A Comparative Modeling and Molecular Docking Study on Mycobacterium Tuberculosis Targets Involved in Peptidoglycan Biosynthesis

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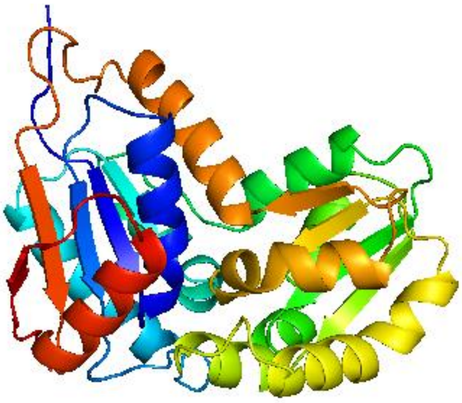
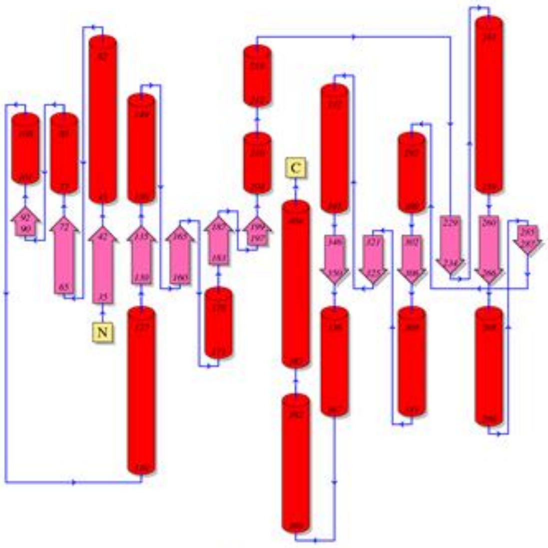


Figure S1. The 3D structure of MurI are presented as colourful structure.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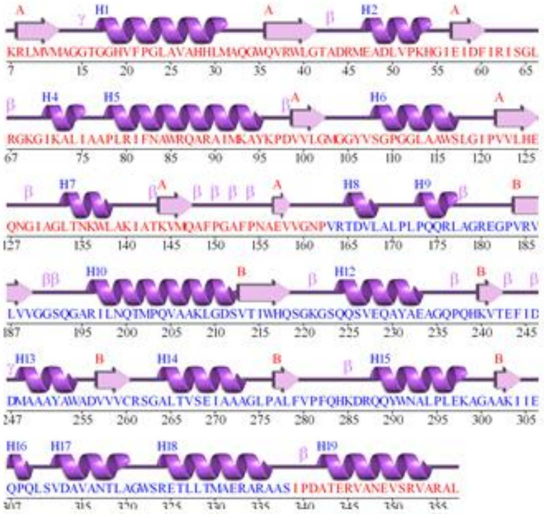
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γ H13 B H14 B β H15 B
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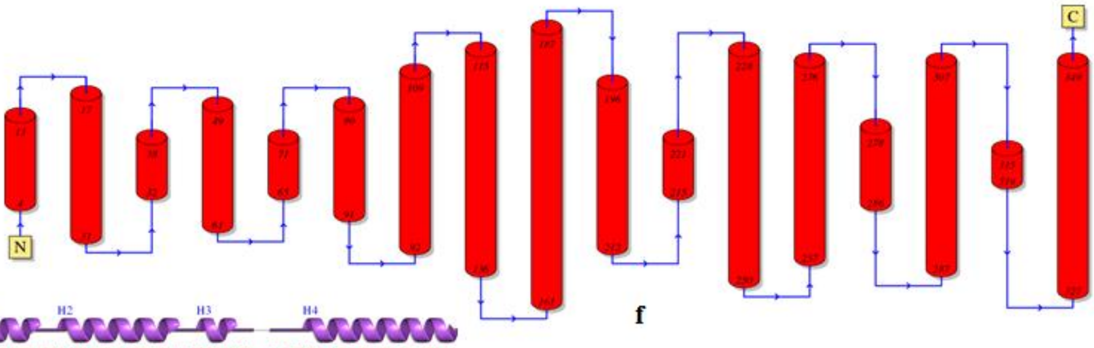
e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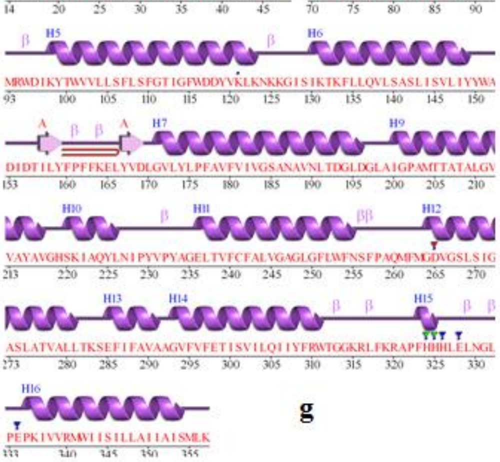
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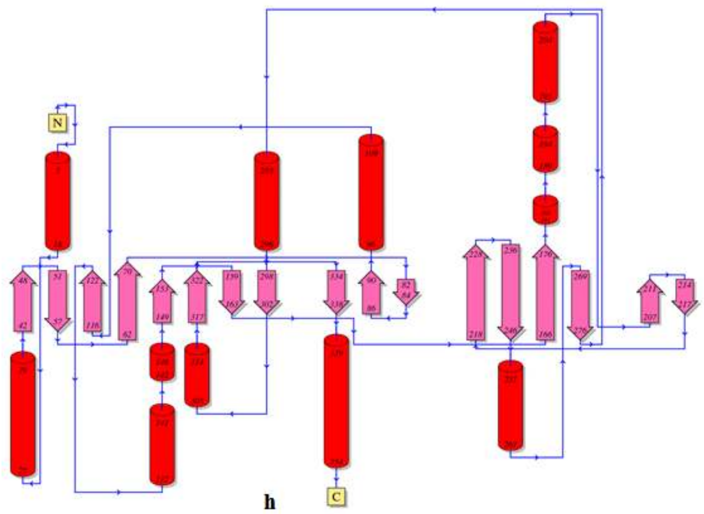
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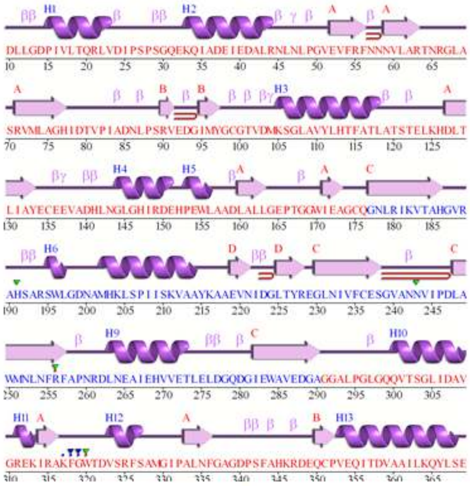
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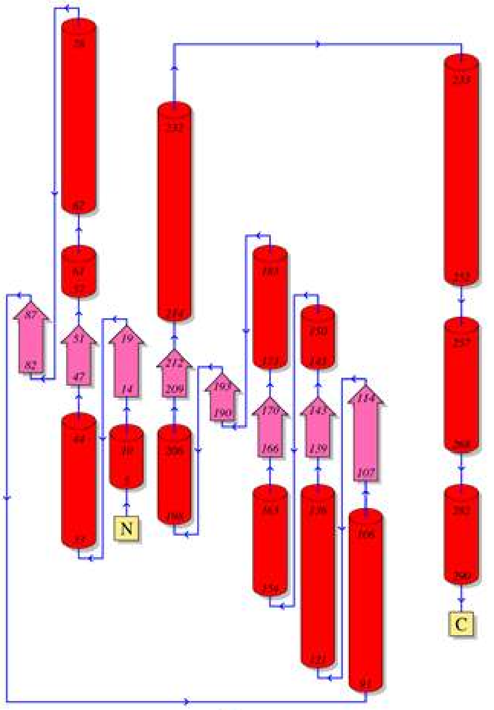
i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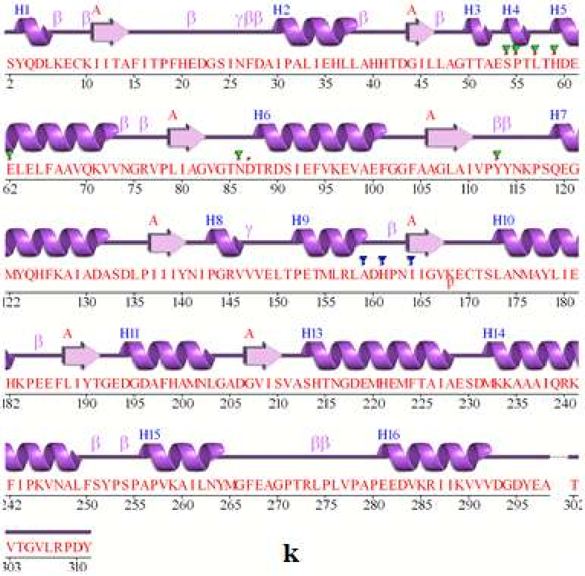
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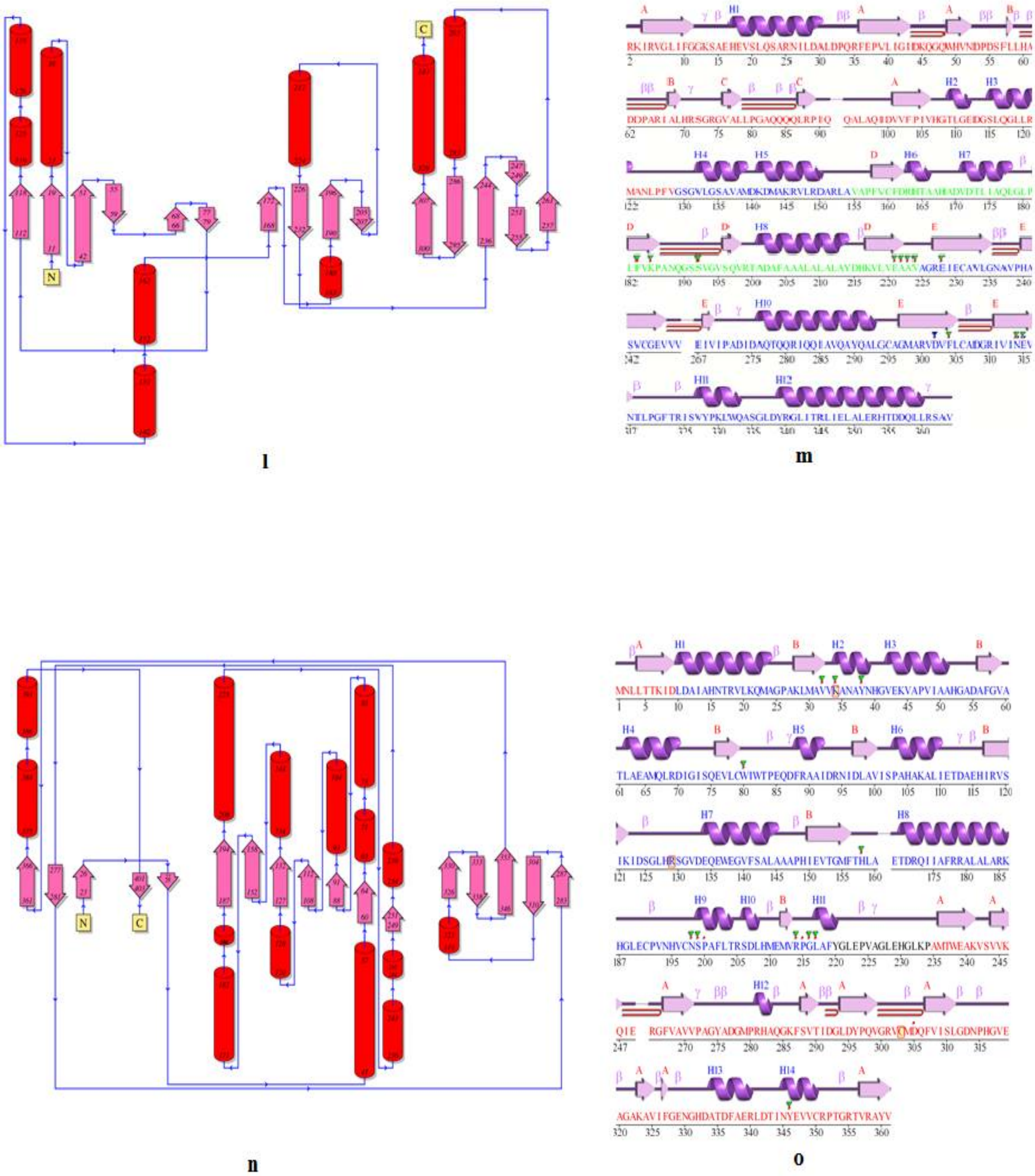


