



## Full wwPDB EM Validation Report ⓘ

Mar 5, 2026 – 08:56 PM UTC

PDB ID : 8WHY / pdb\_00008why  
EMDB ID : EMD-37552  
Title : Cryo- EM structure of Mycobacterium smegmatis 50S ribosomal subunit (body 1) of 70S ribosome and RafH.  
Authors : Kumar, N.; Sharma, S.; Kaushal, P.S.  
Deposited on : 2023-09-23  
Resolution : 2.70 Å(reported)  
Based on initial model : 8WHX

This is a Full wwPDB EM Validation Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

---

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev132  
MolProbity : 4-5-2 with Phenix2.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

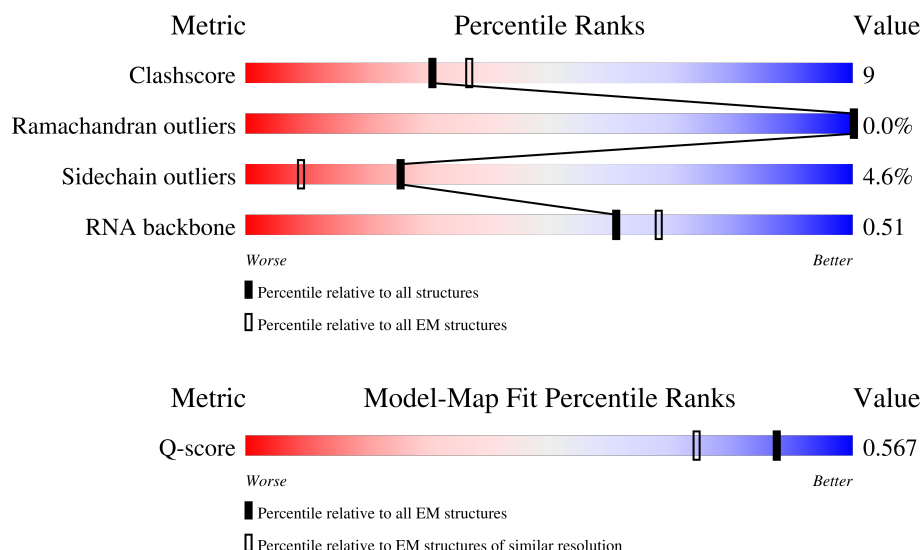
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 2.70 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



| Metric                | Whole archive<br>(#Entries) | EM structures<br>(#Entries) | Similar EM resolution<br>(#Entries, resolution range(Å)) |
|-----------------------|-----------------------------|-----------------------------|----------------------------------------------------------|
| Clashscore            | 229148                      | 23984                       | -                                                        |
| Ramachandran outliers | 224038                      | 23583                       | -                                                        |
| Sidechain outliers    | 223484                      | 23102                       | -                                                        |
| RNA backbone          | 8273                        | 3508                        | -                                                        |
| Q-score               | -                           | 25397                       | 10327 ( 2.20 - 3.20 )                                    |

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion  $< 40\%$ ). The numeric value is given above the bar.

| Mol | Chain | Length | Quality of chain                                                                                   |
|-----|-------|--------|----------------------------------------------------------------------------------------------------|
| 1   | E     | 278    | <br>85% 13% .. |
| 2   | F     | 217    | <br>80% 19% .  |
| 3   | G     | 215    | <br>76% 20% .. |

Continued on next page...

Continued from previous page...

| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|------------------|
| 4   | H     | 187    |                  |
| 5   | I     | 179    |                  |
| 6   | J     | 151    |                  |
| 7   | M     | 147    |                  |
| 8   | N     | 122    |                  |
| 9   | O     | 147    |                  |
| 10  | Q     | 199    |                  |
| 11  | R     | 127    |                  |
| 12  | S     | 113    |                  |
| 13  | T     | 129    |                  |
| 14  | U     | 103    |                  |
| 15  | V     | 153    |                  |
| 16  | W     | 100    |                  |
| 17  | X     | 105    |                  |
| 18  | Z     | 88     |                  |
| 19  | 1     | 64     |                  |
| 20  | 2     | 77     |                  |
| 21  | 3     | 61     |                  |
| 22  | 5     | 57     |                  |
| 23  | 6     | 55     |                  |
| 24  | 7     | 47     |                  |
| 25  | 8     | 64     |                  |
| 26  | 4     | 75     |                  |
| 27  | A     | 3119   |                  |
| 28  | B     | 118    |                  |

## 2 Entry composition

There are 28 unique types of molecules in this entry. The entry contains 89672 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called 50S ribosomal protein L2.

| Mol | Chain | Residues | Atoms |      |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 1   | E     | 275      | Total | C    | N   | O   | S | 0       | 0     |
|     |       |          | 2110  | 1298 | 438 | 370 | 4 |         |       |

- Molecule 2 is a protein called 50S ribosomal protein L3.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 2   | F     | 214      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1587  | 982 | 310 | 290 | 5 |         |       |

- Molecule 3 is a protein called 50S ribosomal protein L4.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 3   | G     | 209      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1569  | 969 | 295 | 303 | 2 |         |       |

- Molecule 4 is a protein called 50S ribosomal protein L5.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 4   | H     | 181      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1436  | 901 | 269 | 260 | 6 |         |       |

- Molecule 5 is a protein called 50S ribosomal protein L6.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 5   | I     | 165      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1260  | 792 | 229 | 238 | 1 |         |       |

- Molecule 6 is a protein called 50S ribosomal protein L9.

| Mol | Chain | Residues | Atoms |     |    |    |   | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 6   | J     | 41       | Total | C   | N  | O  | S | 0       | 0     |
|     |       |          | 308   | 195 | 55 | 57 | 1 |         |       |

- Molecule 7 is a protein called 50S ribosomal protein L13.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 7   | M     | 146      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1130  | 722 | 207 | 200 | 1 |         |       |

- Molecule 8 is a protein called 50S ribosomal protein L14.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 8   | N     | 122      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 938   | 586 | 179 | 170 | 3 |         |       |

- Molecule 9 is a protein called 50S ribosomal protein L15.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 9   | O     | 145      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1078  | 676 | 205 | 194 | 3 |         |       |

- Molecule 10 is a protein called 50S ribosomal protein L17.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 10  | Q     | 118      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 928   | 583 | 180 | 163 | 2 |         |       |

- Molecule 11 is a protein called 50S ribosomal protein L18.

| Mol | Chain | Residues | Atoms |     |     |     | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|-------|
| 11  | R     | 124      | Total | C   | N   | O   | 0       | 0     |
|     |       |          | 941   | 577 | 195 | 169 |         |       |

- Molecule 12 is a protein called 50S ribosomal protein L19.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 12  | S     | 113      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 907   | 570 | 171 | 165 | 1 |         |       |

- Molecule 13 is a protein called 50S ribosomal protein L20.

| Mol | Chain | Residues | Atoms |     |     |     | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|-------|
| 13  | T     | 124      | Total | C   | N   | O   | 0       | 0     |
|     |       |          | 988   | 613 | 203 | 172 |         |       |

- Molecule 14 is a protein called 50S ribosomal protein L21.

| Mol | Chain | Residues | Atoms |     |     |     | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|-------|
| 14  | U     | 100      | Total | C   | N   | O   | 0       | 0     |
|     |       |          | 754   | 478 | 137 | 139 |         |       |

- Molecule 15 is a protein called 50S ribosomal protein L22.

| Mol | Chain | Residues | Atoms |     |     |     | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|-------|
| 15  | V     | 113      | Total | C   | N   | O   | 0       | 0     |
|     |       |          | 864   | 538 | 170 | 156 |         |       |

- Molecule 16 is a protein called 50S ribosomal protein L23.

| Mol | Chain | Residues | Atoms |     |     |     | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|-------|
| 16  | W     | 97       | Total | C   | N   | O   | 0       | 0     |
|     |       |          | 756   | 479 | 138 | 139 |         |       |

- Molecule 17 is a protein called 50S ribosomal protein L24.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 17  | X     | 93       | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 710   | 443 | 133 | 132 | 2 |         |       |

- Molecule 18 is a protein called 50S ribosomal protein L27.

| Mol | Chain | Residues | Atoms |     |     |    | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|----|---------|-------|
| 18  | Z     | 77       | Total | C   | N   | O  | 0       | 0     |
|     |       |          | 574   | 355 | 121 | 98 |         |       |

- Molecule 19 is a protein called 50S ribosomal protein L28.

| Mol | Chain | Residues | Atoms |     |     |    |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|----|---|---------|-------|
| 19  | 1     | 63       | Total | C   | N   | O  | S | 0       | 0     |
|     |       |          | 470   | 283 | 103 | 80 | 4 |         |       |

- Molecule 20 is a protein called 50S ribosomal protein L29.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 20  | 2     | 63       | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 527   | 322 | 102 | 102 | 1 |         |       |

- Molecule 21 is a protein called 50S ribosomal protein L30.

| Mol | Chain | Residues | Atoms |     |    |    | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---------|-------|
| 21  | 3     | 58       | Total | C   | N  | O  | 0       | 0     |
|     |       |          | 470   | 290 | 94 | 86 |         |       |

- Molecule 22 is a protein called 50S ribosomal protein L32.

| Mol | Chain | Residues | Atoms |     |    |    |   | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 22  | 5     | 54       | Total | C   | N  | O  | S | 0       | 0     |
|     |       |          | 423   | 260 | 93 | 69 | 1 |         |       |

- Molecule 23 is a protein called 50S ribosomal protein L33A.

| Mol | Chain | Residues | Atoms |     |    |    |   | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 23  | 6     | 49       | Total | C   | N  | O  | S | 0       | 0     |
|     |       |          | 405   | 248 | 82 | 71 | 4 |         |       |

- Molecule 24 is a protein called 50S ribosomal protein L34.

| Mol | Chain | Residues | Atoms |     |    |    |   | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 24  | 7     | 45       | Total | C   | N  | O  | S | 0       | 0     |
|     |       |          | 372   | 222 | 96 | 53 | 1 |         |       |

- Molecule 25 is a protein called 50S ribosomal protein L35.

| Mol | Chain | Residues | Atoms |     |     |    | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|----|---------|-------|
| 25  | 8     | 63       | Total | C   | N   | O  | 0       | 0     |
|     |       |          | 502   | 302 | 115 | 85 |         |       |

- Molecule 26 is a protein called 50S ribosomal protein L31.

| Mol | Chain | Residues | Atoms |     |    |    |   | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 26  | 4     | 48       | Total | C   | N  | O  | S | 0       | 0     |
|     |       |          | 364   | 225 | 63 | 71 | 5 |         |       |

- Molecule 27 is a RNA chain called 23S rRNA.

| Mol | Chain | Residues | Atoms |       |       |       |      | AltConf | Trace |
|-----|-------|----------|-------|-------|-------|-------|------|---------|-------|
| 27  | A     | 3017     | Total | C     | N     | O     | P    | 0       | 0     |
|     |       |          | 64799 | 28881 | 11918 | 20983 | 3017 |         |       |

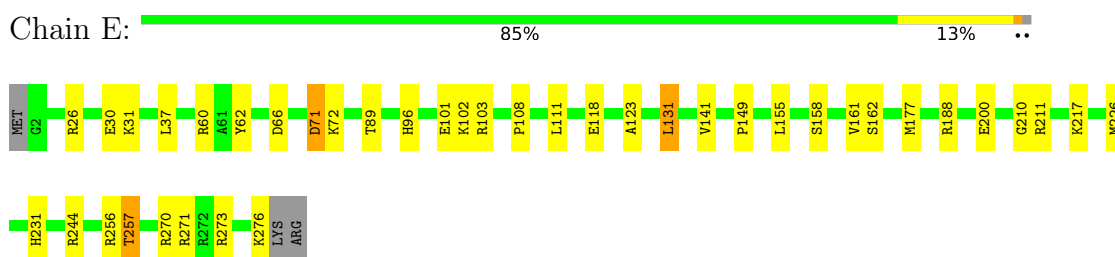
- Molecule 28 is a RNA chain called 5S rRNA.

| Mol | Chain | Residues | Atoms |      |     |     |     | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|-----|---------|-------|
|     |       |          | Total | C    | N   | O   | P   |         |       |
| 28  | B     | 117      | 2502  | 1117 | 465 | 803 | 117 | 0       | 0     |

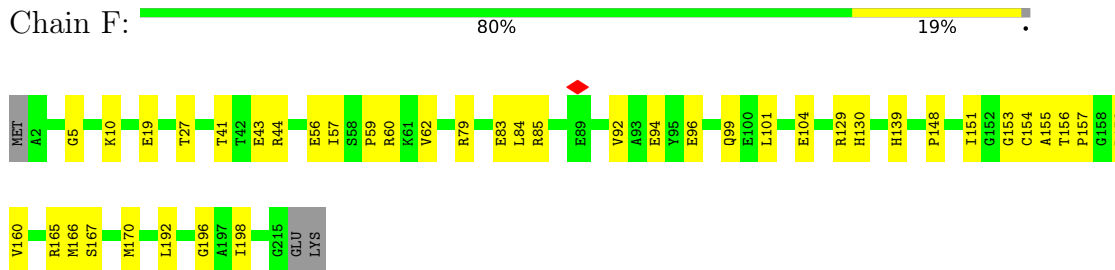
### 3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

