# Supporting Information

**Baker et al. 10.1073/pnas.1309947110**

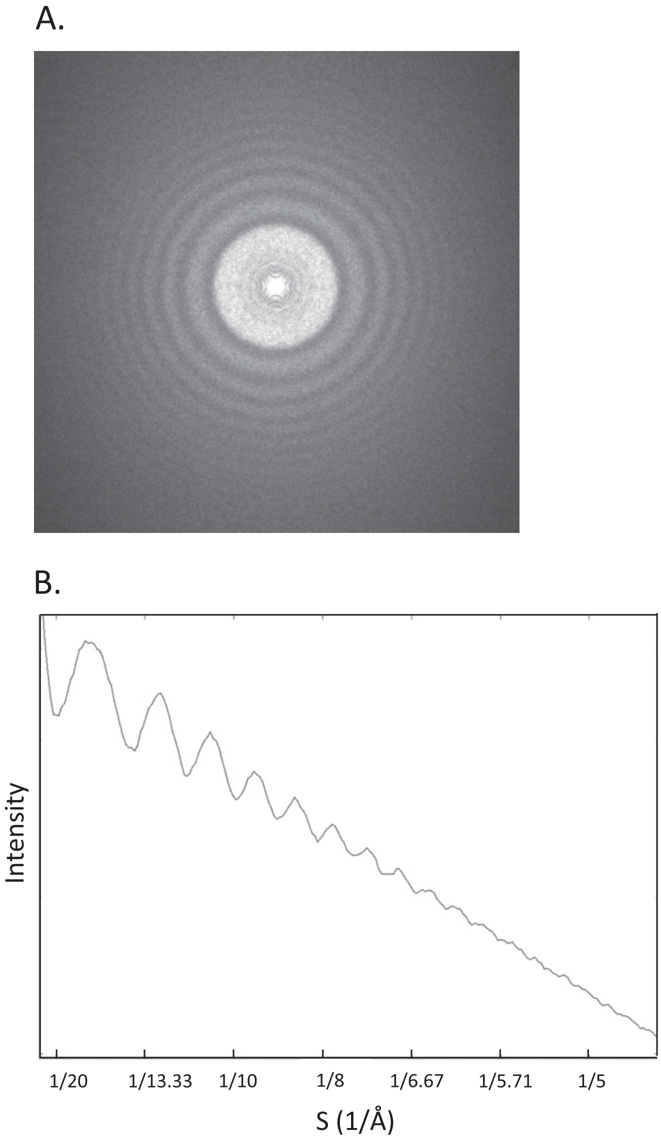

**Fig. S1.** Image quality assessment. (*A*) 2D average power spectra of ε15 particles in a micrograph. (*B*) 1D rotational average of (*A*) showing signal beyond 5 Å resolution.

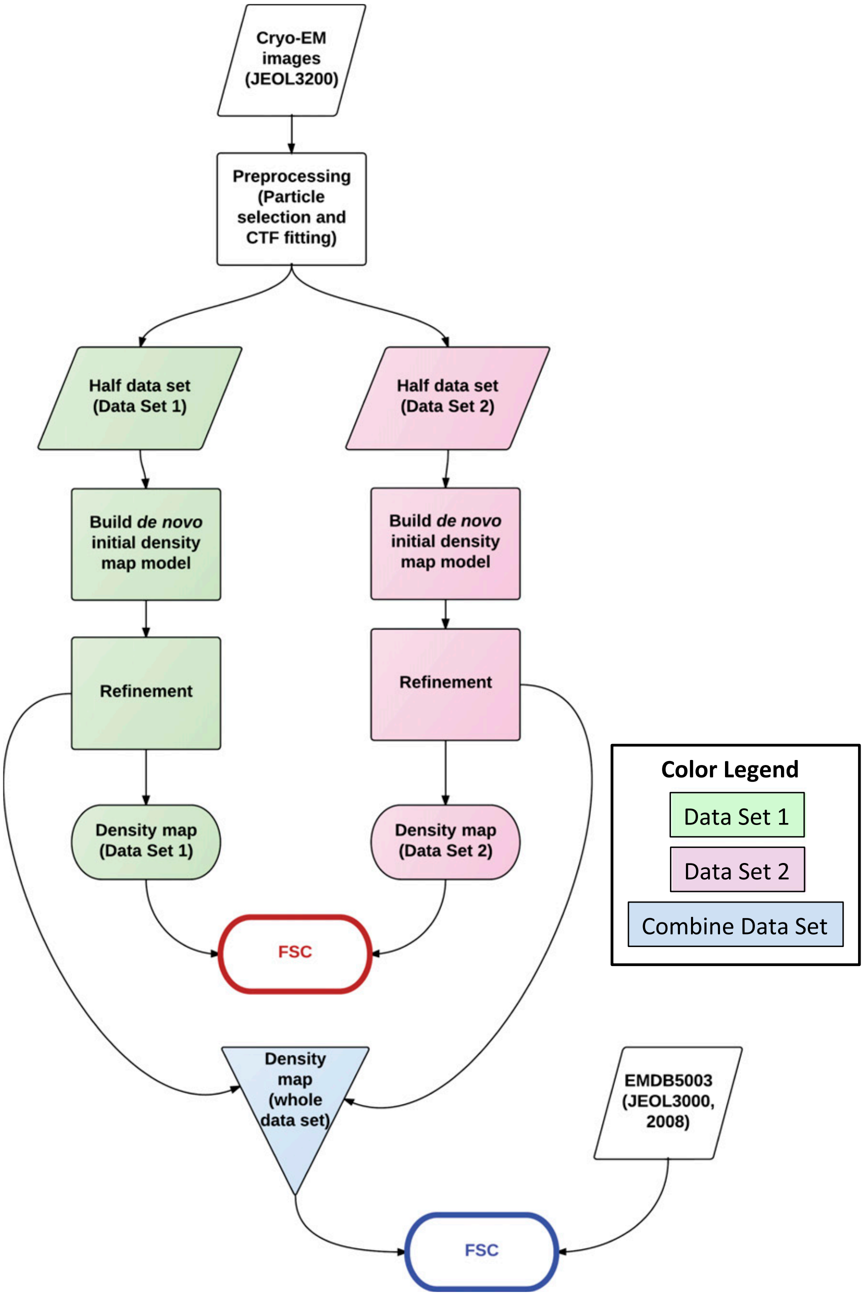

**Fig. S2.** Image processing. The image processing protocol is shown and colored to represent the different portions of the reconstruction process. The data used in this study were split following preprocessing. Dataset 1 and Dataset 2 were both processed independently using the same parameters. A Fourier Shell Correlation (FSC) was computed between the two datasets (shown in red process bubble), which corresponds to the red curve in Fig. 1*C*. To further validate our resolution estimate, an FSC curve was computed for combined data set against the previously published results (Electron Microscopy Data Bank ID code 5003) (shown in the blue process bubble), which corresponds to the blue curve in Fig. 1*C*.