l m

n o

Figure S2. The secondary structure of the modeled protein /template, MurG (d)/1F0K (e), MraY (f) /4J72 (g), DapE (h)/ 3TX8 (i), DapA (j)/ 4FHA (k), Ddl (l)/ 3RFC (m), Alr (n)/ 2DY3 (o).

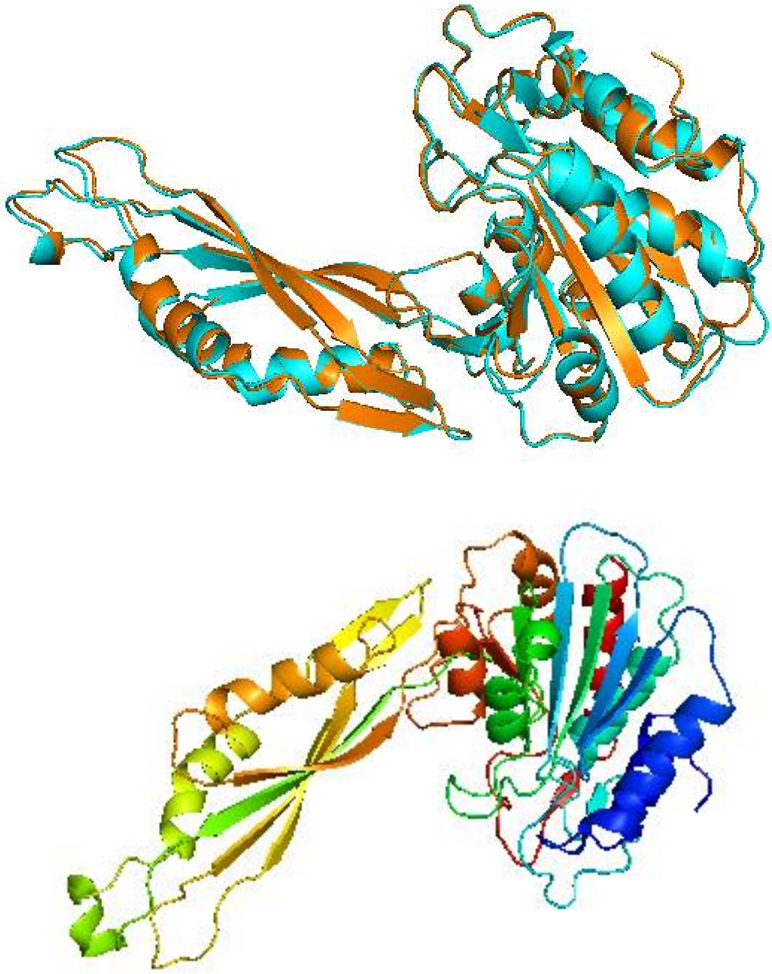


Figure S3c. Superimposition of model target protein, DapE, and template protein, 3TX8, are demonstrated in orange and cyan color in top and the 3D structures of the modeled DapE are presented as colorful structure in below respectively.

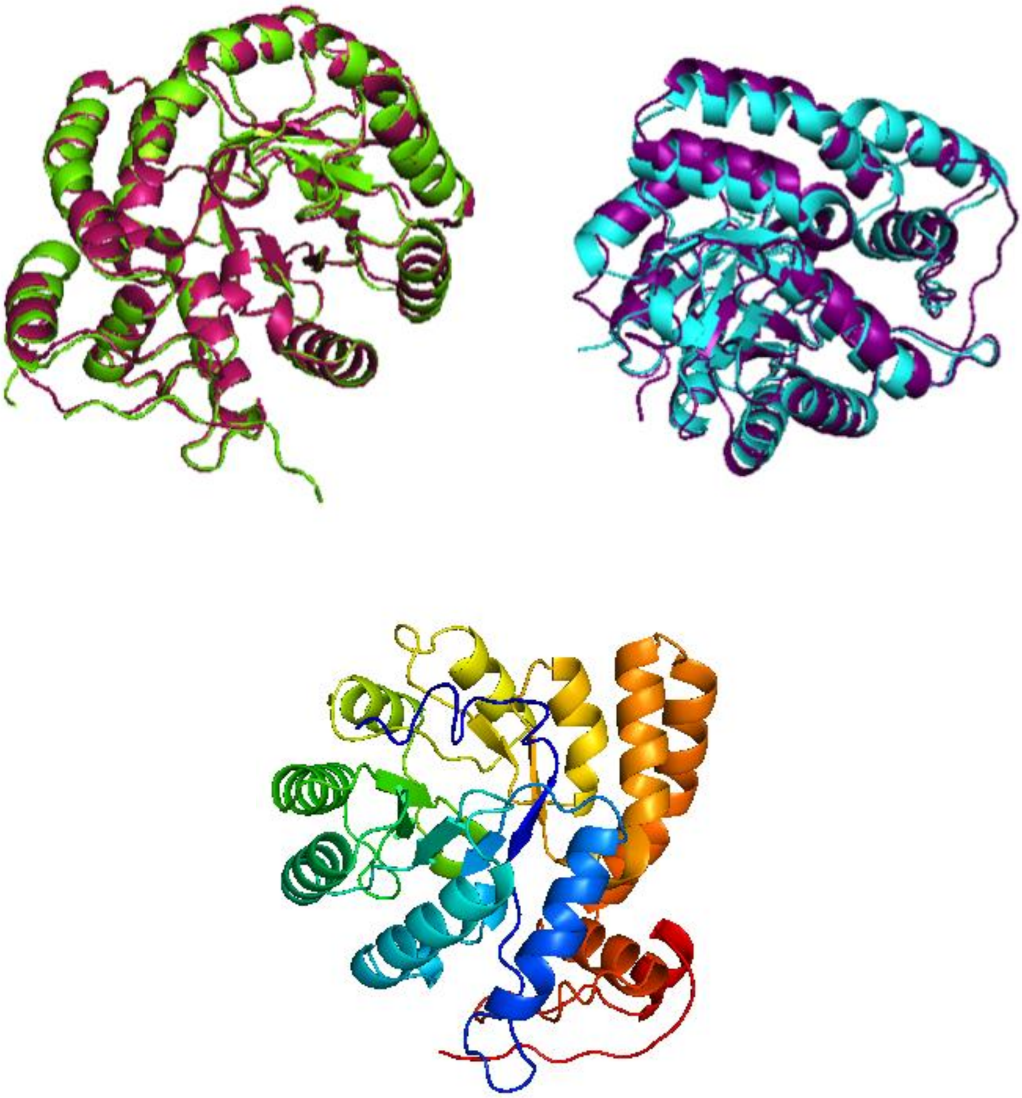


Figure S3d. Superimposition of model target/template protein, dapA/4FHA in warm pink/chartreuse color (top and left hand side), and target/template protein, dapA/1XXX in deep purple/cyan color (top and right side), and the 3D structures of the modeled dapA are presented as colorful structure in below.