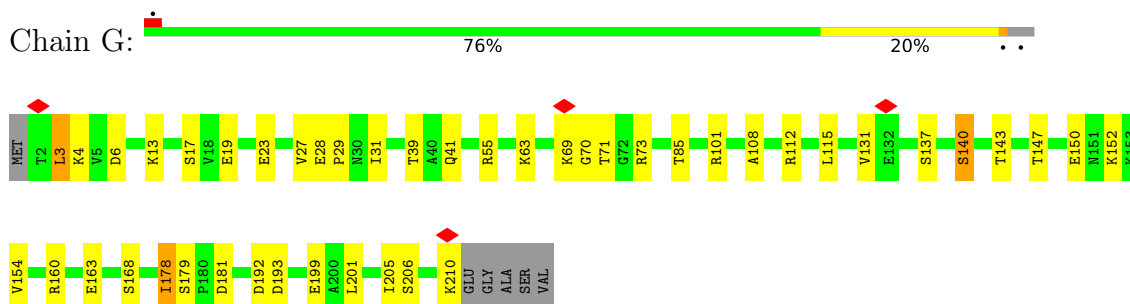
- Molecule 1: 50S ribosomal protein L2



- Molecule 2: 50S ribosomal protein L3



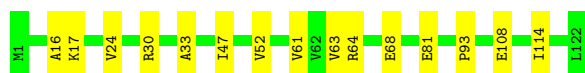
- Molecule 3: 50S ribosomal protein L4



- Molecule 4: 50S ribosomal protein L5

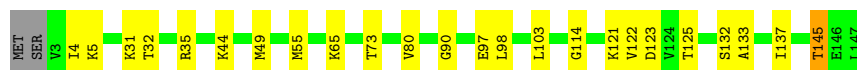






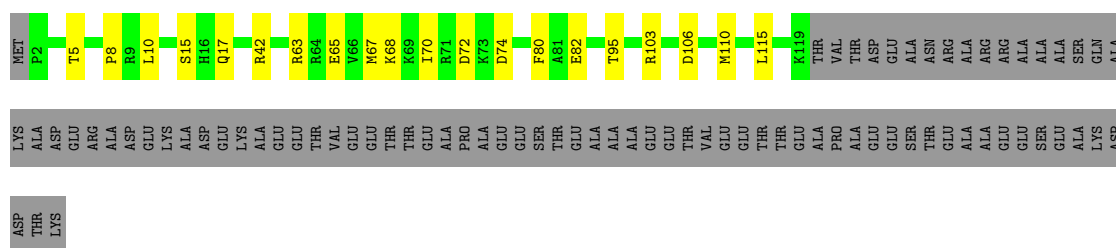
- Molecule 9: 50S ribosomal protein L15

Chain O: 82% 16% ..



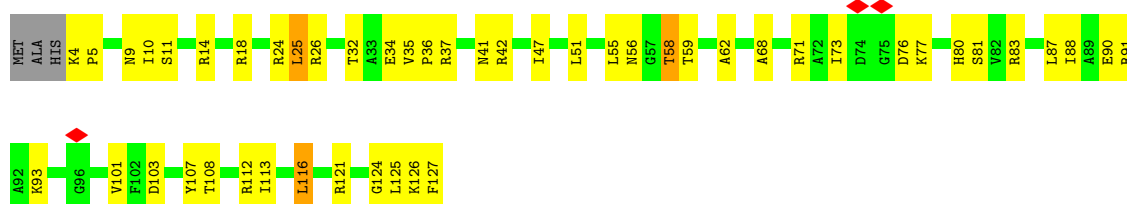
- Molecule 10: 50S ribosomal protein L17

Chain Q: 49% 10% 41%



- Molecule 11: 50S ribosomal protein L18

Chain R: 59% 36% ..



- Molecule 12: 50S ribosomal protein L19

Chain S: 81% 17% .



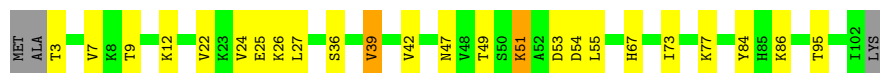
- Molecule 13: 50S ribosomal protein L20

Chain T: 79% 16% ..



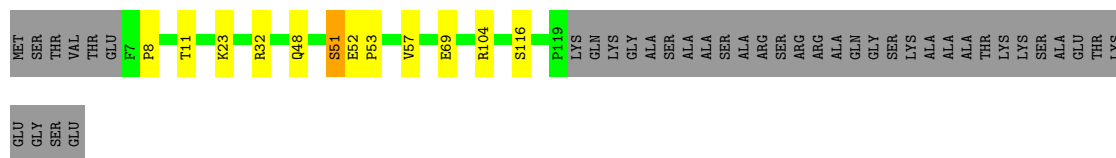
- Molecule 14: 50S ribosomal protein L21

Chain U:  74% 21% . .



- Molecule 15: 50S ribosomal protein L22

Chain V:  66% 7% . 26%



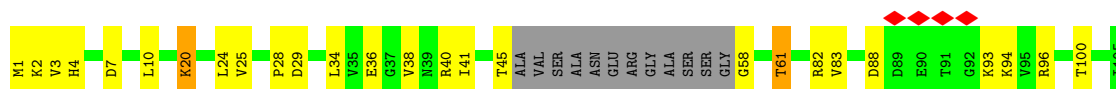
- Molecule 16: 50S ribosomal protein L23

Chain W:  80% 16% . .



- Molecule 17: 50S ribosomal protein L24

Chain X:  64% 23% . 11%



- Molecule 18: 50S ribosomal protein L27

Chain Z:  70% 16% . 13%



- Molecule 19: 50S ribosomal protein L28

Chain 1:  84% 12% . .



- Molecule 20: 50S ribosomal protein L29

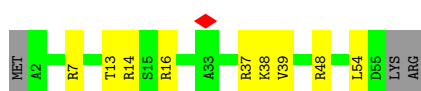
Chain 2:  62% 18% . 18%



- Molecule 21: 50S ribosomal protein L30



- Molecule 22: 50S ribosomal protein L32



- Molecule 23: 50S ribosomal protein L33A



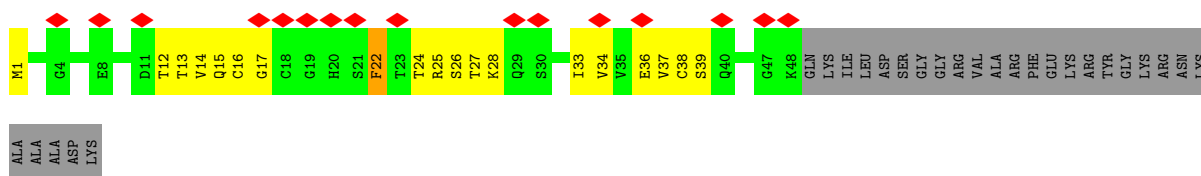
- Molecule 24: 50S ribosomal protein L34



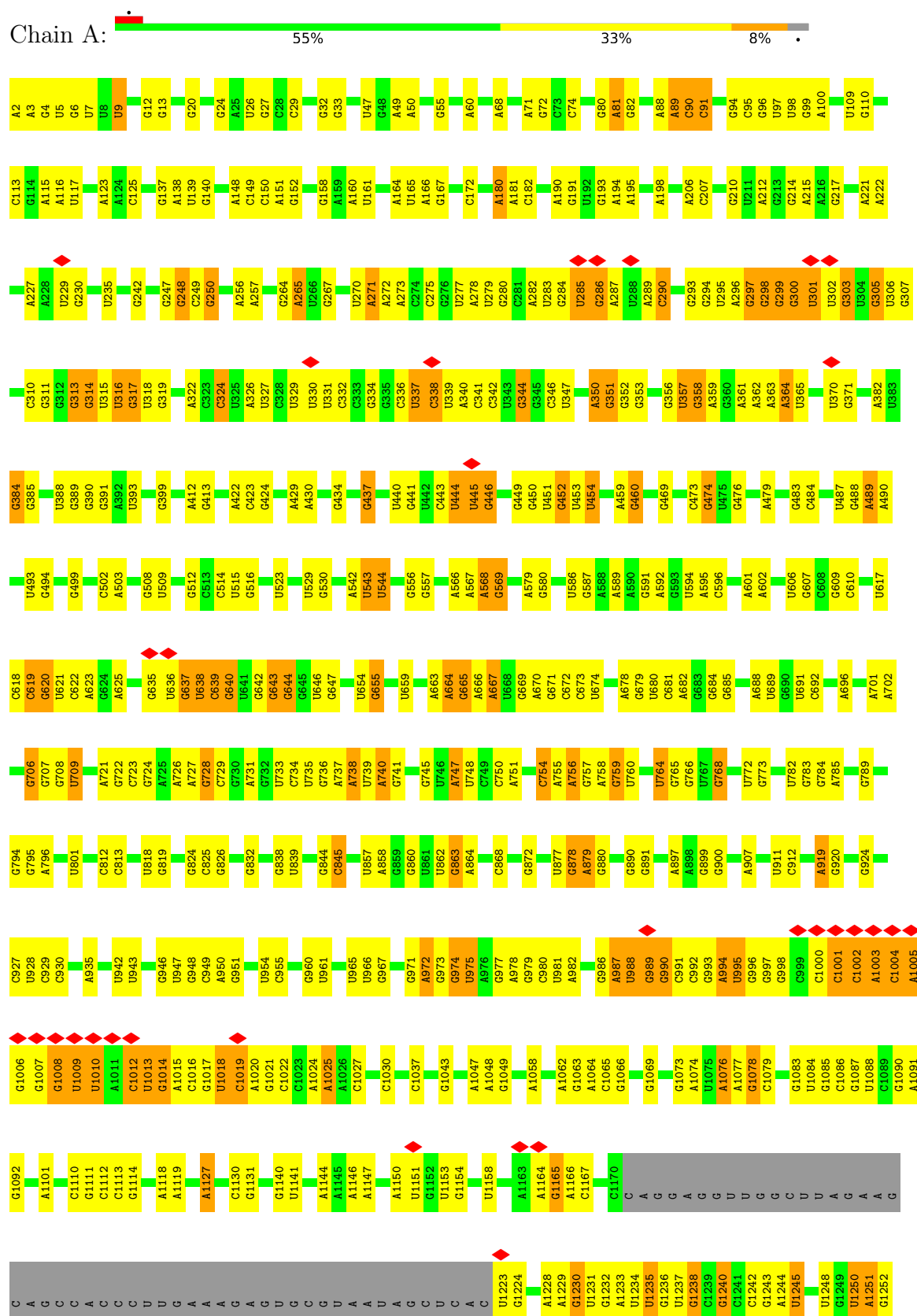
- Molecule 25: 50S ribosomal protein L35



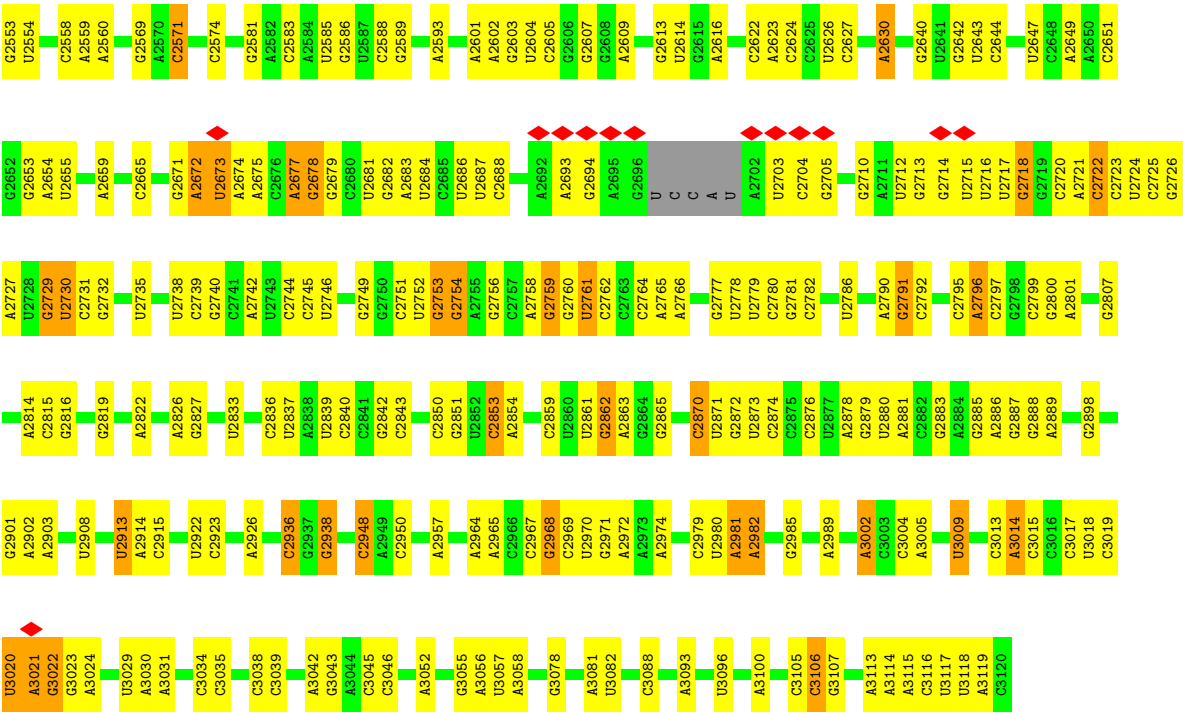
- Molecule 26: 50S ribosomal protein L31



