



STRUCTURAL BIOLOGY  
COMMUNICATIONS

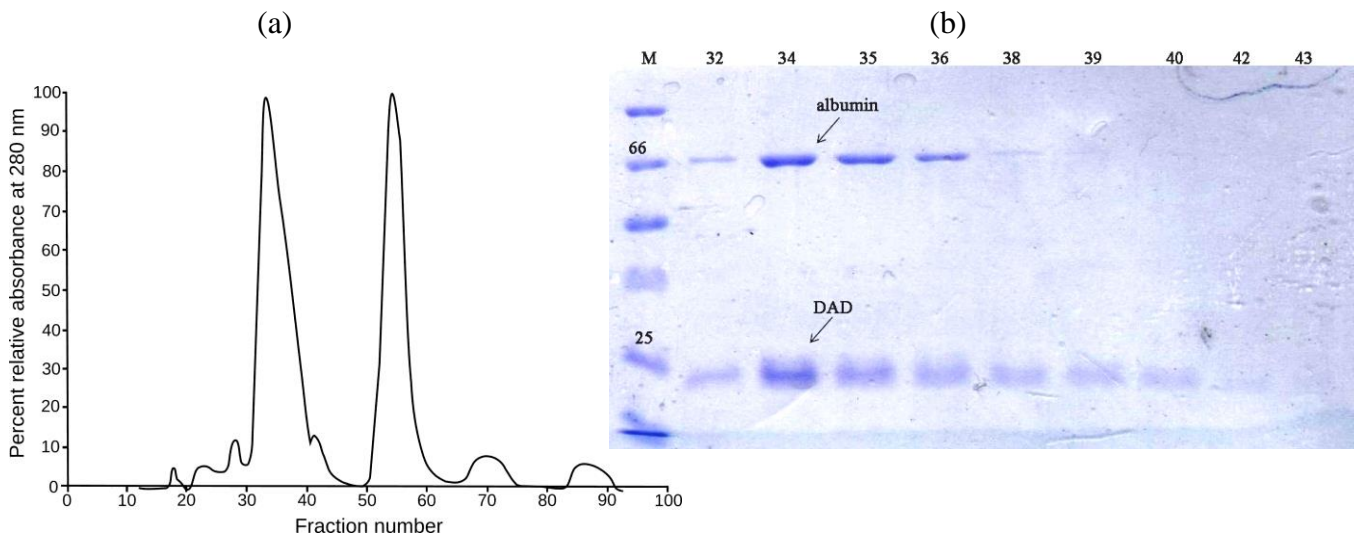
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**Supporting information for article:**

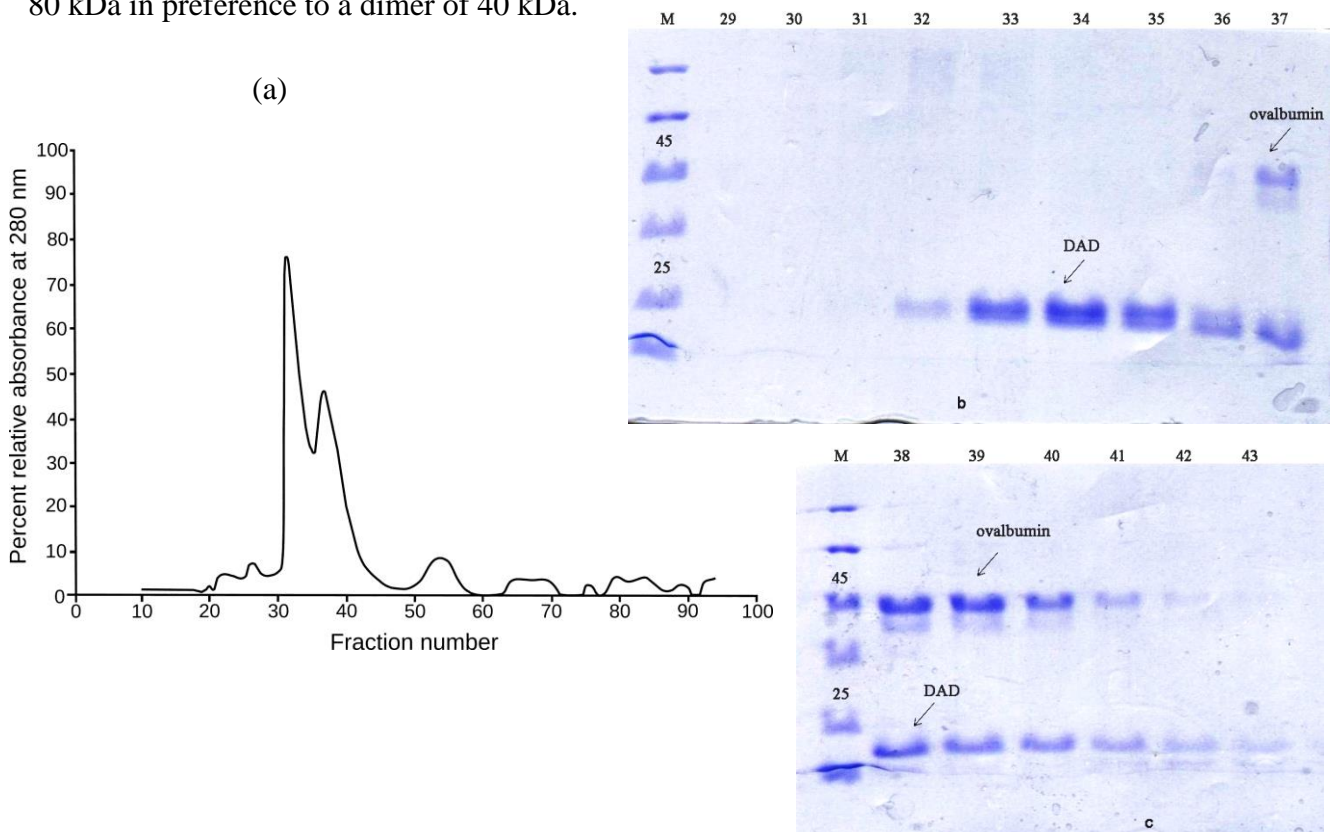
**Extension of resolution and oligomerisation state studies of 2,4'-  
dihydroxyacetophenone dioxygenase from *Alcaligenes* sp. 4HAP**