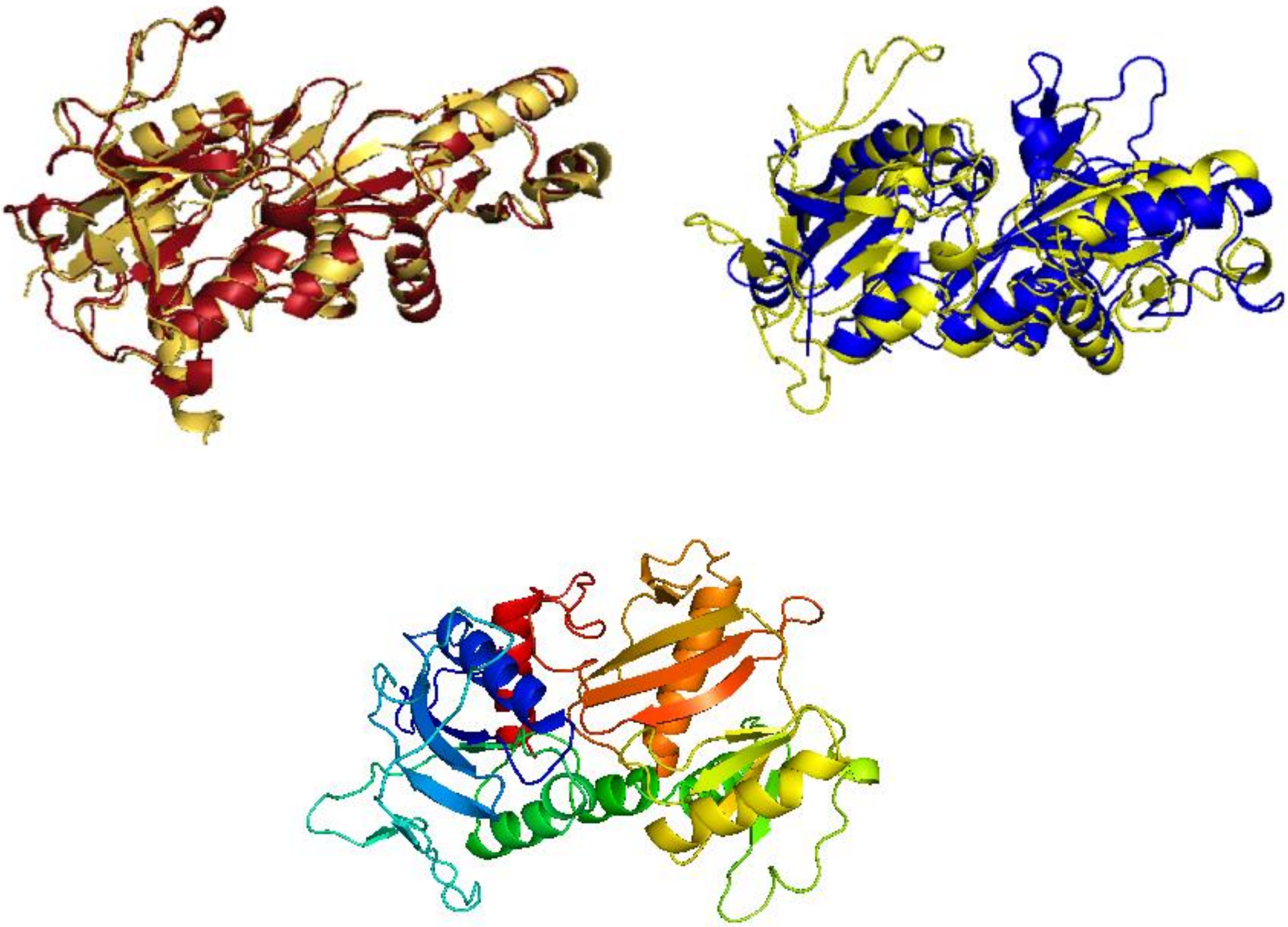
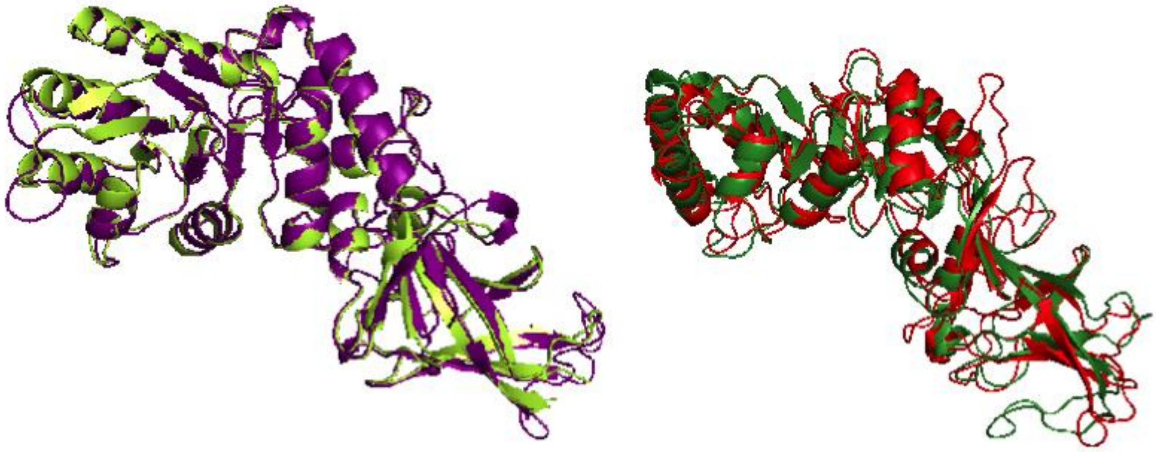


Figure S3e. Superimposition of model target/template protein, Ddl/3RFC in firebrick and pale yellow color (top and left side) and target/template protein Ddl/3LWB in yellow/blue color (top and right hand side) and the 3D structures of the modeled Ddl are presented as colorful structure in below are demonstrated respectively.



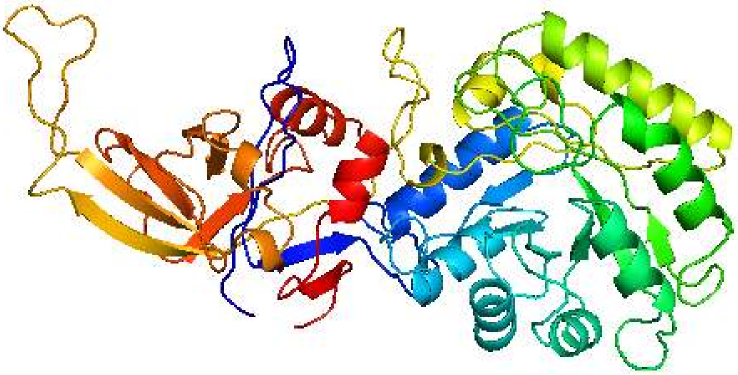


Figure S3f. Superimposition of model target/template protein, Alr/2DY3 in deep purple/Limon color (top and left hand side) and target/template protein Alr/1XFC in red/green color (top and right side) and the 3D structures of the modeled Alr are presented as colorful structure in below respectively.

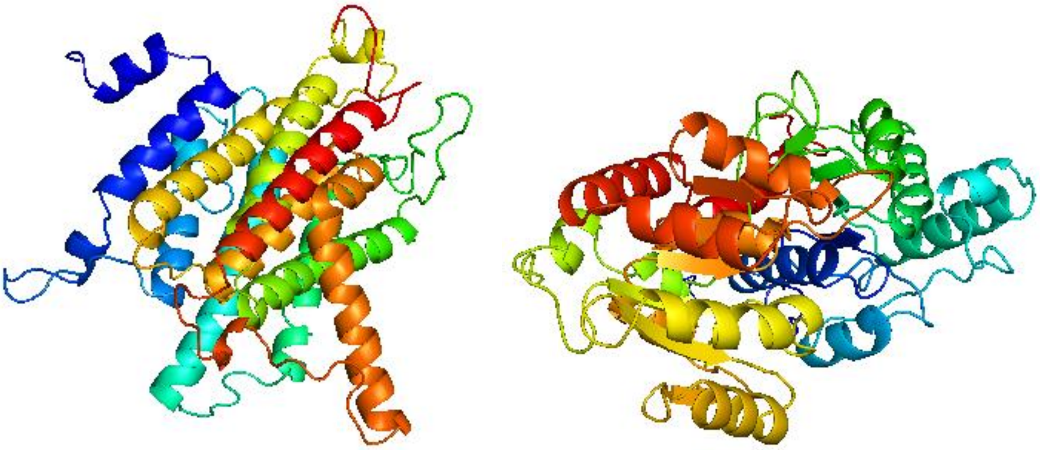
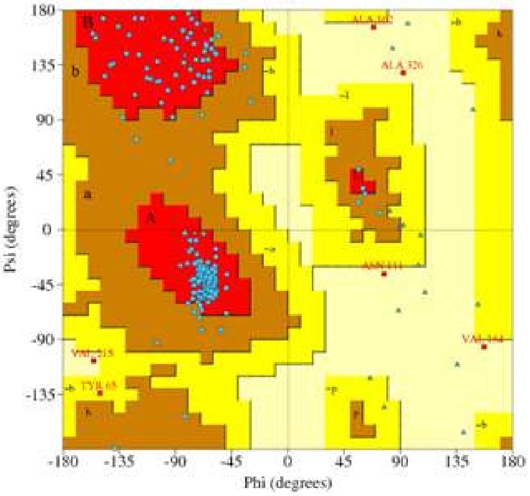


