|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
|  **Protein (Virus)** | **RMSDa (Å2)** | **Aligned Residues** | **Identitya (%)** | **Conserved Disulfides** | **Nascent length** | **Mature length** | **Localization Signal** |
| CPXV203 (CPXV) | - | - | - | 5/5 | 225 | 209 | KTEL |
| CrmD-CTD (CPXV)b | 2.8 | 136 | 12 | 3/5 | 320b | 300b | - |
| A41 (VACV) | 3.9 | 134 | 15 | 4/5 | 219 | 199 | - |
| vCCI (ECTV) | 3.0 | 143 | 14 | 4/5 | 247 | 231 | - |
| vCCI (RPV) | 3.1 | 139 | 15 | 4/5 | 258 | 242 | - |
| vCCI (CPXV) | 3.1 | 139 | 14 | 4/5 | 246 | 224 | - |

**Table S3. Structural comparison of CPXV203 with vCCI-like CKBPs.**

**General comparison**

**Electrostatics and 2o structure comparison**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
|  **Protein (Virus)** | **CKB Patch** | **CKB loop (2-3)**  |  | **7-9 Junction**  |  | **vCCI 13-14** |  |
|  | **-sheet IIc** | **Chargec** | **Lengthd** | **Lengthd** | **-strandd,e** | **(/** | **Lengthd** |
| CPXV203 (CPXV) | Neutral | Neutral | 6: R38-G43 | 19: D110-Y128 | 9: F118-S126 |  | 29: E152-L180 |
| CrmD-CTD (CPXV)g | Neutral | Neutral | 3: I184-S186 | 20: N247-H266 | 4: S252-L255 |  | 27: N288-P314 |
| A41 (VACV) | NEGATIVE | Neutral | 2: K39-Y40 | 32: E113-M144 | - |  | 32: E165-F196 |
| vCCI (ECTV) | NEGATIVE | NEGATIVE | 15: S52-P66 | 29: S140-S168 | - |  | 37: M191-L227 |
| vCCI (RPV) | NEGATIVE | NEGATIVE | 25: E53-P77 | 29: S151-I179 | - |  | 37: M202-L238 |
| vCCI (CPXV) | NEGATIVE | NEGATIVE | 14: E46-P59 | 29: S133-I161 | - |  | 37: M184-L220 |

Structures used in this analysis: 3ONA, 2VGA, 2GRK, 2FFK, 1CQ3. Chain A from each structure was used in this analysis.

aThe Dali server identified poxvirus CKB proteins as structurally similar to CPXV203. RMSD and identity are derived from Dali structural alignment.

bC-terminal domain (CTD) of ECTV CrmD (fusion of TNFR to SECRET domain).

cThe electrostatic surface for each molecule was evaluated using APBS within PyMOL.

dLength:boundaries; 2o structure defined by STRIDE.

e-strand not present in vCCI-like proteins that extends -sheet II.

fPrimary 2o structure within this region.

gUnlike the other proteins, the CrmD-CTD authors [1] used nascent protein residue numbering.