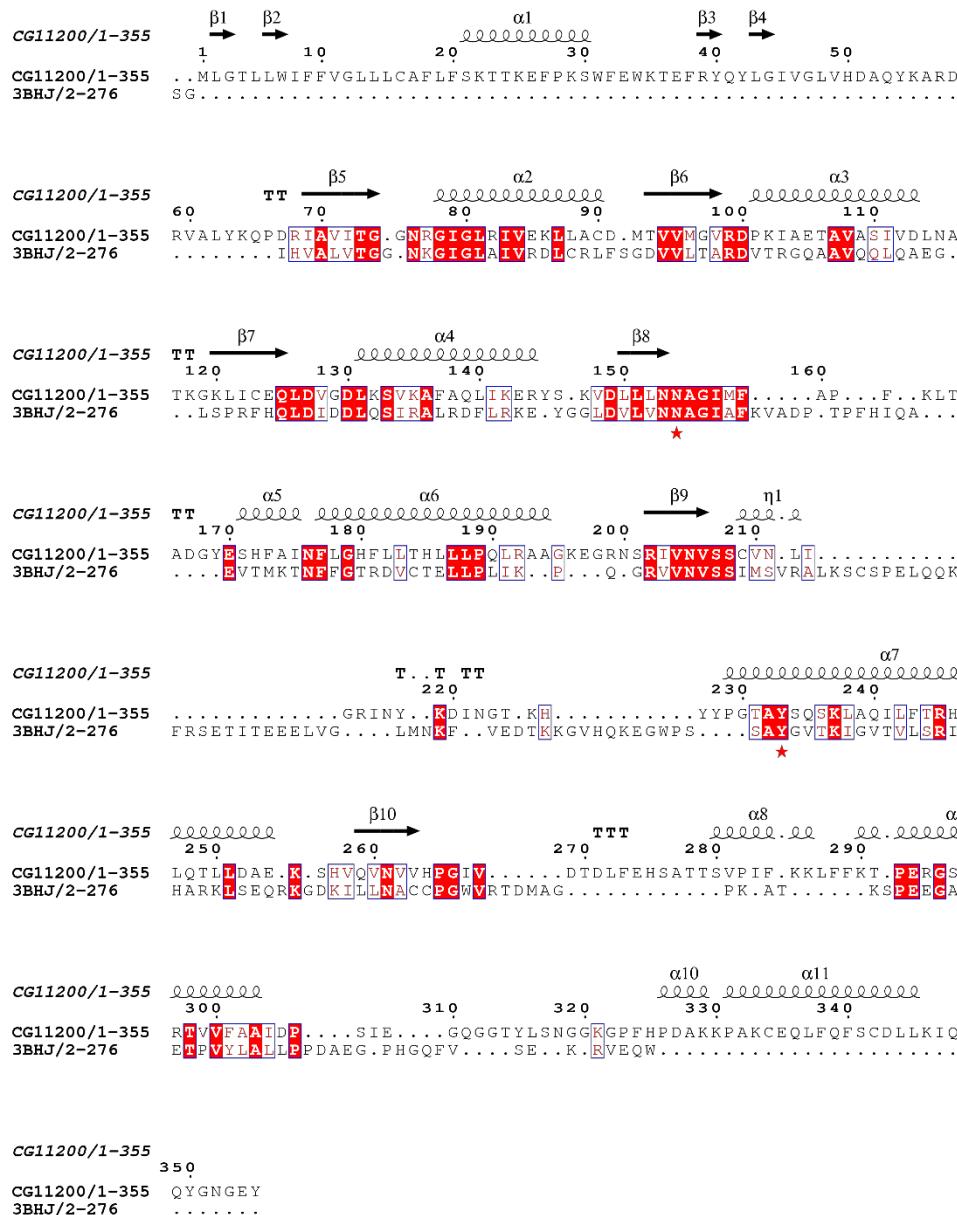
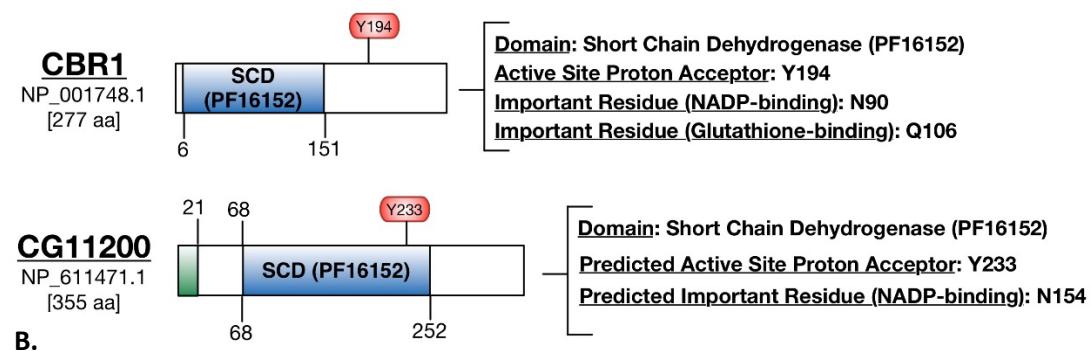