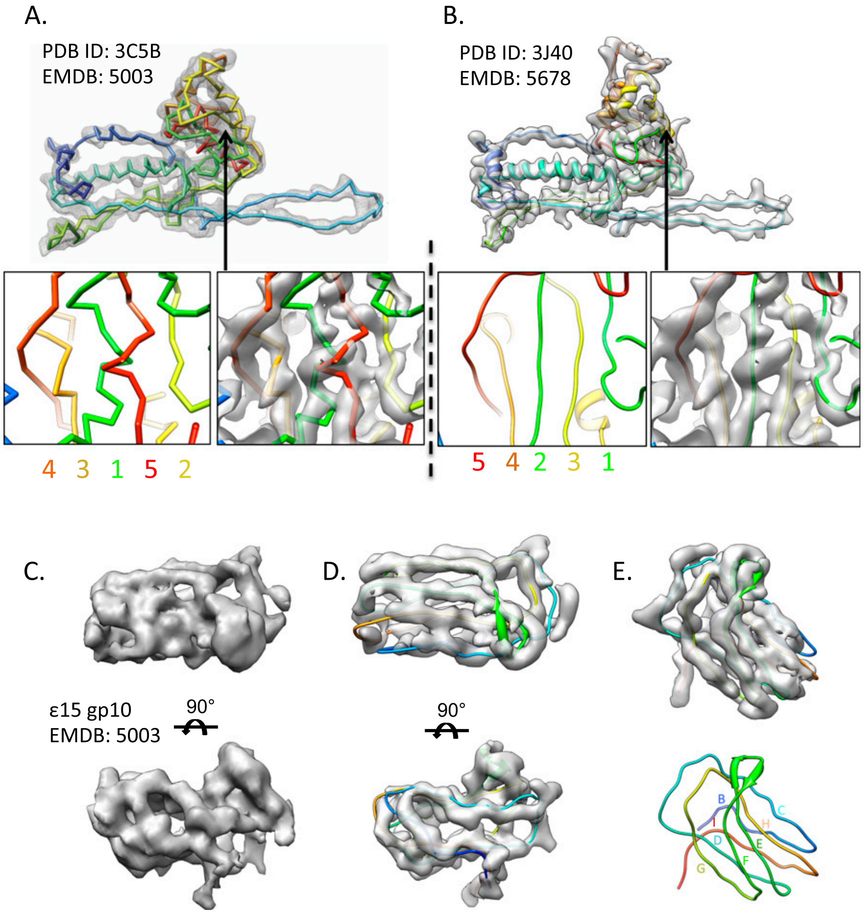

**Fig. S3.** Comparison of the ε15 datasets. (*A*) The previously published gp7 density map and model (represented in rainbow) is shown highlighting the strand order in the A-domain (panel cutout). (*B*) The current density map and model for gp7 is shown, revealing improved density connectivity and resolvability. Strand order for both Fig. S3 *A* and *B* is shown below the panel insets and colored based on the rainbow representation of the model. The previous and current hexon subunit-averaged density maps of gp10 are shown in (*C*) and (*D*), respectively. A top view is shown above with a side view. In *E*, the jellyroll fold of gp10 is shown with and without density.

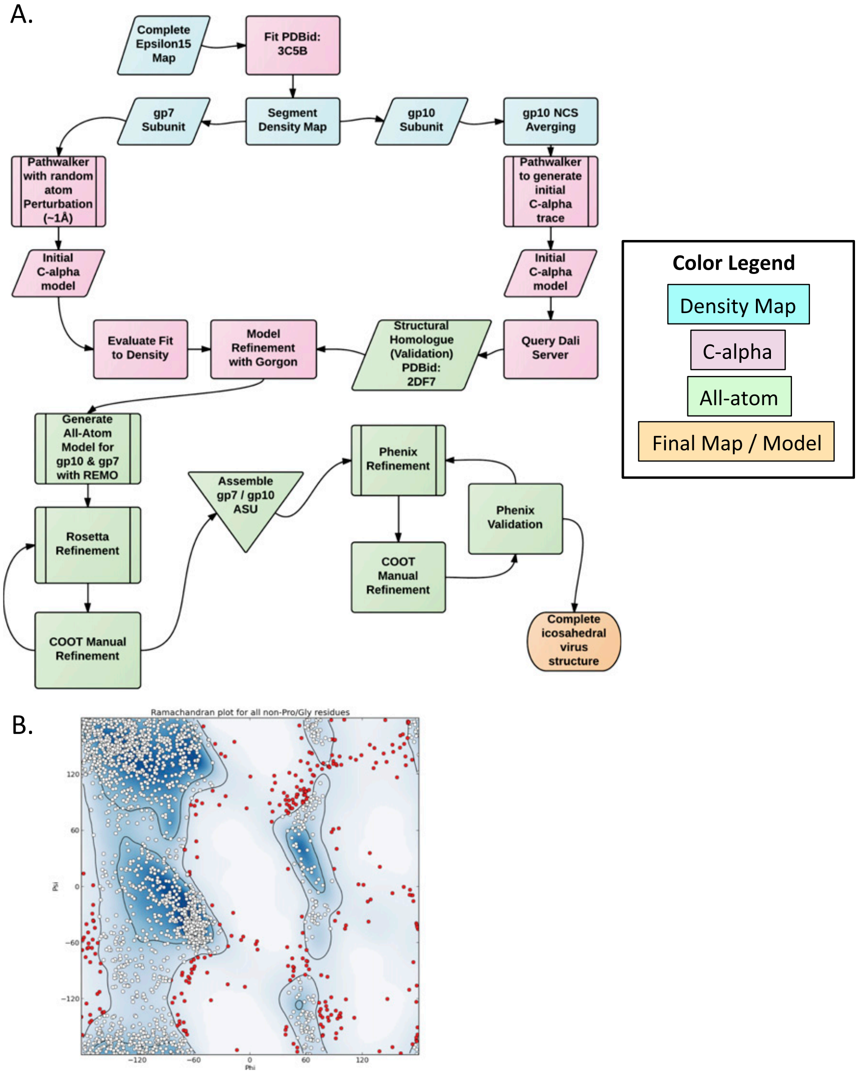

**Fig. S4.** Molecular modeling. (*A*) The molecular modeling protocol used to generate the final molecular model for gp7 and gp10 are shown. Following segmentation of the individual subunits, Pathwalker was used to generate the initial Cα trace (procedures colored in pink). Once an all-atom model was generated by REMO, the refinement process was started, first using COOT and ROSETTA for individual subunits and then PHENIX for the larger complexes. (*B*) The Ramachandran plot for the entire asymmetric unit is shown.