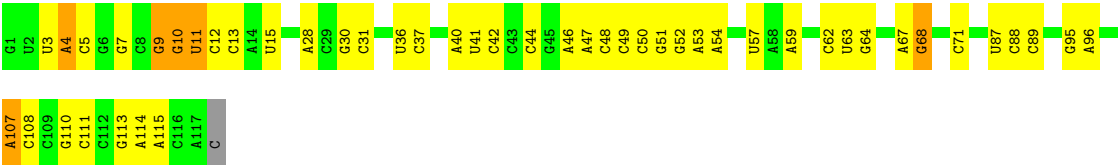
- Molecule 27: 23S rRNA



|       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |
|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|
| G2466 | U2467 | U2383 | U2384 | U2385 | U2386 | U2387 | U2388 | U2389 | U2390 | U2391 | U2392 | U2393 | U2394 | U2395 | U2396 | U2397 | U2398 | U2399 | U2400 | U2401 | U2402 | U2403 | U2404 | U2405 | U2406 | U2407 | U2408 | U2409 | U2410 | U2411 | U2412 | U2413 | U2414 | U2415 | U2416 | U2417 | U2421 | U2422 | U2425 | U2426 | U2427 | U2434 | U2435 | U2436 | U2437 | U2438 | U2439 | U2447 | U2448 | U2449 | U2457 | U2458 | U2459 | U2460 | U2461 | U2462 | U2463 | U2464 | U2465 |
| G2466 | U2467 | U2383 | U2384 | U2385 | U2386 | U2387 | U2388 | U2389 | U2390 | U2391 | U2392 | U2393 | U2394 | U2395 | U2396 | U2397 | U2398 | U2399 | U2400 | U2401 | U2402 | U2403 | U2404 | U2405 | U2406 | U2407 | U2408 | U2409 | U2410 | U2411 | U2412 | U2413 | U2414 | U2415 | U2416 | U2417 | U2421 | U2422 | U2425 | U2426 | U2427 | U2434 | U2435 | U2436 | U2437 | U2438 | U2439 | U2447 | U2448 | U2449 | U2457 | U2458 | U2459 | U2460 | U2461 | U2462 | U2463 | U2464 | U2465 |
| C2322 | G2323 | A2324 | U2325 | A2326 | G2327 | G2328 | G2329 | U2330 | U2331 | U2332 | G2333 | U2334 | G2335 | U2336 | U2337 | G2338 | G2339 | A2340 | U2341 | A2342 | G2343 | G2344 | U2345 | G2346 | G2347 | G2348 | A2349 | G2350 | A2351 | G2352 | U2353 | G2354 | U2355 | G2356 | A2357 | G2358 | G2359 | G2360 | U2361 | G2362 | A2363 | G2364 | A2365 | G2366 | G2367 | G2368 | G2369 | A2370 | G2371 | U2372 | G2373 | U2374 | G2375 | G2376 | G2377 | G2378 | G2379 | G2380 | U2381 |
| C2322 | G2323 | A2324 | U2325 | A2326 | G2327 | G2328 | G2329 | U2330 | U2331 | U2332 | G2333 | U2334 | G2335 | U2336 | U2337 | G2338 | G2339 | A2340 | U2341 | A2342 | G2343 | G2344 | U2345 | G2346 | G2347 | G2348 | A2349 | G2350 | A2351 | G2352 | U2353 | G2354 | U2355 | G2356 | A2357 | G2358 | G2359 | G2360 | U2361 | G2362 | A2363 | G2364 | A2365 | G2366 | G2367 | G2368 | G2369 | A2370 | G2371 | U2372 | G2373 | U2374 | G2375 | G2376 | G2377 | G2378 | G2379 | G2380 | U2381 |
| G2096 | G2097 | U2098 | G2099 | G2105 | A2106 | A2107 | A2108 | A2109 | A2113 | A2114 | G2130 | G2137 | G2138 | G2139 | G2140 | G2141 | G2145 | A2146 | U2147 | G2148 | A2152 | G2153 | G2154 | A2160 | A2161 | A2162 | U2163 | U2170 | G2171 | U2179 | U2180 | G2181 | G2182 | G2189 | A2190 | A2191 | A2194 | U2195 | G2196 | G2211 | A2212 | U2215 | G2216 | U2217 | G2218 | U2219 | G2220 | A2221 |       |       |       |       |       |       |       |       |       |       |       |
| G2096 | G2097 | U2098 | G2099 | G2105 | A2106 | A2107 | A2108 | A2109 | A2113 | A2114 | G2130 | G2137 | G2138 | G2139 | G2140 | G2141 | G2145 | A2146 | U2147 | G2148 | A2152 | G2153 | G2154 | A2160 | A2161 | A2162 | U2163 | U2170 | G2171 | U2179 | U2180 | G2181 | G2182 | G2189 | A2190 | A2191 | A2194 | U2195 | G2196 | G2211 | A2212 | U2215 | G2216 | U2217 | G2218 | U2219 | G2220 | A2221 |       |       |       |       |       |       |       |       |       |       |       |
| A1980 | U1986 | U1989 | A2000 | A2001 | A2002 | A2003 | A2004 | C2007 | A2008 | U2011 | C2012 | G2013 | G2014 | U2015 | G2016 | C2017 | G2018 | A2019 | A2020 | C2025 | A2026 | A2029 | C2030 | U2033 | C2043 | A2046 | U2061 | A2064 | A2065 | G2066 | A2070 | A2071 | G2074 | G2075 | C2085 | U2086 | C2087 | C2088 | C2089 | U2090 | U2091 | U2092 | G2093 | G2094 | G2095 |       |       |       |       |       |       |       |       |       |       |       |       |       |       |
| A1980 | U1986 | U1989 | A2000 | A2001 | A2002 | A2003 | A2004 | C2007 | A2008 | U2011 | C2012 | G2013 | G2014 | U2015 | G2016 | C2017 | G2018 | A2019 | A2020 | C2025 | A2026 | A2029 | C2030 | U2033 | C2043 | A2046 | U2061 | A2064 | A2065 | G2066 | A2070 | A2071 | G2074 | G2075 | C2085 | U2086 | C2087 | C2088 | C2089 | U2090 | U2091 | U2092 | G2093 | G2094 | G2095 |       |       |       |       |       |       |       |       |       |       |       |       |       |       |
| U1864 | A1865 | G1866 | G1867 | U1870 | G1871 | A1872 | A1873 | U1876 | G1885 | C1888 | G1892 | G1893 | A1895 | U1898 | G1899 | C1900 | C1901 | C1902 | A1907 | A1908 | G1921 | G1922 | G1923 | G1933 | G1937 | G1938 | U1946 | U1947 | A1948 | C1949 | C1953 | C1954 | A1955 | G1961 | A1962 | U1964 | A1973 | A1974 | A1975 | A1976 | C1977 | U1981 |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |
| U1864 | A1865 | G1866 | G1867 | U1870 | G1871 | A1872 | A1873 | U1876 | G1885 | C1888 | G1892 | G1893 | A1895 | U1898 | G1899 | C1900 | C1901 | C1902 | A1907 | A1908 | G1921 | G1922 | G1923 | G1933 | G1937 | G1938 | U1946 | U1947 | A1948 | C1949 | C1953 | C1954 | A1955 | G1961 | A1962 | U1964 | A1973 | A1974 | A1975 | A1976 | C1977 | U1981 |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |
| C1718 | G1724 | G1725 | C1726 | A1727 | U1728 | A1729 | A1731 | G1736 | A1737 | G1738 | G1754 | A1755 | G1756 | U1757 | G1758 | A1759 | U1767 | U1771 | G1772 | U1781 | U1782 | G1786 | A1787 | G1788 | U1789 | A1790 | A1791 | A1792 | U1798 | A1803 | G1804 | G1805 | A1808 | U1809 | A1810 | C1813 | G1825 | A1826 | G1840 | U1854 | A1859 | G1860 |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |
| C1718 | G1724 | G1725 | C1726 | A1727 | U1728 | A1729 | A1731 | G1736 | A1737 | G1738 | G1754 | A1755 | G1756 | U1757 | G1758 | A1759 | U1767 | U1771 | G1772 | U1781 | U1782 | G1786 | A1787 | G1788 | U1789 | A1790 | A1791 | A1792 | U1798 | A1803 | G1804 | G1805 | A1808 | U1809 | A1810 | C1813 | G1825 | A1826 | G1840 | U1854 | A1859 | G1860 |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |
| G1629 | U1630 | A1631 | G1632 | U1633 | C1634 | G1639 | A1640 | U1641 | G1642 | G1647 | A1648 | C1649 | G1650 | C1651 | A1652 | G1653 | G1654 | A1655 | A1656 | G1657 | U1658 | U1659 | A1660 | U1665 | A1666 | G1670 | A1673 | G1674 | U1675 | G1676 | G1677 | U1678 | A1679 | U1680 | U1681 | A1690 | A1691 | G1696 | G1703 | U1704 | C1705 | A1706 | G1707 | A1710 | G1711 | A1714 | A1715 | U1716 | U1717 |       |       |       |       |       |       |       |       |       |       |
| G1629 | U1630 | A1631 | G1632 | U1633 | C1634 | G1639 | A1640 | U1641 | G1642 | G1647 | A1648 | C1649 | G1650 | C1651 | A1652 | G1653 | G1654 | A1655 | A1656 | G1657 | U1658 | U1659 | A1660 | U1665 | A1666 | G1670 | A1673 | G1674 | U1675 | G1676 | G1677 | U1678 | A1679 | U1680 | U1681 | A1690 | A1691 | G1696 | G1703 | U1704 | C1705 | A1706 | G1707 | A1710 | G1711 | A1714 | A1715 | U1716 | U1717 |       |       |       |       |       |       |       |       |       |       |
| A     | C     | C     | G     | U     | G     | A     | C     | G     | C     | A     | C     | U     | U     | U     | C     | G     | G     | G     | U     | U     | U     | G     | G     | C     | C     | U     | U     | U     | G     | G     | G     | C     | U1608 | G1609 | A1610 | A1611 | U1612 | G1613 | G1614 | G1615 | A1616 | C1617 | U1618 | U1619 | U1620 | C1621 | G1622 | U1623 | U1624 | G1625 | U1627 | A1628 |       |       |       |       |       |       |       |
| A     | C     | C     | G     | U     | G     | A     | C     | G     | C     | A     | C     | U     | U     | U     | C     | G     | G     | G     | U     | U     | U     | G     | G     | C     | C     | U     | U     | U     | G     | G     | G     | C     | U1608 | G1609 | A1610 | A1611 | U1612 | G1613 | G1614 | G1615 | A1616 | C1617 | U1618 | U1619 | U1620 | C1621 | G1622 | U1623 | U1624 | G1625 | U1627 | A1628 |       |       |       |       |       |       |       |
| G1379 | G1386 | A1387 | U1388 | U1389 | C1393 | A1394 | G1398 | A1399 | G1400 | C1403 | C1404 | G1407 | C1408 | A1415 | A1416 | U1427 | C1430 | U1431 | C1435 | C1436 | C1441 | A1442 | G1443 | U1444 | C1445 | C1446 | G1447 | C1448 | U1459 | C1465 | U1466 | U1467 | A1468 | A1469 | G1476 | C1477 | G1478 | G1479 | A1480 | C1485 | G1486 |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |
| G1379 | G1386 | A1387 | U1388 | U1389 | C1393 | A1394 | G1398 | A1399 | G1400 | C1403 | C1404 | G1407 | C1408 | A1415 | A1416 | U1427 | C1430 | U1431 | C1435 | C1436 | C1441 | A1442 | G1443 | U1444 | C1445 | C1446 | G1447 | C1448 | U1459 | C1465 | U1466 | U1467 | A1468 | A1469 | G1476 | C1477 | G1478 | G1479 | A1480 | C1485 | G1486 |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |
| U1487 | A1493 | U1494 | A1499 | A1500 | C1501 | G1502 | G1507 | A1508 | U1509 | A1510 | U1511 | G1522 | U1523 | U1524 | U1529 | G1530 | C1531 | G1532 | U1533 | C1534 | C1535 | U1536 | U1537 | A1539 | U1540 | G1541 | A1542 | A1543 | U1544 | C1545 | C1546 | G1547 | C1548 | G1550 | U1551 | A1552 | C1553 | U1554 | A1555 | A1556 | C1557 | C1558 | A1559 | U1560 | C1561 | C1562 | A     | A     | A     | A     | C     | C     |       |       |       |       |       |       |       |
| U1487 | A1493 | U1494 | A1499 | A1500 | C1501 | G1502 | G1507 | A1508 | U1509 | A1510 | U1511 | G1522 | U1523 | U1524 | U1529 | G1530 | C1531 | G1532 | U1533 | C1534 | C1535 | U1536 | U1537 | A1539 | U1540 | G1541 | A1542 | A1543 | U1544 | C1545 | C1546 | G1547 | C1548 | G1550 | U1551 | A1552 | C1553 | U1554 | A1555 | A1556 | C1557 | C1558 | A1559 | U1560 | C1561 | C1562 | A     | A     | A     | A     | C     | C     |       |       |       |       |       |       |       |



• Molecule 28: 5S rRNA



## 4 Experimental information

| Property                             | Value                                | Source    |
|--------------------------------------|--------------------------------------|-----------|
| EM reconstruction method             | SINGLE PARTICLE                      | Depositor |
| Imposed symmetry                     | POINT, C1                            | Depositor |
| Number of particles used             | 110934                               | Depositor |
| Resolution determination method      | FSC 0.143 CUT-OFF                    | Depositor |
| CTF correction method                | NONE; CTF correction in Relion 3.1.4 | Depositor |
| Microscope                           | FEI TITAN KRIOS                      | Depositor |
| Voltage (kV)                         | 300                                  | Depositor |
| Electron dose ( $e^-/\text{\AA}^2$ ) | 1.34                                 | Depositor |
| Minimum defocus (nm)                 | 1800                                 | Depositor |
| Maximum defocus (nm)                 | 3000                                 | Depositor |
| Magnification                        | Not provided                         |           |
| Image detector                       | FEI FALCON III (4k x 4k)             | Depositor |
| Maximum map value                    | 0.280                                | Depositor |
| Minimum map value                    | -0.042                               | Depositor |
| Average map value                    | 0.002                                | Depositor |
| Map value standard deviation         | 0.011                                | Depositor |
| Recommended contour level            | 0.045                                | Depositor |
| Map size ( $\text{\AA}$ )            | 406.6, 406.6, 406.6                  | wwPDB     |
| Map dimensions                       | 380, 380, 380                        | wwPDB     |
| Map angles ( $^\circ$ )              | 90.0, 90.0, 90.0                     | wwPDB     |
| Pixel spacing ( $\text{\AA}$ )       | 1.07, 1.07, 1.07                     | Depositor |

