

S2 Table. Structural homologues of *Ab-WbjB*

PDB file	Dali Z-score ^a	r.m.s.d (Å) ^b	sequence identity (%)	enzyme name	source organism	quaternary structure	Coenzyme/ substrate
3vvb	39.4	1.0	68	CapE	<i>S. aureus</i>	hexamer	NADP
2gn4	38.1	2.1	39	UDP-GlcNAc-8-dehydratase/ FlaA1	<i>H. pylori</i>	hexamer	NADP
2hun	27.0	2.3	23	DTDP-glucose 4,6-dehydratase	<i>P. horikoshii</i>	dimer	NAD
1wvg	26.1	2.8	20	CDP-glucose 4,6-dehydratase	<i>S. typhi</i>	tetramer	APR/CXY
1rkk	25.6	2.7	22	CDP-glucose 4,6-dehydratase	<i>Y. pseudotuberculosis</i>	tetramer	NAD
3lu1	25.2	2.8	22	WbgU	<i>P. shigelloides</i>	dimer	NAD/ UDP-GalNAc
2pzm	24.9	2.3	21	putative nucleotide sugar epimerase/ dehydratase	<i>B. bronchiseptica</i>	dimer	NAD/ UDP
1gla	24.3	2.8	23	DTDP-glucose 4,6-dehydratase	<i>S. enterica</i>	dimer	NAD/ sulphate ion
3ehe	22.9	2.9	23	UDP-glucose 4-epimerase	<i>A. fulgidus</i>	dimer	NAD

^a Statistical significance of best alignment as calculated by DALI. This score includes weighting according to sequence identity levels.

^b Position deviation over main-chain Cα atoms as calculated within DALI