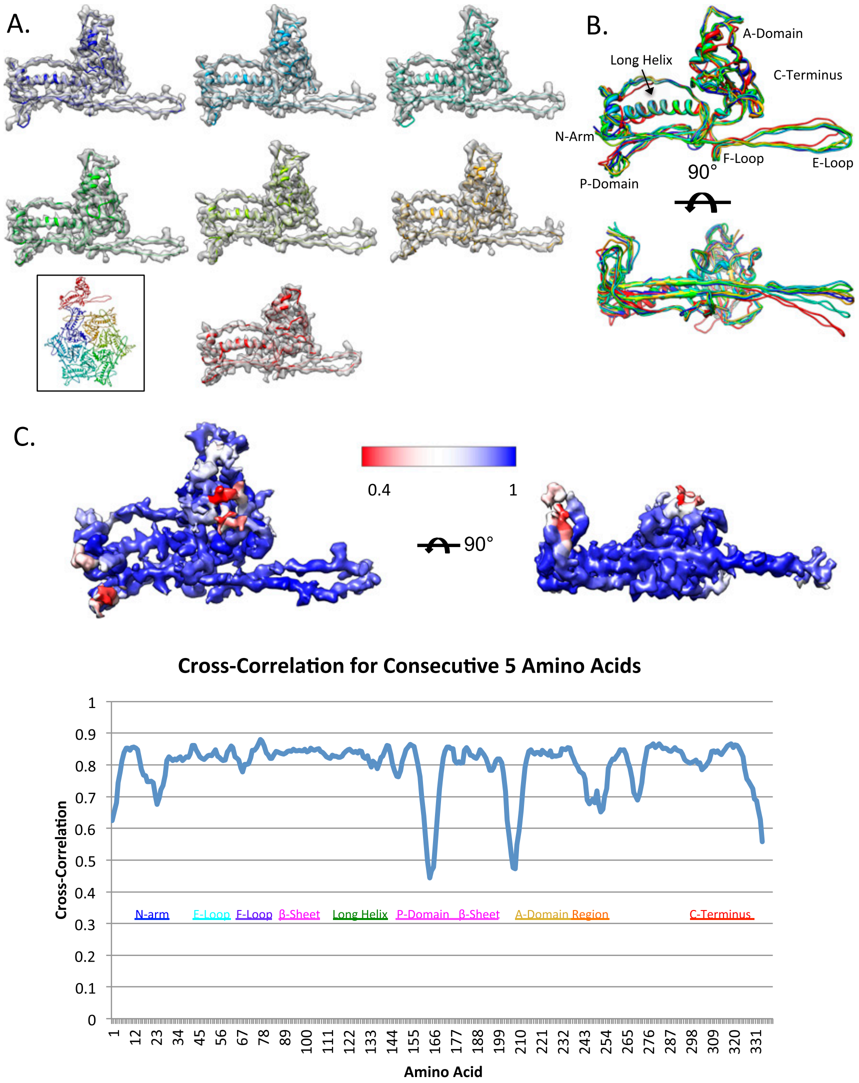

**Fig. S5.** Structure of gp7. (*A*) Seven individual gp7 subunits were generated and refined using the density map as a constraint. These subunits are shown with the corresponding density. (*B*) Overlapping of seven gp7 subunit models from one asymmetric unit illustrates model differences. Individual domains in gp7 are labeled. The red penton subunit shows the highest variation of structure. (*C*) The average density map and model correlation (five amino acids window) for gp7 is shown. The correlation values are mapped on to the density map (*Left*), where red indicates poor correlation and blue indicates good correlation. These values are shown in the plot on the right.

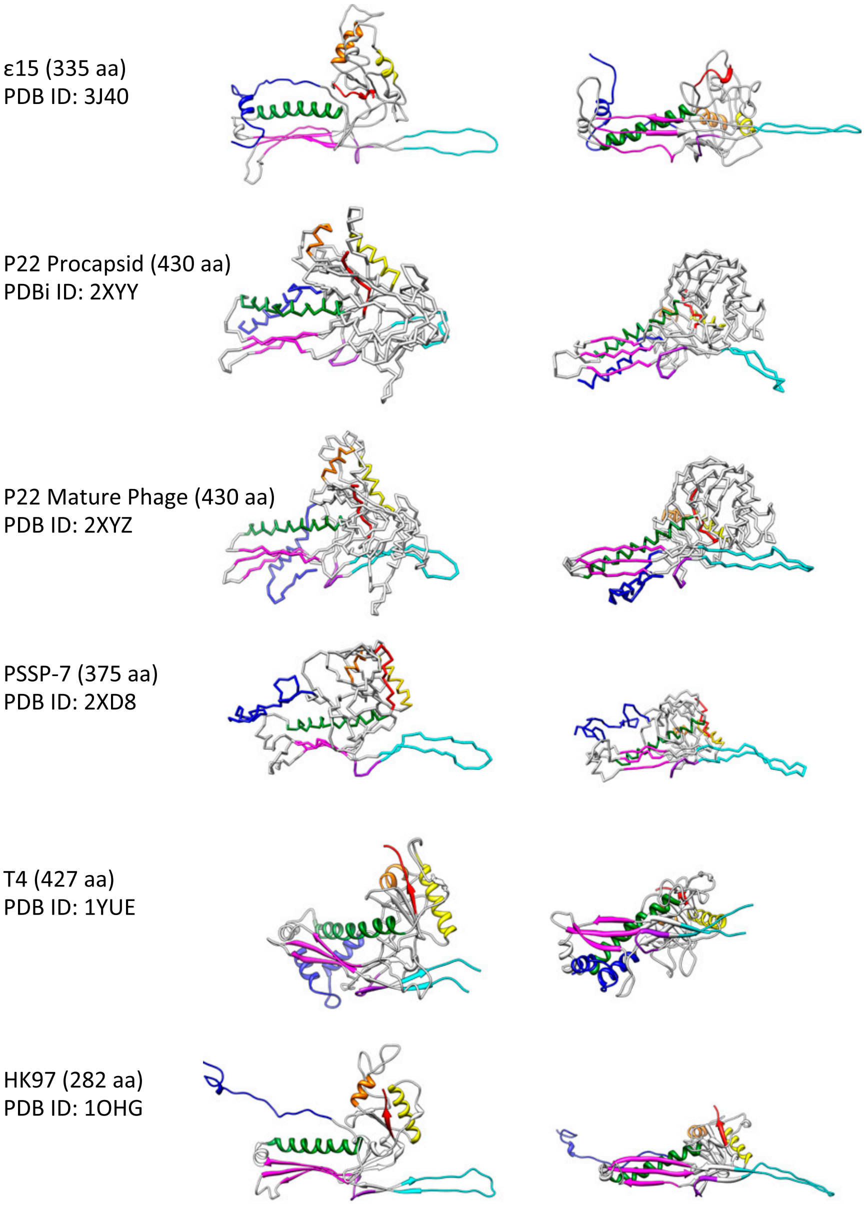

**Fig. S6.** Structural homologs of gp7. Two views of bacteriophage capsid protein structures are shown, colored by their functional domains. These functional domains are shown in Fig. 2*B*.