A.



C.

CG11200/1-355 1 --MLGTLLWIFFVGLLLCAFLFSKTTKEFPKSWEWKTEFRYQYLGIVGLVHDAQYKARDRVALYKQPDRIAVIT73
3BHJ/2-276 2 SG-----IHVALVT10

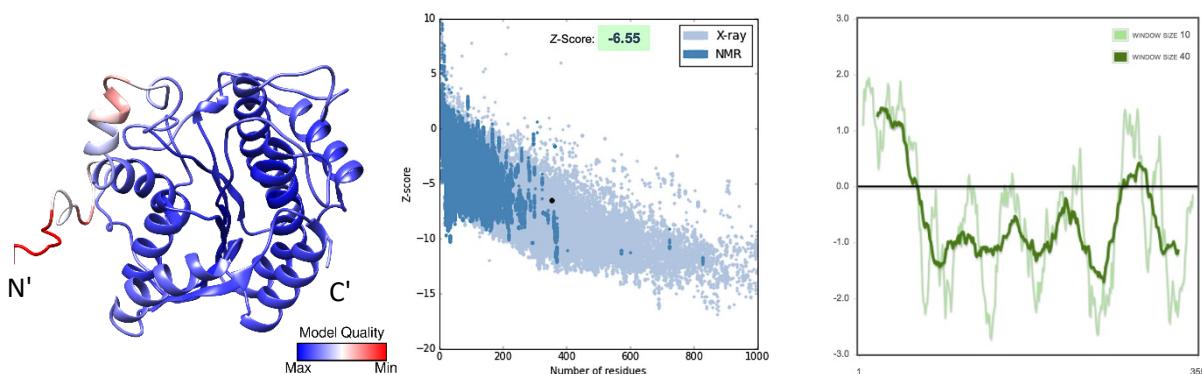
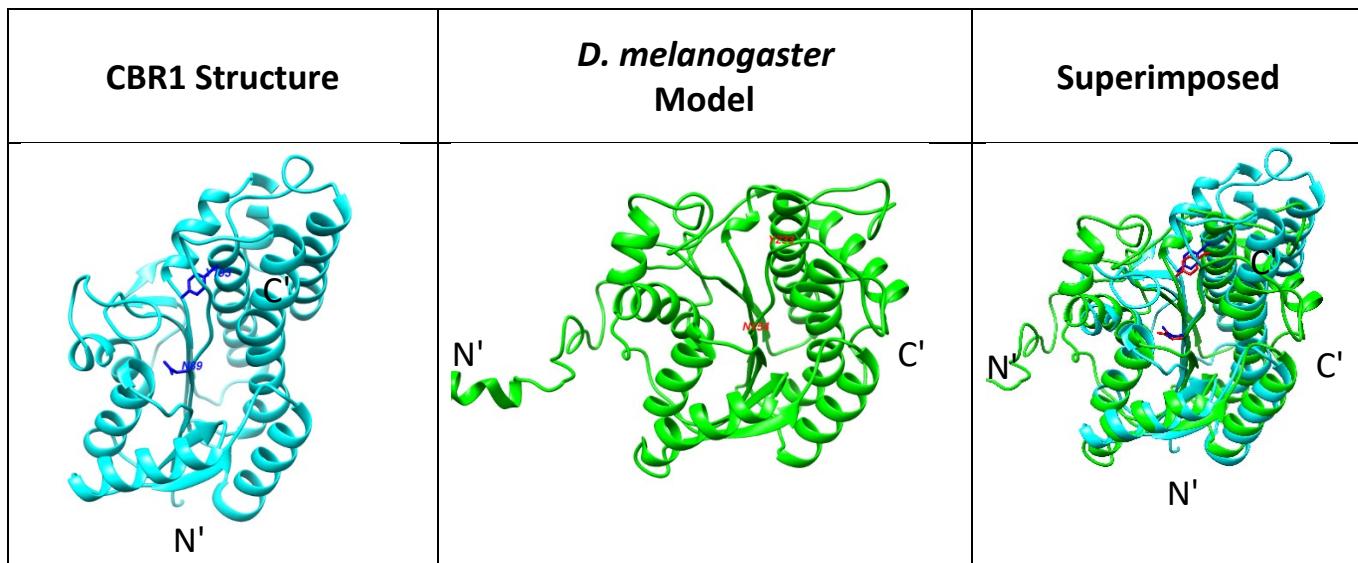
CG11200/1-355 74 G-GNRGIGLRIVEKLLACD-MTVVMGVDRDPKIAETAVASIVDLNATKGKLICEQLDVGDLKSVKAFAQLIKERYS146
3BHJ/2-276 11 GG-NKGIGLAIVRDLCRLFSGDVVLTAEDVTRGQAAVQQLQAEG--LSPREHOLDIDDLQSIRALRDFLKE-Y80

