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Serial macromolecular crystallography at ALBA Synchrotron Light Source. Erratum

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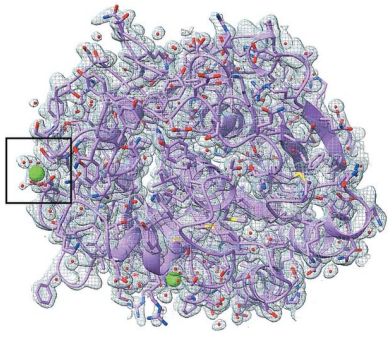
A revised version of Table 2 of Martin-Garcia *et al.* [*J. Synchrotron Rad.* (2022). **29**, 896–907] is provided.

The PDB code for phycocyanin given in Table 2 in the paper by Martin-Garcia *et al.* (2022) was incorrectly given as 7s4z. The correct code is 7s50. The full correct table is shown below.

Table 2
Data refinement statistics (values in parentheses are for the high-resolution shell).

	Lysozyme	Proteinase K	Phycocyanin	α-Spectrin-SH3	Insulin
Resolution range (Å)	35.35–2.1 (2.16–2.10)	44.21–1.9 (1.95–1.9)	43.4–2.1 (2.16–2.1)	32.6–2.1 (2.16–2.1)	24.35–1.71
Completeness (%)	100 (100)	100 (100)	99.2 (90.0)	99.1 (88.1)	99.7 (96.0)
No. of reflections, working set	6723 (479)	19879 (1431)	22830 (1530)	4110 (264)	8163 (584)
No. of reflections, test set	741 (59)	1071 (79)	1185 (78)	503 (33)	908 (56)
R_{work} (%)	17.9	16.5	30.5	19.4	24.0
R_{free} (%)	23.2	19.6	34.7	23.9	25.8
No. of atoms					
Protein	1001	2068	2488	462	808
Ions	1	2	2	0	3
Ligands	0	4	138	0	0
Water	17	89	43	5	15
Total	1019	2163	2671	467	826
R.m.s. deviations					
Bonds (Å)	0.010	0.011	0.005	0.012	0.006
Angles (°)	1.582	1.596	1.162	1.826	1.271
Average *B*-factors (Å^2)					
Protein	46.9	30.4	53.9	62.1	33.0
Ions	64.5	33.0	92.8	0	35.1
Ligands	0	55.3	57.6	0	0
Water	40.0	35.1	47.4	59.7	34.2
Ramachandran plot					
Favoured (%)	96.1	96.0	97.6	98.2	94.7
Allowed (%)	3.9	3.6	2.1	1.8	4.3
PDB code	7s4w	7s4z	7s50	7s4r	7s4y



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