|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **EC23 RMSDs** | **4** | **7** | **6** | **8**  **(chains A&B)** | **A1**  **(chains A&B)** | **A1**  **(chains C&D)** | **A8** | **B** | **B** | **B7**  **(crystal form 1)** | **B7**  **(crystal form 2)** |
| **4** |  | 1.3 Å  (389) | 4.7 Å  (391) | 3.9 Å  (385) | 4.4 Å (389) | 4.6 Å (386) | 6.2 Å (393) | 2.1 Å  (390) | 4.1 Å  (393) | 1.6 Å (377) | 1.4 Å (356) |
| **7** | 1.3 Å  (389) |  | 4.7 Å  (398) | 4.0 Å  (391) | 4.5 Å (408) | 4.7 Å (404) | 6.1 Å (406) | 2.1 Å  (380) | 4.0 Å  (401) | 2.2 Å (384) | 2.0 Å (370) |
| **6** | 4.7 Å  (391) | 4.7 Å  (398) |  | 1.0 Å  (398) | 3.2 Å (393) | 2.9 Å (371) | 3.6 Å (368) | 4.1 Å  (406) | 1.9 Å  (392) | 4.1 Å (401) | 3.9 Å (398) |
| **8**  **(chains A&B)** | 3.9 Å  (385) | 4.0 Å  (391) | 1.0 Å  (398) |  | 3.3 Å (395) | 2.9 Å (370) | 3.9 Å (369) | 3.5 Å  (405) | 1.9 Å  (395) | 3.4 Å (398) | 3.3 Å (397) |
| **A1**  **(chains A&B)** | 4.4 Å (389) | 4.5 Å (408) | 3.2 Å (393) | 3.3 Å (395) |  | 0.8 Å (385) | 2.9 Å (407) | 4.4 Å  (402) | 3.4 Å  (408) | 4.1 Å (381) | 4.0 Å (380) |
| **A1**  **(chains C&D)** | 4.6 Å (386) | 4.7 Å (404) | 2.9 Å (371) | 2.9 Å (370) | 0.8 Å (385) |  | 2.3 Å (403) | 4.5 Å  (398)) | 3.1 Å  (394) | 3.9 Å (358) | 3.8 Å (363) |
| **A8** | 6.2 Å (393) | 6.1 Å (406) | 3.6 Å (368) | 3.9 Å (369) | 2.9 Å (407) | 2.3 Å (403) |  | 5.9 Å  (405) | 3.3 Å  (373) | 5.3 Å (367) | 5.3 Å (374) |
| **B** | 2.1 Å  (390) | 2.1 Å  (380) | 4.1 Å  (406) | 3.5 Å  (405) | 4.4 Å  (402) | 4.5 Å  (398) | 5.9 Å  (405) |  | 3.7 Å  (408) | 1.8 Å  (399) | 1.6 Å  (393) |
| **B** | 4.1 Å  (393) | 4.0 Å  (401) | 1.9 Å  (392) | 1.9 Å  (395) | 3.4 Å  (408) | 3.1 Å  (394) | 3.3 Å  (373) | 3.7 Å  (408) |  | 4.0 Å  (404) | 3.9 Å  (404) |
| **B7**  **(crystal form 1)** | 1.6 Å (377) | 2.2 Å (384) | 4.1 Å (401) | 3.4 Å (398) | 4.1 Å (381) | 3.9 Å (358) | 5.3 Å (367) | 1.8 Å  (399) | 4.0 Å  (404) |  | 0.8 Å (391) |
| **B7**  **(crystal form 2)** | 1.4 Å (356) | 2.0 Å (370) | 3.9 Å (398) | 3.3 Å (397) | 4.0 Å (380) | 3.8 Å (363) | 5.3 Å (374) | 1.6 Å  (393) | 3.9 Å  (404) | 0.8 Å (391) |  |

#### Figure 1—source data 4. Overall structural similarity between -, -, and -Pcdh EC2:EC3interface regions

Root mean square deviations over aligned C’s (RMSDs) between pairs of interacting EC2–3:EC2–3 regions from the Pcdh *trans* dimer structures are shown. The number of aligned C’s for each pair is given in parentheses. The 4EC1–4, 7EC1–5, 6EC1–4, 8EC1–4, and B3EC1–4 structures correspond to PDBs: 5DZW, 5DZV, 5DZX, 5DZY, and 5K8R. RMSDs between pairs of dimers from the same subfamily are shaded by subfamily.