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

| Mol | Chain | Bond lengths |         | Bond angles |                 |
|-----|-------|--------------|---------|-------------|-----------------|
|     |       | RMSZ         | # Z  >5 | RMSZ        | # Z  >5         |
| 1   | E     | 0.20         | 0/2153  | 0.27        | 0/2895          |
| 2   | F     | 0.21         | 0/1609  | 0.35        | 0/2165          |
| 3   | G     | 0.20         | 0/1592  | 0.34        | 0/2153          |
| 4   | H     | 0.14         | 0/1458  | 0.35        | 0/1962          |
| 5   | I     | 0.13         | 0/1281  | 0.34        | 0/1733          |
| 6   | J     | 0.17         | 0/311   | 0.47        | 0/419           |
| 7   | M     | 0.19         | 0/1157  | 0.29        | 0/1567          |
| 8   | N     | 0.19         | 0/946   | 0.27        | 0/1268          |
| 9   | O     | 0.17         | 0/1091  | 0.37        | 0/1457          |
| 10  | Q     | 0.21         | 0/945   | 0.35        | 0/1267          |
| 11  | R     | 0.19         | 0/950   | 0.47        | 0/1276          |
| 12  | S     | 0.19         | 0/921   | 0.37        | 0/1236          |
| 13  | T     | 0.21         | 0/1000  | 0.30        | 0/1341          |
| 14  | U     | 0.19         | 0/764   | 0.24        | 0/1030          |
| 15  | V     | 0.21         | 0/878   | 0.32        | 0/1192          |
| 16  | W     | 0.22         | 0/766   | 0.38        | 0/1030          |
| 17  | X     | 0.17         | 0/716   | 0.33        | 0/957           |
| 18  | Z     | 0.18         | 0/583   | 0.32        | 0/782           |
| 19  | 1     | 0.16         | 0/478   | 0.32        | 0/641           |
| 20  | 2     | 0.19         | 0/530   | 0.37        | 0/708           |
| 21  | 3     | 0.20         | 0/473   | 0.38        | 0/635           |
| 22  | 5     | 0.15         | 0/427   | 0.26        | 0/572           |
| 23  | 6     | 0.25         | 0/413   | 0.59        | 1/553 (0.2%)    |
| 24  | 7     | 0.20         | 0/375   | 0.28        | 0/493           |
| 25  | 8     | 0.13         | 0/507   | 0.25        | 0/672           |
| 26  | 4     | 0.14         | 0/372   | 0.35        | 0/503           |
| 27  | A     | 0.22         | 0/72557 | 0.30        | 0/113208        |
| 28  | B     | 0.15         | 0/2799  | 0.27        | 0/4362          |
| All | All   | 0.21         | 0/98052 | 0.31        | 1/148077 (0.0%) |

There are no bond length outliers.

All (1) bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms   | Z     | Observed(°) | Ideal(°) |
|-----|-------|-----|------|---------|-------|-------------|----------|
| 23  | 6     | 18  | CYS  | CB-CA-C | -5.33 | 110.42      | 116.54   |

There are no chirality outliers.

There are no planarity outliers.

## 5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|-----|-------|-------|----------|----------|---------|--------------|
| 1   | E     | 2110  | 0        | 2165     | 23      | 0            |
| 2   | F     | 1587  | 0        | 1630     | 33      | 0            |
| 3   | G     | 1569  | 0        | 1607     | 30      | 0            |
| 4   | H     | 1436  | 0        | 1463     | 46      | 0            |
| 5   | I     | 1260  | 0        | 1300     | 57      | 0            |
| 6   | J     | 308   | 0        | 323      | 10      | 0            |
| 7   | M     | 1130  | 0        | 1167     | 11      | 0            |
| 8   | N     | 938   | 0        | 1000     | 9       | 0            |
| 9   | O     | 1078  | 0        | 1151     | 15      | 0            |
| 10  | Q     | 928   | 0        | 972      | 14      | 0            |
| 11  | R     | 941   | 0        | 979      | 35      | 0            |
| 12  | S     | 907   | 0        | 938      | 13      | 0            |
| 13  | T     | 988   | 0        | 1038     | 15      | 0            |
| 14  | U     | 754   | 0        | 802      | 13      | 0            |
| 15  | V     | 864   | 0        | 903      | 8       | 0            |
| 16  | W     | 756   | 0        | 802      | 11      | 0            |
| 17  | X     | 710   | 0        | 760      | 16      | 0            |
| 18  | Z     | 574   | 0        | 591      | 11      | 0            |
| 19  | 1     | 470   | 0        | 484      | 9       | 0            |
| 20  | 2     | 527   | 0        | 538      | 11      | 0            |
| 21  | 3     | 470   | 0        | 497      | 8       | 0            |
| 22  | 5     | 423   | 0        | 463      | 6       | 0            |
| 23  | 6     | 405   | 0        | 411      | 50      | 0            |
| 24  | 7     | 372   | 0        | 406      | 7       | 0            |
| 25  | 8     | 502   | 0        | 541      | 13      | 0            |
| 26  | 4     | 364   | 0        | 352      | 16      | 0            |
| 27  | A     | 64799 | 0        | 32602    | 886     | 0            |
| 28  | B     | 2502  | 0        | 1274     | 27      | 0            |
| All | All   | 89672 | 0        | 57159    | 1269    | 0            |

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 9.

All (1269) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

| Atom-1           | Atom-2           | Interatomic distance (Å) | Clash overlap (Å) |
|------------------|------------------|--------------------------|-------------------|
| 23:6:19:LYS:HE3  | 23:6:45:CYS:SG   | 1.61                     | 1.39              |
| 23:6:6:ASP:O     | 23:6:7:VAL:HG13  | 1.22                     | 1.28              |
| 23:6:20:HIS:CG   | 27:A:2624:C:H5'  | 1.78                     | 1.18              |
| 23:6:20:HIS:CD2  | 27:A:2624:C:H5'  | 1.93                     | 1.03              |
| 23:6:19:LYS:CE   | 23:6:45:CYS:SG   | 2.46                     | 1.02              |
| 27:A:2971:G:H21  | 27:A:2981:A:N6   | 1.58                     | 1.01              |
| 27:A:1540:U:H3   | 27:A:1632:G:H1   | 1.01                     | 1.00              |
| 27:A:337:U:H3    | 27:A:344:G:H1    | 1.10                     | 0.99              |
| 27:A:1754:G:H1   | 27:A:1759:A:N6   | 1.61                     | 0.98              |
| 23:6:6:ASP:O     | 23:6:7:VAL:CG1   | 2.12                     | 0.97              |
| 27:A:2971:G:N2   | 27:A:2981:A:H62  | 1.62                     | 0.96              |
| 27:A:2971:G:H21  | 27:A:2981:A:H62  | 0.95                     | 0.91              |
| 27:A:1754:G:N2   | 27:A:1759:A:N1   | 2.18                     | 0.91              |
| 27:A:2086:U:H3   | 27:A:2096:G:H1   | 0.90                     | 0.88              |
| 23:6:19:LYS:HD2  | 23:6:44:ASN:OD1  | 1.72                     | 0.87              |
| 27:A:334:G:H1    | 27:A:347:U:H3    | 1.23                     | 0.87              |
| 27:A:1542:A:H61  | 27:A:1628:A:H1'  | 1.41                     | 0.85              |
| 27:A:337:U:O2    | 27:A:344:G:N2    | 2.09                     | 0.84              |
| 27:A:1547:G:H1   | 27:A:1623:U:H3   | 0.85                     | 0.84              |
| 23:6:16:GLU:OE1  | 23:6:50:PRO:HG2  | 1.78                     | 0.83              |
| 10:Q:103:ARG:HD3 | 10:Q:110:MET:HE2 | 1.61                     | 0.82              |
| 27:A:2671:G:H1   | 27:A:2675:A:H62  | 1.26                     | 0.82              |
| 27:A:989:G:O6    | 27:A:990:G:N2    | 2.13                     | 0.82              |
| 27:A:747:A:N6    | 27:A:768:G:O2'   | 2.14                     | 0.81              |
| 27:A:2674:A:N6   | 27:A:2725:C:O2   | 2.14                     | 0.80              |
| 4:H:87:ARG:H     | 4:H:90:MET:HE2   | 1.47                     | 0.79              |
| 27:A:1550:G:H1   | 27:A:1620:U:H3   | 1.27                     | 0.79              |
| 27:A:217:G:H22   | 27:A:235:U:H4'   | 1.47                     | 0.78              |
| 23:6:21:ARG:HG3  | 23:6:43:PRO:HD2  | 1.64                     | 0.78              |
| 18:Z:64:PRO:HB3  | 27:A:759:G:H1    | 1.48                     | 0.77              |
| 17:X:10:LEU:HD23 | 17:X:20:LYS:HG3  | 1.66                     | 0.77              |
| 6:J:2:LYS:HA     | 6:J:2:LYS:HE2    | 1.66                     | 0.77              |
| 27:A:1541:G:H22  | 27:A:1631:A:H61  | 1.31                     | 0.77              |
| 27:A:365:U:H3    | 27:A:437:G:H1    | 1.32                     | 0.76              |
| 23:6:20:HIS:ND1  | 27:A:2624:C:H5'  | 2.00                     | 0.76              |
| 27:A:2333:G:O2'  | 27:A:2343:G:OP2  | 2.03                     | 0.76              |
| 11:R:71:ARG:NH2  | 28:B:28:A:OP1    | 2.19                     | 0.76              |

*Continued on next page...*

*Continued from previous page...*

| Atom-1           | Atom-2           | Interatomic distance (Å) | Clash overlap (Å) |
|------------------|------------------|--------------------------|-------------------|
| 4:H:83:GLN:N     | 4:H:83:GLN:OE1   | 2.17                     | 0.75              |
| 27:A:643:G:O2'   | 27:A:644:G:OP1   | 2.04                     | 0.75              |
| 11:R:34:GLU:OE2  | 11:R:34:GLU:N    | 2.17                     | 0.75              |
| 27:A:2343:G:H1   | 27:A:2401:U:H3   | 1.35                     | 0.75              |
| 27:A:1556:A:N1   | 27:A:1615:G:O6   | 2.20                     | 0.74              |
| 27:A:2386:U:OP1  | 27:A:2393:A:O2'  | 2.05                     | 0.74              |
| 23:6:17:VAL:HG12 | 23:6:17:VAL:O    | 1.86                     | 0.74              |
| 20:2:9:GLU:OE2   | 20:2:9:GLU:N     | 2.21                     | 0.74              |
| 25:8:19:THR:OG1  | 27:A:745:G:OP1   | 2.05                     | 0.74              |
| 27:A:329:U:O2    | 27:A:446:G:O6    | 2.05                     | 0.74              |
| 4:H:147:GLU:OE1  | 26:4:27:THR:OG1  | 2.06                     | 0.73              |
| 12:S:52:GLY:H    | 12:S:56:GLU:HG2  | 1.53                     | 0.73              |
| 10:Q:10:LEU:HB2  | 10:Q:17:GLN:HG3  | 1.71                     | 0.73              |
| 18:Z:14:ARG:NH2  | 27:A:2503:G:N7   | 2.34                     | 0.73              |
| 3:G:150:GLU:OE2  | 3:G:150:GLU:N    | 2.21                     | 0.73              |
| 5:I:151:ARG:NH2  | 27:A:2967:C:O2   | 2.21                     | 0.73              |
| 16:W:18:GLU:OE2  | 16:W:18:GLU:N    | 2.21                     | 0.73              |
| 19:1:41:ARG:HG2  | 19:1:43:GLY:H    | 1.52                     | 0.72              |
| 4:H:68:THR:HG21  | 4:H:96:VAL:HG21  | 1.70                     | 0.72              |
| 15:V:69:GLU:N    | 15:V:69:GLU:OE1  | 2.23                     | 0.72              |
| 27:A:1540:U:O4   | 27:A:1632:G:O6   | 2.06                     | 0.72              |
| 11:R:77:LYS:HB3  | 11:R:112:ARG:HD3 | 1.71                     | 0.72              |
| 27:A:1147:A:N6   | 27:A:1243:G:O2'  | 2.22                     | 0.72              |
| 3:G:23:GLU:OE2   | 3:G:23:GLU:N     | 2.20                     | 0.72              |
| 2:F:104:GLU:OE2  | 2:F:104:GLU:N    | 2.18                     | 0.72              |
| 27:A:1854:U:HO2' | 27:A:1977:C:HO2' | 1.36                     | 0.72              |
| 27:A:2552:A:H2'  | 27:A:2553:G:C8   | 2.25                     | 0.71              |
| 27:A:1755:A:O2'  | 27:A:1758:G:N2   | 2.21                     | 0.71              |
| 23:6:20:HIS:CE1  | 27:A:2624:C:H5'  | 2.26                     | 0.71              |
| 28:B:67:A:H4'    | 28:B:68:G:H5'    | 1.71                     | 0.71              |
| 2:F:19:GLU:N     | 2:F:19:GLU:OE2   | 2.23                     | 0.71              |
| 27:A:2862:G:O2'  | 27:A:3002:A:N6   | 2.23                     | 0.71              |
| 20:2:9:GLU:HA    | 20:2:12:GLU:HG2  | 1.73                     | 0.70              |
| 1:E:271:ARG:NH2  | 27:A:2016:G:OP2  | 2.24                     | 0.70              |
| 13:T:25:ARG:NH1  | 27:A:2245:C:OP1  | 2.24                     | 0.70              |
| 9:O:32:THR:HG22  | 9:O:35:ARG:H     | 1.57                     | 0.70              |
| 27:A:2756:G:O2'  | 27:A:2881:A:N1   | 2.23                     | 0.70              |
| 12:S:26:ASN:OD1  | 12:S:26:ASN:N    | 2.24                     | 0.70              |
| 17:X:24:LEU:HD12 | 17:X:25:VAL:HG23 | 1.74                     | 0.70              |
| 4:H:20:ARG:HG2   | 4:H:35:ILE:HG21  | 1.72                     | 0.70              |
| 8:N:93:PRO:HG3   | 8:N:114:ILE:HG12 | 1.74                     | 0.69              |

