330 A. Dataset Statistics

As described in Section 3.1.1, we used protein sequences 332 reviewed by experts and reported to Swiss-Prot (Consortium, 333 2022). This dataset, denoted as 'split100', was curated by 334 CLEAN (Yu et al., 2023) and divided into two subsets: 335 split30 and split50. We used split30 and split50 as training sets, while NEW-392 and Price-149 served as independent 337 test sets. Table 1 details the number of proteins in each 338 dataset and the number of EC numbers at each hierarchical 339 level. 340

341 One of the challenges in EC number prediction is the sparse 342 annotation of many classes, especially for level 4. Table 1 343 shows that in split100 dataset, each level 4 EC number has 344 an average of 46 positive proteins out of 227,362. Addi-345 tionally, more than a quarter of level 4 EC numbers have 346 only one positive protein, indicating severe class imbalance. 347 Furthermore, novel proteins may belong to previously undefined EC numbers that are unseen to the model. 349

B. Model Architecture

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352 All of the models used identical architecture, which consists 353 of encoder network that maps feature to initial representa-354 tion using pretrained model, and projection network that 355 maps initial representation to final representation vectors 356 which are ready for use in inference phase. We used pre-357 trained ESM-2-650M (Lin et al., 2023) model as encoder 358 network that acquires initial representation $r \in \mathcal{R}^{D_E}$ from 359 the sequence of protein, with weight parameters frozen. 360 Projection network then maps r into final representation 361 $f \in \mathcal{R}^{D_o}$, which is acquired by following equations: 362

$$f = W_3(\operatorname{Mod}_2(\operatorname{Mod}_1(r))) \tag{3}$$

$$Mod_i(\cdot) = ReLU(Dropout(LayerNorm(W_i(\cdot))))$$
(4)

Linear matrix $W_1 \in \mathcal{R}^{D_E \times D_h}, W_2 \in \mathcal{R}^{D_h \times D_h}, W_3 \in \mathcal{R}^{D_h \times D_o}$ are trained to get task-appropriate representation f.

C. Hyperparameters

Hyperparameters are given in table 2. We trained models
were trained up to 3000 epochs, and the model with the
lowest validation loss was selected for testing.

D. Experimental Results

380 D.1. Weight Grid Search for Levels 2 and 1

We conducted a grid search to optimize weights for each hierarchical level (λ_l), starting with level 3 and progressing to levels 2 and 1, while keeping the λ_4 fixed at 1. For each level, we selected the weight with the highest AUPRC from cross-validation. For level 3, λ_3 of 0.02 yielded the highest AUPRC for level 4 (Figure 2). Consequently, we fixed λ_3 and λ_4 at 0.02 and 1, respectively, and proceeded to optimize the λ_2 , as shown in Figure 8.



Figure 8. Grid search on the weight for level 2, λ_2

With λ_2 of 0.001 achieving the highest AUPRC for predicting level 4 EC numbers, we fixed λ_2 , λ_3 , λ_4 , at 0.001, 0.02, and 1, respectively. We then conducted a grid search to optimize λ_1 , as depicted in Figure 9.



Figure 9. Grid search on the weight for level 1, λ_1

DATASET	# Proteins	LEVEL	# EC Numbers	# PROTEIN-EC NUMBER PAIRS	Avg. Proteins per EC Numbers	# Single-protein EC Numbers
Split30	10,202	Level 1	7	10,427	1,490	C
		Level 2	72	10,504	146	6
		Level 3	240	10,555	44	26
		Level 4	3,576	11,033	3	2,051
Split50	29,942	Level 1	7	30,543	4,363	0
		Level 2	72	30,772	427	3
		Level 3	251	30,916	123	16
		Level 4	4,709	32,027	7	2,168
Split100	227,362	Level 1	7	232,306	33,187	0
		Level 2	72	233,878	3,248	1
		Level 3	253	234,855	928	7
		Level 4	5,242	241,025	46	1,360
NEW-392	392	Level 1	7	396	57	0
		Level 2	28	397	14	4
		Level 3	57	399	7	17
		Level 4	177	503	3	89
Price-149	149	Level 1	6	149	25	0
		Level 2	19	149	8	4
		Level 3	27	149	6	8
		Level 4	56	152	3	27

Table 1. Dataset statistics.

Table 2. Hyperparameters for model architecture and training.

	Hyperparameter	VALUE
MODEL ARCHITECTURE	DROPOUT	0.3
	D_E	1280
	D_h	512
	D_o	256
TRAINING	BATCH SIZE	SPLIT30: 6000, SPLIT50: 10000
	Optimizer	AdamW
	LEARNING RATE	5.00E-04
	WEIGHT DECAY	1.00E-03
	Contrastive loss temperature $ au$	0.1

The optimized weights for each level (λ_l) are illustrated in Figure 10. As the number of unique EC numbers decreases logarithmically, the weights for each hierarchical level also decrease logarithmically.

comparable or slightly better performance on all levels, most noticeable when extended to level 3. We conclude that effectiveness of hierarchical CL can be generalized on larger EC number datasets.

D.2. Experimental Results on Split50 Dataset

Figure 11 shows performances on grid search for the weight on level 3 (λ_3), starting with weight for level 4 (λ_4) as 1. Similar to performance on split30 dataset, there exists an optimal point of weight λ_3 and λ_4 for performance on level 3 and level 4. Raising weight for level 3 λ_3 gives slight performance gain in level 3 while performance on level 4 is not lost. Figure 12 shows performances on split50 dataset when extending HMC to all levels. λ_l weights follows that from split30. Extending HMC to higher levels gives



Figure 10. Optimized weights for each level (λ_l) .



Figure 11. HMC for level 3 and level 4 in split50 dataset.



Figure 12. HMC from level 1 to level 4 in split50 dataset. Extending HMC for higher levels improves the model performance.

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