Supplemental Materials

3D-QSAR and Molecular recognition of Klebsiella pneumoniae NDM-1 inhibitors

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Figure S1 The structure-activity relationship based on all available experimental data.
Figure S2 Key residues for molecular recognition NDM-1 by Cmpd #17 were obtained by energy decomposition method (A) and proximity principle within 0.4nm (B), as well as the structure of NDM-1-Cmpd #17 complex.
| Cmpd # | IC₅₀ a (nM) | pIC₅₀ | CoMFA | CoMSIA |
|--------|-------------|-------|-------|-------|
|        |             |       | Pred. b | Res. c | Error Rate | Pred. | Res. | Error Rate |
| **Training Set** | | | | | | | | |
| 1      | 7.9 | 5.102 | 5.148 | 0.046 | 0.9% | 5.054 | -0.048 | -0.9% |
| 2      | 56  | 4.252 | 4.228 | -0.024 | -0.6% | 4.206 | -0.046 | -1.1% |
| 3      | 81  | 4.092 | 4.148 | 0.056 | 1.4% | 4.090 | -0.002 | 0.0% |
| 4      | 53  | 4.276 | 4.288 | 0.012 | 0.3% | 4.206 | -0.07 | -1.6% |
| 5      | 20  | 4.699 | 4.556 | -0.143 | -3.0% | 4.723 | 0.024 | 0.5% |
| 10     | 52  | 4.284 | 4.192 | -0.092 | -2.1% | 4.229 | -0.055 | -1.3% |
| 11     | 21  | 4.678 | 4.653 | -0.025 | -0.5% | 4.723 | 0.045 | 1.0% |
| 12     | 20  | 4.699 | 4.789 | 0.090 | 1.9% | 4.804 | 0.105 | 2.2% |
| 13     | 13  | 4.886 | 4.906 | 0.020 | 0.4% | 4.881 | -0.005 | -0.1% |
| 14     | 120 | 3.921 | 3.875 | -0.046 | -1.2% | 3.858 | -0.065 | -1.7% |
| 16     | 1.5 | 5.824 | 5.733 | -0.091 | -1.6% | 5.742 | -0.082 | -1.4% |
| 17     | 5.0 | 5.301 | 5.339 | 0.038 | 0.7% | 5.383 | 0.082 | 1.5% |
| 18     | 182 | 3.740 | 3.788 | 0.048 | 1.3% | 3.635 | -0.105 | -2.8% |
| 20     | 235 | 3.629 | 3.577 | -0.052 | -1.4% | 3.573 | -0.056 | -1.5% |
| 21     | 68  | 4.167 | 4.079 | -0.088 | -2.1% | 4.235 | 0.068 | 1.6% |
| 22     | 263 | 3.580 | 3.572 | -0.008 | -0.2% | 3.639 | 0.059 | 1.6% |
| 23     | 249 | 3.604 | 3.548 | -0.056 | -1.6% | 3.665 | 0.061 | 1.7% |
| **Test Set** | | | | | | | | |
| 6      | 48  | 4.319 | 4.281 | -0.038 | -0.9% | 4.282 | -0.037 | -0.9% |
| 7      | 55  | 4.260 | 4.130 | -0.130 | -3.1% | 4.130 | -0.13 | -3.1% |
| 8      | 92  | 4.036 | 4.251 | 0.215 | 5.3% | 4.251 | 0.215 | 5.3% |
| 9      | 135 | 3.87 | 4.100 | 0.230 | 5.9% | 4.100 | 0.23 | 5.9% |
| 15     | 5   | 5.301 | 5.226 | -0.075 | -1.4% | 5.226 | -0.075 | -1.4% |
| 19     | 113 | 3.947 | 3.950 | 0.003 | 0.1% | 3.950 | 0.003 | 0.1% |

a Experimental data obtained from references 28 and 29. b Pred. (Predicted values) stands for predicted pIC₅₀ values. c Res. (Residual values) stands for residual values between experimental and predicted pIC₅₀ values.
| System | Donor       | Acceptor    | Distance (Å) | Angle (°) | Occupancy (%) |
|--------|-------------|-------------|--------------|-----------|---------------|
| NDM-1  | S145-OG-HG  | D192-OD2    | 2.607±0.09   | 12.17±6.55 | 99.89         |
|        | S249-OG-HG  | D90-OD2     | 2.647±0.10   | 12.85±6.92 | 99.54         |
|        | T190-OG1-HG1| D192-OD1    | 2.649±0.10   | 17.31±9.12 | 99.43         |
|        | S213-OG-HG  | D254-OD2    | 2.654±0.10   | 14.68±7.98 | 91.01         |
|        | R85-NH2-HH21| D82-OD2     | 2.772±0.09   | 25.60±8.91 | 89.09         |
|        | R234-NH2-HH22| D267-OD2  | 2.794±0.09   | 18.25±9.65 | 67.65         |
|        | N146-ND2-HD21| S160-OG   | 2.875±0.08   | 18.60±9.93 | 66.77         |
|        | H228-ND1-HD1| D225-OD1    | 2.806±0.10   | 29.31±13.37| 65.63         |
|        | H228-ND1-HD1| D225-OD2    | 2.806±0.10   | 30.73±13.93| 63.90         |
|        | R234-NH1-HH11| D267-OD1  | 2.803±0.09   | 16.79±8.79 | 61.37         |
|        | S145-OG-HG  | D192-OD2    | 2.631±0.10   | 12.25±6.53 | 99.76         |
|        | T190-OG1-HG1| D192-OD1    | 2.649±0.10   | 18.46±9.51 | 99.12         |
|        | R85-NH2-HH21| D82-OD2     | 2.773±0.09   | 26.31±8.66 | 95.83         |
|        | R234-NH2-HH22| D267-OD2  | 2.788±0.09   | 17.46±9.06 | 94.08         |
|        | T62-OG1-HG1  | N76-OD1     | 2.746±0.11   | 17.36±9.84 | 91.90         |
|        | R234-NH1-HH11| D267-OD1  | 2.804±0.10   | 16.12±8.39 | 86.68         |
|        | T119-OG1-HG1  | D90-OD1     | 2.801±0.11   | 19.89±10.37 | 78.87         |
|        | S213-OG-HG  | D254-OD1    | 2.655±0.11   | 14.31±7.83 | 74.85         |
|        | Q37-NE2-HE21  | N76-OD1     | 2.851±0.08   | 25.89±13.15 | 73.00         |
|        | H228-ND1-HD1  | D225-OD2    | 2.803±0.10   | 26.17±12.75 | 65.46         |
|        | N146-ND2-HD21 | S160-OG   | 2.876±0.08   | 20.89±10.58 | 64.98         |
|        | R85-NE-HE    | D82-OD2     | 2.854±0.09   | 31.59±7.53 | 63.25         |
| H228-ND1-HD1 | D225-OD1 | Distance | Angle |
|--------------|----------|----------|-------|
| 2.80±0.10    | 30.52±14.74 | 60.88    |

*a* Distance stands for the average distance between the H-bond donor atom and the acceptor atom. 
*b* Angle stands for the average angle of the donor atom, hydrogen atom and acceptor atom. 
*c* Occupancy is the ratio of the snapshots with H-bond to all MD conformations.