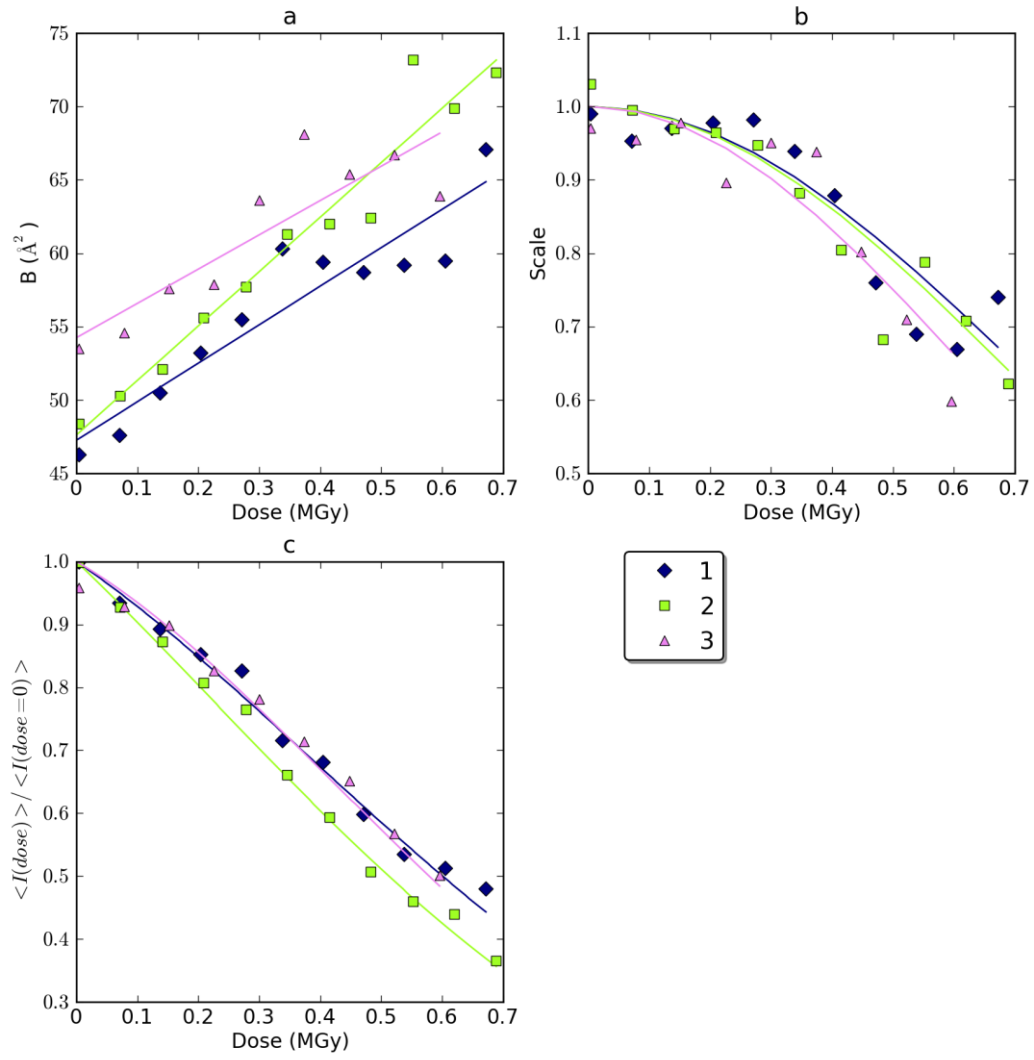
Bovine pancreatic trypsin, orthorhombic, low density form

