

**Table S1.** Proposed hydrogen bonds between methyltransferase and cofactor based on the crystal structure of each methyltransferase with bound AdoHcy

Enzyme	PDB	Substrate	<sup>a</sup> Amino acid CO <sub>2</sub> H			<sup>a</sup> Amino acid NH <sub>2</sub>			Nucleoside OH	N6	N1	N3
			L1	L4	X	L1	L4	X				
Hhal	1MHT	DNA C (C5)	L <sub>21</sub> G <sub>23</sub>	S <sub>305</sub>					E <sub>40</sub>	D <sub>60</sub>	I <sub>61</sub>	W <sub>41</sub>
DNMT2	1G55	DNA C (C5)	V <sub>13</sub> G <sub>15</sub>	S <sub>376</sub>			S <sub>76</sub>		D <sub>34</sub>	E <sub>88</sub>	I <sub>57</sub>	Y <sub>10</sub>
PvuII	1BOO	DNA C (N4)	G <sub>273</sub> S <sub>276</sub>					F <sub>250</sub>	H <sub>246</sub> E <sub>294</sub>	D <sub>34</sub>	S <sub>33</sub>	
TaqI	1AQI	DNA A (N6)		T <sub>23</sub>		E <sub>45</sub> A <sub>47</sub> C <sub>48</sub>			E <sub>71</sub>	D <sub>89</sub>	F <sub>90</sub>	I <sub>72</sub>
<sup>b</sup> DpnM	2DPM	DNA A (N6)	E <sub>41</sub> G <sub>46</sub> A <sub>48</sub>	K <sub>21</sub>		E <sub>41</sub> F <sub>43</sub>	D <sub>194</sub>		W <sub>17</sub> D <sub>62</sub>	D <sub>177</sub>	F <sub>178</sub>	F <sub>63</sub>
T4dam	1Q0T	DNA A (N6)	S <sub>37</sub>	K <sub>11</sub>			D <sub>171</sub>		Y <sub>7</sub> D <sub>50</sub> Q <sub>52</sub>	F <sub>184</sub>	F <sub>157</sub>	
<sup>b,d</sup> RsrI	1NW5	DNA A (N6)		K <sub>227</sub> S <sub>253</sub>			D <sub>65</sub>		H <sub>223</sub> D <sub>271</sub>	D <sub>46</sub>	C <sub>47</sub>	A <sub>272</sub>
<sup>d</sup> RsrI	1NW7	DNA A (N6)					D <sub>65</sub>	P <sub>66</sub>	H <sub>223</sub> D <sub>271</sub>	D <sub>46</sub>	C <sub>47</sub>	A <sub>272</sub>
<sup>b</sup> MboII	1G60	DNA A (N6)	T <sub>225</sub> S <sub>223</sub>	K <sub>197</sub>			D <sub>30</sub>		D <sub>241</sub>	N <sub>11</sub>	C <sub>12</sub>	M <sub>242</sub>
<sup>b</sup> FtsJ	1EIZ	RNA	G <sub>63</sub> G <sub>64</sub> G <sub>65</sub>	S <sub>33</sub>		D <sub>57</sub> G <sub>59</sub>	D <sub>124</sub>		A <sub>61</sub> D <sub>83</sub>	D <sub>99</sub>		F <sub>100</sub>
Ermc	1QAN	RNA A (N6)		I <sub>13</sub>	N <sub>101</sub>	G <sub>38</sub>			E <sub>59</sub>	D <sub>84</sub>		I <sub>85</sub>
Vp39	1AV6	RNA OH	G <sub>72</sub> H <sub>74</sub>	Q <sub>39</sub>		D <sub>68</sub>	G <sub>138</sub>		D <sub>95</sub> R <sub>97</sub>	V <sub>116</sub>		
Cher	1AF7	Protein E (O)		T <sub>94</sub> R <sub>98</sub>		A <sub>123</sub> E <sub>129</sub>		R <sub>230</sub>	D <sub>154</sub>	A <sub>38</sub> N <sub>212</sub>		
Prmt1	1ORI	Protein R (N)		R <sub>54</sub>					H <sub>45</sub> E <sub>100</sub>	E <sub>29</sub>	V <sub>128</sub>	
Prmt3	1F3L	Protein R (N)			R <sub>236</sub>	D <sub>258</sub>			D <sub>282</sub>	E <sub>311</sub>	I <sub>310</sub>	
PIMT	1DL5	Protein D-NH <sub>2</sub>	G <sub>85</sub> G <sub>87</sub>			G <sub>83</sub>			E <sub>107</sub>	D <sub>134</sub>	G <sub>135</sub>	V <sub>106</sub>
<sup>c</sup> HPIMT	1I1N	Protein D-NH <sub>2</sub>	S <sub>88</sub>	S <sub>59</sub> H <sub>64</sub>					D <sub>109</sub>	D <sub>141</sub>	T <sub>216</sub>	G <sub>142</sub>