Figure S3g. The 3D structures of MraY (left hand side) and MurG (right side) are presented as colorful structure.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VAL 344
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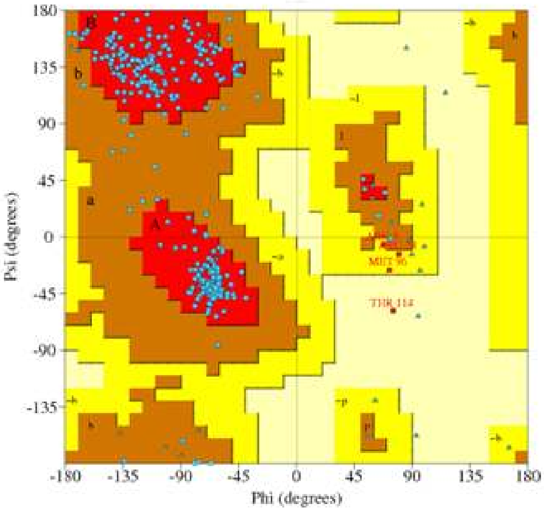
C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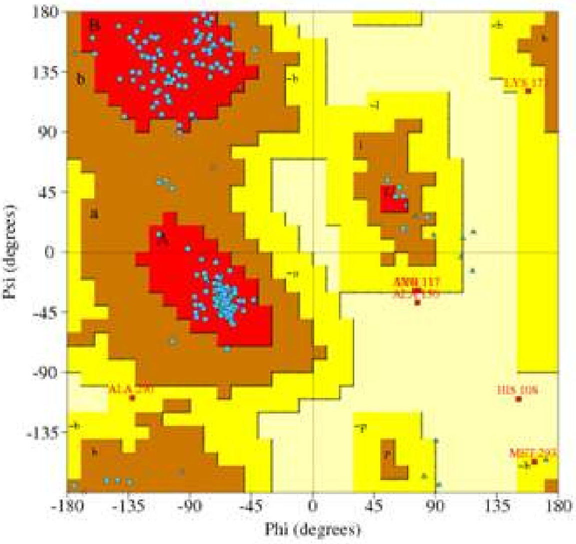
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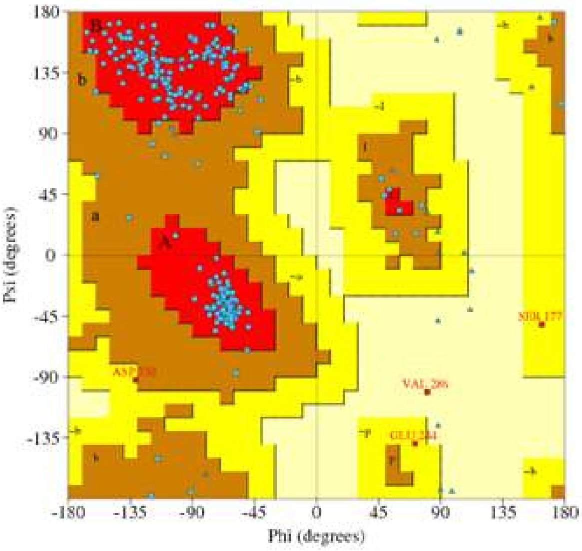
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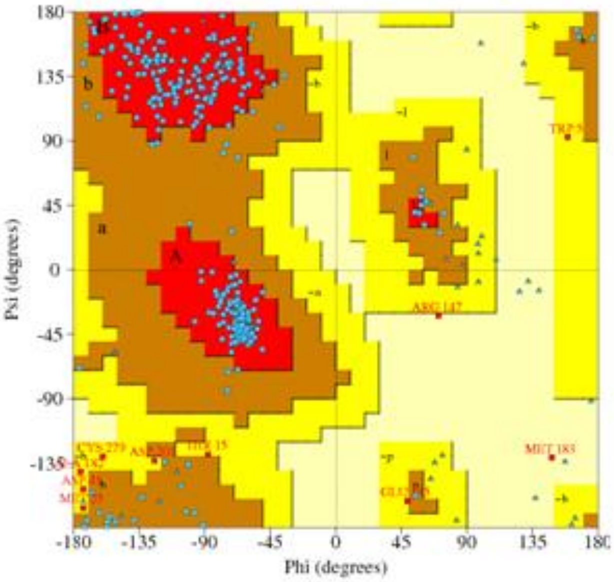
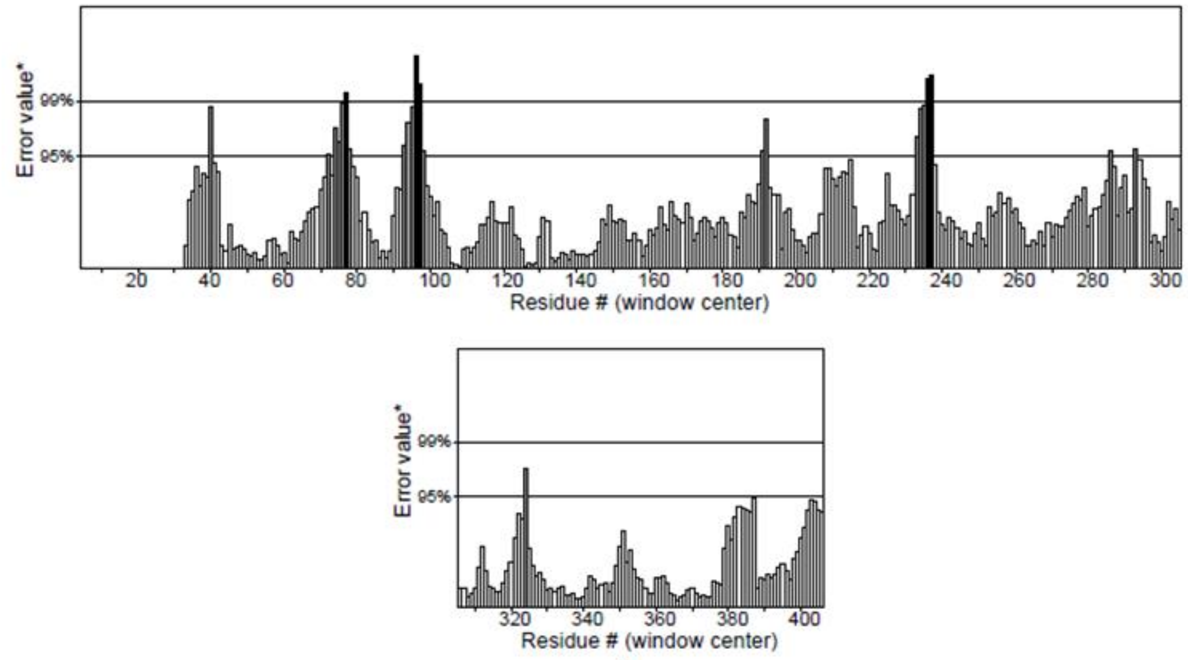


G

Figure S4. Ramachandran plots generated via PROCHECK for mraY (C), dapE (D), dapA (E), Ddl (F) and Alr (G) modeled proteins. The residues in most favored, allowed, and disallowed regions are presented in red, yellow and beige color, respectively.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Residue # (window center)

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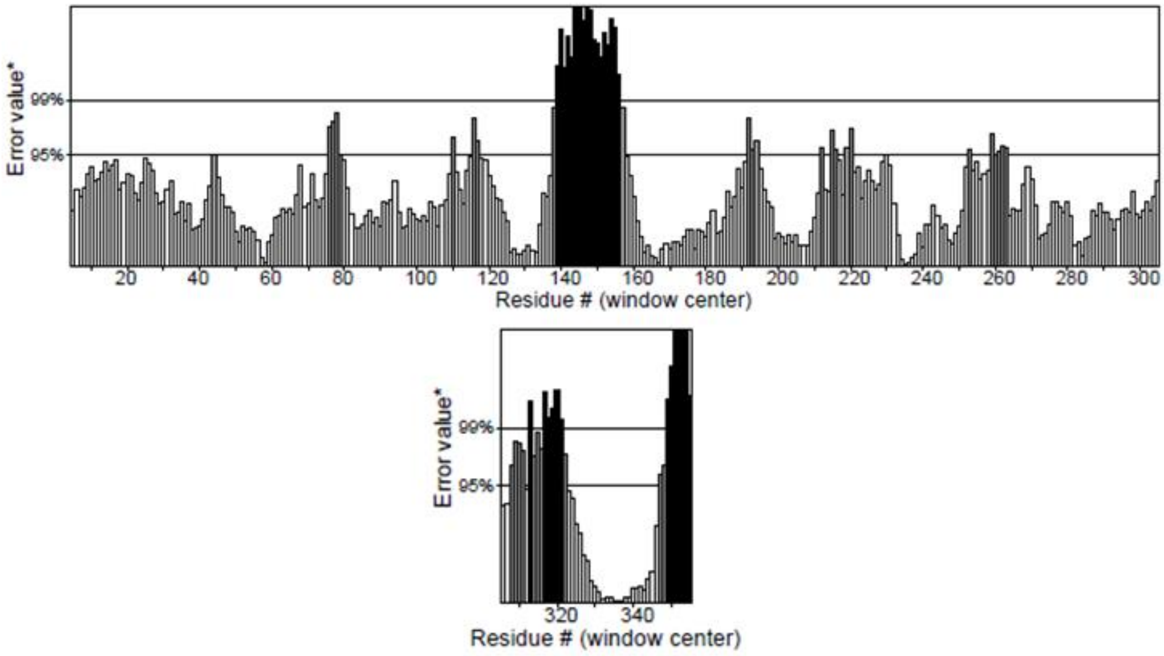
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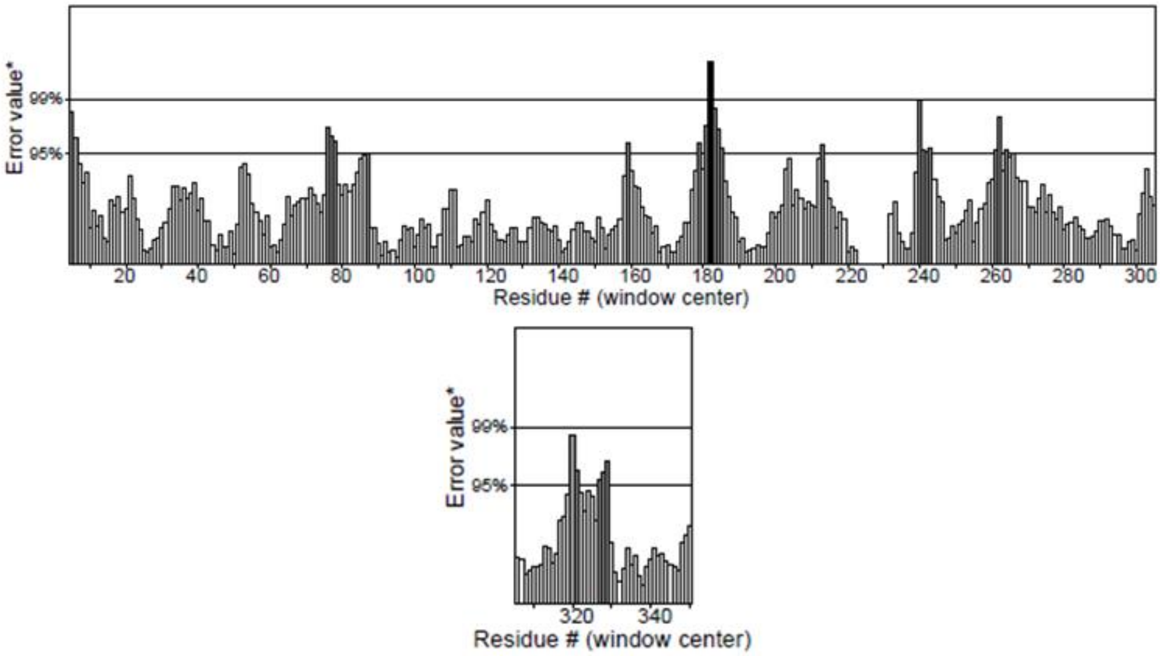
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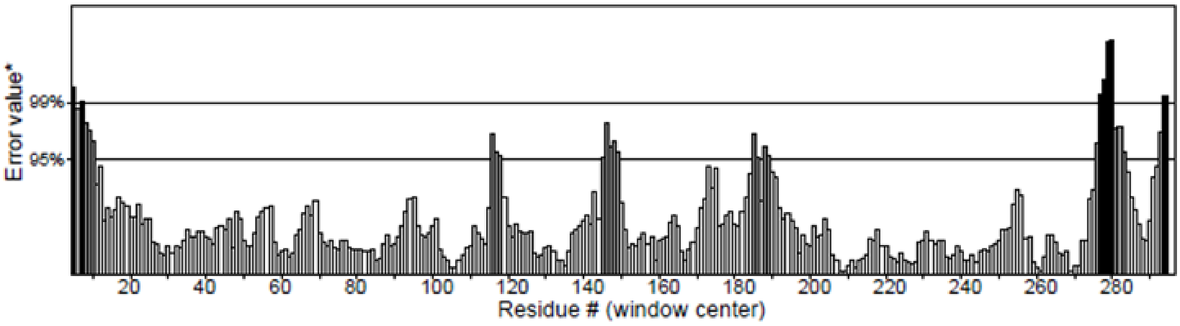
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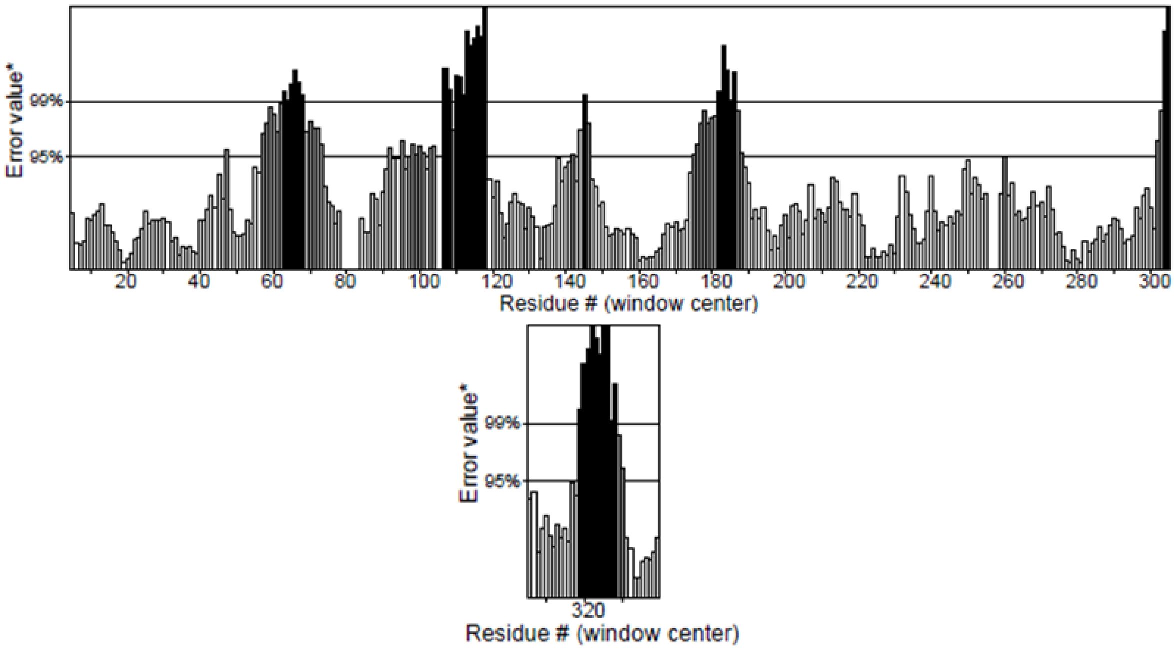