CG11200/1-355 147 -KV DLLLNNAAGIMF---AP---F---KLTADGYESHF A I N F L G H F L L T H L L P Q L R A A G K E G R N S R I V N V S S C V 210
3BHJ/2-276 81 GGL D V L V N N A G I A F K V A D P - T P F H I Q A - - - E V T M K T N F F G T R D V C T E L L P L I K --P--Q-GRVVNVSSIM141

CG11200/1-355 211 N-LI-----GRINY-KDINGT-KH-----YYPGTAYSQSKLAQILFTRH246
3BHJ/2-276 142 SVRALKSCSPELQQKF RSET I TEEELVG---LMNF---VEDTKKGVHQKEGWPS---SAYGVTKIGVTVL SRI 206

CG11200/1-355 247 LQTLLDAE-K-SHVQVN VVHPGIV-----DTDLFEHSATTSPVIF-KKLFFKT-PERGSRTVVFAAIDP---S307
3BHJ/2-276 207 HARKLSEQRKGD KILLNACCPGWVRTDMAG-----PK-AT-----KSPEEQAEIPVYLA L P P D A E G 262

CG11200/1-355 308 I E -----GQGGTYLSNGGKGPFH P DAKKPAKCEQLFQFSCDLLKIQQYGNGEY
3BHJ/2-276 263 -PHQQFV-----SE-K-IVEQW-----355
3BHJ/2-276 276

D.**E.**

F.	Length (AA)	Domain Architecture (Pfam, range)	Functional Residues (aligned matches in <i>D. melanogaster</i>)	Sequence ID%	Structural Overlap (RMSD)
Carbonyl reductase 1 (CBR1, NP_001748.1, PDB: 3BHJ)	277	Short chain dehydrogenase domain (PF16152) 6-151	N90 and Y194		
CBR (CG11200, NP_611471.1)	355	Short chain dehydrogenase domain (PF16152) 68-252	N154 and Y233	20% ID 33% SIM	1.153 Å

S11 Fig. Sequence and structural details of the modeled fly CBR1 candidate. A. Domain architecture of CBR1 and CG11200 and known/predicted functional residues B. Pairwise alignment of CG11200 and 3BHJ generated from structural superposition showing shared secondary structure elements and known/predicted functional residues (marked with red asterisks) C. Pairwise alignment of CG11200 and 3BHJ generated from structural superposition with conserved residues highlighted using the physicochemical color scheme (CLUSTALX) D. Validation of the CG11200 model: ProQ2 quality score mapped to a 3D model of CG11200 (left); ProSA global quality score ranking (middle) and per-residue quality graph (right) E. CPA1 (3BHJ, cyan-blue) superimposed on the predicted structure of CG11200 (green-red) with potential matches for conserved functional residues highlighted F. Summary of features shared by CBR1 and potential *D. melanogaster* ortholog CG11200.