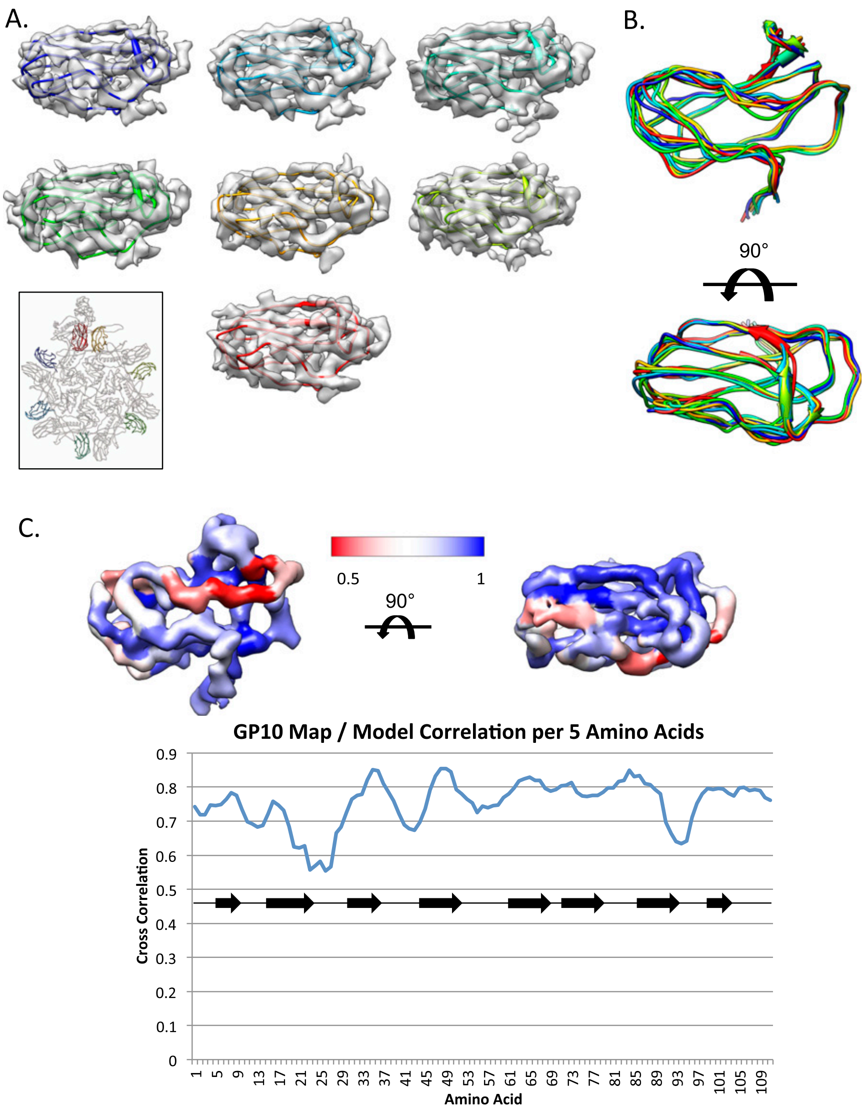

**Fig. S7.** Structure of gp10. (*A*) Seven individual gp10 subunits from an asymmetric unit are shown with the corresponding density. (*B*) Two views of the seven gp10 subunits are shown superimposed. (*C*) The average density map and model correlation (five amino acids window) for gp10 is shown. The correlation values are mapped on to the density map (*Left*), where red indicates poor correlation and blue indicates good correlation. These values are shown in the plot on the right.

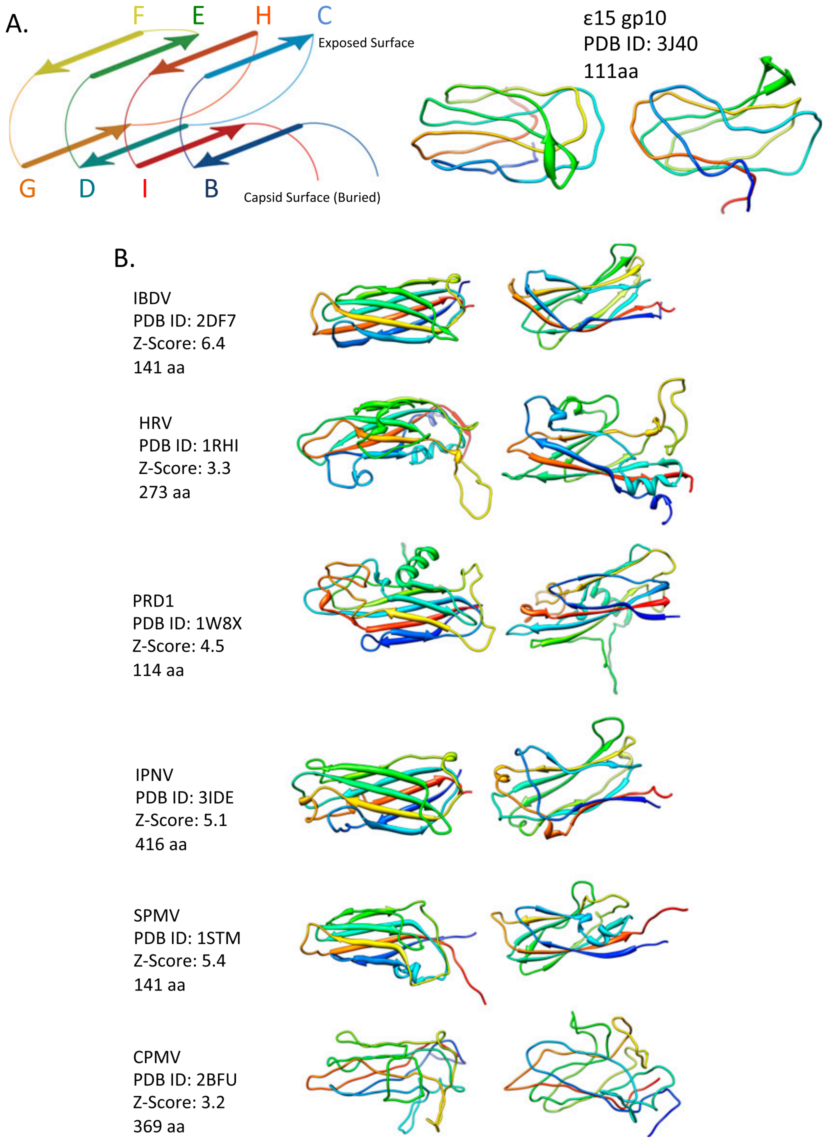

**Fig. S8.** Structural homologs of gp10. A rainbow colored cartoon (*A*, *Left*) illustrates the fold of gp10 (*A*, *Right*). Similar jellyroll folds from DALI are shown in (*B*) in two views and are identified by their Protein Data Bank (PDB) IDs and numbers of amino acids in the jellyroll fold.

