*ESM 3*. Global model-fits and latent factor correlations for the test structural models in the domains General Health, COVID-19-IP and ECAP

| | $\chi^2$ | *df* | *p* | TLI | CFI | RMSEA | SRMR | $r_{GH, COVID-19-IP}$ / $r_{GH, ECAP}$ / $r_{COVID-19-IP, ECAP}$ |
|---|---|---|---|---|---|---|---|---|
| **General Health** | | | | | | | | |
| 1-DIM | 689.78 | 54 | <.001 | .833 | .864 | .185 | ,093 | |
| 3-DIM | 390.11 | 51 | <.001 | .906 | .927 | .139 | .070 | .731, .648, 1.049 |
| Bi-factor[a] | - | - | - | - | - | - | - | |
| 3-DIM[GH-MOD-DEV; b] | 247.90 | 52 | <.001 | .909 | .929 | .148 | .077 | .697, .687, .830 |
| 3-DIM[GH-MOD-CON, c] | 183.45 | 52 | <.001 | .901 | .918 | .122 | .078 | .691, .502, .665 |
| 3-DIM[GH-MOD] | 357.78 | 52 | <.001 | .912 | .931 | .135 | .071 | .673, .576, .739 |
| Bi-factor[3DIM-GH-MOD] | 162.60 | 62 | <.001 | .961 | .974 | .090 | .041 | |
| **COVID-19-IP** | | | | | | | | |
| 1-DIM | 305.95 | 54 | <.001 | .924 | .938 | .117 | .068 | |
| 3-DIM | 199.30 | 51 | <.001 | .953 | .963 | .092 | .055 | .921, .733, .891 |
| Bi-factor[3DIM] | - | - | - | - | - | - | - | |
| Bi-factor[3DIM-GH-MOD] | 190.57 | 62 | <.001 | .966 | .968 | .078 | .069 | |

**ECAP**

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| 1-DIM | 434.26 | 54 | <.001 | .901 | .919 | .143 | .064 | |
| 3-DIM | 331.69 | 51 | <.001 | .923 | .940 | .127 | .056 | .879, .784, .950 |
| 3-DIM[ECAP-MOD-DEV; b)] | 172.38 | 51 | <.001 | .950 | .961 | .117 | .055 | .757, .676, .784 |
| 3-DIM [ECAP-MOD-CON; c)] | 110.98 | 51 | <.001 | .959 | .968 | .083 | .053 | .863, .785, .856 |
| 3-DIM[ECAP-MOD] | 222.04 | 51 | <.001 | .953 | .946 | .099 | .047 | .796, .722, .812 |
| Bifactor[3DIM-GH-MOD] | 355.22 | 62 | <.001 | .934 | .938 | .117 | .077 | |
| Bifactor[3DIM-ECAP-MOD] | 148.80 | 42 | <.001 | .964 | .977 | .086 | .035 | |

*Notes:* GHP = General Health Prevention, ECAP = Early Childhood Allergy Prevention, COVID-19-IP = COVID-19 infection prevention; [a)] Not estimable (Matrix not positive definite); [b)] Developmental sample: $n = 173$; Confirmatory/cross-validation sample: $n = 170$