

Supplementary Information

Crystal structure of tyrosine decarboxylase and identification of key residues involved in conformational swing and substrate binding

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Table S1 Primers used in this study.

| | | | |
|---------|------------------------|---------|------------------------|
| H98A-F | TGGGGTGC AATGAATTCAGAG | S586G-F | CGCGCTGGTGT TATGACGCCG |
| H98A-R | ATTCATTGCACCCCAATAACG | S586G-R | CATAACACCAGCGCGAATGAT |
| M99A-F | GGTCACGCAAATTCAGAGACC | S586V-F | CGCGCTGTTGTTATGACGCCG |
| M99A-R | TGAATTTGCGTGACCCCAATA | S586V-R | CATAACAACAGCGCGAATGAT |
| N100A-F | CACATGGCATCAGAGACCCTA | S586L-F | CGCGCTCTGGTTATGACGCCG |
| N100A-R | CTCTGATGCCATGTGACCCCA | S586L-R | CATAACCAGAGCGCGAATGAT |
| S101A-F | ATGAATGCAGAGACCCTAATG | S586I-F | CGCGCTATTGTTATGACGCCG |
| S101A-R | GGTCTCTGCATTCATGTGACC | S586I-R | CATAACAATAGCGCGAATGAT |
| E102A-F | AATTCAGCAACCCTAATGCCT | S586M-F | CGCGCTATGGTTATGACGCCG |
| E102A-R | TAGGGTTGCTGAATTCATGTG | S586M-R | CATAACCATAGCGCGAATGAT |
| T103A-F | TCAGAGGCACTAATGCCTGCT | S586P-F | CGCGCTCCGGTTATGACGCCG |
| T103A-R | CATTAGTGCCTCTGAATTCAT | S586P-R | CATAACCGGAGCGCGAATGAT |
| K240A-F | CAAACGGCACATTATTCTTGG | S586F-F | CGCGCTTTTGT TATGACGCCG |
| K240A-R | ATAATGTGCCGTTTGTGGTAC | S586F-R | CATAACAAAAGCGCGAATGAT |
| H241A-F | ACGAAGGCATATTCTTGGATC | S586W-F | CGCGCTTGGGTTATGACGCCG |
| H241A-R | AGAATATGCCTTCGTTTGTGG | S586W-R | CATAACCCAAGCGCGAATGAT |
| V294A-F | GTTGGTGCAGCCGGATCAACT | S586C-F | CGCGCTTGTGTTATGACGCCG |
| V294A-R | TCCGGCTGCACCAACCACGCC | S586C-R | CATAACACAAGCGCGAATGAT |
| A295F-F | GGTGTGTTTGGATCAACTGAA | S586T-F | CGCGCTACCGTTATGACGCCG |
| A295F-R | TGATCCAAACACACCAACCAC | S586T-R | CATAACGGTAGCGCGAATGAT |
| G296F-F | GTGGCCTTTTCAACTGAAGAA | S586N-F | CGCGCTAATGTTATGACGCCG |
| G296F-R | AGTTGAAAAGGCCACACCAAC | S586N-R | CATAACATTAGCGCGAATGAT |
| S297A-F | GCCGGAGCAACTGAAGAAGGT | S586Q-F | CGCGCTCAGGTTATGACGCCG |
| S297A-R | TTCAGTTGCTCCGGCCACACC | S586Q-R | CATAACCTGAGCGCGAATGAT |
| T298A-F | GGATCAGCAGAAGAAGGTGCC | S586Y-F | CGCGCTTATGTTATGACGCCG |
| T298A-R | TTCTTCTGCTGATCCGGCCAC | S586Y-R | CATAACATAAGCGCGAATGAT |
| E299A-F | TCAACTGCAGAAGGTGCCGTT | S586K-F | CGCGCTAAAGTTATGACGCCG |
| E299A-R | ACCTTCTGCAGTTGATCCGGC | S586K-R | CATAACTTTAGCGCGAATGAT |
| Y331A-F | GCTGCAGCAGGTGGATATGCT | S586R-F | CGCGCTCGTGTTATGACGCCG |
| Y331A-R | TCCACCTGCTGCAGCATCTAC | S586R-R | CATAACACGAGCGCGAATGAT |
| H391A-F | GATCCCGCAAAGATGGGATAT | S586H-F | CGCGCTCATGTTATGACGCCG |
| H391A-R | CATCTTTGCGGGATCAATTGT | S586H-R | CATAACATGAGCGCGAATGAT |
| G394F-F | AAGATGTTTTATGTACCATAC | S586D-F | CGCGCTGATGTTATGACGCCG |
| G394F-R | TACATAAAACATCTTATGGGG | S586D-R | CATAACATCAGCGCGAATGAT |

