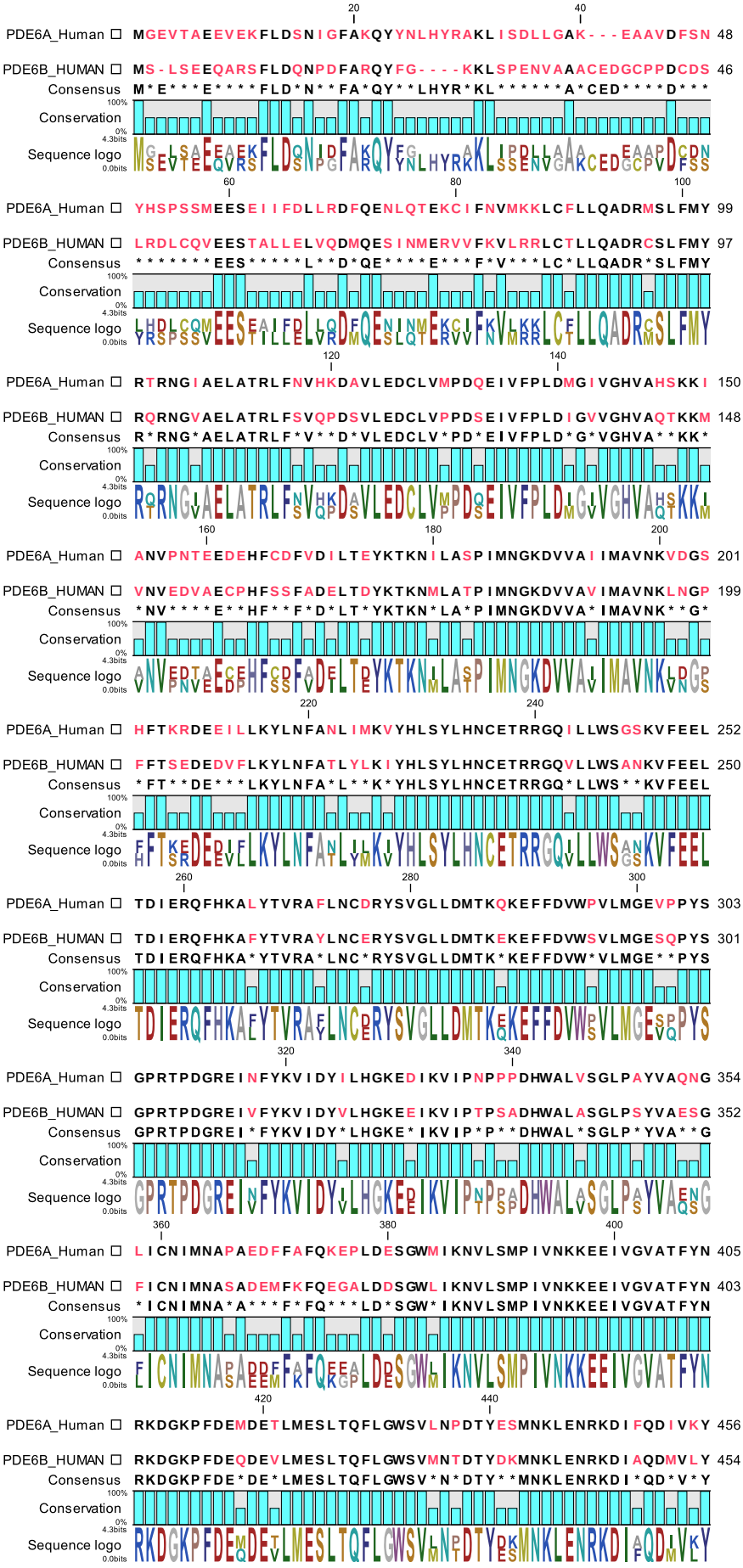
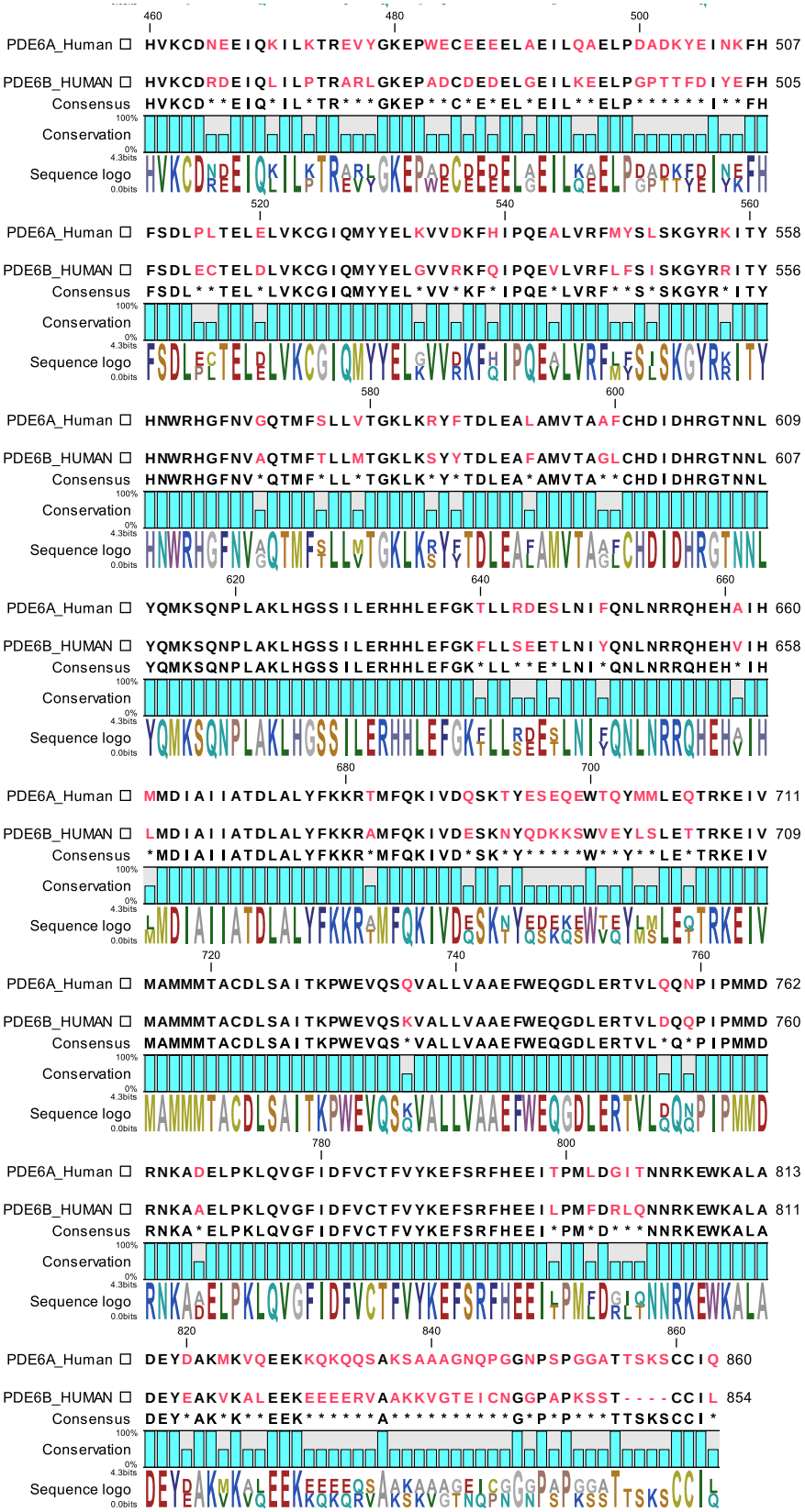
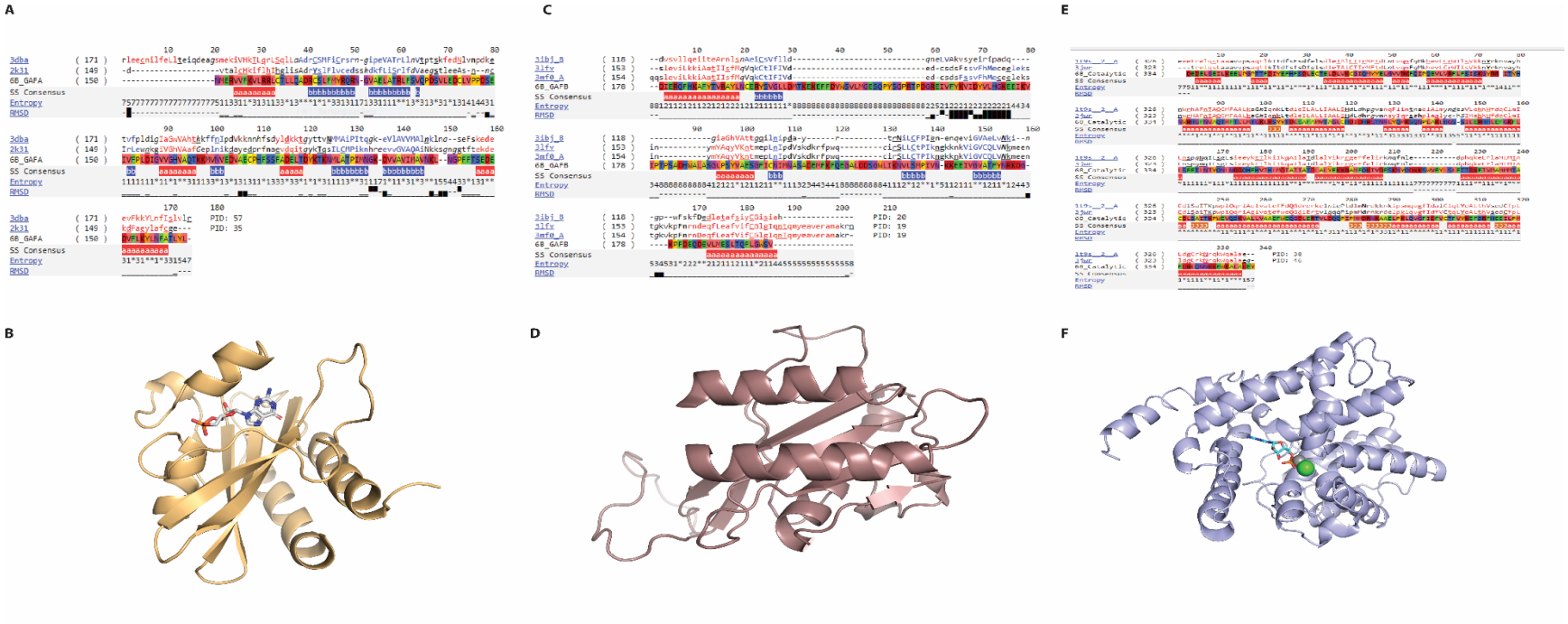

PDE6A_Human MGEVTAEEVEKFLDSNIGFAKQYYNLHYRAKLISDLLGAK---EAAVDFSN 48
PDE6B_HUMAN MS-LSEEQARSFLDQNPDFARQYFG----KKLSPENVAAACEDGCPPDCDS 46
Consensus M*E***E*****FLD*N**FA*QY**LHYR*KL******A*CED****D***
Conservation
Sequence logo
PDE6A_Human YHSPSSMEESEIIFDLLRDFQENLQTEKCIFNVMKKLCFLLQADRMSLFMY 99
PDE6B_HUMAN LRDLCQVEESTALLELVQDMQESINMERVVFKVLRRLCTLLQADRCSLFMY 97