*Continued on next page...*

*Continued from previous page...*

| Atom-1           | Atom-2           | Interatomic distance (Å) | Clash overlap (Å) |
|------------------|------------------|--------------------------|-------------------|
| 20:2:13:LEU:HB3  | 20:2:17:GLU:HG3  | 1.72                     | 0.69              |
| 2:F:153:GLY:HA3  | 2:F:157:PRO:HG2  | 1.74                     | 0.69              |
| 23:6:20:HIS:NE2  | 27:A:2624:C:OP1  | 2.26                     | 0.69              |
| 3:G:163:GLU:OE2  | 3:G:163:GLU:N    | 2.25                     | 0.69              |
| 23:6:16:GLU:OE1  | 23:6:50:PRO:CG   | 2.40                     | 0.69              |
| 23:6:20:HIS:CG   | 27:A:2624:C:C5'  | 2.68                     | 0.68              |
| 27:A:2343:G:H2'  | 27:A:2344:G:C8   | 2.29                     | 0.68              |
| 27:A:1532:G:O2'  | 27:A:1803:A:N1   | 2.21                     | 0.68              |
| 11:R:83:ARG:O    | 11:R:87:LEU:HD22 | 1.94                     | 0.68              |
| 19:1:57:LYS:NZ   | 27:A:488:G:N7    | 2.41                     | 0.68              |
| 27:A:664:A:H3'   | 27:A:665:G:H8    | 1.57                     | 0.68              |
| 2:F:96:GLU:OE1   | 2:F:99:GLN:NE2   | 2.25                     | 0.68              |
| 3:G:199:GLU:OE2  | 3:G:199:GLU:N    | 2.20                     | 0.68              |
| 5:I:90:ILE:HD13  | 5:I:95:TYR:HB2   | 1.74                     | 0.68              |
| 27:A:2470:A:H2'  | 27:A:2471:A:H8   | 1.58                     | 0.68              |
| 4:H:102:ARG:NH2  | 26:4:1:MET:SD    | 2.67                     | 0.68              |
| 27:A:2970:U:N3   | 27:A:2980:U:O4   | 2.19                     | 0.68              |
| 1:E:270:ARG:HD3  | 1:E:273:ARG:HH22 | 1.59                     | 0.68              |
| 23:6:19:LYS:HG3  | 23:6:45:CYS:SG   | 2.34                     | 0.67              |
| 27:A:1554:U:H2'  | 27:A:1555:A:C8   | 2.28                     | 0.67              |
| 3:G:160:ARG:NH2  | 27:A:706:G:O2'   | 2.27                     | 0.67              |
| 27:A:857:U:H2'   | 27:A:858:A:C8    | 2.29                     | 0.67              |
| 11:R:127:PHE:O   | 27:A:2601:A:O2'  | 2.12                     | 0.67              |
| 27:A:947:U:H2'   | 27:A:948:G:H8    | 1.58                     | 0.67              |
| 14:U:26:LYS:HA   | 14:U:95:THR:HG23 | 1.76                     | 0.67              |
| 19:1:24:ARG:NH1  | 27:A:469:G:OP1   | 2.27                     | 0.67              |
| 27:A:1621:C:H2'  | 27:A:1622:G:H8   | 1.60                     | 0.67              |
| 27:A:1543:A:N1   | 27:A:1628:A:O2'  | 2.24                     | 0.67              |
| 27:A:2671:G:H1   | 27:A:2675:A:N6   | 1.92                     | 0.67              |
| 1:E:72:LYS:NZ    | 1:E:101:GLU:OE1  | 2.23                     | 0.66              |
| 5:I:108:LEU:HD21 | 5:I:153:ARG:HD2  | 1.77                     | 0.66              |
| 27:A:1754:G:N1   | 27:A:1759:A:N6   | 2.25                     | 0.66              |
| 27:A:327:U:O2    | 27:A:449:G:N2    | 2.28                     | 0.66              |
| 27:A:858:A:O2'   | 27:A:1877:U:OP1  | 2.14                     | 0.66              |
| 27:A:1229:A:H8   | 27:A:1230:G:H1'  | 1.60                     | 0.66              |
| 27:A:2364:C:H2'  | 27:A:2365:A:C8   | 2.30                     | 0.66              |
| 9:O:97:GLU:N     | 9:O:97:GLU:OE1   | 2.28                     | 0.66              |
| 27:A:285:U:H3'   | 27:A:286:G:H4'   | 1.78                     | 0.66              |
| 27:A:2407:C:N4   | 27:A:2408:G:O6   | 2.28                     | 0.66              |
| 27:A:2285:G:O6   | 27:A:2675:A:N1   | 2.29                     | 0.66              |
| 1:E:71:ASP:OD1   | 1:E:71:ASP:N     | 2.29                     | 0.65              |

*Continued on next page...*

*Continued from previous page...*

| Atom-1           | Atom-2           | Interatomic distance (Å) | Clash overlap (Å) |
|------------------|------------------|--------------------------|-------------------|
| 27:A:666:A:N6    | 27:A:2258:U:OP1  | 2.29                     | 0.65              |
| 27:A:2342:A:N6   | 27:A:2390:U:O2'  | 2.30                     | 0.65              |
| 27:A:1541:G:H22  | 27:A:1631:A:N6   | 1.95                     | 0.65              |
| 27:A:2372:U:H2'  | 27:A:2373:G:C8   | 2.32                     | 0.65              |
| 26:4:16:CYS:SG   | 26:4:17:GLY:N    | 2.70                     | 0.65              |
| 27:A:567:A:H4'   | 27:A:568:A:H5'   | 1.79                     | 0.65              |
| 27:A:994:A:H5''  | 27:A:1014:G:H21  | 1.62                     | 0.65              |
| 15:V:53:PRO:O    | 15:V:57:VAL:HG23 | 1.97                     | 0.64              |
| 27:A:1530:G:N2   | 27:A:1805:G:H1   | 1.94                     | 0.64              |
| 5:I:15:VAL:HG12  | 5:I:28:GLY:HA2   | 1.77                     | 0.64              |
| 23:6:28:ASN:ND2  | 27:A:2509:C:OP2  | 2.30                     | 0.64              |
| 3:G:41:GLN:HG2   | 27:A:709:U:H1'   | 1.79                     | 0.64              |
| 5:I:150:ARG:NE   | 5:I:163:VAL:O    | 2.30                     | 0.64              |
| 2:F:148:PRO:O    | 27:A:2735:U:O2'  | 2.16                     | 0.64              |
| 18:Z:11:ARG:O    | 18:Z:14:ARG:NH1  | 2.30                     | 0.64              |
| 5:I:64:SER:O     | 27:A:2972:A:O2'  | 2.12                     | 0.64              |
| 3:G:179:SER:OG   | 3:G:181:ASP:OD1  | 2.16                     | 0.63              |
| 27:A:990:G:O6    | 27:A:1018:U:O4   | 2.16                     | 0.63              |
| 27:A:2094:G:HO2' | 27:A:2095:G:H8   | 1.45                     | 0.63              |
| 6:J:10:GLU:HG3   | 6:J:11:HIS:CE1   | 2.33                     | 0.63              |
| 27:A:1146:A:N3   | 27:A:2710:G:O2'  | 2.29                     | 0.63              |
| 2:F:43:GLU:OE1   | 2:F:43:GLU:N     | 2.32                     | 0.63              |
| 4:H:143:SER:HA   | 4:H:148:ILE:HD11 | 1.81                     | 0.63              |
| 9:O:65:LYS:HB2   | 27:A:2640:G:H5'' | 1.80                     | 0.63              |
| 17:X:24:LEU:HD23 | 17:X:36:GLU:HG2  | 1.80                     | 0.63              |
| 7:M:56:VAL:HB    | 7:M:124:VAL:HG12 | 1.79                     | 0.63              |
| 27:A:1547:G:O6   | 27:A:1623:U:O4   | 2.15                     | 0.63              |
| 27:A:2879:G:O2'  | 27:A:2888:G:O6   | 2.12                     | 0.63              |
| 23:6:20:HIS:CE1  | 27:A:2624:C:C5'  | 2.82                     | 0.63              |
| 4:H:136:THR:HG21 | 27:A:2527:G:H21  | 1.64                     | 0.63              |
| 23:6:17:VAL:HG21 | 23:6:49:GLN:HG3  | 1.80                     | 0.63              |
| 27:A:681:C:H2'   | 27:A:682:A:H8    | 1.62                     | 0.63              |
| 27:A:1690:A:H2'  | 27:A:1691:A:C8   | 2.33                     | 0.63              |
| 27:A:2339:G:H1   | 27:A:2387:U:H3   | 1.47                     | 0.63              |
| 5:I:77:VAL:O     | 5:I:81:THR:HG23  | 1.98                     | 0.62              |
| 27:A:1076:A:O2'  | 27:A:2681:U:O2'  | 2.16                     | 0.62              |
| 4:H:76:ARG:NH1   | 4:H:89:GLY:O     | 2.32                     | 0.62              |
| 5:I:98:GLN:HE22  | 5:I:105:GLU:HB3  | 1.64                     | 0.62              |
| 7:M:71:LYS:NZ    | 27:A:1140:G:OP1  | 2.32                     | 0.62              |
| 21:3:31:ILE:HG22 | 21:3:32:ARG:HG3  | 1.80                     | 0.62              |
| 27:A:998:G:H1    | 27:A:1010:U:H3   | 1.47                     | 0.62              |

*Continued on next page...*

*Continued from previous page...*

| Atom-1           | Atom-2           | Interatomic distance (Å) | Clash overlap (Å) |
|------------------|------------------|--------------------------|-------------------|
| 22:5:16:ARG:NH2  | 27:A:1379:G:OP1  | 2.23                     | 0.62              |
| 27:A:947:U:H2'   | 27:A:948:G:C8    | 2.34                     | 0.62              |
| 27:A:2224:C:O2'  | 27:A:2913:U:OP2  | 2.17                     | 0.62              |
| 26:4:15:GLN:N    | 26:4:33:ILE:O    | 2.33                     | 0.62              |
| 27:A:2323:G:N2   | 27:A:2412:U:O2   | 2.25                     | 0.62              |
| 27:A:341:C:C4    | 27:A:342:C:N4    | 2.68                     | 0.62              |
| 27:A:1009:U:H2'  | 27:A:1010:U:C6   | 2.33                     | 0.62              |
| 11:R:34:GLU:HG2  | 11:R:35:VAL:HG23 | 1.80                     | 0.62              |
| 27:A:1610:C:H2'  | 27:A:1611:A:C8   | 2.34                     | 0.62              |
| 27:A:2356:G:H2'  | 27:A:2380:G:H1   | 1.64                     | 0.62              |
| 27:A:247:G:OP2   | 27:A:249:C:N4    | 2.33                     | 0.62              |
| 27:A:284:G:H1'   | 27:A:303:G:C2    | 2.35                     | 0.61              |
| 27:A:1073:G:O2'  | 27:A:1076:A:N6   | 2.32                     | 0.61              |
| 23:6:40:LYS:NZ   | 27:A:2571:C:OP1  | 2.33                     | 0.61              |
| 27:A:1825:C:N4   | 27:A:1840:G:OP2  | 2.21                     | 0.61              |
| 27:A:2019:A:H2'  | 27:A:2020:A:C8   | 2.35                     | 0.61              |
| 27:A:2470:A:H2'  | 27:A:2471:A:C8   | 2.34                     | 0.61              |
| 1:E:257:THR:OG1  | 27:A:2014:G:O2'  | 2.17                     | 0.61              |
| 27:A:997:G:H2'   | 27:A:998:G:C8    | 2.35                     | 0.61              |
| 27:A:1076:A:H2'  | 27:A:1077:A:C8   | 2.35                     | 0.61              |
| 27:A:3014:A:N6   | 27:A:3113:A:OP2  | 2.34                     | 0.61              |
| 27:A:2353:U:N3   | 27:A:2354:G:O6   | 2.34                     | 0.61              |
| 5:I:60:ARG:NH1   | 27:A:1153:U:OP1  | 2.33                     | 0.61              |
| 5:I:150:ARG:HD2  | 5:I:163:VAL:HG23 | 1.83                     | 0.61              |
| 27:A:341:C:N4    | 27:A:342:C:N4    | 2.48                     | 0.61              |
| 27:A:993:G:N1    | 27:A:1015:A:OP2  | 2.21                     | 0.61              |
| 27:A:1854:U:O2'  | 27:A:1977:C:O2'  | 2.16                     | 0.61              |
| 27:A:2761:U:H2'  | 27:A:2762:C:C6   | 2.36                     | 0.61              |
| 4:H:15:TYR:HA    | 4:H:19:ILE:HB    | 1.83                     | 0.61              |
| 4:H:40:LYS:HE2   | 4:H:164:VAL:HG11 | 1.82                     | 0.61              |
| 27:A:625:A:N6    | 27:A:647:G:O2'   | 2.34                     | 0.61              |
| 27:A:2674:A:OP1  | 27:A:2721:A:O2'  | 2.14                     | 0.61              |
| 5:I:144:GLN:OE1  | 27:A:2968:G:N2   | 2.34                     | 0.61              |
| 27:A:2088:C:H2'  | 27:A:2089:C:C6   | 2.36                     | 0.60              |
| 4:H:63:ASP:OD2   | 4:H:157:ARG:NE   | 2.35                     | 0.60              |
| 23:6:20:HIS:ND1  | 27:A:2624:C:C5'  | 2.64                     | 0.60              |
| 2:F:83:GLU:OE2   | 27:A:2859:C:O2'  | 2.15                     | 0.60              |
| 2:F:60:ARG:NH2   | 27:A:3052:A:OP1  | 2.35                     | 0.60              |
| 27:A:1076:A:HO2' | 27:A:2681:U:HO2' | 1.46                     | 0.60              |
| 27:A:137:G:H21   | 27:A:1524:G:H1'  | 1.66                     | 0.60              |
| 20:2:7:PRO:HD3   | 20:2:56:ARG:HD3  | 1.82                     | 0.60              |

