**Supplementary information**

*In silico* targeting of the long noncoding RNA MALAT1

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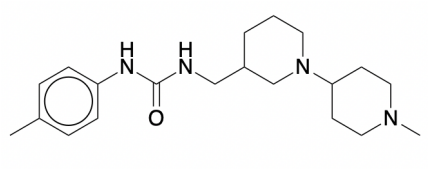
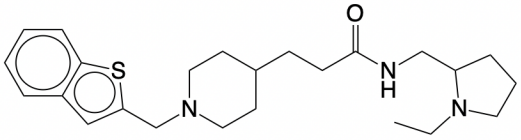
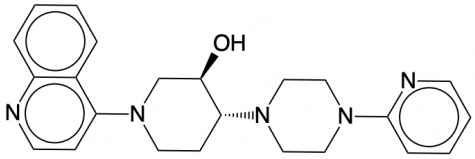
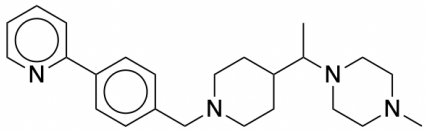
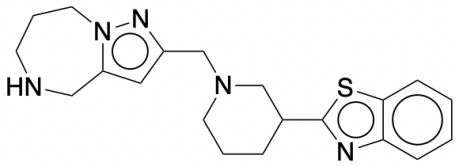
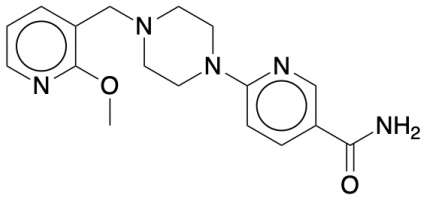
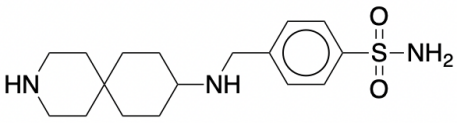
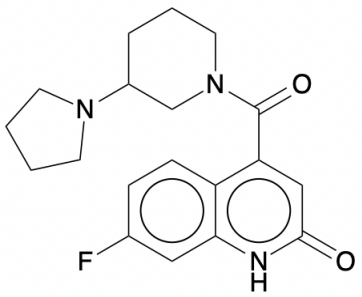
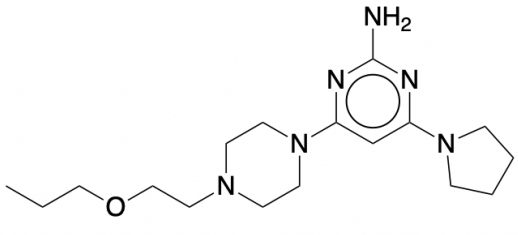
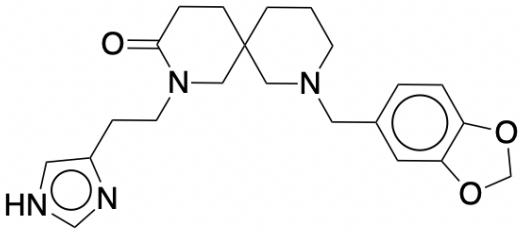
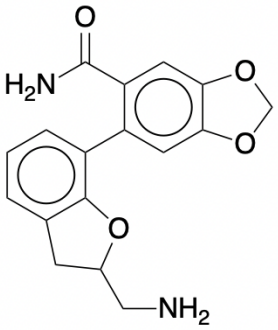
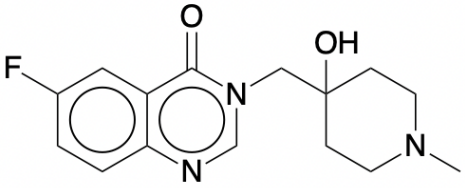
Supplementary information content:

**Table S1: Structure, chemical name and docking scores of *in-silico* docking top hits.**

| Study ID | Structure | Chemical Name | XP Glide Score | Target Site |
|---|---|---|---|---|
| MTC01 |  | N-[(1'-methyl-1,4'-bipiperidin-3-yl)methyl]-N'-(4-methylphenyl)urea | -7.844 | 2 |
| MTC02 |  | 3-[1-(1-benzothien-2-ylmethyl)-4-piperidinyl]-N-[(1-ethyl-2-pyrrolidinyl)methyl]propanamide | -6.956 | 3 |
| MTC03 |  | (3R*,4R*)-4-[4-(2-pyridinyl)-1-piperazinyl]-1-(4-quinolinyl)-3-piperidinol | N/A | Non-specific |
| MTC04 |  | 1-methyl-4-{1-[1-(4-pyridin-2-ylbenzyl)piperidin-4-yl]ethyl}piperazine | -7.557 | 3 |