Consensus *******EES*****L**D*QE****E***F*V***LC*LLQADR*SLFMY
Conservation
Sequence logo
PDE6A_Human RTRNGIAELATRLFNVHKDAVLEDCLVMPDQEIVFPLDMGIVGHVAHSKKI 150
PDE6B_HUMAN RQRNGVAELATRLFSVQPDSVLEDCLVPPDSEIVFPLDIGVVGHVAQTKKM 148
Consensus R*RNG*AELATRLF*V**D*VLEDCLV*PD*EIVFPLD*G*VGHVA***KK*
Conservation
Sequence logo
PDE6A_Human ANVPNTEEDEHFCDFVDILTEYKTKNILASPIMNGKDVVAIIMAVNKVDGS 201
PDE6B_HUMAN VNVEDVAECPHFSSFADELTDYKTKNMLATPIMNGKDVVAVIMAVNKLNGP 199
Consensus *NV****E**HF**F*D*LT*YKTKN*LA*PIMNGKDVVA*IMAVNK**G*
Conservation
Sequence logo
PDE6A_Human HFTKRDEEILLKYLNFANLIMKVYHLSYLHNCETRRGQILLWSGSKVFEEL 252
PDE6B_HUMAN FFTSEDEDVFLKYLNFATLYLKIYHLSYLHNCETRRGQVLLWSANKVFEEL 250
Consensus *FT**DE***LKYLNFA*L**K*YHLSYLHNCETRRGQ*LLWS**KVFEEL
Conservation
Sequence logo
PDE6A_Human TDIERQFHKALYTVRAFLNCDRYSVGLLDMTKQKEFFDVWPVLMGEVPPYS 303
PDE6B_HUMAN TDIERQFHKAFYTVRAYLNCERYSVGLLDMTKEKEFFDVWSVLMGESQPYS 301
Consensus TDIERQFHKA*YTVRA*LNC*RYSVGLLDMTK*KEFFDVW*VLMGE**PYS
Conservation
Sequence logo
PDE6A_Human GPRTPDGREINFYKVIDYILHGKEDIKVIPNPPDHWALVSGLPAYVAQNG 354