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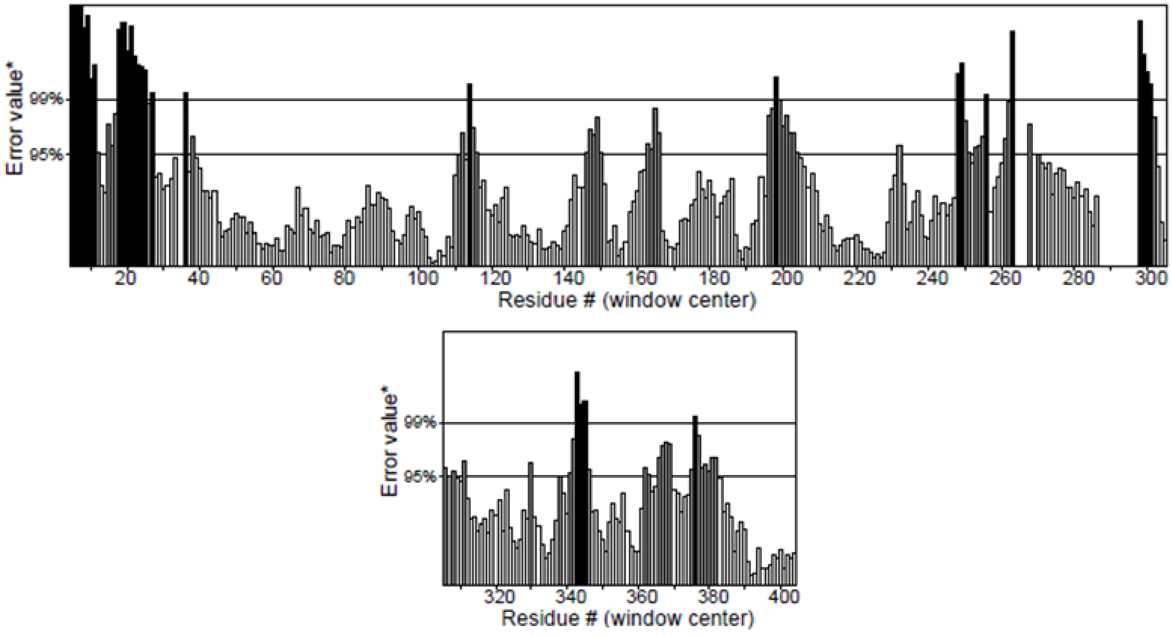


F

Figure S5. The ERRAT score of the MraY (A), MurG (B), DapE (C), DapA (D), Ddl (E) and Alr (F) protein models.

Table S3. Secondary structure comparsion between ,modeled targets and templates.

	Number of amino acid residues%				
Target/Template	**Helix**	**Strand**	**Others**	**RMSD (A^0)**	**Similarity%**
MurI	44.3	16.2	39.5	0.2	58
2JFU	43	16.5	40.5		
MurG	41	14.1	44.9	0.3	52
1F0K	43.9	15.7	40.4		
MraY	61.9	0	38.1	0.35	56
4J72	69.7	1.9	28.4		
DapE	26.8	26.3	46.9	0.26	43
3TX8	26.1	25.6	48.3		
DapA	45.7	11.7	42.6	0.21	55
4FHA	45.8	10.8	43.4		
Ddl	26.8	22.7	50.5	0.44	63
3RFC	33.1	26.2	40.7		
Alr	24.8	18.1	57.1	0.29	58
2DY3	29.9	23.4	46.7		

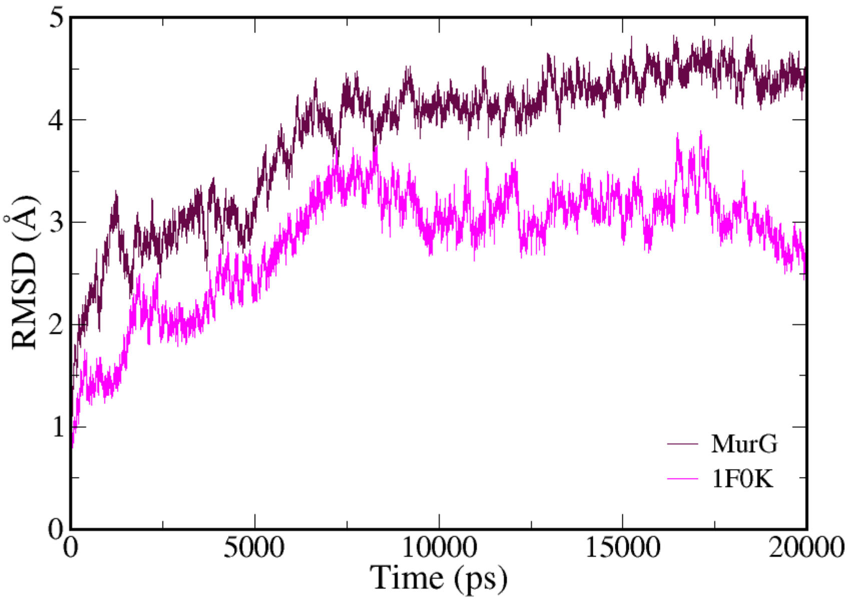


Figure S6. The RMSD plot of the modeled MurG (target – maroon) and 1F0K (template – magneta) is presented over the 20 ns MD trajectory.

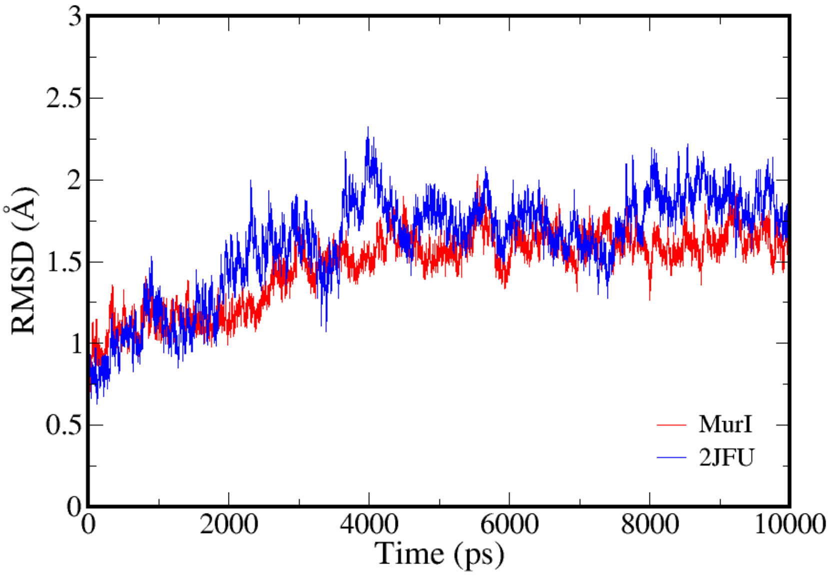


Figure S6-1. The RMSD plot of the modeled MurI (target – red) and 2JFU (template – blue) over the 10 ns MD trajectory.

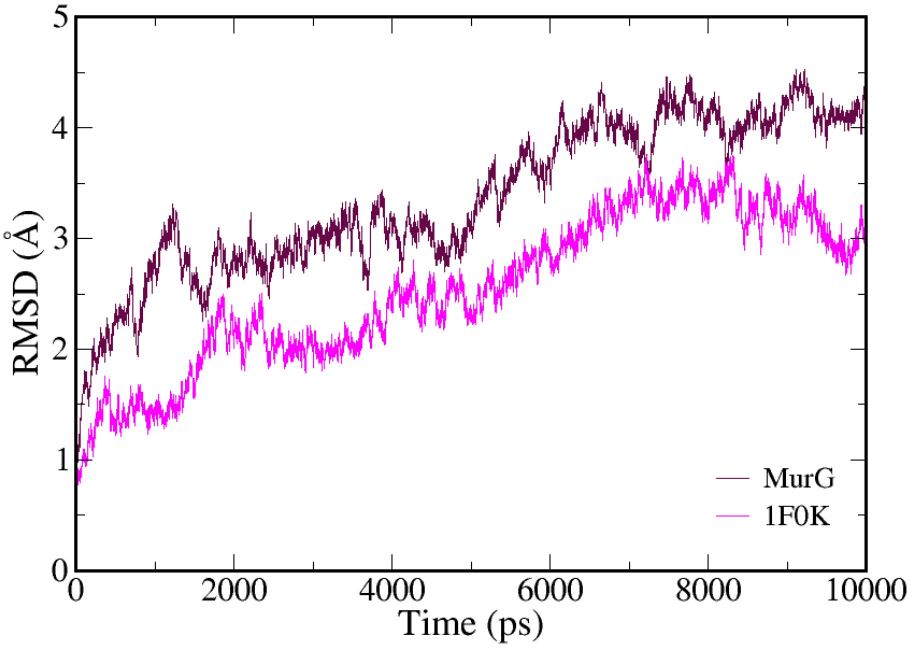


Figure S6-2. The RMSD plot of the modeled MurG (target – maroon) and 1F0K (template – magneta) is presented over the 10 ns MD trajectory.

