**Table S1: List of templates assigned for M1AP by structural modeling algorithms.** The methods used to obtain the structures are given with resolution (the smaller the better) and Ramachandran outliers (the smaller the better) indicating the quality of the structures.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Algorithm | Templates | Method | Resolution (Å) | Ramachandran outliers (%) |
| GalaxyWeb | 5Y3R\_B, **1JEY\_B** | Cryo-EM, **X-ray** | 6.60, **2.50** | 2.4, **0.6** |
| I-TASSER | 1JEQ\_A1, **1JEY\_B**, 1RS0\_A, **2I6Q\_A**, 2XWB\_F, **3S5H\_A**, 5GJV\_F, **5Y58\_A**, 5Y58\_B, **6CIN\_A** | X-ray, **X-ray**, X-ray, **X-ray**, X-ray, **X-ray**, Cryo-EM, **X-ray**, X-ray, **X-ray** | 2.70, **2.50**, 2.60, **2.10**, 3.49, **1.60**, 3.60, **2.80**, 2.80, **2.60** | 2.1, **0.6**, 0.6, **0.0**, 1.3, **0.2**, 2.0, **0.0**, 0.0, **0.0** |
| Phyre2 | 1JEY\_B, **6FPZ\_A**, 1JEY\_A, **1JEQ\_A**, 1JEY\_B1 | X-ray, **X-ray**, X-ray, **X-ray**, X-ray | 2.50, **2.20**, 2.50, **2.70**, 2.50 | 0.6, **0.0**, 0.6, **2.1**, 0.6 |
| PRIMO | 4ACQ\_A, **5AH5\_A**, 5CK3\_B, **5CK4\_A**, 6H3V\_A | X-ray, **X-ray**, X-ray, **X-ray**, X-ray | 4.30, **2.10**, 3.20, **1.89**, 2.90 | 4.4, **0.3**, 1.5, **0.0**, 0.4 |
| RaptorX | 1T6B\_Y, **3N2N\_A**, 4WFQ\_A, **4HQK\_A**, 4C29\_A, **1JEQ\_A**, 1JEQ\_B, **5Y58\_B**, 5Y58\_A, **5KXF\_A**, 3MBO\_A, **3USQ\_A**, 3LRX\_A, **3PM6\_A**, 5GVV\_A | X-ray, **X-ray**, X-ray, **X-ray**, X-ray, **X-ray**, X-ray, **X-ray**, X-ray, **X-ray**, X-ray, **X-ray**, X-ray, **X-ray**, X-ray | 2.50, **1.80**, 2.40, **2.25**, 2.20, **2.70**, 2.70, **2.80**, 2.80, **2.70**, 3.31, **2.40**, 2.60, **2.20**, 1.95 | 0.5, **0.0**, 0.5, **0.0**, 0.0, **2.1**, 2.1, **0.0**, 0.0, **0.0**, 1.2, **1.2**, 0.5, **0.2**, 0.3 |
| Robetta | 1JEQ\_A, **1PCX\_A**, 2I6Q\_A, **4CNB\_B**, 4FX5\_A, **4KXF\_D**, 5BP4\_A, **5CIO\_B**, 5O85\_C, **5OQJ\_A**, 6CIN\_A, **6CIN\_B**, 6CIN\_C, **6CIO\_D**, 6HYT\_D, **6I2S\_A**, 6MG0\_A, **6MG0\_B**, 6NMI\_E, **6R2C\_A**, 6R2C\_B, **6R2C\_C**, 6UIM\_A | X-ray, **X-ray**, X-ray, **X-ray**, X-ray, **X-ray**, X-ray, **X-ray**, X-ray, **Cryo-EM**, X-ray, **X-ray**, X-ray, **X-ray**, X-ray, **X-ray**, X-ray, **X-ray**, Cryo-EM, **X-ray**, X-ray, **X-ray**, X-ray | 2.70, **2.50**, 2.10, **1.80**, 1.73, **3.20**, 3.75, **2.50**, 3.40, **4.70**, 2.60, **2.60**, 2.60, **3.00**, 2.33, **2.40**, 6.00, **6.00**, 3.70, **2.09**, 2.09, **2.09**, 2.75 | 2.1, **0.7**, 0.0, **0.9**, 0.0, **0.1**, 1.8, **0.0**, 0.6, **1.2**, 0.0, **0.0**, 0.0, **0.0**, 0.2, **0.1**, 0.1, **0.1**, 0.2, **0.0**, 0.0, **0.0**, 0.5 |
| Robetta-domain‡ | 1SHU\_X, **2I6Q\_A**, 2ODP\_A, **2XWJ\_I**, 3HRZ\_D, **4CN8\_A**, 4CN9\_A, **4CNB\_A**, 4CNB\_B, **4FX5\_A**, 5NUS\_A, **5O85\_C**, 5OQJ\_A, **5Y58\_D**, 6QDX\_A, **6QDX\_B**, 6QE0\_A, **6QT8\_A**, 6QTB\_A, **6QTA\_A**, 6QTB\_D | X-ray, **X-ray**, X-ray, **X-ray**, X-ray, **X-ray**, X-ray, **X-ray**, X-ray, **X-ray**, X-ray, **X-ray**, Cryo-EM, **X-ray**, X-ray, **X-ray**, X-ray, **X-ray**, X-ray, **X-ray**, X-ray | 1.50, **2.10**, 1.90, **4.00**, 2.20, **2.45**, 1.90, **1.95**, 1.95, **1.73**, 2.20, **3.40**, 4.70, **2.80**, 2.10, **2.10**, 1.39, **2.33**, 1.89, **1.89**, 1.89 | 0.0, **0.0**, 0.2, **1.3**, 0.2, **0.5**, 0.5, **0.3**, 0.3, **0.0**, 0.0, **0.6**, 1.2, **0.0**, 0.0, **0.0**, 0.0, **0.0**, 0.0, **0.3**, 0.0 |

† In “Templates”, the four characters before the underscore indicate the PDB ID, and the letter after the underscore indicates the protein chain. If there is a number after the chain identifier, it refers to the domain fold in their library.

**‡** Robetta-domain automatically used these templates to model amino acids 1-270 of M1AP and used *ab initio* modeling to model amino acids 265-530.