<sup>c</sup> PIMT	1JG1	Protein D-NH <sub>2</sub>	S <sub>102</sub> N <sub>105</sub>			E <sub>97</sub> G <sub>99</sub>			E <sub>121</sub>	D <sub>148</sub>	L <sub>221</sub>	
<sup>b</sup> DOT1L	1NW3	Protein K (N)	Q <sub>168</sub>	T <sub>139</sub>		D <sub>161</sub> G <sub>163</sub>			E <sub>186</sub>	D <sub>222</sub>		F <sub>223</sub>
<sup>b</sup> HemK	1NV8	Protein Q (N)	G <sub>129</sub>	N <sub>197</sub>		D <sub>127</sub>			D <sub>151</sub>			
CmaAI	1KPG	Lipid C=C			Y <sub>33</sub> S <sub>34</sub>	G <sub>72</sub>	I <sub>136</sub>		G <sub>74</sub> T <sub>90</sub> L <sub>94</sub> Q <sub>95</sub>	E <sub>124</sub>		
CmaA2	1KPI	Lipid C=C			Y <sub>41</sub> S <sub>42</sub>	G <sub>80</sub>	L <sub>144</sub>		G <sub>82</sub> T <sub>102</sub> L <sub>103</sub> Q <sub>107</sub>	E <sub>132</sub>		W <sub>131</sub>
PcaA	1L1E	Lipid C=C			Y <sub>33</sub> S <sub>34</sub>	G <sub>72</sub>	I <sub>136</sub>		G <sub>74</sub> T <sub>94</sub> L <sub>95</sub> Q <sub>99</sub>	W <sub>123</sub>	E <sub>124</sub>	
ChOMT	1FP1	Small		K <sub>274</sub>		D <sub>215</sub>			D <sub>240</sub>	D <sub>260</sub>		
IOMT	1FP2	Small		K <sub>253</sub>		D <sub>194</sub>			D <sub>219</sub>	D <sub>293</sub>		
<sup>b</sup> COMT	1VID	Small			V <sub>42</sub>	G <sub>60</sub> S <sub>72</sub>	D <sub>141</sub>		E <sub>90</sub>	S <sub>119</sub>	S <sub>119</sub>	
Gamt	1KHH	Small	M <sub>70</sub> I <sub>72</sub> A <sub>73</sub>				D <sub>134</sub>		G <sub>60</sub> E <sub>89</sub> C <sub>90</sub>	E <sub>117</sub>		W <sub>116</sub>
Pnmt	1HNH	Small	Y <sub>85</sub>	Y <sub>35</sub> Y <sub>40</sub>		G <sub>79</sub> S <sub>80</sub>	A <sub>181</sub>		D <sub>81</sub> G <sub>101</sub>	D <sub>158</sub>		V <sub>159</sub>
<sup>b</sup> COMT	1KYZ	Small		K <sub>265</sub>		D <sub>206</sub>			D <sub>231</sub>	D <sub>251</sub>		
Gnmt	1NBH	Small			W <sub>30</sub> R <sub>40</sub>	A <sub>64</sub>	L <sub>136</sub>		D <sub>85</sub>	N <sub>116</sub>		W <sub>117</sub>
Hnmt	1JQD	Small	E <sub>65</sub>	E <sub>28</sub> H <sub>29</sub>		G <sub>60</sub> D <sub>67</sub>	H <sub>140</sub> I <sub>142</sub>		E <sub>89</sub> Q <sub>94</sub>	S <sub>120</sub>	S <sub>121</sub>	S <sub>120</sub>
<sup>b</sup> SAMT	1M6E	Small	N <sub>65</sub>			D <sub>57</sub>			D <sub>98</sub>	S <sub>129</sub>		

<sup>a</sup> The residues contacting the methionine moiety are grouped according to their position in the type I AdoMet-dependent methyltransferase fold: L1 indicates the loop following strand β1, L4 the loop following β4 and X indicates residues outside the conserved domain. Residues forming side chain interactions are written in black, main chain interactions in blue and water mediated interactions in magenta. Conserved residues are highlighted in yellow.

<sup>b</sup> 2DPM, 1NW5, 1G60, 1EIZ, 1NW3, 1NV8, 1VID, 1KYZ and 1M6E were solved with bound AdoMet and 1IM8 was solved with AdoHcy.

<sup>c</sup> Hydrogen bonds with adenine N<sup>7</sup> were predicted: made by the main chain of Thr 216 in 1I1N and Ile 221 in 1JG1.

<sup>d</sup> AdoMet and AdoHcy have different conformations and different interactions with M.RsrI in 1NW5 and 1NW7, therefore both structures are included.