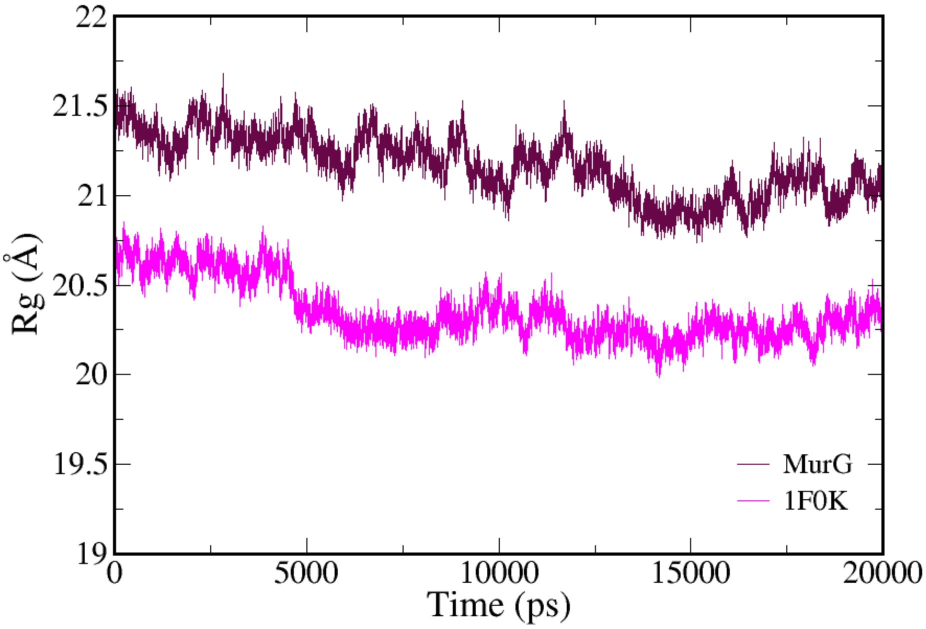


Figure S7. The plot of Radius of gyration (R_g) the modeled MurG (target – maroon) and 1F0K (template – magneta) is presented over the 20 ns MD trajectory.

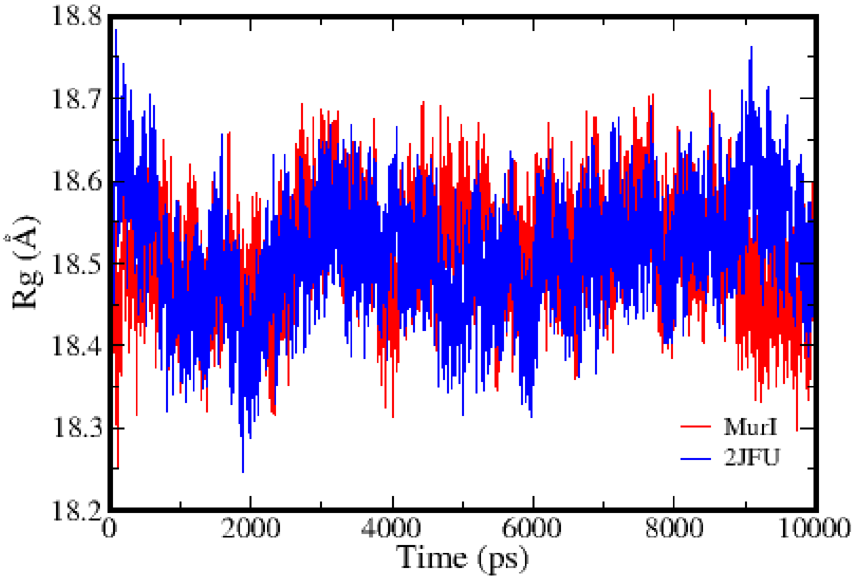


Figure S7-1. The plot of Radius of gyration (R_g) of the modeled MurI (target - red) and 2JFU (template - blue) is presented over the 10 ns MD trajectory.

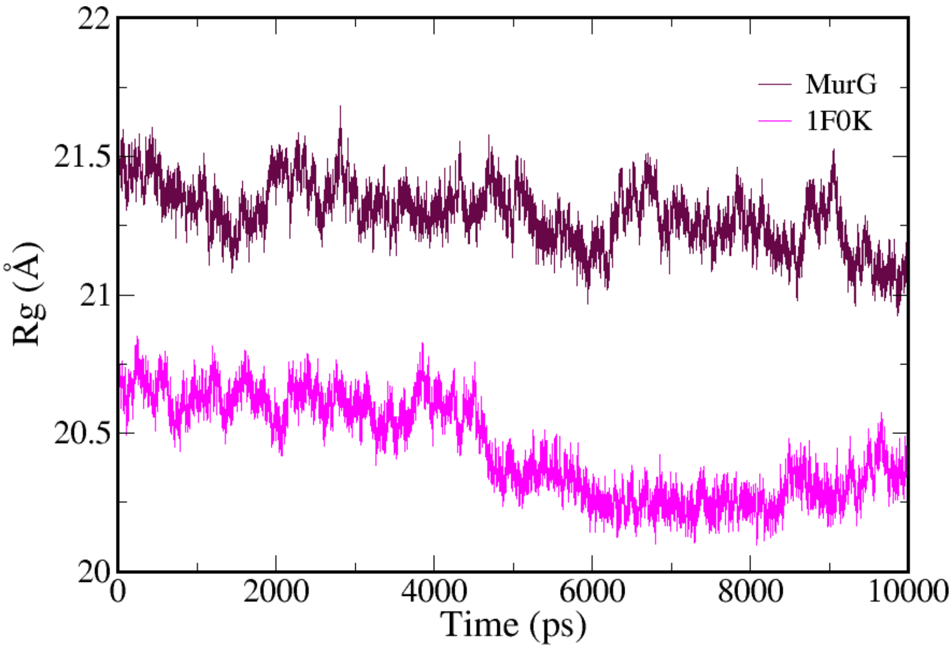


Figure S7-2. The plot of Radius of gyration (R_g) the modeled MurG (target – maroon) and 1F0K (template – magneta) is presented over the 10 ns MD trajectory.

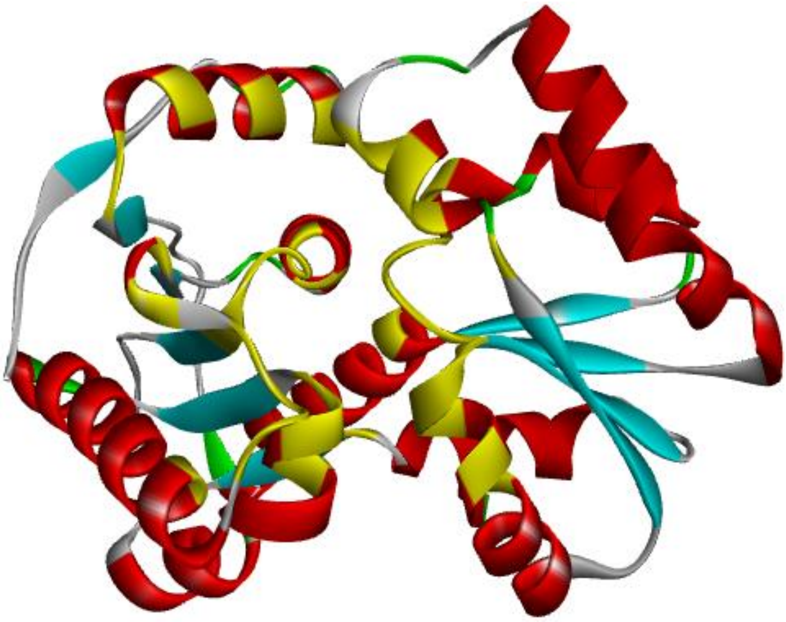
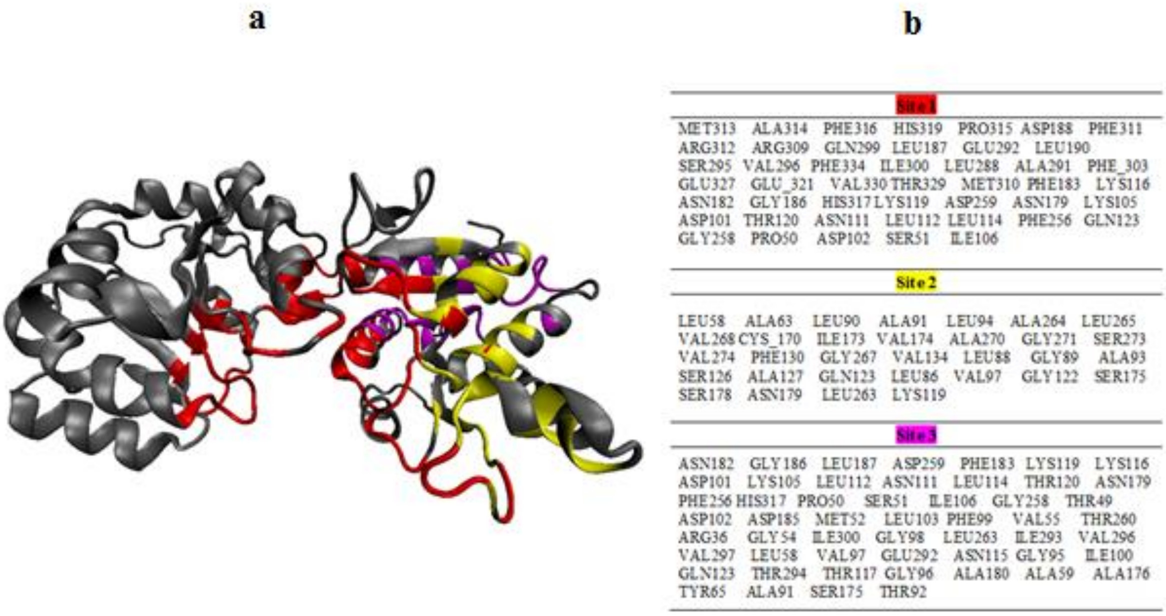


Figure S8. The common 40 amino acid residues obtained using Metapocket and POOL program as highlighted in yellow.