PDE6B_HUMAN GPRTPDGREIVFYKVIDYVLHGKEEIKVIPTPSADHWALASGLPSYVAESG 352
Consensus GPRTPDGREI*FYKVIDY*LHGKE*IKVIP*P**DHWAL*SGLP*YVA**G
Conservation
Sequence logo
PDE6A_Human LICNIMNAPAEDFFAFQKEPLDESGWMIKNVLSMPIVNKKEEIVGVATFYN 405
PDE6B_HUMAN FICNIMNASADEMFKFQEGALDDSGWLIKNVLSMPIVNKKEEIVGVATFYN 403
Consensus *ICNIMNA*A***F*FQ***LD*SGW*IKNVLSMPIVNKKEEIVGVATFYN
Conservation
Sequence logo
PDE6A_Human RKDGKPFDEMDETLMESLTQFLGWSVLNPDTYESMNKLENRKDIFQDIVKY 456
PDE6B_HUMAN RKDGKPFDEQDEVLMESLTQFLGWSVMNTDTYDKMNKLENRKDIAQDMVLY 454
Consensus RKDGKPFDE*DE*LMESLTQFLGWSV*N*DTY**MNKLENRKDI*QD*V*Y
Conservation
Sequence logo

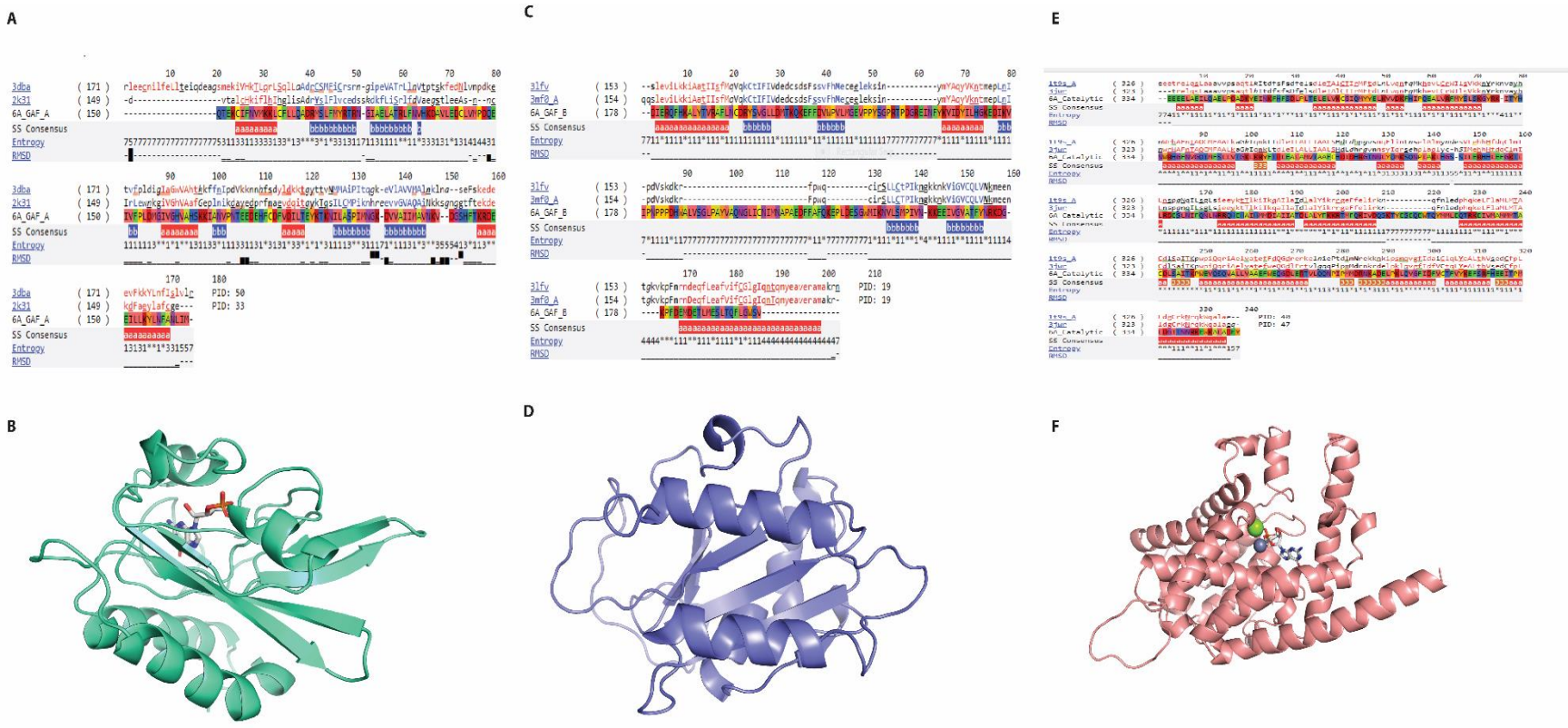



Supplementary Figure 1: Sequence alignment of Human PDE6α and PDE6β chains using CLC workbench. Identical residues among both the chains are shown in black color while consensus residues, conservation bars plots (0-100) and sequence logos are also given at the bottom to highlight conservation in both the chain's amino acid sequence.