**Table S1. Culled list of gp10 structural similarities**

| Chain | Z | rmsd | lali | Nres | %id | Description |
|---|---|---|---|---|---|---|
| 1gui-A | 5.6 | 2.7 | 91 | 155 | 4 | LAMINARINASE 16A |
| 1o6u-A | 5.4 | 2.9 | 86 | 393 | 3 | SEC14-LIKE PROTEIN 2 |
| 1pgw-1 | 5.2 | 3 | 95 | 185 | 3 | BEAN POD MOTTLE VIRUSSMALL (S) SUBUNIT |
| 3fbm-A | 5.1 | 2.7 | 90 | 428 | 7 | POLYPROTEIN |
| 3gza-A | 5.1 | 3.2 | 90 | 438 | 6 | PUTATIVE ALPHA-L-FUCOSIDASE |
| 4ind-M | 5 | 2.9 | 86 | 377 | 7 | C381 TURRET PROTEIN |
| 3j31-P | 5 | 3.1 | 87 | 373 | 7 | A223 PENTON BASE |
| 1ny7-1 | 5 | 3.3 | 98 | 189 | 5 | COWPEA MOSAIC VIRUS,SMALL (S) SUBUNIT |
| 3nru-H | 5 | 3.3 | 96 | 157 | 2 | EPHRIN RECEPTOR |
| 3ide-B | 4.9 | 2.8 | 93 | 416 | 8 | CAPSID PROTEIN VP2 |
| 2q1f-A | 4.9 | 3 | 94 | 991 | 3 | CHONDROITINASE |
| 1bmv-1 | 4.9 | 3.1 | 94 | 185 | 3 | PROTEIN (ICOSAHEDRALVIRUS - A DOMAIN) |
| 4i0w-B | 4.9 | 3.3 | 91 | 464 | 4 | PROTEASE CSPB |
| 2vvd-A | 4.9 | 3.3 | 101 | 162 | 8 | SPIKE PROTEIN P1 |
| 1us2-A | 4.8 | 2.9 | 92 | 507 | 9 | ENDO-BETA-1,4-XYLANASE |
| 2wak-A | 4.8 | 2.9 | 94 | 156 | 6 | TUMOR NECROSIS FACTORLIGAND SUPERFAMILY MEMBER |
| 4h3w-A | 4.7 | 3.1 | 93 | 313 | 3 | HYPOTHETICAL PROTEIN |
| 3p6b-B | 4.7 | 3.2 | 100 | 186 | 8 | CELLULOSE 1,4-BETA-CELLOBIOSIDASE |
| 1gu3-A | 4.7 | 3.2 | 92 | 142 | 9 | ENDOGLUCANASE C |
| 1pmh-X | 4.6 | 2.8 | 91 | 183 | 5 | BETA-1,4-MANNANASE |
| 1oh4-A | 4.6 | 3 | 93 | 174 | 4 | BETA-MANNOSIDASE |
| 1gny-A | 4.6 | 3.1 | 95 | 153 | 11 | XYLANASE 10C |
| 3afg-B | 4.6 | 3.2 | 89 | 507 | 7 | SUBTILISIN-LIKE SERINE PROTEASE |
| 4agx-A | 4.5 | 3 | 87 | 159 | 7 | VP1 PROTEIN |
| 1nqd-B | 4.5 | 3.1 | 87 | 114 | 3 | CLASS 1 COLLAGENASE |
| 2o8o-B | 4.5 | 3.1 | 87 | 114 | 3 | COLLAGENASE |
| 1nlq-B | 4.5 | 3.3 | 81 | 97 | 9 | NUCLEOPLASMIN-LIKE PROTEIN |
| 3a7q-A | 4.5 | 3.3 | 100 | 685 | 5 | REELIN |
| 1gwl-A | 4.5 | 3.6 | 87 | 141 | 7 | NON-CATALYTIC PROTEIN1 |
| 2wnv-E | 4.4 | 2.8 | 83 | 129 | 8 | COMPLEMENT C1Q SUBCOMPONENT SUBUNIT A |
| 3k4z-A | 4.4 | 3.1 | 95 | 275 | 8 | GLYCOSIDE HYDROLASE FAMILY 9 |
| 1uww-B | 4.4 | 3.2 | 95 | 179 | 4 | ENDOGLUCANASE |
| 2wo2-A | 4.4 | 3.2 | 95 | 178 | 3 | EPHRIN TYPE-A RECEPTOR |
| 1dyo-A | 4.4 | 3.3 | 97 | 156 | 5 | ENDO-1,4-BETA-XYLANASE Y |
| 2vmi-A | 4.4 | 3.3 | 90 | 146 | 8 | FIBRONECTIN TYPE IIIDOMAIN PROTEIN |
| 1ot5-A | 4.4 | 3.3 | 92 | 477 | 7 | KEXIN |
| 2zew-B | 4.4 | 3.3 | 92 | 147 | 8 | S-LAYER ASSOCIATED MULTIDOMAIN ENDOGLUCANASE |
| 1stm-C | 4.4 | 3.3 | 91 | 141 | 2 | SATELLITE PANICUM MOSAIC VIRUS |
| 1v0a-A | 4.4 | 3.4 | 93 | 170 | 11 | ENDOGLUCANASE H |
| 1nuk-A | 4.4 | 3.4 | 91 | 169 | 4 | PROTEIN (TYROSINE-PROTEIN KINASE RECEPTOR EPH) |
| 3lxu-X | 4.4 | 4 | 93 | 1,217 | 6 | TRIPEPTIDYL-PEPTIDASE2 |
| 3skj-E | 4.3 | 3.2 | 94 | 176 | 3 | ANTIBODY, LIGHT CHAIN |
| 4gwm-B | 4.3 | 3.4 | 97 | 554 | 6 | MEPRIN A SUBUNIT BETA |
| 4d93-A | 4.3 | 4.1 | 85 | 1,276 | 5 | THIOESTER-CONTAININGPROTEIN I |
| 3jqw-A | 4.2 | 2.9 | 83 | 117 | 5 | COLH PROTEIN |
| 1yq5-A | 4.2 | 3 | 90 | 144 | 3 | MINOR CAPSID PROTEIN |
| 2d6m-A | 4.2 | 3.2 | 91 | 151 | 2 | LECTIN, GALACTOSE BINDING, SOLUBLE 9 |
| 2c9a-A | 4.2 | 3.3 | 92 | 259 | 5 | RECEPTOR-TYPE TYROSINE-PROTEIN PHOSPHATASE MU |
| 4fo9-A | 4.2 | 3.4 | 91 | 261 | 7 | E3 SUMO-PROTEIN LIGASE PIAS2 |
| 2v4v-A | 4.2 | 3.4 | 90 | 129 | 7 | GH59 GALACTOSIDASE |
| 2df7-A | 4.2 | 3.4 | 88 | 420 | 2 | STRUCTURAL POLYPROTEIN VP2 |
| 3acf-A | 4.2 | 3.5 | 96 | 193 | 6 | BETA-1,4-ENDOGLUCANASE |
| 1w9w-A | 4.2 | 3.5 | 88 | 134 | 5 | BH0236 PROTEIN |
| 1shw-B | 4.2 | 3.5 | 95 | 181 | 2 | EPHRIN-A5 |
| 3hjr-A | 4.2 | 3.6 | 93 | 593 | 8 | EXTRACELLULAR SERINEPROTEASE |
| 1laj-A | 4.2 | 3.7 | 93 | 174 | 8 | CAPSID PROTEIN |
| 1p8j-G | 4.2 | 3.8 | 91 | 467 | 4 | FURIN PRECURSOR |
| 1f15-A | 4.2 | 3.9 | 93 | 157 | 8 | COAT PROTEIN |
| 3lkj-B | 4.1 | 3 | 87 | 132 | 9 | CD40 LIGAND |
| 1vtz-w | 4.1 | 3 | 92 | 184 | 9 | COAT PROTEIN |
| 3rqv-L | 4.1 | 3.1 | 92 | 184 | 9 | COAT PROTEIN |
| 1uyx-B | 4.1 | 3.4 | 86 | 130 | 7 | CELLULASE B |
| 1kfx-L | 4.1 | 3.4 | 97 | 640 | 5 | M-CALPAIN LARGE SUBUNIT |

