S1 Fig

TgPcr2 sequence and predicted structure

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   1 MWSLLGFSEESPPEESQDATAASPPTPSHQDVPASPSATEGKEVAGVASS
  51 ASPETMADAPSDSPPATPTSGGGFWSFWGASTPAEAEPAATTPVSSTAAA
 101 VETPDSGISETPGPSGVSSSAAESGGDEKQKKKKKKESGKGGEAVAEKKK
 151 KKKESEKGGEMVAEKKKGESEEMSSKLVSGSDVEAFRARLEQIELQKKAK
 201 EEAKVKRKEDEKKQKEEKREQRGREEEREKKKQEKEAARIAELKRLEEE
 251 LKRTQELAEELEKQNEERKNKRKGDRGESSSRGSSSSPSSGRSRREASEE
 301 RRKAREEREKRRREEQAGLEELLEATERELTETARSLQESIDRQREEREE
 351 LERRRQAQVKREMEIRQLAEEATRALEAQQQAARAAAAPAPPGASKGQPP
 401 APSLVSPADVKARNFMVALLKRDGGPSLPPPELEQRRLAEPARGETSGAK
 451 AEDRQAPELSRKGAAAPTAGRVLAETEVTEGDESMLRPFLAKRGDSVGDE
 501 YQEAQYTQQHVIFRGPAFRAFHELVNATKEINHLKEQVEAASRDEEEITT
 551 LRERLQTLLDKETKNSESHLERACAIRQALNSISIVFRAAQRRLKTLFFT
 601 KLNAAAGAAMPRAVGTSAALRAILGGDSKVTRLGVGLLREVVLRHLRQAW
 651 NQWTRYVKPRDAPPGRGAGTGIGTLEDEKATAAIMALREVEDEAEALKKY
 701 NEEEKRKLAEVASRLERWRRQLVAAHDAVIHLRENETKRCKSGVREKERG
 751 DRRRPRTSSTLDSAEDDAQAPDVLTRLNALVHTEMHRLGLRFENPRAGFG
 801 GDSTPHLETRNRDPFRRIPRSFQTENIGHLRLLHGDANGSFPEDRLSSFL
 851 ESRTSDNGSVRSARGRGVRRRRSLDENGNKALSGTESDTSSVSESISSGR
 901 SSSTSSEGSGALSSSEKRRASSRMSGENPSRRNNTVDEGGRRKKNFDKAC
 951 EDAEITHDLAPATRGQPSKSGDQASSQVSVVKGTLPASRIVKTRPKPPPP
1001 PGASEPATFGGGQQRKLQPASGTETSQDDLESAPSTRSSCSGKGPKGTGA
1051 PTGSTVIYADAHHTQASAKAKNAVQAKVKMERDRQRTATIVVGAGPPILA
1101 PKSLVNGPKSGPKPKQ
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S1 Fig. Pcr2 sequence and Alphafold prediction of Pcr2 structure. Residues predicted to form alpha-helices (pLDDT>70) are highlighted in green.