BPTOL



# Bacteriorhodopsin

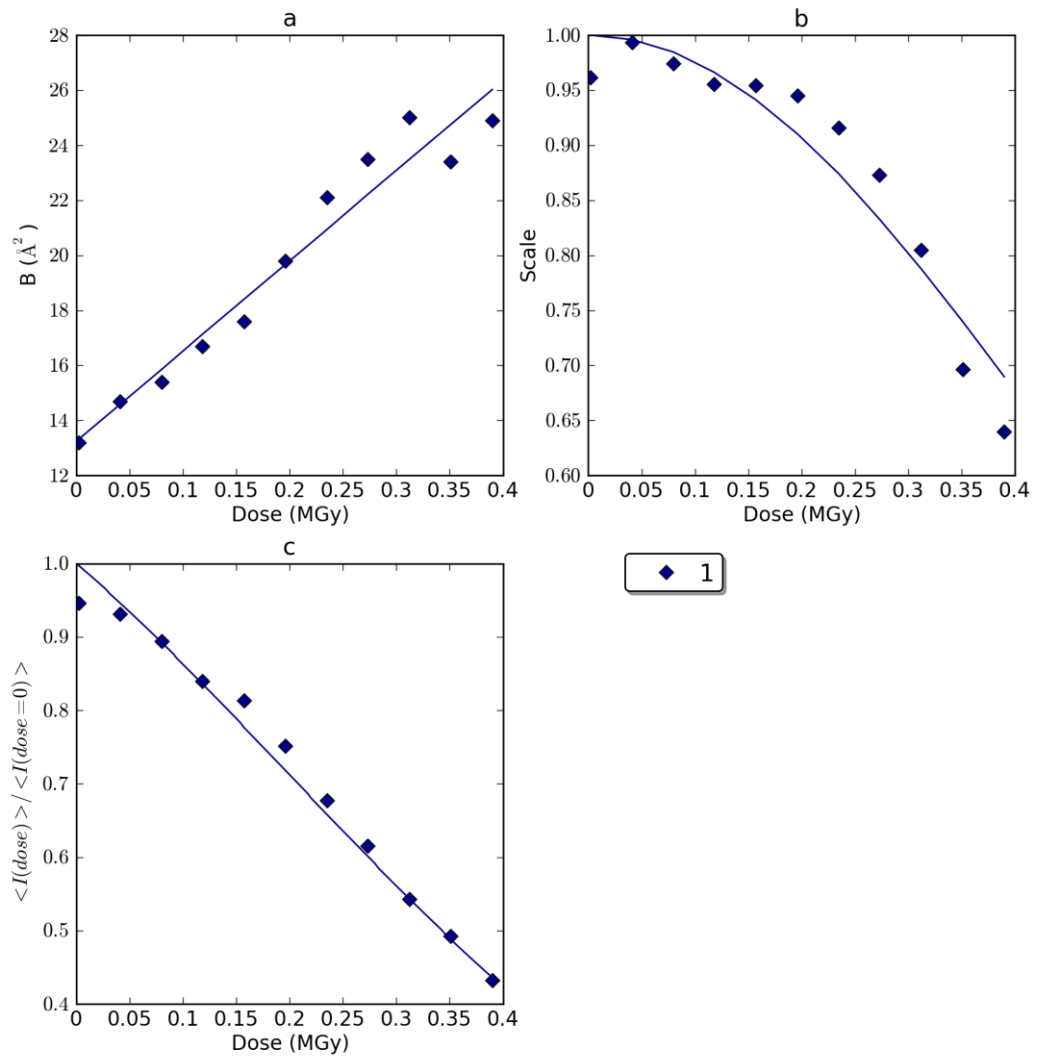
bR





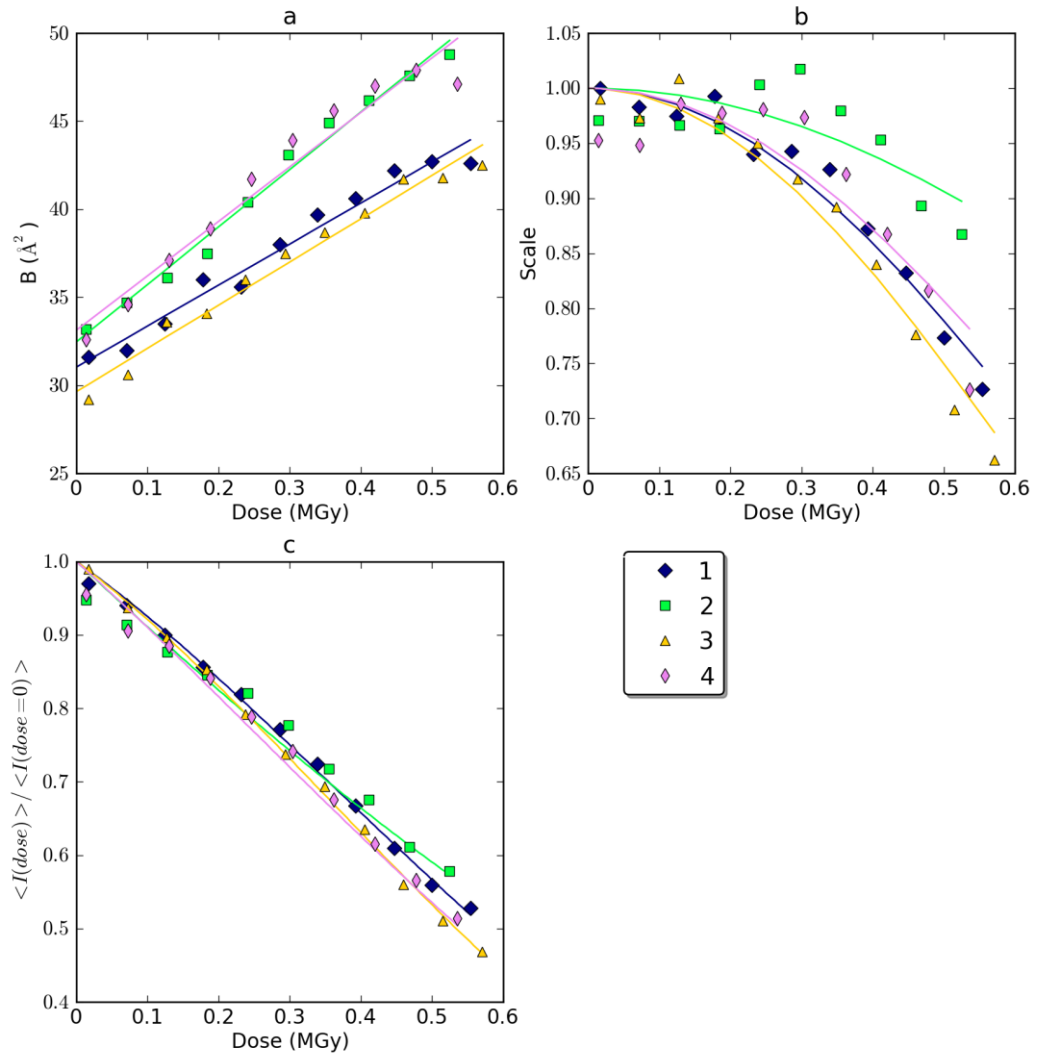
# Triosephosphate isomerase

TIM



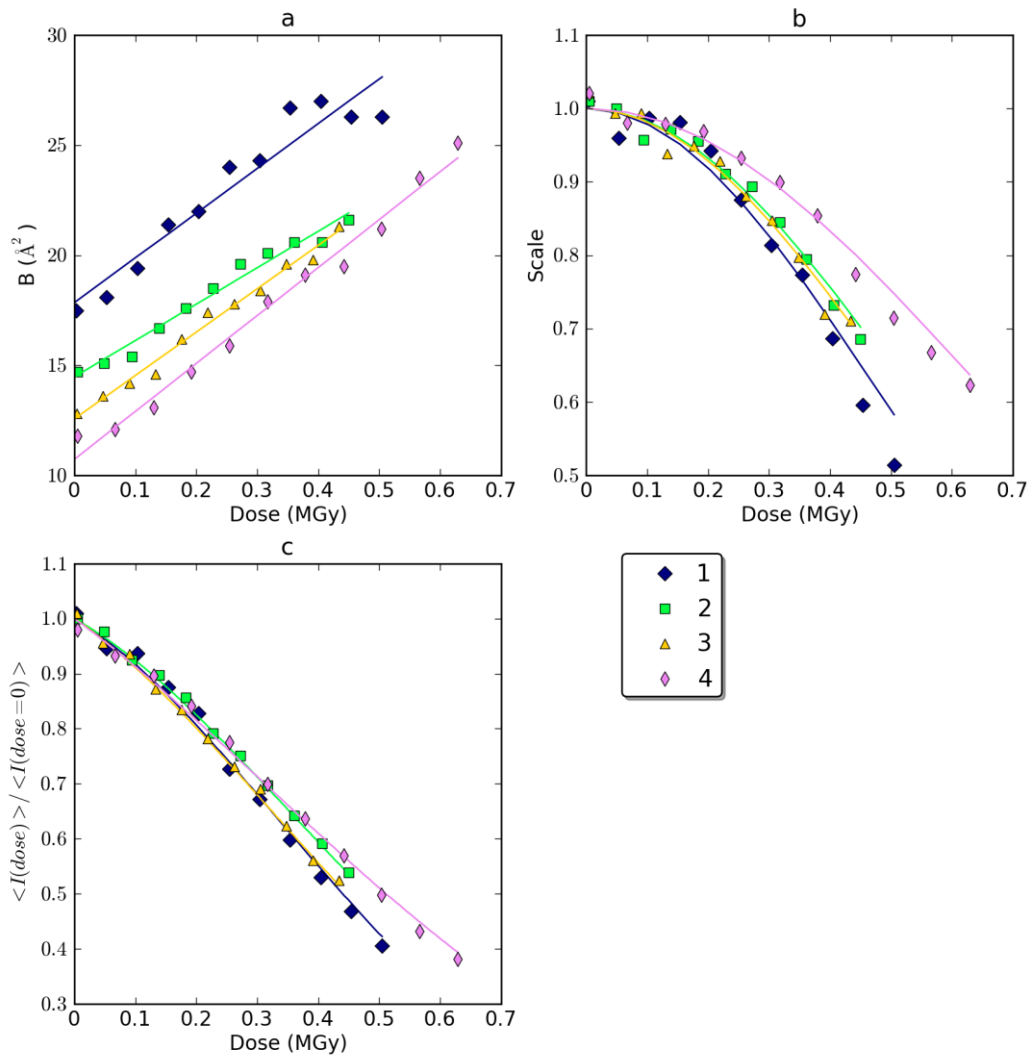
# Thermolysin

THER



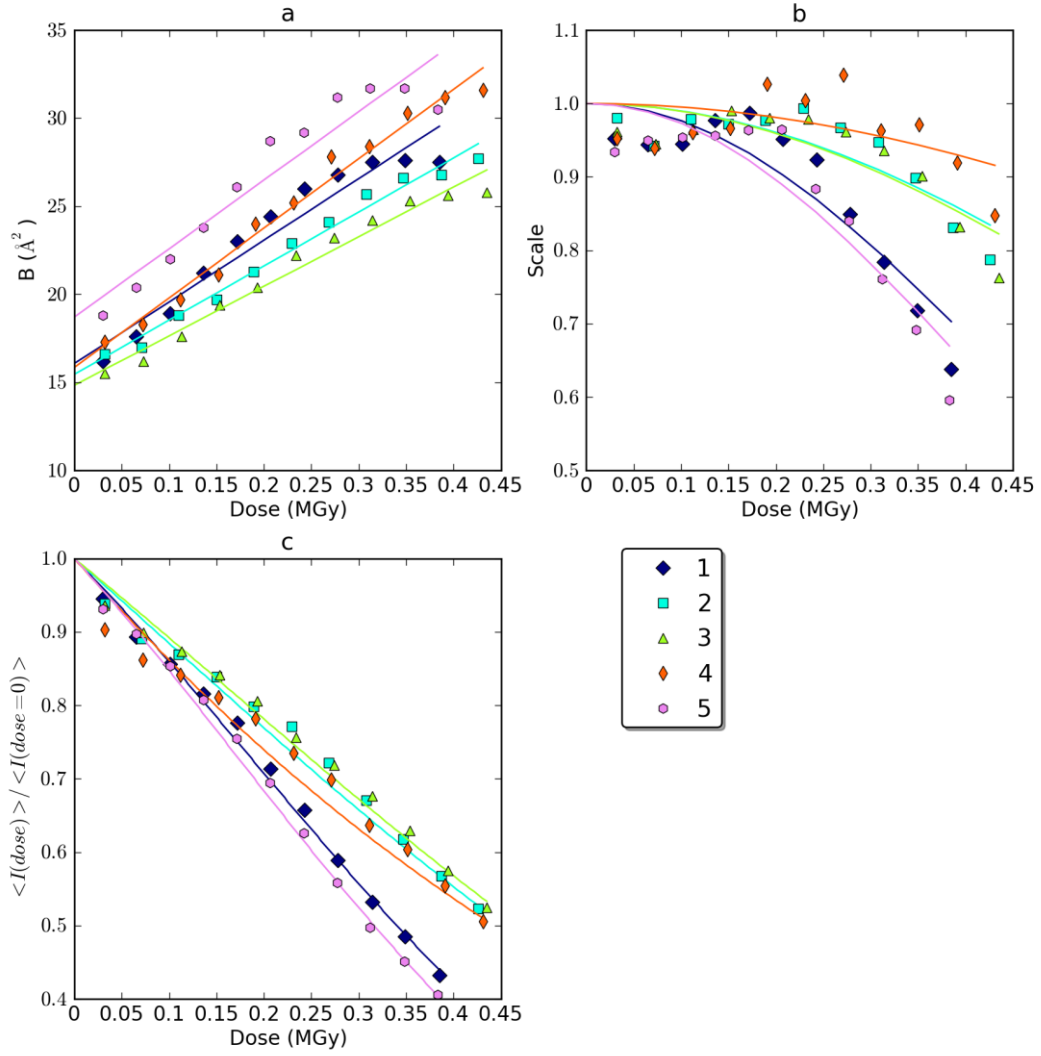
# Thaumatococcus

THAU



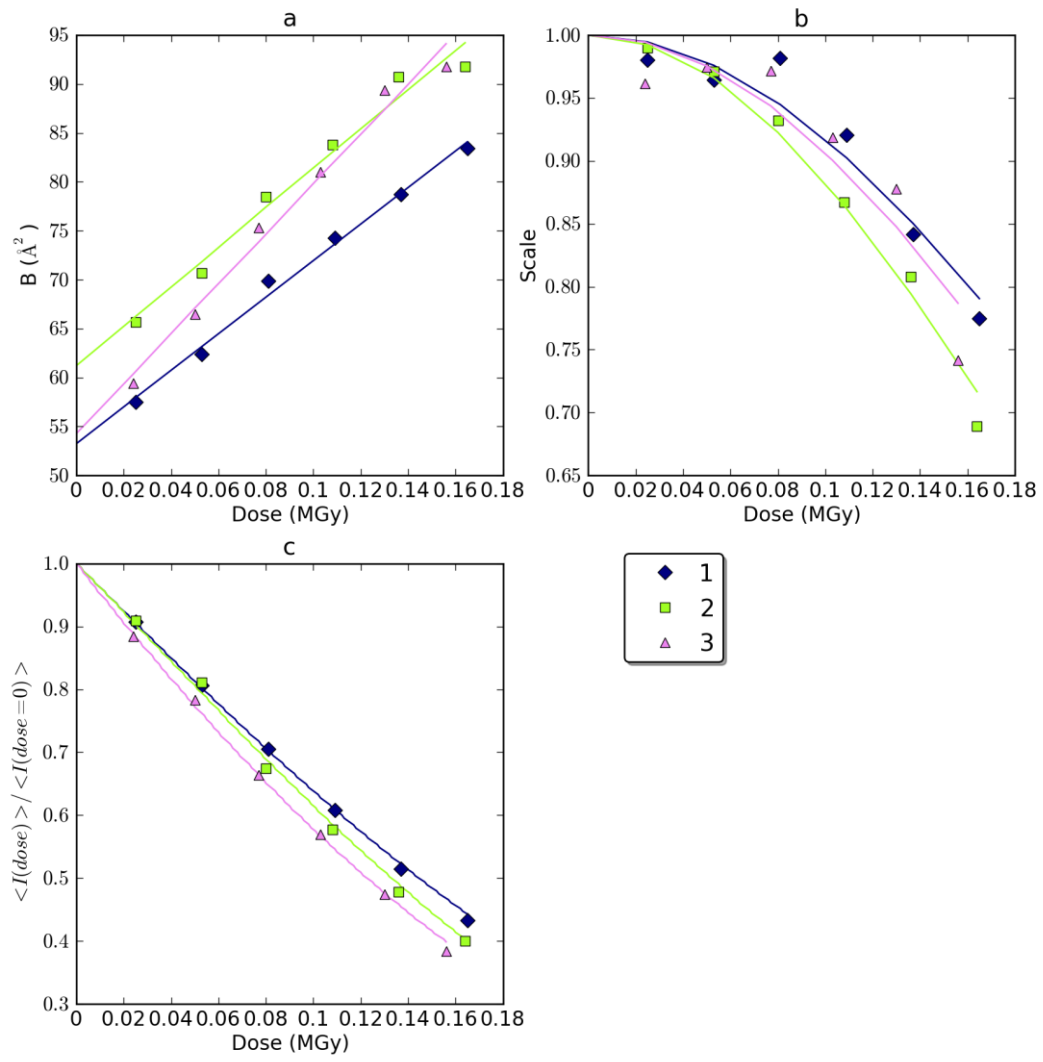
# Feruloyl esterase module of xylanase

FAE



