

Table S2. Quantitative structural similarity.

Protein Pair	Lm Length	Mm Length	Aligned Length	RMSD	Sequence Identity	TM-score (Lm ref)	TM-score (Mm ref)
<i>LmDF1a</i> vs MmDF1	625	559	259	3.94	0.718	0.367	0.408
<i>LmDF1b</i> vs MmDF1	614	559	283	4.12	0.668	0.407	0.445
<i>LmDF2</i> vs MmDF2	639	579	249	3.32	0.791	0.363	0.4
<i>LmDF3</i> vs MmDF3	629	585	272	4.3	0.746	0.384	0.411
<i>LmDC1</i> vs MmDC1	669	736	258	5.05	0.659	0.33	0.302
<i>LmDC2</i> vs MmDC2	1356	1445	1065	4.14	0.649	0.731	0.687

*0.0 < TM-score < 0.30, random structural similarity; *0.5 < TM-score < 1.00, in about the same fold.