| | | | | |
|---|---|---|---|---|
| MTC05 |  | 2-{[3-(1,3-benzothiazol-2-yl)-1-piperidinyl]methyl}-5,6,7,8-tetrahydro-4H-pyrazolo[1,5-a][1,4]diazepine dihydrochloride | -6.806 | 3 |
| MTC06 |  | 6-{4-[(2-methoxypyridin-3-yl)methyl]piperazin-1-yl}nicotinamide | -7.547 | 1 |
| MTC07 |  | 4-[(3-azaspiro[5.5]undec-9-ylamino)methyl]benzene sulfonamide dihydrochloride | -7.395 | 2 |
| MTC08 |  | 7-fluoro-4-{[3-(1-pyrrolidinyl)-1-piperidinyl]carbonyl}-2(1H)-quinolinone | -6.538 | 1 |

| | | | | |
|---|---|---|---|---|
| MTC09 |  | 4-[4-(2-propoxyethyl)piperazin-1-yl]-6-pyrrolidin-1-ylpyrimidin-2-amine | N/A | Non-specific |
| MTC10 |  | 8-(1,3-benzodioxol-5-ylmethyl)-2-[2-(1H-imidazol-4-yl)ethyl]-2,8-diazaspiro[5.5]undecan-3-one | -8.717 | 3 |
| MTC11 |  | 6-[2-(aminomethyl)-2,3-dihydro-1-benzofuran-7-yl]-1,3-benzodioxole-5-carboxamide | -6.795 | 1 |
| MTC12 |  | 6-fluoro-3-[(4-hydroxy-1-methylpiperidin-4-yl)methyl]quinazolin-4(3H)-one | -6.687 | 1 |

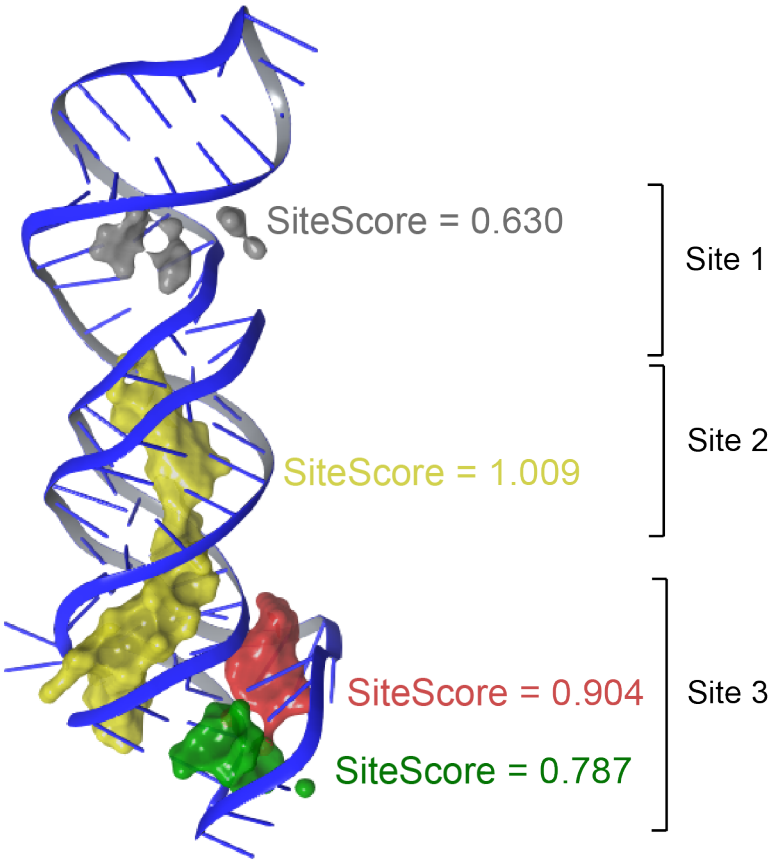



**Figure S1: Sitemap prediction of pockets on MALAT1 triple helix.** Sitemap was used to identify targetable sites within MALAT1 triple helix (PDB ID: 4plx). Four regions were identified (*yellow, red, green and grey*) and ranked based on their SiteScore, that assesses a site's propensity for ligand binding. Three docking sites were chosen based on the Sitemap results.