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SER295 VAL296 PHE334 ILE300 LEU288 ALA291 PHE_303
GLU327 GLU_321 VAL330 THR329 MET310 PHE183 LYS116
ASN182 GLY186 HIS317 LYS119 ASP259 ASN179 LYS105
ASP101 THR120 ASN111 LEU112 LEU114 PHE256 GLN123
GLY258 PRO50 ASP102 SER51 ILE106

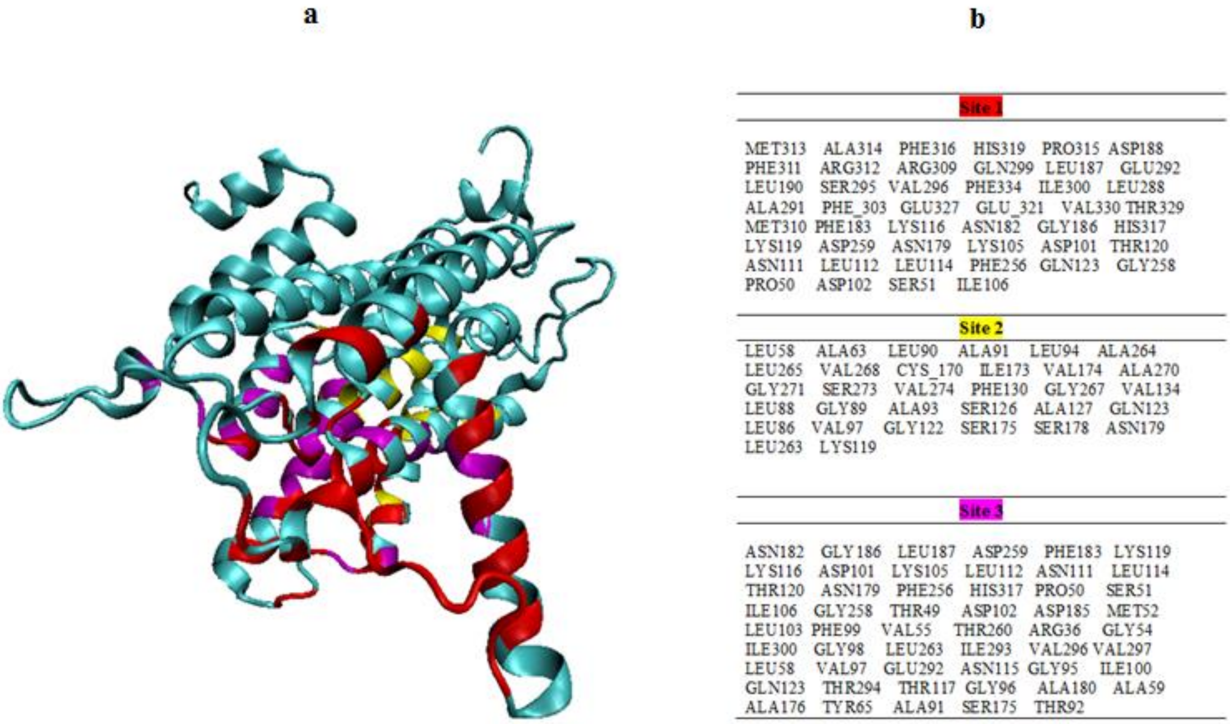
Site 2

LEU58 ALA63 LEU90 ALA91 LEU94 ALA264 LEU265
VAL268 CYS_170 ILE173 VAL174 ALA270 GLY271 SER273
VAL274 PHE130 GLY267 VAL134 LEU88 GLY89 ALA93
SER126 ALA127 GLN123 LEU86 VAL97 GLY122 SER175
SER178 ASN179 LEU263 LYS119

Site 3

ASN182 GLY186 LEU187 ASP259 PHE183 LYS119 LYS116
ASP101 LYS105 LEU112 ASN111 LEU114 THR120 ASN179
PHE256 HIS317 PRO50 SER51 ILE106 GLY258 THR49
ASP102 ASP185 MET52 LEU103 PHE99 VAL55 THR260
ARG36 GLY54 ILE300 GLY98 LEU263 ILE293 VAL296
VAL297 LEU58 VAL97 GLU292 ASN115 GLY95 ILE100
GLN123 THR294 THR117 GLY96 ALA180 ALA59 ALA176
TYR65 ALA91 SER175 THR92

Figure S8-1. **a.** The identified potential binding site 1, 2 and 3 amino acid residues of the modeled MurG marked in red, yellow and magenta color respectively. **b.** The three possible binding site residues of the modeled MurG were identified with Metapocket.



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ALA291 PHE_303 GLU327 GLU_321 VAL330 THR329
MET310 PHE183 LYS116 ASN182 GLY186 HIS317
LYS119 ASP259 ASN179 LYS105 ASP101 THR120
ASN111 LEU112 LEU114 PHE256 GLN123 GLY258
PRO50 ASP102 SER51 ILE106

Site 2

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GLY271 SER273 VAL274 PHE130 GLY267 VAL134
LEU88 GLY89 ALA93 SER126 ALA127 GLN123
LEU86 VAL97 GLY122 SER175 SER178 ASN179
LEU263 LYS119

Site 3

ASN182 GLY186 LEU187 ASP259 PHE183 LYS119
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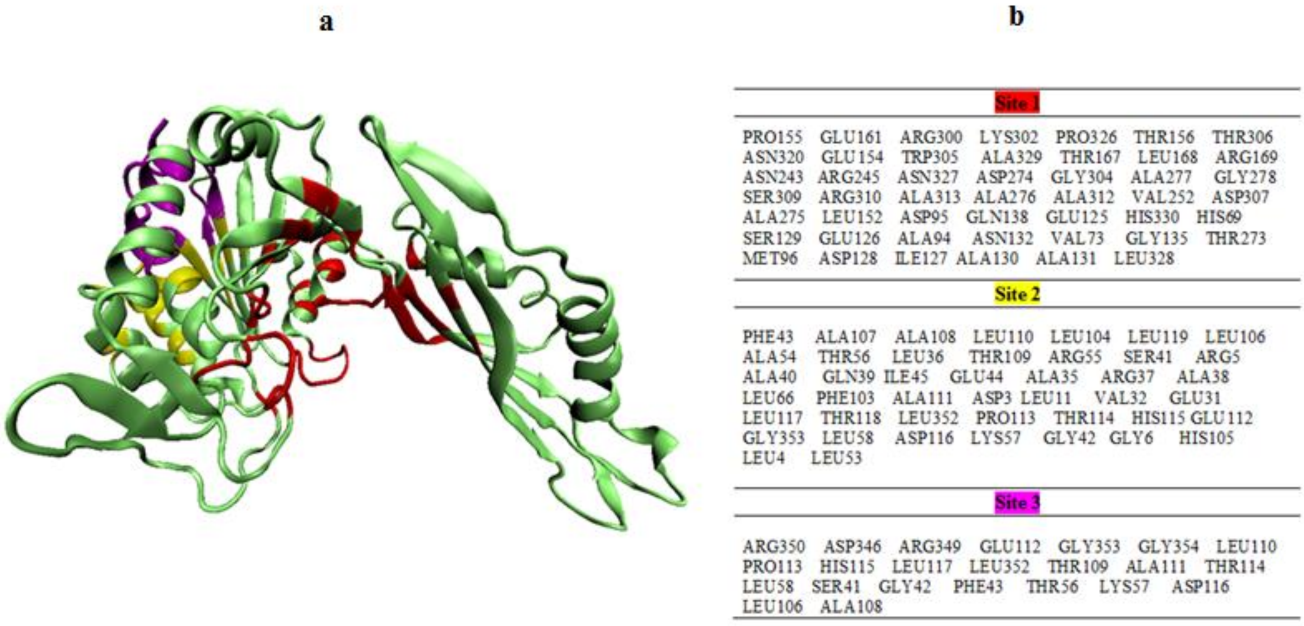
ALA176 TYR65 ALA91 SER175 THR92

Figure S8-2. **a.** The identified potential binding site 1, 2 and 3 amino acid residues of the modeled MraY marked in red, yellow and magenta color respectively. **b.** The three possible binding site residues of the modeled MraY were identified with Metapocket.



Site 1

PRO155 GLU161 ARG300 LYS302 PRO326 THR156 THR306
ASN320 GLU154 TRP305 ALA329 THR167 LEU168 ARG169
ASN243 ARG245 ASN327 ASP274 GLY304 ALA277 GLY278
SER309 ARG310 ALA313 ALA276 ALA312 VAL252 ASP307
ALA275 LEU152 ASP95 GLN138 GLU125 HIS330 HIS69
SER129 GLU126 ALA94 ASN132 VAL73 GLY135 THR273
MET96 ASP128 ILE127 ALA130 ALA131 LEU328

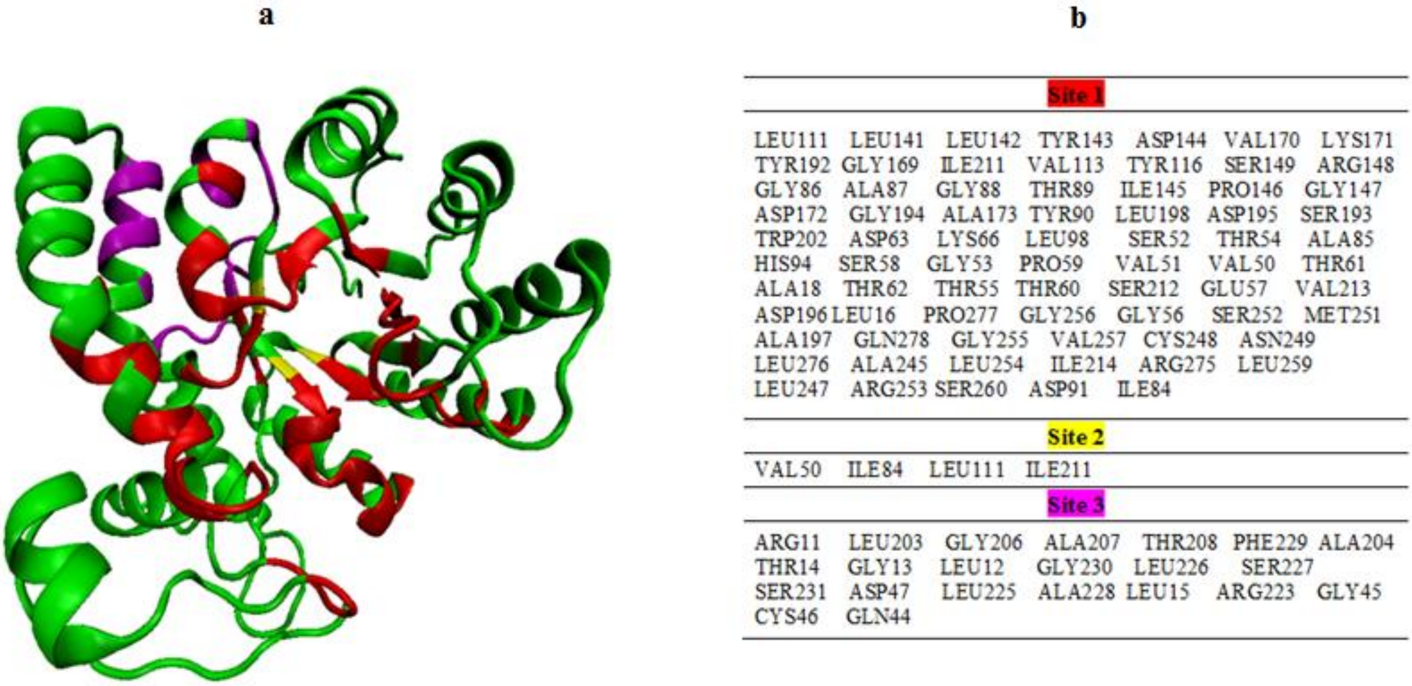
Site 2

PHE43 ALA107 ALA108 LEU110 LEU104 LEU119 LEU106
ALA54 THR56 LEU36 THR109 ARG55 SER41 ARG5
ALA40 GLN39 ILE45 GLU44 ALA35 ARG37 ALA38
LEU66 PHE103 ALA111 ASP3 LEU11 VAL32 GLU31
LEU117 THR118 LEU352 PRO113 THR114 HIS115 GLU112
GLY353 LEU58 ASP116 LYS57 GLY42 GLY6 HIS105
LEU4 LEU53

Site 3

ARG350 ASP346 ARG349 GLU112 GLY353 GLY354 LEU110
PRO113 HIS115 LEU117 LEU352 THR109 ALA111 THR114
LEU58 SER41 GLY42 PHE43 THR56 LYS57 ASP116
LEU106 ALA108

Figure S8-3. **a.** The identified potential binding site 1, 2 and 3 amino acid residues of the modeled DapE marked in red, yellow and magenta color respectively. **b.** The three possible binding site residues of the modeled DapE were identified with Metapocket.