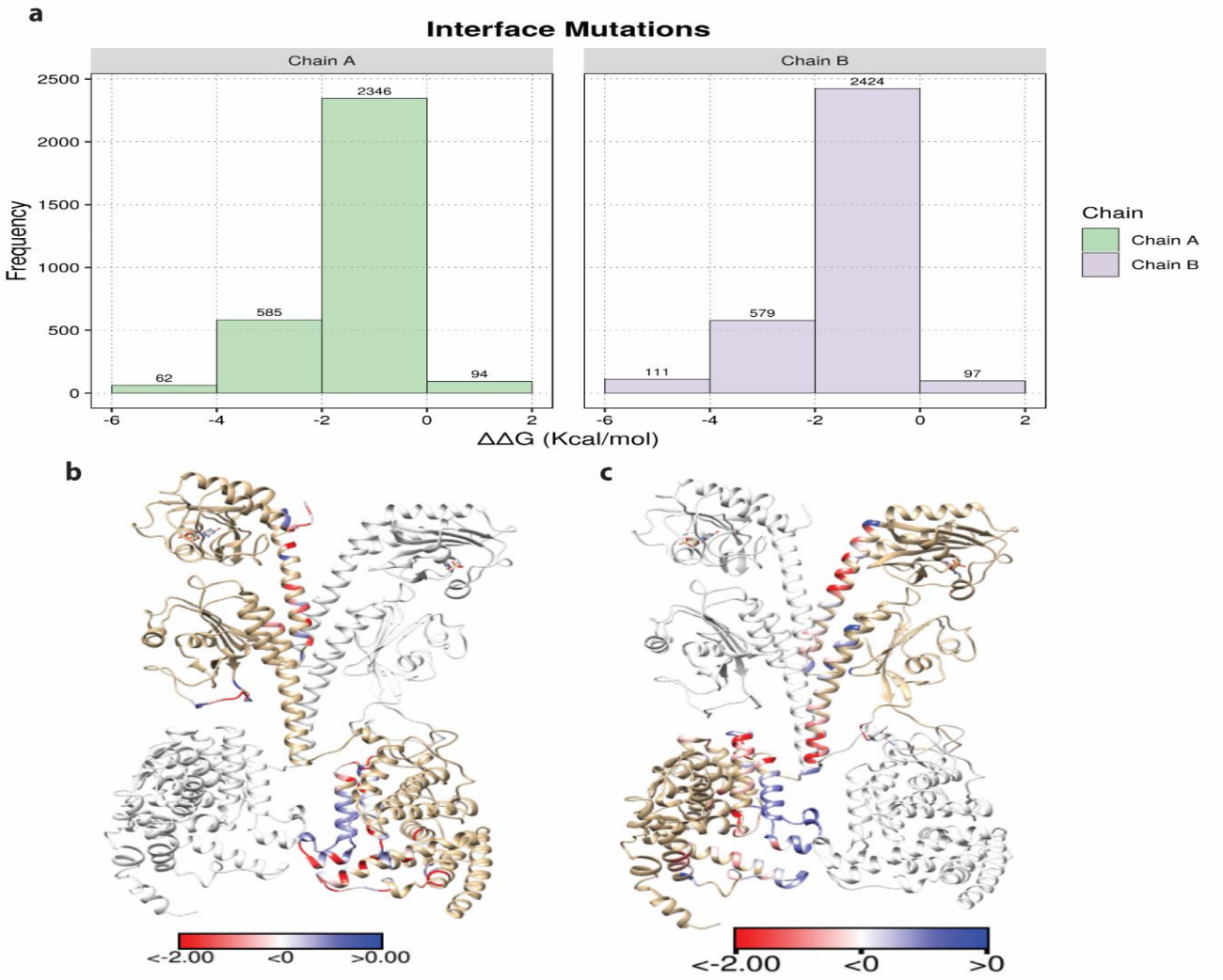



Supplementary Figure 2:Fugue Alignment and homology model of Gaf-A (A, B), Gaf-B (C, D) and catalytic domain (E, F) of PDE6α chain.

Supplementary figure 3




Supplementary Figure 3: Fugue Alignment and homology model of Gaf-A (A, B), Gaf-B (C, D) and catalytic domain (E, F) of PDE6β chain.




Supplementary Figure 4: a) Frequency distribution graphs illustrating the distribution of effects of saturation mutagenesis of dimeric interface residues of PDE6 αβ in terms of ΔΔG values predicted through mCSM-PPI b) Heatmap of the mCSM-PPI predicted changes upon mutation in residues present at heterodimeric interface of PDE6αβ. Energy changes calculated by mCSM-PPI are depicted as a colored gradient scale that starts from blue and turns white to red indicating the average effect from stabilizing (>0.00 kcal/mol) shown in blue to slightly destabilizing (≥-2.0 kcal/mol) shown as white to highly destabilizing (<-2.00 kcal/mol) as red.