*Continued on next page...*

*Continued from previous page...*

| Atom-1          | Atom-2           | Interatomic distance (Å) | Clash overlap (Å) |
|-----------------|------------------|--------------------------|-------------------|
| 26:4:13:THR:O   | 26:4:33:ILE:N    | 2.32                     | 0.60              |
| 2:F:5:GLY:HA3   | 2:F:84:LEU:HD21  | 1.83                     | 0.60              |
| 21:3:15:ALA:O   | 21:3:20:ARG:NH1  | 2.35                     | 0.60              |
| 27:A:911:U:H2'  | 27:A:912:C:C6    | 2.37                     | 0.60              |
| 4:H:61:ILE:HD12 | 4:H:72:PRO:HG2   | 1.83                     | 0.60              |
| 5:I:33:LEU:HD11 | 5:I:137:ILE:HG13 | 1.84                     | 0.60              |
| 5:I:46:ALA:H    | 5:I:51:ILE:HA    | 1.66                     | 0.59              |
| 27:A:1541:G:H1  | 27:A:1631:A:H62  | 1.51                     | 0.59              |
| 2:F:154:CYS:O   | 27:A:2277:G:H5'  | 2.03                     | 0.59              |
| 1:E:60:ARG:HA   | 27:A:1788:G:H5'  | 1.83                     | 0.59              |
| 4:H:12:LYS:HG2  | 4:H:16:ARG:HH12  | 1.66                     | 0.59              |
| 13:T:33:ARG:NH2 | 27:A:672:C:OP1   | 2.36                     | 0.59              |
| 23:6:35:ARG:NH1 | 23:6:53:GLU:O    | 2.35                     | 0.59              |
| 27:A:217:G:N2   | 27:A:235:U:H4'   | 2.18                     | 0.59              |
| 27:A:310:C:H2'  | 27:A:311:G:H8    | 1.67                     | 0.59              |
| 27:A:664:A:H3'  | 27:A:665:G:C8    | 2.38                     | 0.59              |
| 27:A:2363:A:H2' | 27:A:2364:C:C6   | 2.38                     | 0.59              |
| 9:O:133:ALA:O   | 9:O:137:ILE:HG13 | 2.03                     | 0.59              |
| 27:A:1118:A:H2' | 27:A:1119:A:C8   | 2.37                     | 0.59              |
| 27:A:543:U:H3'  | 27:A:544:U:H5''  | 1.84                     | 0.59              |
| 27:A:2323:G:H1  | 27:A:2412:U:H3   | 1.48                     | 0.59              |
| 12:S:48:ARG:NH1 | 12:S:97:TYR:OH   | 2.32                     | 0.59              |
| 17:X:82:ARG:NH2 | 27:A:382:A:OP2   | 2.36                     | 0.59              |
| 26:4:15:GLN:HB3 | 26:4:34:VAL:HA   | 1.85                     | 0.59              |
| 27:A:429:A:H2'  | 27:A:430:A:C8    | 2.38                     | 0.59              |
| 27:A:1284:A:H2' | 27:A:1285:G:C8   | 2.38                     | 0.58              |
| 11:R:87:LEU:HA  | 11:R:90:GLU:OE1  | 2.03                     | 0.58              |
| 13:T:36:LYS:NZ  | 27:A:1367:G:N7   | 2.50                     | 0.58              |
| 27:A:1621:C:H2' | 27:A:1622:G:C8   | 2.38                     | 0.58              |
| 12:S:73:PHE:HB3 | 12:S:80:ILE:HD11 | 1.84                     | 0.58              |
| 27:A:2371:G:H2' | 27:A:2372:U:C6   | 2.38                     | 0.58              |
| 27:A:1529:U:H3' | 27:A:1530:G:H8   | 1.69                     | 0.58              |
| 27:A:1556:A:C2  | 27:A:1615:G:N1   | 2.70                     | 0.58              |
| 27:A:1710:A:N6  | 27:A:1716:A:OP2  | 2.36                     | 0.58              |
| 7:M:60:ASP:OD1  | 7:M:60:ASP:N     | 2.37                     | 0.58              |
| 8:N:108:GLU:CD  | 8:N:108:GLU:H    | 2.11                     | 0.58              |
| 27:A:256:A:H2'  | 27:A:257:A:H8    | 1.68                     | 0.58              |
| 27:A:2716:U:H2' | 27:A:2717:U:C6   | 2.39                     | 0.58              |
| 11:R:11:SER:HB2 | 28:B:31:C:H5'    | 1.84                     | 0.58              |
| 26:4:14:VAL:HB  | 26:4:22:PHE:HB3  | 1.83                     | 0.58              |
| 27:A:2113:A:H2' | 27:A:2114:A:C8   | 2.38                     | 0.58              |

*Continued on next page...*

*Continued from previous page...*

| Atom-1           | Atom-2           | Interatomic distance (Å) | Clash overlap (Å) |
|------------------|------------------|--------------------------|-------------------|
| 27:A:2729:G:H2'  | 27:A:2800:G:N1   | 2.19                     | 0.58              |
| 27:A:279:U:H2'   | 27:A:280:G:H8    | 1.69                     | 0.58              |
| 27:A:665:G:N2    | 27:A:2255:A:OP1  | 2.36                     | 0.58              |
| 27:A:1284:A:H2'  | 27:A:1285:G:H8   | 1.67                     | 0.58              |
| 5:I:75:ASN:ND2   | 27:A:2971:G:OP1  | 2.31                     | 0.58              |
| 10:Q:70:ILE:HG22 | 10:Q:72:ASP:H    | 1.69                     | 0.58              |
| 11:R:83:ARG:HH22 | 11:R:87:LEU:HD11 | 1.69                     | 0.58              |
| 27:A:1236:G:H2'  | 27:A:1237:U:O4'  | 2.03                     | 0.58              |
| 27:A:2090:U:O2   | 27:A:2093:G:N2   | 2.37                     | 0.58              |
| 28:B:5:C:OP1     | 28:B:62:C:O2'    | 2.21                     | 0.58              |
| 27:A:265:A:N1    | 27:A:515:U:O2'   | 2.34                     | 0.58              |
| 27:A:639:C:HO2'  | 27:A:640:G:H8    | 1.51                     | 0.58              |
| 27:A:988:U:O2'   | 27:A:990:G:O4'   | 2.22                     | 0.58              |
| 27:A:2351:A:N3   | 27:A:2396:A:O2'  | 2.36                     | 0.58              |
| 27:A:2902:A:H2'  | 27:A:2903:A:C8   | 2.38                     | 0.58              |
| 2:F:44:ARG:NH1   | 27:A:3009:U:OP1  | 2.37                     | 0.57              |
| 5:I:98:GLN:HA    | 5:I:126:VAL:HG11 | 1.86                     | 0.57              |
| 24:7:27:THR:HG23 | 24:7:30:GLY:H    | 1.69                     | 0.57              |
| 25:8:12:LYS:NZ   | 27:A:249:C:O2    | 2.37                     | 0.57              |
| 27:A:1018:U:O2   | 27:A:1019:C:N4   | 2.36                     | 0.57              |
| 27:A:2356:G:H2'  | 27:A:2380:G:H22  | 1.69                     | 0.57              |
| 27:A:256:A:H2'   | 27:A:257:A:C8    | 2.39                     | 0.57              |
| 27:A:738:A:O2'   | 27:A:740:A:OP1   | 2.23                     | 0.57              |
| 27:A:2043:C:O2'  | 27:A:2195:U:OP2  | 2.23                     | 0.57              |
| 6:J:10:GLU:HG3   | 6:J:11:HIS:ND1   | 2.19                     | 0.57              |
| 7:M:45:THR:HG22  | 7:M:47:ASN:H     | 1.69                     | 0.57              |
| 27:A:1529:U:H3'  | 27:A:1530:G:C8   | 2.39                     | 0.57              |
| 27:A:1530:G:H21  | 27:A:1805:G:H22  | 1.51                     | 0.57              |
| 27:A:1533:U:OP2  | 27:A:1535:C:N4   | 2.37                     | 0.57              |
| 27:A:1544:U:O4   | 27:A:1626:G:O6   | 2.22                     | 0.57              |
| 17:X:4:HIS:NE2   | 27:A:81:A:OP1    | 2.38                     | 0.57              |
| 27:A:1468:A:H2'  | 27:A:1469:A:C8   | 2.39                     | 0.57              |
| 27:A:966:U:H2'   | 27:A:967:G:H8    | 1.69                     | 0.57              |
| 27:A:701:A:H2'   | 27:A:702:A:C8    | 2.40                     | 0.57              |
| 27:A:1020:A:H2'  | 27:A:1021:G:C8   | 2.40                     | 0.57              |
| 14:U:25:GLU:OE2  | 27:A:1111:G:N2   | 2.37                     | 0.56              |
| 27:A:2106:A:H3'  | 27:A:2107:G:H5'' | 1.87                     | 0.56              |
| 27:A:2682:G:O2'  | 27:A:2684:U:O4   | 2.23                     | 0.56              |
| 27:A:81:A:N1     | 27:A:96:G:O2'    | 2.36                     | 0.56              |
| 27:A:2070:A:H2'  | 27:A:2071:A:C8   | 2.40                     | 0.56              |
| 27:A:2285:G:N2   | 27:A:2286:A:O2'  | 2.33                     | 0.56              |

*Continued on next page...*

*Continued from previous page...*

| Atom-1           | Atom-2           | Interatomic distance (Å) | Clash overlap (Å) |
|------------------|------------------|--------------------------|-------------------|
| 11:R:58:THR:OG1  | 11:R:59:THR:N    | 2.36                     | 0.56              |
| 27:A:789:G:H2'   | 27:A:919:A:H61   | 1.69                     | 0.56              |
| 27:A:987:A:H2'   | 27:A:988:U:H5'   | 1.87                     | 0.56              |
| 27:A:2482:U:O2'  | 27:A:2651:C:OP2  | 2.23                     | 0.56              |
| 27:A:2515:U:H2'  | 27:A:2516:U:C6   | 2.40                     | 0.56              |
| 27:A:2674:A:N6   | 27:A:2725:C:C2   | 2.68                     | 0.56              |
| 27:A:3022:G:H2'  | 27:A:3023:G:O4'  | 2.06                     | 0.56              |
| 27:A:726:A:H2'   | 27:A:727:A:C8    | 2.40                     | 0.56              |
| 27:A:2403:U:O4   | 27:A:2404:G:N2   | 2.38                     | 0.56              |
| 5:I:104:LEU:HG   | 5:I:106:PHE:HE1  | 1.70                     | 0.56              |
| 27:A:49:A:H2'    | 27:A:50:A:C8     | 2.41                     | 0.56              |
| 27:A:1500:A:O2'  | 27:A:1511:U:O2   | 2.22                     | 0.56              |
| 27:A:1620:U:H2'  | 27:A:1621:C:C6   | 2.41                     | 0.56              |
| 27:A:2729:G:H2'  | 27:A:2800:G:H1   | 1.71                     | 0.56              |
| 27:A:2249:G:H2'  | 27:A:2250:A:C8   | 2.41                     | 0.56              |
| 27:A:1791:A:H2'  | 27:A:1792:A:C8   | 2.40                     | 0.56              |
| 5:I:153:ARG:HE   | 5:I:154:ARG:H    | 1.53                     | 0.56              |
| 14:U:77:LYS:NZ   | 27:A:1110:C:OP1  | 2.38                     | 0.56              |
| 27:A:672:C:H2'   | 27:A:673:C:C6    | 2.41                     | 0.56              |
| 27:A:2883:G:N2   | 27:A:2886:A:OP2  | 2.24                     | 0.56              |
| 22:5:37:ARG:HD3  | 22:5:54:LEU:HD13 | 1.88                     | 0.56              |
| 27:A:2085:C:HO2' | 27:A:2086:U:H6   | 1.54                     | 0.56              |
| 27:A:2384:C:H5'' | 27:A:2387:U:O4   | 2.06                     | 0.56              |
| 1:E:26:ARG:HH22  | 1:E:30:GLU:HG2   | 1.71                     | 0.55              |
| 23:6:17:VAL:O    | 23:6:19:LYS:HG2  | 2.05                     | 0.55              |
| 27:A:502:C:H2'   | 27:A:503:A:C8    | 2.41                     | 0.55              |
| 27:A:1024:A:H2'  | 27:A:1027:C:H5   | 1.71                     | 0.55              |
| 9:O:98:LEU:HD22  | 9:O:103:LEU:HD12 | 1.89                     | 0.55              |
| 26:4:26:SER:OG   | 26:4:27:THR:N    | 2.38                     | 0.55              |
| 27:A:1476:G:H2'  | 27:A:1477:C:C6   | 2.40                     | 0.55              |
| 27:A:1690:A:H2'  | 27:A:1691:A:H8   | 1.71                     | 0.55              |
| 27:A:1758:G:H2'  | 27:A:1759:A:C8   | 2.42                     | 0.55              |
| 4:H:168:THR:OG1  | 4:H:169:ASN:OD1  | 2.24                     | 0.55              |
| 27:A:339:U:H2'   | 27:A:340:A:C8    | 2.42                     | 0.55              |
| 27:A:654:U:H1'   | 27:A:664:A:H1'   | 1.87                     | 0.55              |
| 27:A:857:U:H2'   | 27:A:858:A:H8    | 1.71                     | 0.55              |
| 27:A:1612:U:H2'  | 27:A:1613:G:C8   | 2.41                     | 0.55              |
| 12:S:33:GLU:OE1  | 12:S:36:LYS:NZ   | 2.39                     | 0.55              |
| 27:A:740:A:O2'   | 27:A:741:G:OP2   | 2.22                     | 0.55              |
| 27:A:2671:G:N2   | 27:A:2675:A:N7   | 2.42                     | 0.55              |
| 1:E:108:PRO:HD2  | 1:E:111:LEU:HD22 | 1.88                     | 0.55              |