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Cooper**

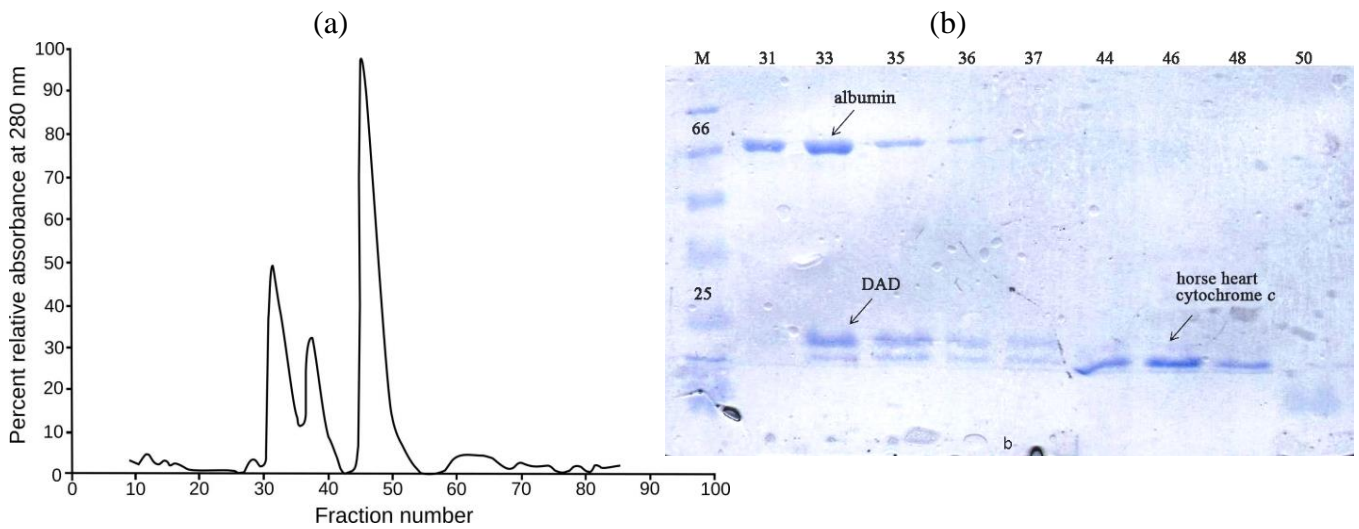
**Fig. S1** (a) A chromatogram showing the gel filtration of full-length DAD, albumin (66 kDa) and horse heart cytochrome *c* (13.4 kDa). The peak due to the full-length DAD enzyme is overlapped with that of the albumin, as confirmed by SDS-PAGE shown in (b). It was difficult to identify which protein came out earlier in this peak. The fraction size for gel-filtration was 2 ml in all runs.



**Fig. S2.** (a) A chromatogram showing the gel filtration of full-length DAD and ovalbumin (44 kDa). The SDS-PAGE gels shown in (b) and (c) confirm that the majority of the DAD protein eluted appreciably earlier than ovalbumin, further suggesting that full-length DAD can form a tetramer of 80 kDa in preference to a dimer of 40 kDa.



**Fig. S3.** (a) A chromatogram showing the gel filtration of chymotrypsinolysed DAD, albumin (66 kDa), and horse heart cytochrome *c* (13.4 kDa). The peak of chymotrypsinolysed DAD lies between those of the albumin and horse heart cytochrome *c*, as confirmed by the SDS-PAGE shown in (b). This suggests that the chymotrypsinolysed DAD is a dimer of 40 kDa.



**Fig. S4.** Sedimentation velocity scans raw (black lines) and fitted (colored lines) data. The first 20 scans for native DAD and the first 34 scans for chymotrypsinolysed DAD are shown from 100 scans. Both samples had a protein concentration of 0.8 mg/ml. Data were fitted using *SEDFIT* v14.81 and displayed by the use of *OriginPro* 9.1.