**Table S1. Cont.**

| Chain | Z | rmsd | lali | Nres | %id | Description |
|---|---|---|---|---|---|---|
| 1wme-A | 4.1 | 3.4 | 94 | 434 | 5 | PROTEASE |
| 4acq-A | 4.1 | 3.6 | 85 | 1,270 | 6 | ALPHA-2-MACROGLOBULIN |
| 1k5m-A | 4.1 | 3.6 | 89 | 283 | 7 | COAT PROTEIN VP1 (P1D) |
| 2jd9-A | 4.1 | 3.6 | 87 | 139 | 2 | YECBM32 |
| 3km5-B | 4 | 2.8 | 90 | 173 | 10 | LYSINE SPECIFIC CYSTEINE PROTEASE |
| 1ule-B | 4 | 2.9 | 85 | 150 | 2 | GALECTIN-2 |
| 3nap-C | 4 | 3 | 94 | 276 | 5 | CAPSID PROTEIN |
| 2w87-B | 4 | 3 | 87 | 138 | 11 | ESTERASE D |
| 2ygm-A | 4 | 3.1 | 91 | 351 | 5 | BLOOD GROUP A-AND B-CLEAVING ENDO-BETA-GALACTOSID |
| 2vng-B | 4 | 3.1 | 90 | 173 | 10 | CPE0329 |
| 4d8m-A | 4 | 3.4 | 95 | 585 | 6 | PESTICIDAL CRYSTAL PROTEIN CRY5BA |
| 4aw7-A | 4 | 3.5 | 86 | 565 | 2 | GH86A BETA-PORPHYRANASE |
| 2zs6-B | 4 | 3.6 | 83 | 420 | 6 | HEMAGGLUTININ COMPONENTS HA3 |
| 1c3h-E | 3.9 | 2.6 | 81 | 137 | 10 | 30 KD ADIPOCYTE COMPLEMENT-RELATED PROTEIN |
| 2qfe-A | 3.9 | 3 | 84 | 139 | 2 | CALPAIN-7 |
| 1fpn-3 | 3.9 | 3.1 | 93 | 237 | 4 | COAT PROTEIN VP1 |
| 2w47-A | 3.9 | 3.2 | 83 | 135 | 11 | LIPOLYTIC ENZYME, G-D-S-L |
| 3k75-B | 3.9 | 3.3 | 84 | 151 | 6 | DNA REPAIR PROTEIN XRCC1 |
| 1hn0-A | 3.9 | 3.4 | 91 | 971 | 7 | CHONDROITIN ABC LYASEI |
| 3km9-B | 3.9 | 3.4 | 83 | 1,459 | 11 | COMPLEMENT C5 |
| 1gr3-A | 3.8 | 2.8 | 81 | 132 | 7 | COLLAGEN X |
| 1o91-A | 3.8 | 2.9 | 82 | 131 | 5 | COLLAGEN ALPHA 1(VIII) CHAIN |
| 2vtx-D | 3.8 | 3 | 75 | 89 | 4 | NPM-A PROTEIN |
| 1b35-C | 3.8 | 3 | 93 | 282 | 5 | PROTEIN (CRICKET PARALYSIS VIRUS, VP1) |
| 4bcu-A | 3.8 | 3.1 | 90 | 188 | 9 | COAT PROTEIN |
| 2w91-A | 3.8 | 3.1 | 93 | 635 | 10 | ENDO-BETA-*N*-ACETYLGLUCOSAMINIDASE D |
| 3jr0-A | 3.8 | 3.1 | 85 | 156 | 6 | GENE 9 PROTEIN |
| 1w8x-N | 3.8 | 3.2 | 81 | 114 | 7 | MAJOR CAPSID PROTEIN(PROTEIN P3) |
| 2buk-A | 3.8 | 3.4 | 91 | 184 | 8 | COAT PROTEIN |
| 1ciy-A | 3.8 | 3.5 | 89 | 577 | 4 | CRYIA(A) |
| 2cdo-A | 3.8 | 3.6 | 81 | 138 | 10 | BETA-AGARASE 1 |
| 3cih-A | 3.8 | 3.7 | 85 | 714 | 7 | PUTATIVE ALPHA-RHAMNOSIDASE |
| 3g6j-B | 3.8 | 4.2 | 86 | 903 | 5 | COMPLEMENT C3 BETA CHAIN |
| 2wq4-A | 3.7 | 2.7 | 82 | 134 | 11 | LECTIN |
| 2wdb-A | 3.7 | 2.9 | 83 | 139 | 6 | HYALURONOGLUCOSAMINIDASE |
| 2k46-A | 3.7 | 3.2 | 90 | 190 | 4 | MGC80075 PROTEIN |
| 3afk-A | 3.7 | 3.3 | 84 | 168 | 2 | ANTI-TUMOR LECTIN |
| 1u5i-A | 3.7 | 3.3 | 94 | 625 | 2 | CALPAIN 2, LARGE [CATALYTIC] SUBUNIT PRECURSOR |
| 2w3j-A | 3.7 | 3.3 | 83 | 137 | 5 | CARBOHYDRATE BINDINGMODULE |
| 1d4m-1 | 3.7 | 3.3 | 90 | 284 | 4 | PROTEIN (COXSACKIEVIRUS A9) |
| 1zba-2 | 3.7 | 3.4 | 95 | 207 | 14 | COAT PROTEIN VP1 |
| 2vzp-B | 3.7 | 3.4 | 86 | 127 | 7 | EXO-BETA-D-GLUCOSAMINIDASE |
| 1aym-1 | 3.7 | 3.4 | 90 | 285 | 6 | HUMAN RHINOVIRUS 16 COAT PROTEIN |
| 1qxp-B | 3.7 | 3.4 | 97 | 788 | 8 | MU-LIKE CALPAIN |
| 2v5d-A | 3.7 | 3.4 | 89 | 722 | 4 | O-GLCNACASE NAGJ |
| 3rjr-C | 3.7 | 3.5 | 91 | 343 | 9 | TRANSFORMING GROWTH FACTOR BETA-1 |
| 2quo-A | 3.7 | 3.6 | 85 | 123 | 1 | HEAT-LABILE ENTEROTOXIN B CHAIN |
| 1dlc-A | 3.7 | 3.7 | 89 | 584 | 7 | DELTA-ENDOTOXIN CRYIIIA |
| 1ddl-A | 3.7 | 3.8 | 91 | 188 | 5 | RNA (5′-R(P*UP*UP*UP*UP*UP*UP*U)-3′) |
| 2obe-A | 3.7 | 3.9 | 88 | 915 | 1 | HEXON |
| 2xom-A | 3.6 | 3 | 83 | 145 | 10 | ARABINOGALACTAN ENDO-1,4-BETA-GALACTOSIDASE |
| 1df0-A | 3.6 | 3.1 | 90 | 624 | 2 | M-CALPAIN |
| 4gh4-B | 3.6 | 3.4 | 94 | 207 | 13 | CAPSID PROTEIN VP1 |
| 1gqp-B | 3.6 | 3.4 | 95 | 188 | 5 | DOC1/APC10 |
| 3pof-B | 3.6 | 3.4 | 77 | 114 | 6 | MANNAN-BINDING LECTINSERINE PROTEASE 1 |
| 2p1b-A | 3.6 | 3.4 | 76 | 100 | 4 | NUCLEOPHOSMIN |
| 1wmx-B | 3.6 | 3.5 | 94 | 195 | 7 | COG3291: FOG: PKD REPEAT |
| 3toj-B | 3.6 | 3.7 | 93 | 197 | 5 | SET1/ASH2 HISTONE METHYLTRANSFERASE COMPLEX SUBUN |
| 1wck-A | 3.5 | 2.8 | 77 | 136 | 6 | BCLA PROTEIN |
| 1gmm-A | 3.5 | 2.9 | 78 | 126 | 6 | CBM6 |
| 2qdn-A | 3.5 | 2.9 | 81 | 123 | 10 | GITR LIGAND |
| 1iqa-A | 3.5 | 2.9 | 85 | 156 | 11 | RECEPTOR ACTIVATOR OFNUCLEAR FACTOR KAPPA B |