*Continued on next page...*

*Continued from previous page...*

| Atom-1          | Atom-2           | Interatomic distance (Å) | Clash overlap (Å) |
|-----------------|------------------|--------------------------|-------------------|
| 27:A:2677:A:O2' | 27:A:2796:A:N3   | 2.40                     | 0.55              |
| 27:A:2815:C:H2' | 27:A:2816:G:C8   | 2.42                     | 0.55              |
| 11:R:68:ALA:HA  | 11:R:71:ARG:HB2  | 1.89                     | 0.55              |
| 17:X:94:LYS:NZ  | 27:A:80:G:OP1    | 2.30                     | 0.55              |
| 27:A:1393:C:H2' | 27:A:1394:A:H8   | 1.72                     | 0.55              |
| 5:I:89:GLU:HA   | 5:I:131:LYS:HA   | 1.89                     | 0.55              |
| 7:M:98:THR:HB   | 7:M:124:VAL:HG23 | 1.87                     | 0.55              |
| 11:R:9:ASN:ND2  | 28:B:59:A:N3     | 2.55                     | 0.55              |
| 25:8:34:GLU:HB2 | 27:A:2644:C:OP1  | 2.06                     | 0.55              |
| 27:A:1016:C:H2' | 27:A:1017:G:O4'  | 2.07                     | 0.55              |
| 27:A:1640:A:H2' | 27:A:1642:G:N7   | 2.21                     | 0.55              |
| 27:A:621:U:H2'  | 27:A:622:C:C6    | 2.42                     | 0.55              |
| 27:A:1233:A:H2' | 27:A:1234:U:O4'  | 2.07                     | 0.55              |
| 27:A:2366:C:H2' | 27:A:2367:G:O4'  | 2.06                     | 0.55              |
| 27:A:3014:A:O2' | 27:A:3015:C:H5'' | 2.07                     | 0.55              |
| 15:V:48:GLN:O   | 15:V:51:SER:OG   | 2.25                     | 0.55              |
| 23:6:20:HIS:NE2 | 27:A:2624:C:H5'  | 2.22                     | 0.55              |
| 27:A:681:C:H2'  | 27:A:682:A:C8    | 2.41                     | 0.55              |
| 27:A:2294:A:H2' | 27:A:2295:C:C6   | 2.42                     | 0.55              |
| 27:A:2297:U:H2' | 27:A:2298:U:C6   | 2.42                     | 0.54              |
| 27:A:329:U:O2   | 27:A:446:G:C6    | 2.60                     | 0.54              |
| 27:A:1165:G:O2' | 27:A:1228:A:N6   | 2.31                     | 0.54              |
| 27:A:2510:A:H4' | 27:A:2511:A:O4'  | 2.07                     | 0.54              |
| 4:H:81:ILE:O    | 4:H:86:LEU:N     | 2.39                     | 0.54              |
| 11:R:126:LYS:N  | 11:R:126:LYS:HE2 | 2.22                     | 0.54              |
| 27:A:1804:G:H2' | 27:A:1805:G:C8   | 2.43                     | 0.54              |
| 3:G:71:THR:HB   | 3:G:73:ARG:HG3   | 1.89                     | 0.54              |
| 27:A:1165:G:H4' | 27:A:1166:A:H5'  | 1.88                     | 0.54              |
| 4:H:95:ARG:NH1  | 27:A:2538:A:OP1  | 2.40                     | 0.54              |
| 27:A:2552:A:H2' | 27:A:2553:G:H8   | 1.71                     | 0.54              |
| 27:A:2872:G:H2' | 27:A:2873:U:C6   | 2.43                     | 0.54              |
| 5:I:140:GLN:NE2 | 27:A:2969:C:O2   | 2.41                     | 0.54              |
| 27:A:90:C:H2'   | 27:A:91:C:O4'    | 2.07                     | 0.54              |
| 27:A:639:C:O2'  | 27:A:640:G:H8    | 1.91                     | 0.54              |
| 27:A:928:U:H2'  | 27:A:929:C:C6    | 2.42                     | 0.54              |
| 27:A:1167:C:H1' | 27:A:1231:U:H4'  | 1.90                     | 0.54              |
| 27:A:1551:U:H2' | 27:A:1552:A:O4'  | 2.07                     | 0.54              |
| 3:G:192:ASP:OD1 | 9:O:5:LYS:NZ     | 2.40                     | 0.54              |
| 16:W:19:LYS:NZ  | 27:A:1455:U:OP1  | 2.35                     | 0.54              |
| 27:A:1705:C:H2' | 27:A:1706:A:H8   | 1.71                     | 0.54              |
| 27:A:2386:U:OP1 | 27:A:2394:A:H5'' | 2.07                     | 0.54              |

*Continued on next page...*

*Continued from previous page...*

| Atom-1           | Atom-2           | Interatomic distance (Å) | Clash overlap (Å) |
|------------------|------------------|--------------------------|-------------------|
| 2:F:155:ALA:HB2  | 27:A:2796:A:N7   | 2.23                     | 0.54              |
| 3:G:31:ILE:HD11  | 9:O:4:ILE:HD12   | 1.88                     | 0.54              |
| 27:A:357:U:H4'   | 27:A:358:G:O5'   | 2.08                     | 0.54              |
| 27:A:673:C:H2'   | 27:A:674:U:C6    | 2.43                     | 0.54              |
| 27:A:1717:U:H5'' | 27:A:1718:C:H5   | 1.73                     | 0.54              |
| 5:I:108:LEU:HD11 | 5:I:153:ARG:HB2  | 1.90                     | 0.54              |
| 27:A:2538:A:H2'  | 27:A:2539:G:H8   | 1.72                     | 0.54              |
| 6:J:1:MET:N      | 6:J:21:VAL:O     | 2.40                     | 0.53              |
| 27:A:2344:G:H4'  | 27:A:2391:G:H22  | 1.71                     | 0.53              |
| 27:A:2364:C:H2'  | 27:A:2365:A:H8   | 1.71                     | 0.53              |
| 27:A:326:A:N6    | 27:A:449:G:H1    | 2.06                     | 0.53              |
| 5:I:96:ARG:HH22  | 5:I:98:GLN:HB3   | 1.72                     | 0.53              |
| 16:W:9:ASP:OD1   | 16:W:9:ASP:N     | 2.37                     | 0.53              |
| 27:A:1234:U:H2'  | 27:A:1235:U:H6   | 1.73                     | 0.53              |
| 27:A:3017:C:H2'  | 27:A:3018:U:H6   | 1.72                     | 0.53              |
| 5:I:104:LEU:HD21 | 5:I:132:PHE:HE2  | 1.74                     | 0.53              |
| 26:4:28:LYS:HG3  | 26:4:33:ILE:HD11 | 1.90                     | 0.53              |
| 27:A:750:C:H2'   | 27:A:751:A:C8    | 2.44                     | 0.53              |
| 12:S:1:MET:SD    | 12:S:1:MET:N     | 2.68                     | 0.53              |
| 27:A:277:U:H2'   | 27:A:278:A:C8    | 2.43                     | 0.53              |
| 27:A:3117:U:H2'  | 27:A:3118:U:C6   | 2.44                     | 0.53              |
| 28:B:113:G:H2'   | 28:B:114:A:H8    | 1.73                     | 0.53              |
| 27:A:138:A:H2'   | 27:A:139:U:O2    | 2.09                     | 0.53              |
| 27:A:1509:U:H2'  | 27:A:1510:A:O4'  | 2.08                     | 0.53              |
| 27:A:1630:U:H2'  | 27:A:1631:A:H8   | 1.74                     | 0.53              |
| 27:A:1624:U:O2'  | 27:A:1625:G:N7   | 2.42                     | 0.53              |
| 27:A:3023:G:H2'  | 27:A:3024:A:O4'  | 2.09                     | 0.53              |
| 23:6:39:LYS:HA   | 23:6:50:PRO:HA   | 1.90                     | 0.53              |
| 28:B:37:C:N3     | 28:B:50:C:O2'    | 2.38                     | 0.53              |
| 5:I:119:PRO:HD2  | 5:I:122:ILE:HD11 | 1.91                     | 0.52              |
| 27:A:440:U:H2'   | 27:A:441:G:C8    | 2.44                     | 0.52              |
| 27:A:1809:U:H2'  | 27:A:1810:A:C8   | 2.44                     | 0.52              |
| 27:A:1937:U:H2'  | 27:A:1938:G:O4'  | 2.09                     | 0.52              |
| 27:A:2553:G:H2'  | 27:A:2554:U:C6   | 2.43                     | 0.52              |
| 28:B:10:G:O2'    | 28:B:11:U:OP1    | 2.23                     | 0.52              |
| 16:W:95:LEU:O    | 16:W:95:LEU:HD12 | 2.09                     | 0.52              |
| 18:Z:15:ASP:OD1  | 18:Z:16:SER:N    | 2.42                     | 0.52              |
| 27:A:429:A:H2'   | 27:A:430:A:H8    | 1.74                     | 0.52              |
| 27:A:691:U:H2'   | 27:A:692:C:C6    | 2.45                     | 0.52              |
| 27:A:2385:G:OP2  | 27:A:2387:U:N3   | 2.41                     | 0.52              |
| 2:F:27:THR:OG1   | 2:F:196:GLY:O    | 2.25                     | 0.52              |

*Continued on next page...*

*Continued from previous page...*

| Atom-1           | Atom-2           | Interatomic distance (Å) | Clash overlap (Å) |
|------------------|------------------|--------------------------|-------------------|
| 11:R:56:ASN:HB3  | 11:R:58:THR:HG22 | 1.91                     | 0.52              |
| 12:S:36:LYS:HD2  | 12:S:36:LYS:C    | 2.34                     | 0.52              |
| 27:A:502:C:H2'   | 27:A:503:A:H8    | 1.75                     | 0.52              |
| 27:A:736:G:N2    | 27:A:739:U:OP2   | 2.34                     | 0.52              |
| 8:N:17:LYS:HE3   | 8:N:47:ILE:HG13  | 1.90                     | 0.52              |
| 18:Z:32:LYS:HB3  | 27:A:759:G:C6    | 2.45                     | 0.52              |
| 27:A:190:A:H2'   | 27:A:191:G:N3    | 2.25                     | 0.52              |
| 27:A:356:G:H5''  | 27:A:357:U:OP1   | 2.10                     | 0.52              |
| 27:A:1675:U:O2'  | 27:A:1676:G:N7   | 2.40                     | 0.52              |
| 8:N:30:ARG:HG3   | 27:A:2898:G:H4'  | 1.90                     | 0.52              |
| 27:A:273:A:H62   | 27:A:313:G:H21   | 1.57                     | 0.52              |
| 27:A:663:A:C5    | 27:A:2254:A:C6   | 2.98                     | 0.52              |
| 27:A:1025:A:N3   | 27:A:2488:C:O2'  | 2.40                     | 0.52              |
| 27:A:1556:A:N1   | 27:A:1615:G:C6   | 2.77                     | 0.52              |
| 27:A:363:A:H2'   | 27:A:364:A:O4'   | 2.10                     | 0.52              |
| 27:A:1534:C:H3'  | 27:A:1535:C:O2   | 2.10                     | 0.52              |
| 27:A:2088:C:H2'  | 27:A:2089:C:C5   | 2.45                     | 0.52              |
| 27:A:2363:A:N6   | 27:A:2375:G:O6   | 2.43                     | 0.52              |
| 27:A:2759:G:H2'  | 27:A:2760:G:H8   | 1.73                     | 0.52              |
| 27:A:2815:C:H2'  | 27:A:2816:G:H8   | 1.75                     | 0.52              |
| 11:R:4:LYS:HA    | 11:R:4:LYS:HE2   | 1.92                     | 0.52              |
| 22:5:14:ARG:HB3  | 27:A:13:G:H5''   | 1.92                     | 0.52              |
| 27:A:750:C:H2'   | 27:A:751:A:H8    | 1.75                     | 0.52              |
| 27:A:2329:G:O6   | 27:A:2406:U:O4   | 2.27                     | 0.52              |
| 11:R:14:ARG:NH1  | 28:B:48:C:OP2    | 2.43                     | 0.51              |
| 26:4:15:GLN:NE2  | 26:4:16:CYS:O    | 2.43                     | 0.51              |
| 27:A:334:G:N2    | 27:A:347:U:O2    | 2.30                     | 0.51              |
| 27:A:529:U:H2'   | 27:A:530:G:C8    | 2.45                     | 0.51              |
| 27:A:2248:C:H2'  | 27:A:2249:G:H8   | 1.73                     | 0.51              |
| 27:A:2465:A:H2'  | 27:A:2466:G:C8   | 2.45                     | 0.51              |
| 27:A:2622:C:H2'  | 27:A:2623:A:H8   | 1.76                     | 0.51              |
| 12:S:2:ASN:O     | 12:S:5:ASP:N     | 2.43                     | 0.51              |
| 27:A:818:U:H2'   | 27:A:819:G:O4'   | 2.11                     | 0.51              |
| 27:A:150:C:H2'   | 27:A:151:A:H8    | 1.75                     | 0.51              |
| 27:A:680:U:H2'   | 27:A:681:C:C6    | 2.46                     | 0.51              |
| 27:A:1656:A:H2'  | 27:A:1657:G:C8   | 2.45                     | 0.51              |
| 23:6:24:ILE:HG13 | 25:8:34:GLU:HG2  | 1.92                     | 0.51              |
| 27:A:293:G:H2'   | 27:A:294:G:C8    | 2.45                     | 0.51              |
| 27:A:3018:U:C2   | 27:A:3019:C:C5   | 2.99                     | 0.51              |
| 4:H:44:ASN:ND2   | 27:A:2537:C:O4'  | 2.44                     | 0.51              |
| 27:A:2096:G:H2'  | 27:A:2097:G:H8   | 1.75                     | 0.51              |