| | | | |
|---------|-----------------------|---------|-----------------------|
| Y395A-F | ATGGGAGCAGTACCATACTCG | S586E-F | CGCGCTGAAGTTATGACGCCG |
| Y395A-R | TGGTACTGCTCCCATCTTATG | S586E-R | CATAACTTCAGCGCGAATGAT |
| V396A-F | GGATATGCACCATACTCGGCT | H241R-F | ACGAAGCGTTATTCTTGGATG |
| V396A-R | GTATGGTGCATATCCCATCTT | H241R-R | AGAATAACGCTTCGTTTGTGG |
| P397A-F | TATGTAGCATACTCGGCTGGG | H241w-F | ACGAAGTGGTATTCTTGGATG |
| P397A-R | CGAGTATGCTACATATCCCAT | H241w-R | AGAATACCACTTCGTTTGTGG |
| Y398A-F | GTACCAGCATCGGCTGGGGGC | H241L-F | ACGAAGCTGTATTCTTGGATG |
| Y398A-R | AGCCGATGCTGGTACATATCC | H241L-R | AGAATACAGCTTCGTTTGTGG |
| M505A-F | TTCAATGCAGTTGACTATGTT | H241S-F | ACGAAGAGCTATTCTTGGATG |
| M505A-R | GTCAACTGCATTGAAGTCAGG | H241S-R | AGAATAGCTCTTCGTTTGTGG |
| S586A-F | CGCGCTGCAGTTATGACGCCG | H241D-F | ACGAAGGATTATTCTTGGATG |
| S586A-R | CATAACTGCAGCGCGAATGAT | H241D-R | AGAATAATCCTTCGTTTGTGG |
| M588A-F | TCGGTTGCAACGCCGTATATG | H241F-F | ACGAAGTTTTATTCTTGGATG |
| M588A-R | CGGCGTTGCAACCGAAGCGCG | H241F-R | AGAATAAACTTCGTTTGTGG |
| Y398F-F | GTACCATTTTCGGCTGGGGGC | H241N-F | ACGAAGAATTATTCTTGGATG |
| Y398F-R | AGCCGAAAATGGTACATATCC | H241N-R | AGAATAATTCTTCGTTTGTGG |

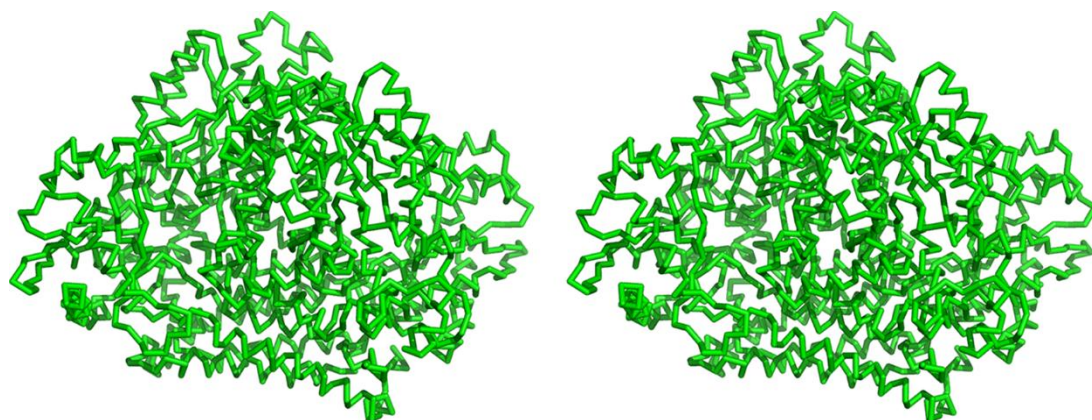


Figure S1 Stereo image of the entire structure of *LbTDC*.