

**Supporting Information S1.** This benchmark dataset  $S$  used in this study contains 207 different viral protein sequences. Among them: 165 belong to one subcellular location, 39 to two locations, and 3 to three locations. Both the accession numbers and sequences are given. None of the proteins included has  $\geq 25\%$  pairwise sequence identity to any other in the same subset (subcellular location) except viral capsid. It was adapted from the benchmark dataset in (Cheng X, Xiao X, Chou K C. *Gene*, 2017, **628**: 315-321) by reorganizing the order of proteins according to the alphabetical order of their accession numbers.

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(1)  $S_1$ : 8 viral capsid proteins

>P0C6L1

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>P32933

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>P32934

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>P32935

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ERLRDLRRKEKNGTHAKAVERGGRKQRKTHGDAQREGVEEEKTSEEPARIGITIEGVMS  
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>P33422

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TKIDVYRDEVPAQIIEVERSLQKELGISREGVAEQTERLRDLRRKEKSETHARVAEKGRR  
KQKRVHGDQKESTEDEKTPEEPTSVGITIEGVMSQKKLLSMIGGVERKMAPIGARESA  
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L

&gt;P33423

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&gt;Q03328

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&gt;Q98829

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**(2) S<sub>2</sub>: 33 host cell membrane proteins**

&gt;O73557

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&gt;P01115

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&gt;P03212

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&gt;P03246

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&gt;P03406

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>P03420

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>P05879

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>P08411

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>P09257

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>P09260

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>P09703

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>P0C2W9

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>P10681

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>P12504

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>P13198

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>P13285

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>P16849

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>P21935

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>P21936

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>P23169

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>P25049

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&gt;P33497

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&gt;P35256

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&gt;P35260

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&gt;P52381

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 VQVEKKKGNYGKCNIIHISTQKAYDLFIGIKIVYCFWGIPTVIFSYFYVIFGKTLRAL  
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&gt;P52382

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&gt;P52638

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>P88963

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>P90489

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>Q86917

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>Q98146

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### (3) S<sub>3</sub>: 20 host endoplasmic reticulum proteins

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>P03087

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>P03093

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>P09712

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>P09713

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>P09729

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>P0C6Y6

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>P11223

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>P11323

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>P13198

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>P14334

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>P21936

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>P52638

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>P59595

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>P59634

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>P59635

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>P90489

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>Q65164

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>Q6RJQ3

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#### (4) $S_4$ : 87 host cytoplasm proteins

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>B2MW49

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>O39521

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>P10208

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>P10216

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>P10220

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>P03213

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>P03264

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>P04485

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>P10188

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>P10189

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>P10190

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>P10201

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>P10202

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>P10205

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>P10208

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>P10209

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>P10216

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>P10220

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>P10226

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>P10231

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>P10233

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>P10238

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>P13288

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>P13292

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>P16753

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