Supplementary Table 4.2.1. Z-DOPE and QMEAN scores for the zebrafish BMP2, BMP4, BMP16 protein models.

Model	**Z-DOPE score**[1]	**QMEAN score**[2]
BMP2a	-0.659	0.669 (-0.96)
BMP2b	-0.746	0.623 (-1.42)
BMP4	-0.710	0.621 (-1.44)
BMP16	-0.260	0.646 (-1.21)

1 – The Z-DOPE score (Benkert et al., 2008) should be negative for acceptable quality models, and <-1 is usually seen for native structures

2 – The QMEAN score (Shen and Sali, 2006) ranges from 0 (worst) to 1 (best). Values in parenthesis are Z-scores based on a distribution of QMEAN scores for a set of experimentally determined structures (Z>-1.5 denote good models).

References:

Benkert P, Tosatto SCE, Schomburg D (2008). QMEAN: A comprehensive scoring function for model quality assessment *Proteins: Structure, Function, and Bioinformatics*. 71:261-277.

Shen MY, Sali A (2006) Statistical potential for assessment and prediction of protein structures. *Protein Sci.* 15: 2507-2524.