**Table S1. Cont.**

| Chain | Z | rmsd | lali | Nres | %id | Description |
|---|---|---|---|---|---|---|
| 1rj7-F | 3.5 | 3 | 85 | 144 | 9 | ECTODYSPLASIN A |
| 1c28-A | 3.5 | 3 | 81 | 123 | 4 | PROTEIN (30 KD ADIPOCYTE COMPLEMENT-RELATED |
| 2qe3-A | 3.5 | 3 | 85 | 140 | 5 | TNF SUPERFAMILY LIGAND TL1A |
| 1sfp-A | 3.5 | 3.1 | 76 | 111 | 9 | ASFP |
| 1nt0-A | 3.5 | 3.1 | 78 | 257 | 5 | MANNOSE-BINDING PROTEIN ASSOCIATED SERINE PROTEAS |
| 3jyb-A | 3.5 | 3.1 | 81 | 138 | 2 | SENSOR PROTEIN |
| 1dg6-A | 3.5 | 3.2 | 87 | 149 | 6 | APO2L/TNF-RELATED APOPOTIS INDUCING LIGAND (TRAIL |
| 1wky-A | 3.5 | 3.2 | 86 | 446 | 5 | ENDO-BETA-1,4-MANNANASE |
| 2v24-A | 3.5 | 3.2 | 91 | 197 | 3 | SPRY DOMAIN-CONTAINING SOCS BOX PROTEIN 4 |
| 1a6c-A | 3.5 | 3.2 | 88 | 513 | 7 | TOBACCO RINGSPOT VIRUS CAPSID PROTEIN |
| 4a6o-A | 3.5 | 3.3 | 82 | 144 | 7 | ALPHA-*N*-ACETYLGLUCOSAMINIDASE FAMILY PROTEIN |
| 1gff-2 | 3.5 | 3.3 | 89 | 177 | 9 | BACTERIOPHAGE G4 CAPSID PROTEINS GPF, GPG, GPJ |
| 1mec-3 | 3.5 | 3.3 | 95 | 231 | 5 | MENGO VIRUS COAT PROTEIN (SUBUNIT VP1) |
| 1tmf-3 | 3.5 | 3.3 | 96 | 232 | 3 | THEILER'S MURINE ENCEPHALOMYELITIS VIRUS |
| 1opo-C | 3.5 | 3.4 | 91 | 268 | 12 | COAT PROTEIN |
| 1qqp-2 | 3.5 | 3.4 | 96 | 216 | 11 | PROTEIN (GENOME POLYPROTEIN) |
| 1ihm-B | 3.5 | 3.5 | 94 | 511 | 4 | CAPSID PROTEIN |
| 2y26-A | 3.5 | 3.5 | 96 | 504 | 4 | COAT PROTEIN |
| 2ypj-A | 3.5 | 3.6 | 87 | 122 | 2 | ENDOGLUCANASE CEL5A |
| 3see-A | 3.4 | 2.7 | 91 | 214 | 2 | HYPOTHETICAL SUGAR BINDING PROTEIN |
| 1bev-1 | 3.4 | 3.1 | 89 | 268 | 7 | BOVINE ENTEROVIRUS COAT PROTEINS VP1 TO VP4 |
| 1m06-G | 3.4 | 3.1 | 89 | 187 | 2 | CAPSID PROTEIN |
| 1nzi-B | 3.4 | 3.1 | 75 | 156 | 8 | COMPLEMENT C1S COMPONENT |
| 1k5j-A | 3.4 | 3.1 | 76 | 94 | 5 | NUCLEOPLASMIN CORE |
| 1y4w-A | 3.4 | 3.2 | 86 | 517 | 6 | EXO-INULINASE |
| 1f49-A | 3.4 | 3.3 | 89 | 1,021 | 3 | BETA-GALACTOSIDASE |
| 3m8l-A | 3.4 | 3.3 | 92 | 534 | 4 | CAPSID PROTEIN |
| 3ecq-B | 3.4 | 3.3 | 89 | 1,347 | 9 | ENDO-ALPHA-*N*-ACETYLGALACTOSAMINIDASE |
| 4dzg-A | 3.4 | 3.3 | 82 | 114 | 7 | PLIG |
| 1lns-A | 3.4 | 3.3 | 88 | 763 | 3 | X-PROLYL DIPEPTIDYL AMINOPETIDASE |
| 2wzr-2 | 3.4 | 3.4 | 94 | 207 | 9 | POLYPROTEIN |
| 3cmg-A | 3.4 | 3.4 | 87 | 661 | 3 | PUTATIVE BETA-GALACTOSIDASE |
| 2ii7-B | 3.4 | 3.5 | 79 | 115 | 3 | ANABAENA SENSORY RHODOPSIN TRANSDUCER PROTEIN |
| 3mo4-A | 3.4 | 3.6 | 88 | 456 | 9 | ALPHA-1,3/4-FUCOSIDASE |
| 2qkg-A | 3.4 | 3.6 | 90 | 589 | 3 | INSECTICIDAL DELTA-ENDOTOXIN CRY8EA1 |
| 1xna-A | 3.4 | 3.6 | 88 | 151 | 6 | PROTEIN (DNA-REPAIR PROTEIN XRCC1) |
| 4es8-A | 3.4 | 3.7 | 91 | 302 | 5 | EPF |
| 1oq1-A | 3.4 | 3.7 | 93 | 223 | 4 | PROTEIN YESU |
| 1sdd-B | 3.4 | 4 | 88 | 601 | 2 | COAGULATION FACTOR V |
| 2r32-A | 3.3 | 2.8 | 71 | 140 | 7 | GCN4-PII/TUMOR NECROSIS FACTOR LIGAND |
| 1rb8-F | 3.3 | 3.1 | 93 | 422 | 9 | CAPSID PROTEIN |
| 3b7m-A | 3.3 | 3.1 | 91 | 216 | 5 | CELLULASE |
| 3ggl-A | 3.3 | 3.2 | 85 | 161 | 12 | PUTATIVE CHITOBIASE |
| 1d2q-A | 3.3 | 3.2 | 85 | 134 | 8 | TNF-RELATED APOPTOSISINDUCING LIGAND |
| 3cji-B | 3.3 | 3.3 | 93 | 238 | 8 | POLYPROTEIN |
| 1rud-1 | 3.3 | 3.3 | 83 | 273 | 7 | RHINOVIRUS 14 |
| 1c8n-C | 3.3 | 3.4 | 95 | 219 | 5 | COAT PROTEIN |
| 1h8t-B | 3.3 | 3.4 | 96 | 252 | 4 | ECHOVIRUS 11 COAT PROTEIN VP1 |
| 4ag4-A | 3.3 | 3.4 | 86 | 340 | 0 | EPITHELIAL DISCOIDINDOMAIN-CONTAINING RECEPTOR 1 |
| 3ut0-A | 3.3 | 3.5 | 95 | 804 | 9 | EXO-1,3/1,4-BETA-GLUCANASE |
| 1al0-G | 3.3 | 3.5 | 95 | 175 | 7 | SCAFFOLDING PROTEIN GPD |
| 1tnv-B | 3.3 | 3.5 | 93 | 186 | 0 | TOBACCO NECROSIS VIRUS (SUBUNIT VP1) |
| 1yjl-A | 3.3 | 3.6 | 84 | 285 | 7 | PEPTIDYL-GLYCINE ALPHA-AMIDATING MONOOXYGENASE |
| 2r0f-A | 3.3 | 3.7 | 87 | 163 | 5 | CGL3 LECTIN |
| 1xpw-A | 3.3 | 3.7 | 80 | 143 | 6 | LOC51668 PROTEIN |
| 4gz9-A | 3.2 | 3 | 80 | 562 | 6 | NEUROPILIN-1 |
| 1k3i-A | 3.2 | 3.1 | 81 | 651 | 7 | GALACTOSE OXIDASE PRECURSOR |
| 1poq-A | 3.2 | 3.1 | 79 | 118 | 5 | YPM |
| 2y38-A | 3.2 | 3.2 | 84 | 341 | 8 | LAMININ SUBUNIT ALPHA-5 |
| 1spp-A | 3.2 | 3.2 | 74 | 109 | 5 | MAJOR SEMINAL PLASMAGLYCOPROTEIN PSP-I |
| 2yue-A | 3.2 | 3.2 | 87 | 168 | 3 | PROTEIN NEURALIZED |
| 2fnj-A | 3.2 | 3.3 | 92 | 217 | 5 | CG2944-PF, ISOFORM F |