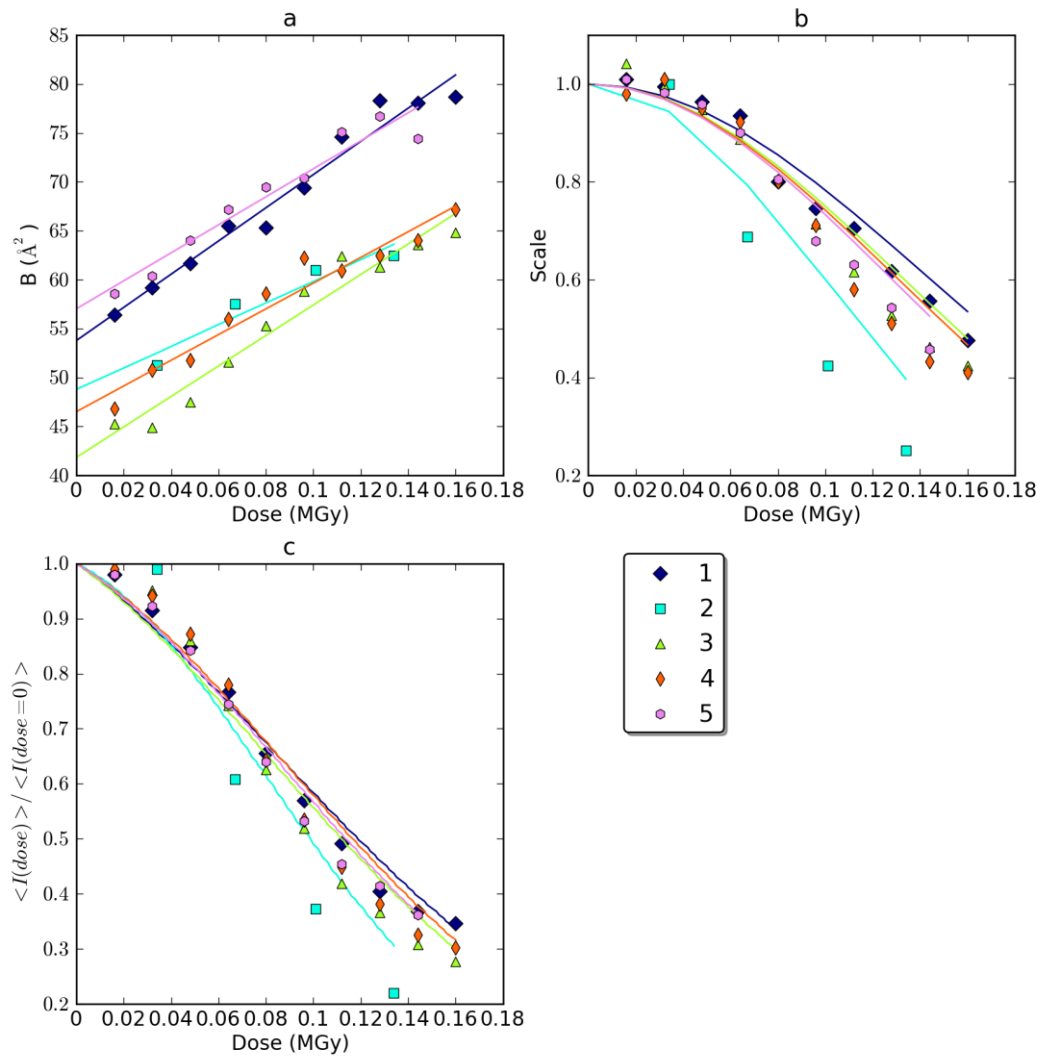
# 6-hydroxy-L-nicotine oxidase

6HLNO



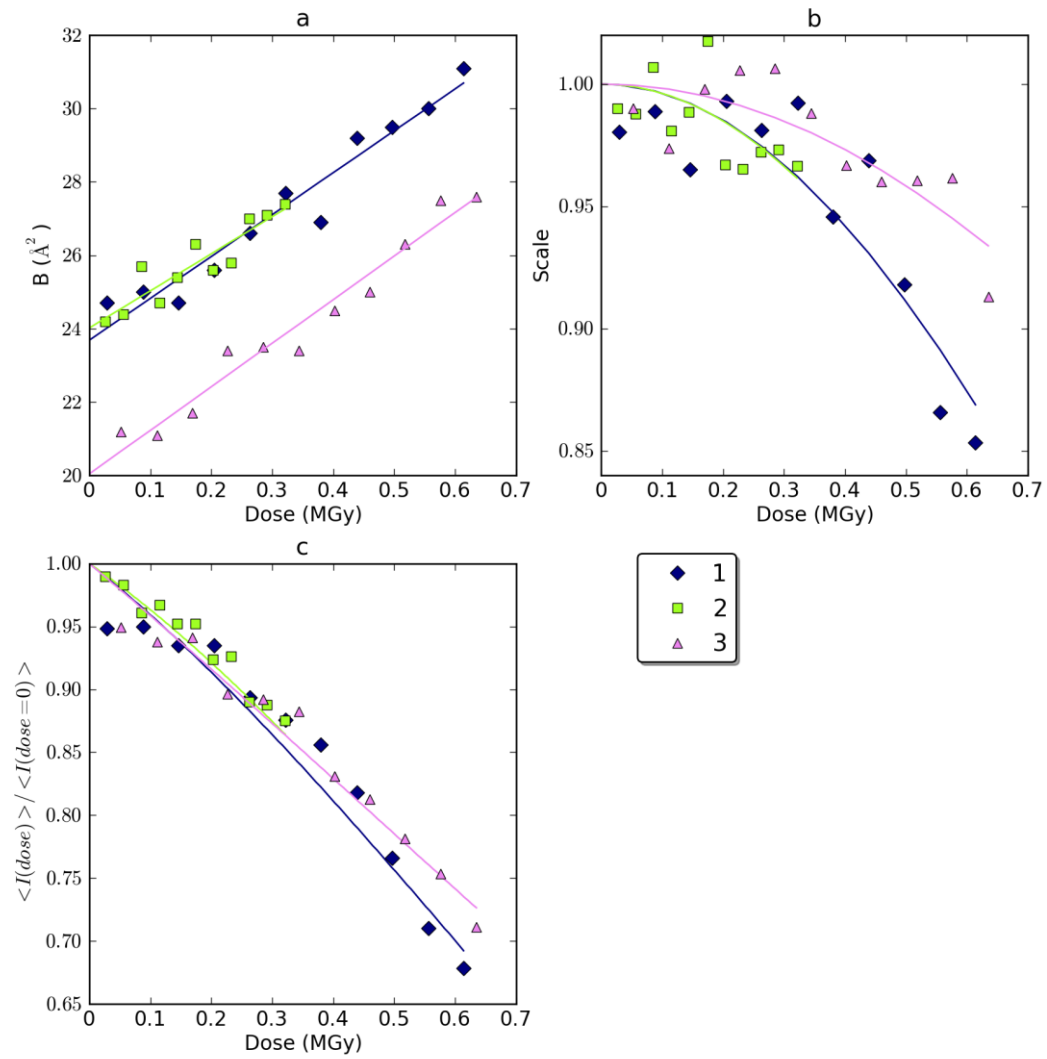
La Crosse orthobunyavirus L-protein polymerase, N-terminal domain

LACV



Thioalkalivibrio nitratireducens Cytochrome c nitrite reductase

TvNiR



Supplementary Table

Data set resolution, initial B-factor (Bo), radiation damage model parameters  $\beta$  and  $\gamma$ , half-dose  $D_{1/2}$  and normalized half-dose  $D_{1/2}^N$  for all data sets.

Protein/Crystal number	Resolution Å	B-factor Å <sup>2</sup>	$\beta$ Å <sup>2</sup> MGy <sup>-1</sup>	$\gamma$ MGy <sup>-1</sup>	$D_{1/2}^H$ MGy	$D_{1/2}$ MGy
Lysozyme monoclinic (LYZM)						
1	1.90	13.3	13.95	1.4	0.452	0.446
2	1.90	13.3	15.23	0.93	0.582	0.568
3	1.90	13.6	14.68	1.1	0.53	0.521
4	1.95	13.4	14.76	0.79	0.65	0.633
5	1.90	14.2	15.12	1.13	0.514	0.508
6	1.90	13.3	14.57	0.9	0.602	0.588
7	2.05	16.4	15.32	0.85	0.615	0.629
Lysozyme tetragonal (LYZT)						
1	1.90	14.1	16.57	2.01	0.328	0.326
2	1.90	14.0	21.02	2.6	0.255	0.254
3	1.90	12.4	21.57	1.81	0.333	0.325
4	1.90	14.6	18.21	1.99	0.324	0.323
5	1.90	13.5	19.38	1.76	0.35	0.345
