Supplementary Table S10. Impact of the number of LoRA modules in the last layers of the ESM-2 model family on MCC2. The bold value indicates the highest value for each SP type from each backbone model. The underlined value indicates the highest value for each SP type among all methods. The SP type marked with the symbol † represents SP types with limited training samples.

Organism	SP type	Archaea					Eukarya	Gram-negative bacteria					Gram-positive bacteria					mean
		Sec/SPI	Sec/SPII	Sec/SPIII†	Tat/SPI	Tat/SPII†	Sec/SPI	Sec/SPI	Sec/SPII	Sec/SPIII†	Tat/SPI	Tat/SPII†	Sec/SPI	Sec/SPII	Sec/SPIII†	Tat/SPI	Tat/SPII†	
Backbone	# of last layers																	
ESM2-150M	1	0.822	0.754	0.176	**0.802**	0.236	0.943	0.807	0.915	0.588	0.919	0.184	0.773	0.849	0.618	0.656	0.094	0.634
	5	0.806	0.826	0.426	0.594	0.677	0.949	0.824	0.935	0.898	0.955	0.453	0.793	0.904	0.969	0.713	0.509	0.764
	10	0.813	0.721	0.371	0.607	0.720	0.951	0.831	0.946	**0.967**	0.959	**0.535**	0.797	0.906	1.000	0.658	0.531	0.769
	15	0.798	0.832	0.176	0.594	0.514	0.955	0.853	**0.949**	0.918	0.962	0.486	0.811	0.930	0.951	0.745	**0.713**	0.761
	20	**0.840**	0.802	0.251	0.638	0.699	**0.956**	0.840	0.945	0.949	**0.965**	0.453	0.850	0.919	0.951	0.855	0.649	0.785
	25	0.781	0.855	0.328	0.736	0.941	0.955	0.815	0.934	0.934	0.950	0.434	0.845	**0.932**	0.969	0.843	0.633	**0.805**
	30	0.819	**0.864**	**0.569**	0.596	0.606	0.948	0.836	0.948	0.943	0.962	0.384	0.834	0.921	1.000	0.916	0.436	0.786
ESM2-650M	1	0.808	0.617	0.176	0.610	0.561	**0.955**	0.823	0.918	0.769	0.958	0.350	0.821	0.875	0.451	0.716	0.569	0.686
	5	0.835	0.690	0.474	0.620	0.561	0.948	0.802	0.918	0.809	0.963	0.487	0.822	0.900	0.636	0.690	0.643	0.737
	10	**0.837**	0.775	0.638	0.539	0.402	0.951	**0.841**	0.931	0.952	0.912	0.170	0.820	0.878	0.831	0.691	0.238	0.713
	15	0.803	0.695	0.655	0.624	0.334	0.939	0.777	0.924	0.968	0.964	0.368	0.803	0.914	0.951	0.779	0.479	0.748
	20	0.810	0.787	0.601	0.638	**0.898**	0.950	0.817	0.928	0.918	0.963	**0.489**	0.825	0.914	1.000	0.806	**0.694**	**0.815**
	25	0.813	0.864	**0.797**	0.594	0.791	0.948	0.805	**0.948**	0.753	0.904	0.399	0.777	**0.923**	0.762	0.753	0.681	0.782
	30	0.782	0.884	0.246	0.597	0.834	0.949	0.833	0.943	0.919	0.957	0.449	0.816	0.912	1.000	0.810	0.635	0.785
	33	0.749	0.798	0.471	0.863	0.887	0.939	0.802	0.939	0.870	0.943	0.458	**0.831**	0.911	0.911	0.732	0.427	0.783
ESM2-3B	1	0.810	0.624	0.325	0.604	0.552	0.961	0.714	0.888	0.584	0.898	0.279	0.778	0.855	0.833	0.537	0.399	0.665
	5	0.804	0.776	0.501	0.572	0.744	0.955	0.780	0.934	0.904	0.871	0.380	0.801	0.878	0.969	0.632	0.531	0.752
	10	0.815	0.720	0.408	0.600	0.765	0.955	0.831	0.939	0.861	0.980	0.654	0.789	0.892	0.916	0.733	0.791	0.791
	15	0.838	0.662	0.467	0.577	0.681	0.948	0.830	0.945	0.922	0.958	0.324	0.804	0.914	1.000	0.686	0.521	0.755
	20	0.853	**0.805**	0.642	0.616	0.792	0.961	**0.852**	0.948	0.860	0.970	0.558	0.813	0.911	1.000	0.746	0.665	0.812
	25	0.803	0.783	0.676	0.599	0.827	0.962	0.836	0.938	0.917	0.961	0.372	0.824	0.897	0.969	0.804	0.595	0.798
	30	0.800	0.777	0.601	**0.623**	**0.880**	0.962	0.825	0.944	0.838	0.966	0.335	0.840	0.905	0.803	0.828	0.680	0.788
	35	0.783	0.730	0.798	0.579	0.850	0.960	0.809	0.945	0.919	0.961	0.520	**0.848**	0.939	1.000	0.850	0.783	**0.830**
	36	0.794	0.737	0.413	0.619	0.819	0.959	0.847	0.949	**0.952**	0.966	0.403	0.826	0.900	1.000	**0.872**	0.530	0.787