Supporting Information

Structural basis of substrate recognition and catalysis by fucosyltransferase 8

Michael Järvå[1,2†], Marija Dramicanin[1,2†], James P. Lingford[1,2], Runyu Mao[1,2], Alan John[1,2], Kate Jarman[1,2], Rhys W. Grinter[3], and Ethan D. Goddard-Borger[1,2*]

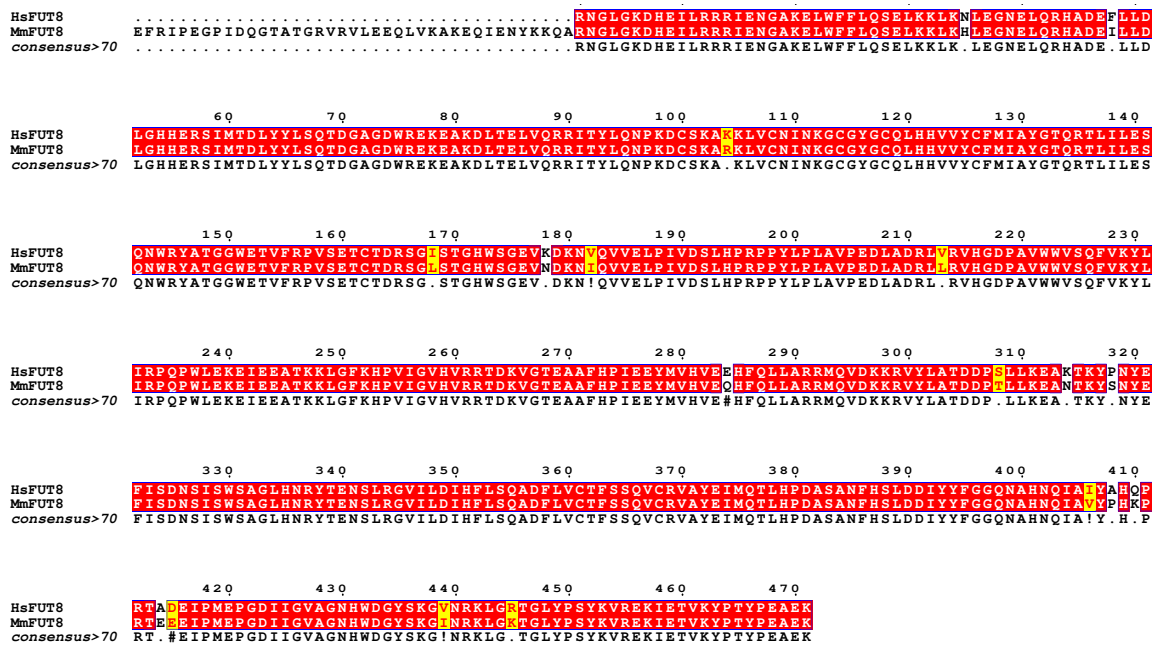
[1] The Walter and Eliza Hall Institute of Medical Research, Parkville, Victoria 3052, Australia.

[2] Department of Medical Biology, University of Melbourne, Parkville, Victoria 3010, Australia.

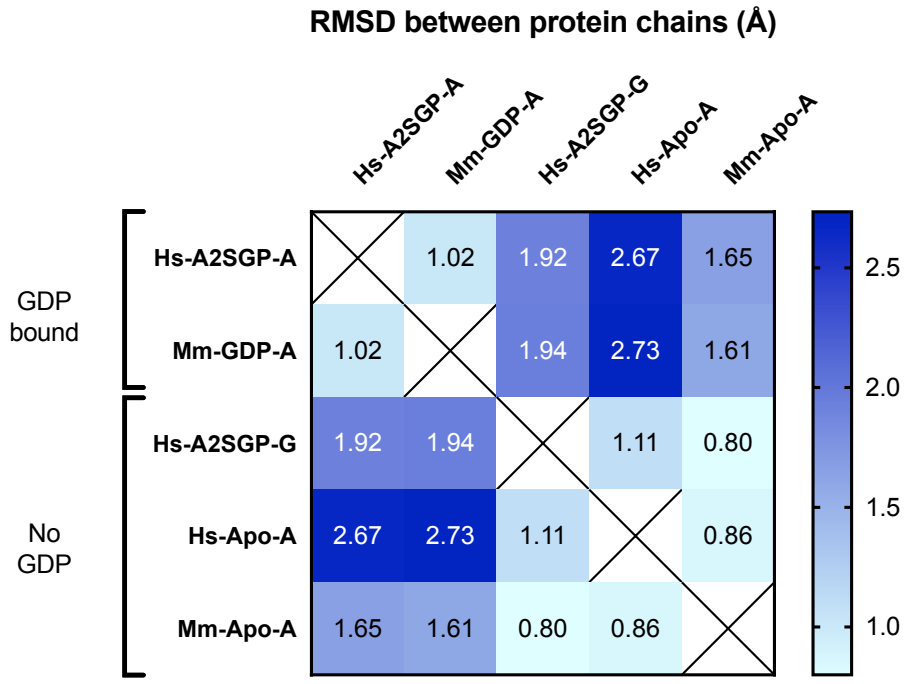
[3] Department of Microbiology, Monash Biomedicine Discovery Institute, Monash University, Clayton, VIC 3800, Australia.