6	1.90	14.9	18.01	2.07	0.315	0.314
7	1.90	14.6	17.3	2.08	0.317	0.316
8	1.90	14.6	16.82	2.01	0.328	0.327
Insulin rhombohedral (INSR)						
1	2.00	20.2	20.25	1.27	0.43	0.447
2	2.35	19.3	25.04	1	0.448	0.498
3	2.00	20.5	25.16	0.6	0.545	0.584
Insulin cubic (INSC)						
1	2.00	16.8	27.43	3.49	0.187	0.198
2	2.00	16.4	25.06	3.18	0.204	0.216
3	2.00	18.1	29.68	3.94	0.171	0.179
4	2.00	17.0	33.71	3.63	0.176	0.186
5	2.00	16.8	35.99	3.32	0.187	0.198
6	2.00	17.8	34.23	4.04	0.16	0.168
7	2.00	17.2	35.52	3.47	0.181	0.191
8	2.00	17.4	33.72	3.55	0.181	0.191
9	2.00	17.3	32.81	3.71	0.176	0.185
10	2.00	17.3	33.65	3.66	0.177	0.187
11	2.00	17.6	30.64	3.76	0.172	0.181
Bovine pancreatic trypsin, trigonal (BPTTR)						
1	2.00	11.4	11.93	1.04	0.587	0.579