**Table S1. Cont.**

| Chain | Z | rmsd | lali | Nres | %id | Description |
|---|---|---|---|---|---|---|
| 4h7m-A | 3.2 | 3.3 | 91 | 226 | 5 | ENDO-1,4-BETA-GLUCANASE |
| 1z7s-3 | 3.2 | 3.3 | 94 | 239 | 3 | HUMAN COXSACKIEVIRUSA21 |
| 3iyp-C | 3.2 | 3.4 | 97 | 252 | 4 | CAPSID PROTEIN |
| 1cov-3 | 3.2 | 3.4 | 97 | 238 | 3 | COXSACKIEVIRUS COAT PROTEIN |
| 1ev1-2 | 3.2 | 3.4 | 98 | 254 | 5 | ECHOVIRUS 1 |
| 3vbf-B | 3.2 | 3.4 | 96 | 245 | 7 | GENOME POLYPROTEIN, CAPSID PROTEIN VP1 |
| 1eah-2 | 3.2 | 3.4 | 97 | 262 | 6 | POLIOVIRUS TYPE 2 COAT PROTEINS VP1 TO VP4 |
| 1qkq-A | 3.2 | 3.5 | 78 | 141 | 3 | EOSINOPHIL LYSOPHOSPHOLIPASE |
| 1mqt-B | 3.2 | 3.5 | 98 | 254 | 4 | POLYPROTEIN |
| 3skv-A | 3.2 | 3.5 | 78 | 354 | 8 | SSFX3 |
| 4fy1-1 | 3.2 | 3.7 | 97 | 217 | 8 | CAPSID PROTEIN |
| 1ncq-A | 3.2 | 3.7 | 91 | 273 | 8 | COAT PROTEIN VP1 |
| 3sam-B | 3.2 | 3.8 | 82 | 544 | 2 | RIFAMPICIN RESISTANCEPROTEIN |
| 1auy-B | 3.2 | 4.4 | 96 | 189 | 4 | TURNIP YELLOW MOSAICVIRUS |
| 4g3y-C | 3.1 | 2.9 | 76 | 147 | 9 | INFLIXIMAB FAB L |
| 4rhv-1 | 3.1 | 3.3 | 88 | 273 | 9 | HUMAN RHINOVIRUS 14 C |
| 3frl-B | 3.1 | 3.3 | 91 | 232 | 2 | LIPL32 |
| 1bzw-A | 3.1 | 3.3 | 95 | 232 | 3 | PROTEIN (PEANUT LECTIN) |
| 1lgn-A | 3.1 | 3.3 | 86 | 204 | 10 | SERUM AMYLOID P COMPONENT |
| 1o59-A | 3.1 | 3.4 | 83 | 318 | 10 | ALLANTOICASE |
| 2zah-C | 3.1 | 3.4 | 94 | 331 | 6 | COAT PROTEIN |
| 2gh8-A | 3.1 | 3.5 | 89 | 544 | 8 | CAPSID PROTEIN |
| 1o8p-A | 3.1 | 3.5 | 81 | 131 | 7 | PUTATUVE ENDO-XYLANASE |
| 4dy5-A | 3.1 | 3.6 | 75 | 111 | 9 | GIFSY-1 PROPHAGE PROTEIN |
| 3iii-A | 3.1 | 3.8 | 86 | 556 | 5 | COCE/NOND FAMILY HYDROLASE |
| 3kb5-A | 3.1 | 3.8 | 89 | 193 | 7 | TRIPARTITE MOTIF-CONTAINING PROTEIN 72 |
| 3kq4-B | 3 | 2.9 | 74 | 457 | 11 | GASTRIC INTRINSIC FACTOR |
| 1ovp-A | 3 | 2.9 | 71 | 114 | 3 | HYPOTHETICAL PROTEINLECB |
| 3nv1-A | 3 | 3 | 75 | 136 | 1 | GALECTIN 9 SHORT ISOFORM VARIANT |
| 1vbc-3 | 3 | 3.2 | 92 | 235 | 4 | POLIOVIRUS TYPE 3 |
| 2wzp-P | 3 | 3.3 | 77 | 298 | 6 | PUTATIVE RECEPTOR BINDING PROTEIN |
| 2w0c-L | 3 | 3.5 | 102 | 335 | 7 | MAJOR CAPSID PROTEINP2 |
| 3k94-B | 3 | 3.5 | 72 | 216 | 1 | THIAMIN PYROPHOSPHOKINASE |
| 3a0n-A | 3 | 3.5 | 93 | 242 | 5 | VAL-1 |
| 2tbv-C | 3 | 3.6 | 95 | 320 | 4 | TOMATO BUSHY STUNT VIRUS |
| 4dmi-B | 3 | 3.7 | 75 | 169 | 11 | CAPSID PROTEIN |
| 1qjz-B | 3 | 3.7 | 94 | 188 | 5 | PHYSALIS MOTTLE VIRUS |
| 2okx-B | 3 | 3.7 | 86 | 954 | 2 | RHAMNOSIDASE B |
| 2v73-A | 3 | 3.8 | 92 | 183 | 4 | PUTATIVE EXO-ALPHA-SIALIDASE |
| 2fbe-C | 3 | 3.9 | 88 | 199 | 11 | PREDICTED: SIMILAR TORET FINGER PROTEIN-LIKE 1 |
| 1p30-A | 3 | 4.1 | 91 | 891 | 4 | HEXON PROTEIN |

A nonredundant list of the top DALI hits above 3.0 for gp10 are shown. “Chain” represents the four letter PDB ID and associated chain ID, “Z” is the DALI Z-score, “rmsd” is the root mean squared deviation between gp10 and the DALI hit over the aligned residues (“lali”). The sequence identity of the aligned residues is shown in the “%id” column; total domain length for the DALI hit is shown in the “nres” column. A short description of the hit is listed under the “Description” column.

## Table S2. Potential salt bridges

| gp7 | gp7 | gp10 | Location | Density observed |
|---|---|---|---|---|
| Ser10 | — | Lys2 | N-arm | +++ |
| Lys20 | Asp48 | — | N-arm:F-loop | +++ |
| Lys33 | Asp232 | — | N-arm:A-domain | ++ |
| Lys51 | — | Asp107 | F-loop | +++ |
| Arg57 | Glu113 | — | E-loop:long helix | +++ |
| Glu62 | Lys124 | — | E-loop:long helix | + |
| Arg66 | Asp96 | — | E-loop:P-domain | – |
| Arg102 | Asp225 | — | P-domain:P-domain | – |
| Asp135 | — | Arg41 | A-domain | +++ |
| His199 | Glu200 | — | P-domain:P-domain | – |
| Arg216 | Glu221 | — | P-domain:P-domain | +++ |
| Asp263 | Lys292 | — | A-domain:A-domain | – |
| Asp269 | Lys284 | — | A-domain:A-domain | – |
| Glu-305 | Lys310 | — | A-domain | +++ |

A list of potential salt bridges was identified using PDBe PISA webserver. Residues for the relevant gp7 and gp10 subunits are indicated. A general location is given for the interaction (relative to gp10 in the case of gp7–gp10 interactions). Interactions across capsomeres are highlighted in red text in the location column. Visible density at the potential salt bridge locations is indicated with a rank for “–“ (no density present) to “+++” where clear density is seen.