[†] These authors contributed equally

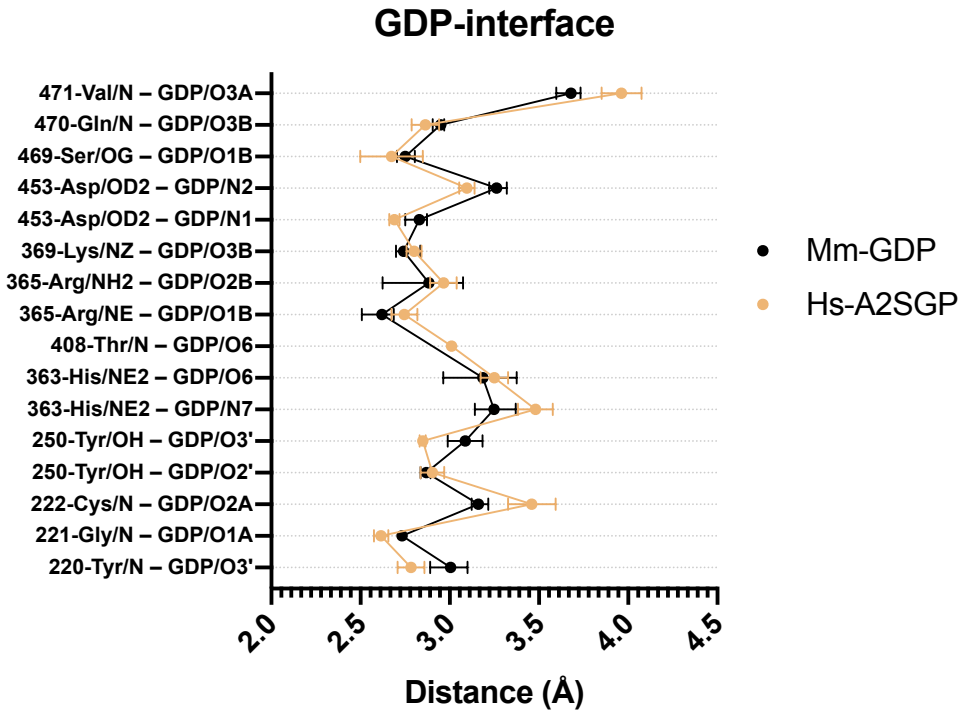
* Correspondence and requests for materials should be addressed to E.D.G.-B. (goddard-borger.e@wehi.edu.au).



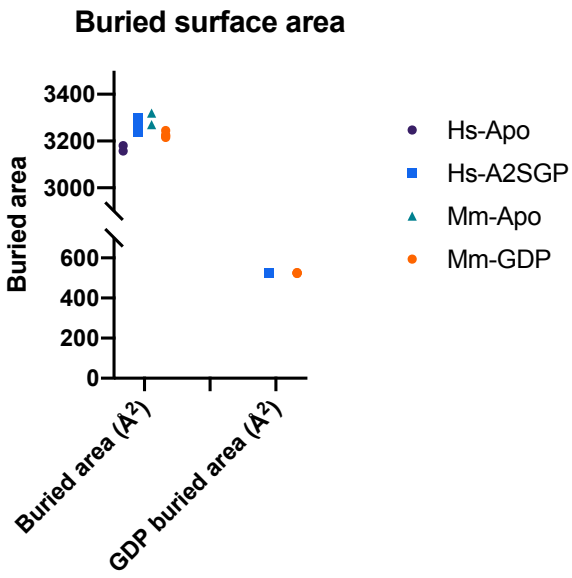
Supplementary Figure 1. Sequence alignment of HsFUT8$_{105-575}$ and MmFut8$_{68-575}$. The proteins are ≈97% identical over this region.



Supplementary Figure 2. Heatmap illustrating the RMSD between protein chains in the FUT8 structures reported in this study.



Supplementary Figure 3. A map of hydrogen bond distances between GDP and FUT8 for all relevant structures reported in this work.



Supplementary Figure 4. Buried surface area of FUT8 upon dimerisation, and of GDP upon binding FUT8, for each of the structures reported in this work.