Site 1

LEU111 LEU141 LEU142 TYR143 ASP144 VAL170 LYS171
TYR192 GLY169 ILE211 VAL113 TYR116 SER149 ARG148
GLY86 ALA87 GLY88 THR89 ILE145 PRO146 GLY147
ASP172 GLY194 ALA173 TYR90 LEU198 ASP195 SER193
TRP202 ASP63 LYS66 LEU98 SER52 THR54 ALA85
HIS94 SER58 GLY53 PRO59 VAL51 VAL50 THR61
ALA18 THR62 THR55 THR60 SER212 GLU57 VAL213
ASP196 LEU16 PRO277 GLY256 GLY56 SER252 MET251
ALA197 GLN278 GLY255 VAL257 CYS248 ASN249
LEU276 ALA245 LEU254 ILE214 ARG275 LEU259
LEU247 ARG253 SER260 ASP91 ILE84

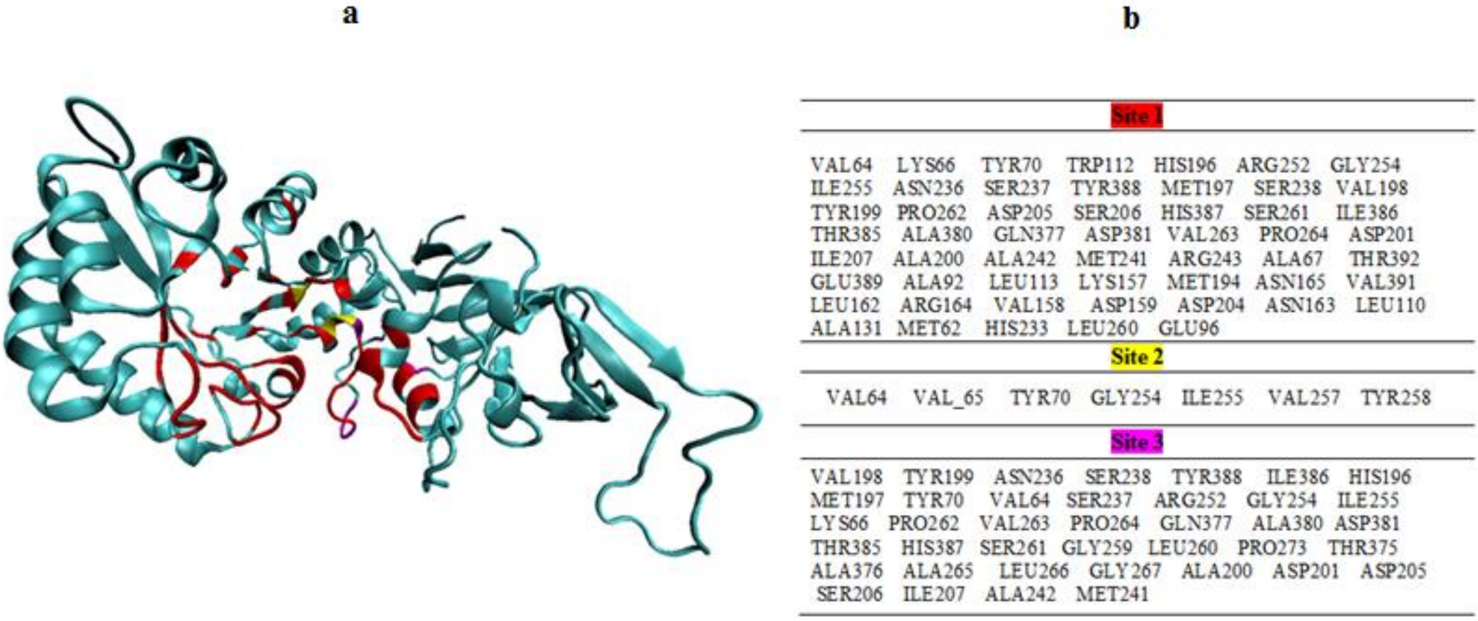
Site 2

VAL50 ILE84 LEU111 ILE211

Site 3

ARG11 LEU203 GLY206 ALA207 THR208 PHE229 ALA204
THR14 GLY13 LEU12 GLY230 LEU226 SER227
SER231 ASP47 LEU225 ALA228 LEU15 ARG223 GLY45
CYS46 GLN44

Figure S8-4. **a.** The identified potential binding site 1, 2 and 3 amino acid residues of the modeled DapA marked in red, yellow and magenta color respectively. **b.** The three possible binding site residues of the modeled DapA were identified with Metapocket



Site 1

VAL64 LYS66 TYR70 TRP112 HIS196 ARG252 GLY254
ILE255 ASN236 SER237 TYR388 MET197 SER238 VAL198
TYR199 PRO262 ASP205 SER206 HIS387 SER261 ILE386
THR385 ALA380 GLN377 ASP381 VAL263 PRO264 ASP201
ILE207 ALA200 ALA242 MET241 ARG243 ALA67 THR392
GLU389 ALA92 LEU113 LYS157 MET194 ASN165 VAL391
LEU162 ARG164 VAL158 ASP159 ASP204 ASN163 LEU110
ALA131 MET62 HIS233 LEU260 GLU96

Site 2

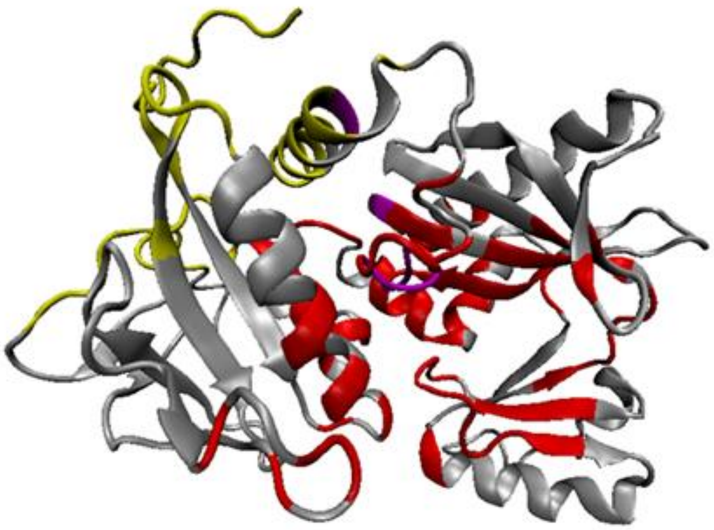
VAL64 VAL_65 TYR70 GLY254 ILE255 VAL257 TYR258

Site 3

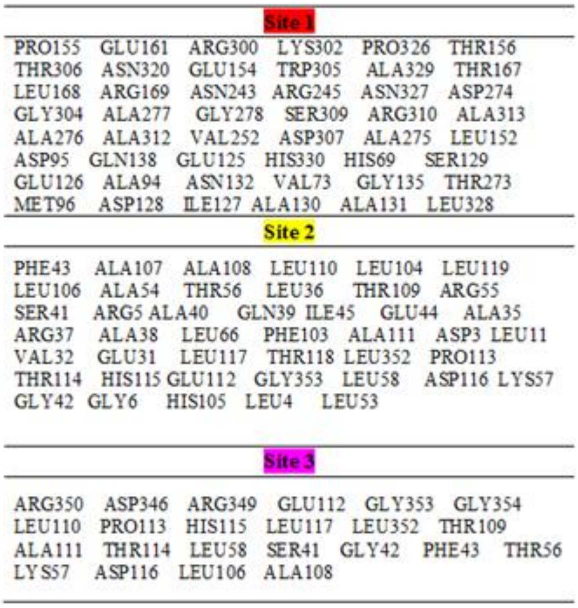
VAL198 TYR199 ASN236 SER238 TYR388 ILE386 HIS196
MET197 TYR70 VAL64 SER237 ARG252 GLY254 ILE255
LYS66 PRO262 VAL263 PRO264 GLN377 ALA380 ASP381
THR385 HIS387 SER261 GLY259 LEU260 PRO273 THR375
ALA376 ALA265 LEU266 GLY267 ALA200 ASP201 ASP205
SER206 ILE207 ALA242 MET241

Figure S8-5. **a.** The identified potential binding site 1, 2 and 3 amino acid residues of the modeled Alr marked in red, yellow and magenta color respectively. **b.** The three possible binding site residues of the modeled Alr were identified with Metapocket.

a



b



Site 1

PRO155 GLU161 ARG300 LYS302 PRO326 THR156
THR306 ASN320 GLU154 TRP305 ALA329 THR167
LEU168 ARG169 ASN243 ARG245 ASN327 ASP274
GLY304 ALA277 GLY278 SER309 ARG310 ALA313
ALA276 ALA312 VAL252 ASP307 ALA275 LEU152
ASP95 GLN138 GLU125 HIS330 HIS69 SER129
GLU126 ALA94 ASN132 VAL73 GLY135 THR273
MET96 ASP128 ILE127 ALA130 ALA131 LEU328

Site 2

PHE43 ALA107 ALA108 LEU110 LEU104 LEU119
LEU106 ALA54 THR56 LEU36 THR109 ARG55
SER41 ARG5 ALA40 GLN39 ILE45 GLU44 ALA35
ARG37 ALA38 LEU66 PHE103 ALA111 ASP3 LEU11
VAL32 GLU31 LEU117 THR118 LEU352 PRO113
THR114 HIS115 GLU112 GLY353 LEU58 ASP116 LYS57
GLY42 GLY6 HIS105 LEU4 LEU53

Site 3

ARG350 ASP346 ARG349 GLU112 GLY353 GLY354
LEU110 PRO113 HIS115 LEU117 LEU352 THR109
ALA111 THR114 LEU58 SER41 GLY42 PHE43 THR56
LYS57 ASP116 LEU106 ALA108

Figure S8-6. **a.** The identified potential binding site 1, 2 and 3 amino acid residues of the modeled Ddl marked in red, yellow and magenta color respectively. **b.** The three possible binding site residues of the modeled Ddl were identified with Metapocket.