2	2.00	13.6	13.06	1.38	0.463	0.463
3	2.00	11.8	12.23	0.75	0.721	0.707
4	2.00	11.7	14.82	1.3	0.468	0.462
5	2.00	11.8	12.52	0.84	0.665	0.654
6	2.00	11.3	13.11	1.21	0.512	0.505
7	2.00	9.8	12.5	0.96	0.609	0.592
Bovine pancreatic trypsin, orthorhombic, high density form (BPTOH)						
1	1.70	9.3	13.54	1.74	0.385	0.365
2	1.70	7.5	15.61	1.8	0.364	0.339
3	1.70	8.6	12.15	1.48	0.446	0.42
Bovine pancreatic trypsin, orthorhombic, low density form (BPTOL)						
1	2.20	12.4	17.85	2.4	0.281	0.286
2	2.20	13.8	24.7	2.73	0.237	0.243
3	2.20	13.4	24.71	2.14	0.284	0.292
4	2.20	13.0	17.18	3.01	0.232	0.232
5	2.20	17.1	20.63	3.83	0.183	0.183
6	2.20	13.6	19.8	2.34	0.28	0.287
7	2.20	13.7	21.43	2.8	0.24	0.245
8	2.20	13.4	19.22	2.82	0.243	0.248
9	2.20	14.6	19.02	3.13	0.224	0.224
10	2.20	14.6	11.91	3.16	0.222	0.222
Bacteriorhodopsin (bR)						
1	3.00	47.3	26.21	0.94	0.45	0.6
2	3.00	47.6	37.08	0.97	0.359	0.512
3	3.00	54.3	23.35	1.07	0.447	0.579
Triosephosphosphate isomerase (TIM)						
1	2.50	13.2	32.8	1.56	0.312	0.342
thermolysin (THER)						
1	2.80	31.0	23.28	0.97	0.47	0.576
2	3.00	32.5	32.62	0.63	0.444	0.634
3	2.90	29.7	24.53	1.07	0.437	0.534
4	2.95	33.1	30.86	0.93	0.411	0.54
Thaumatococcus (THAU)						
1	2.80	17.9	20.31	1.46	0.394	0.44
2	2.50	14.5	16.54	1.32	0.449	0.48
3	2.50	12.6	19.69	1.36	0.412	0.442
4	2.60	10.7	21.76	1.07	0.463	0.512
Feruloyl esterase module of xylanase (FAE)						
1	2.50	16.1	34.98	1.54	0.305	0.34
2	2.50	15.5	30.72	1	0.4	0.453
3	2.50	14.8	28.13	1.03	0.417	0.469
4	2.50	15.9	39.5	0.69	0.374	0.443
5	2.50	18.7	38.84	1.65	0.28	0.316
6-hydroxy-L-nicotine oxidase (6HLNO)						

1	3.60	53.3	186.9	2.94	0.081	0.144
2	3.70	61.2	201.59	3.53	0.073	0.133
3	3.80	54.3	255.2	3.14	0.061	0.123
<i>La Crosse orthobunyavirus</i> L-protein polymerase, N-terminal domain (LACV)						
1	3.90	53.8	170.06	4.96	0.075	0.119
2	3.95	48.8	110.6	7.17	0.077	0.098
3	3.80	41.9	156.18	5.37	0.077	0.112
4	3.80	46.5	131.68	5.47	0.083	0.117
5	3.80	57.0	143.46	5.58	0.079	0.114
<i>Thioalkalivibrio nitratireducens</i> Cytochrome c nitrite reductase (TvNiR)						
1	2.60	23.7	11.4	0.61	0.841	0.961
2	2.60	24.0	10.11	0.62	0.877	0.99
3	2.60	20.0	11.87	0.41	1.006	1.182