Table S1. The sequences of nucleotides and proteins used in this study. Restrictions sites used for cloning are underlined; signal peptides are shaded in grey; His_{10} tags are shaded in yellow; V5 epitope tags are shaded in blue; and factor Xa sites are shaded in pink.

protein	Synthetic dsDNA used for cloning	Protein sequence
HsFUT8	GGATCTCGGTCCGAAACCATGCTACTAGTAAATCAGTCACACCAAGGCTTCA ATAAGGAACACACAAGCAAGATGGTAAGCGCTATTGTTTTATATGTGCTTTT GGCGGCGGCGGCGCATTCTGCCTTTGCGAGAAATGGTCTGGGGAAGGATCAT GAAATCCTGAGGAGGAGGATTGAAAATGGAGCTAAAGAGCTCTGGTTTTTCC TACAGAGTGAATTGAAGAAATTAAAGAACTTAGAAGGAAATGAACTCCAAAG ACATGCAGATGAATTTCTTTTGGATTTAGGACATCATGAAAGGTCTATAATG ACGGATCTATACTACCTCAGTCAGACAGATGGAGCAGGTGATTGGCGGGAAA AAGAGGCCAAAGATCTGACAGAACTGGTTCAGCGGAGAATAACATATCTTCA GAATCCCAAGGACTGCAGCAAAGCCAAAAAGCTGGTGTGTAATATCAACAAA GGCTGTGGCTATGGCTGTCAGCTCCATCATGTGGTCTACTGCTTCATGATTG CATATGGCACCCAGCGAACACTCATCTTGGAATCTCAGAATTGGCGCTATGC TACTGGTGGATGGGAGACTGTATTTAGGCCTGTAAGTGAGACATGCACAGAC AGATCTGGCATCTCCACTGGACACTGGTCAGGTGAAGTGAAGGACAAAAATG TTCAAGTGGTCGAGCTTCCCATTGTAGACAGTCTTCATCCCCGTCCTCCATA TTTACCCTTGGCTGTACCAGAAGACCTCGCAGATCGACTTGTACGAGTGCAT GGTGACCCTGCAGTGTGGTGGGTGTCTCAGTTTGTCAAATACTTGATCCGCC CACAGCCTTGGCTAGAAAAAGAAATAGAAGAAGCCACCAAGAAGCTTGGCTT CAAACATCCAGTTATTGGAGTCCATGTCAGACGCACAGACAAAGTGGGAACA GAAGCTGCCTTCCATCCCATTGAAGAGTACATGGTGCATGTTGAAGAACATT TTCAGCTTCTTGCACGCAGAATGCAAGTGGACAAAAAAAGAGTGTATTTGGC CACAGATGACCCTTCTTTATTAAAGGAGGCAAAAACAAAGTACCCCAATTAT GAATTTATTAGTGATAACTCTATTTCCTGGTCAGCTGGACTGCACAATCGAT ACACAGAAAATTCACTTCGTGGAGTGATCCTGGATATACATTTTCTCTCTCA GGCAGACTTCCTAGTGTGTACTTTTTCATCCCAGGTCTGTCGAGTTGCTTAT GAAATTATGCAAACACTACATCCTGATGCCTCTGCAAACTTCCATTCTTTAG ATGACATCTACTATTTTGGGGGCCAGAATGCCCACAATCAAATTGCCATTTA TGCTCACCAACCCCGAACTGCAGATGAAATTCCCATGGAACCTGGAGATATC ATTGGTGTGGCTGGAAATCATTGGGATGGCTATTCTAAAGGTGTCAACAGGA AATTGGGAAGGACGGGCCTATATCCCTCCTACAAAGTTCGAGAGAAGATAGA AACGGTCAAGTACCCCACATATCCTGAGGCTGAGAAACACCACCATCACCAT CACCATCACCATCACTGACTCGAGGCATG	MLLVNQSHQGFNKEHTSKMVSAIVL YVLLAAAAHSAFARNGLGKDHEILR RRIENGAKELWFFLQSELKKLKNLE GNELQRHADEFLLDLGHHERSIMTD LYYLSQTDGAGDWREKEAKDLTELV QRRITYLQNPKDCSKAKKLVCNINK GCGYGCQLHHVVYCFMIAYGTQRTL ILESQNWRYATGGWETVFRPVSETC TDRSGISTGHWSGEVKDKNVQVVEL PIVDSLHPRPPYLPLAVPEDLADRL VRVHGDPAVWWVSQFVKYLIRPQPW LEKEIEEATKKLGFKHPVIGVHVRR TDKVGTEAAFHPIEEYMVHVEEHFQ LLARRMQVDKKRVYLATDDPSLLKE AKTKYPNYEFISDNSISWSAGLHNR YTENSLRGVILDIHFLSQADFLVCT FSSQVCRVAYEIMQTLHPDASANFH SLDDIYYFGGQNAHNQIAIYAHQPR TADEIPMEPGDIIGVAGNHWDGYSK GVNRKLGRTGLYPSYKVREKIETVK YPTYPEAEKHHHHHHHHH
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