*Continued on next page...*

*Continued from previous page...*

| Atom-1          | Atom-2           | Interatomic distance (Å) | Clash overlap (Å) |
|-----------------|------------------|--------------------------|-------------------|
| 2:F:129:ARG:HA  | 2:F:170:MET:SD   | 2.50                     | 0.51              |
| 13:T:73:ASP:O   | 13:T:114:ARG:NH1 | 2.44                     | 0.51              |
| 27:A:451:U:H2'  | 27:A:452:G:C8    | 2.44                     | 0.51              |
| 27:A:1561:C:H42 | 27:A:1610:C:H42  | 1.58                     | 0.51              |
| 27:A:2330:U:H3' | 27:A:2331:U:C6   | 2.46                     | 0.51              |
| 2:F:56:GLU:HA   | 2:F:56:GLU:OE2   | 2.10                     | 0.51              |
| 2:F:85:ARG:NH2  | 27:A:2862:G:OP1  | 2.32                     | 0.51              |
| 5:I:118:ALA:HB2 | 5:I:124:PHE:CE2  | 2.46                     | 0.51              |
| 27:A:388:U:H2'  | 27:A:389:G:O4'   | 2.11                     | 0.51              |
| 27:A:844:G:H4'  | 27:A:878:G:H5'   | 1.93                     | 0.51              |
| 27:A:1244:A:H4' | 27:A:1245:U:O4'  | 2.11                     | 0.51              |
| 27:A:2340:A:H61 | 27:A:2394:A:H61  | 1.58                     | 0.51              |
| 4:H:126:PRO:O   | 4:H:174:ARG:NH1  | 2.38                     | 0.51              |
| 14:U:47:ASN:OD1 | 14:U:47:ASN:N    | 2.40                     | 0.51              |
| 27:A:293:G:H2'  | 27:A:294:G:H8    | 1.76                     | 0.51              |
| 27:A:3017:C:H2' | 27:A:3018:U:C6   | 2.46                     | 0.51              |
| 11:R:42:ARG:HG3 | 11:R:47:ILE:HD12 | 1.93                     | 0.51              |
| 27:A:736:G:N2   | 27:A:738:A:H3'   | 2.26                     | 0.51              |
| 27:A:1020:A:H2' | 27:A:1021:G:H8   | 1.76                     | 0.51              |
| 27:A:1541:G:H2' | 27:A:1542:A:H8   | 1.75                     | 0.51              |
| 27:A:1808:A:H2' | 27:A:1809:U:H6   | 1.75                     | 0.51              |
| 27:A:2238:A:H2' | 27:A:2239:A:C8   | 2.46                     | 0.51              |
| 5:I:98:GLN:NE2  | 5:I:105:GLU:HB3  | 2.25                     | 0.51              |
| 5:I:99:LEU:HA   | 5:I:104:LEU:HD12 | 1.93                     | 0.51              |
| 14:U:27:LEU:H   | 14:U:95:THR:HG21 | 1.75                     | 0.51              |
| 19:1:45:ASN:OD1 | 19:1:45:ASN:N    | 2.39                     | 0.51              |
| 24:7:42:ARG:NH2 | 27:A:556:G:N7    | 2.43                     | 0.51              |
| 27:A:165:U:H2'  | 27:A:166:A:C8    | 2.46                     | 0.51              |
| 27:A:737:A:N1   | 27:A:2593:A:O2'  | 2.41                     | 0.51              |
| 27:A:1900:C:H2' | 27:A:1901:C:C6   | 2.46                     | 0.51              |
| 11:R:41:ASN:ND2 | 28:B:7:G:O3'     | 2.43                     | 0.50              |
| 27:A:736:G:H1'  | 27:A:740:A:N6    | 2.26                     | 0.50              |
| 27:A:1403:C:H5  | 27:A:1441:C:N3   | 2.10                     | 0.50              |
| 27:A:1547:G:N2  | 27:A:1623:U:O2   | 2.32                     | 0.50              |
| 27:A:979:G:H2'  | 27:A:980:C:C6    | 2.46                     | 0.50              |
| 27:A:3116:C:H2' | 27:A:3117:U:H6   | 1.76                     | 0.50              |
| 5:I:58:ASP:O    | 5:I:63:ARG:NH1   | 2.44                     | 0.50              |
| 27:A:1393:C:H2' | 27:A:1394:A:C8   | 2.47                     | 0.50              |
| 27:A:1541:G:H1  | 27:A:1631:A:N6   | 2.09                     | 0.50              |
| 2:F:154:CYS:HB2 | 27:A:2799:C:H5'  | 1.92                     | 0.50              |
| 27:A:2:A:H2'    | 27:A:3:A:C8      | 2.47                     | 0.50              |

*Continued on next page...*

*Continued from previous page...*

| Atom-1           | Atom-2           | Interatomic distance (Å) | Clash overlap (Å) |
|------------------|------------------|--------------------------|-------------------|
| 27:A:32:G:H1'    | 27:A:542:A:C4    | 2.47                     | 0.50              |
| 27:A:3018:U:H2'  | 27:A:3019:C:C6   | 2.47                     | 0.50              |
| 27:A:453:U:H2'   | 27:A:454:U:C5    | 2.47                     | 0.50              |
| 27:A:2378:U:H2'  | 27:A:2379:G:H8   | 1.77                     | 0.50              |
| 27:A:499:G:OP2   | 27:A:2630:A:O2'  | 2.29                     | 0.50              |
| 27:A:1001:C:C5   | 27:A:1002:C:H1'  | 2.47                     | 0.50              |
| 27:A:1790:A:H2'  | 27:A:1791:A:C8   | 2.45                     | 0.50              |
| 27:A:2791:G:H2'  | 27:A:2792:C:C6   | 2.47                     | 0.50              |
| 2:F:59:PRO:O     | 2:F:62:VAL:HG22  | 2.12                     | 0.50              |
| 27:A:987:A:H2    | 27:A:1021:G:H22  | 1.58                     | 0.50              |
| 27:A:1633:U:H2'  | 27:A:1634:C:C6   | 2.47                     | 0.50              |
| 27:A:2686:U:H2'  | 27:A:2687:U:C6   | 2.46                     | 0.50              |
| 28:B:50:C:H2'    | 28:B:51:G:H8     | 1.77                     | 0.50              |
| 5:I:87:LYS:NZ    | 5:I:89:GLU:HB3   | 2.27                     | 0.50              |
| 27:A:310:C:H2'   | 27:A:311:G:C8    | 2.47                     | 0.50              |
| 27:A:665:G:H22   | 27:A:2255:A:P    | 2.35                     | 0.50              |
| 13:T:119:GLU:OE1 | 13:T:119:GLU:N   | 2.38                     | 0.50              |
| 27:A:139:U:H2'   | 27:A:140:G:O4'   | 2.11                     | 0.50              |
| 27:A:1165:G:HO2' | 27:A:1228:A:H61  | 1.58                     | 0.50              |
| 27:A:2457:U:H2'  | 27:A:2458:G:C8   | 2.47                     | 0.50              |
| 5:I:45:ARG:HA    | 5:I:51:ILE:HG22  | 1.93                     | 0.49              |
| 17:X:2:LYS:O     | 17:X:96:ARG:NH1  | 2.40                     | 0.49              |
| 27:A:1229:A:C8   | 27:A:1230:G:H1'  | 2.45                     | 0.49              |
| 27:A:1756:G:H1'  | 27:A:1758:G:C6   | 2.47                     | 0.49              |
| 27:A:2497:A:H2'  | 27:A:2498:A:C8   | 2.47                     | 0.49              |
| 5:I:81:THR:OG1   | 5:I:82:GLU:OE1   | 2.31                     | 0.49              |
| 21:3:37:ARG:HH22 | 27:A:1043:G:H4'  | 1.77                     | 0.49              |
| 27:A:1288:A:H2'  | 27:A:1289:A:C8   | 2.47                     | 0.49              |
| 27:A:1808:A:H2'  | 27:A:1809:U:C6   | 2.46                     | 0.49              |
| 27:A:2569:G:N3   | 27:A:2605:C:H2'  | 2.27                     | 0.49              |
| 7:M:25:LEU:HA    | 7:M:62:ILE:HD11  | 1.94                     | 0.49              |
| 27:A:929:C:H2'   | 27:A:930:C:H6    | 1.76                     | 0.49              |
| 9:O:90:GLY:HA2   | 9:O:122:VAL:HG22 | 1.94                     | 0.49              |
| 27:A:728:G:H2'   | 27:A:729:C:C6    | 2.47                     | 0.49              |
| 27:A:1446:C:H2'  | 27:A:1448:C:C5   | 2.48                     | 0.49              |
| 27:A:1647:G:OP2  | 27:A:1648:A:O2'  | 2.30                     | 0.49              |
| 27:A:1758:G:H2'  | 27:A:1759:A:H8   | 1.76                     | 0.49              |
| 28:B:10:G:O2'    | 28:B:11:U:H5'    | 2.12                     | 0.49              |
| 27:A:795:G:H2'   | 27:A:796:A:C8    | 2.47                     | 0.49              |
| 27:A:877:U:H4'   | 27:A:878:G:O5'   | 2.13                     | 0.49              |
| 27:A:1002:C:H2'  | 27:A:1003:A:H3'  | 1.93                     | 0.49              |

*Continued on next page...*

*Continued from previous page...*

| Atom-1           | Atom-2           | Interatomic distance (Å) | Clash overlap (Å) |
|------------------|------------------|--------------------------|-------------------|
| 27:A:2344:G:H2'  | 27:A:2345:U:C6   | 2.47                     | 0.49              |
| 27:A:2374:U:H2'  | 27:A:2375:G:H8   | 1.77                     | 0.49              |
| 23:6:8:ARG:N     | 23:6:9:PRO:HD3   | 2.28                     | 0.49              |
| 27:A:271:A:OP2   | 27:A:314:G:N2    | 2.39                     | 0.49              |
| 27:A:619:C:H4'   | 27:A:620:G:C8    | 2.47                     | 0.49              |
| 27:A:665:G:O2'   | 27:A:666:A:O5'   | 2.28                     | 0.49              |
| 27:A:1446:C:H2'  | 27:A:1448:C:H5   | 1.76                     | 0.49              |
| 27:A:277:U:H2'   | 27:A:278:A:H8    | 1.77                     | 0.49              |
| 27:A:543:U:H3'   | 27:A:544:U:C5'   | 2.43                     | 0.49              |
| 27:A:1704:U:H2'  | 27:A:1705:C:C6   | 2.48                     | 0.49              |
| 27:A:2381:A:H4'  | 27:A:2382:G:O5'  | 2.11                     | 0.49              |
| 27:A:2538:A:H2'  | 27:A:2539:G:C8   | 2.48                     | 0.49              |
| 27:A:3078:G:N2   | 27:A:3081:A:OP2  | 2.33                     | 0.49              |
| 2:F:153:GLY:O    | 27:A:2276:G:H4'  | 2.13                     | 0.49              |
| 5:I:104:LEU:HB3  | 5:I:116:ILE:HB   | 1.95                     | 0.49              |
| 6:J:9:VAL:HG12   | 6:J:12:LEU:HB2   | 1.95                     | 0.49              |
| 27:A:479:A:H1'   | 27:A:499:G:O4'   | 2.13                     | 0.49              |
| 27:A:1415:A:H4'  | 27:A:1416:A:H5'  | 1.94                     | 0.49              |
| 27:A:1537:U:H2'  | 27:A:1538:G:C8   | 2.47                     | 0.49              |
| 2:F:156:THR:HB   | 27:A:2795:C:O2'  | 2.13                     | 0.49              |
| 9:O:121:LYS:HZ1  | 9:O:123:ASP:CG   | 2.21                     | 0.49              |
| 13:T:77:ASN:OD1  | 13:T:78:ARG:N    | 2.46                     | 0.49              |
| 25:8:31:HIS:NE2  | 27:A:2616:A:OP2  | 2.25                     | 0.49              |
| 27:A:2086:U:H2'  | 27:A:2087:C:C6   | 2.48                     | 0.49              |
| 27:A:3055:G:H2'  | 27:A:3100:A:H61  | 1.77                     | 0.49              |
| 27:A:3057:U:H2'  | 27:A:3058:A:C8   | 2.48                     | 0.49              |
| 27:A:160:A:OP2   | 27:A:161:U:O2'   | 2.23                     | 0.49              |
| 4:H:80:SER:HB3   | 4:H:88:GLU:HG2   | 1.95                     | 0.48              |
| 7:M:88:THR:OG1   | 7:M:91:GLU:OE1   | 2.31                     | 0.48              |
| 9:O:44:LYS:NZ    | 27:A:919:A:OP1   | 2.46                     | 0.48              |
| 23:6:6:ASP:C     | 23:6:29:ARG:HH11 | 2.20                     | 0.48              |
| 27:A:1091:A:H5'  | 27:A:1303:U:H1'  | 1.95                     | 0.48              |
| 27:A:1710:A:H61  | 27:A:1716:A:H5'' | 1.78                     | 0.48              |
| 1:E:37:LEU:HD13  | 1:E:62:TYR:HB2   | 1.96                     | 0.48              |
| 10:Q:106:ASP:OD2 | 27:A:1867:G:O2'  | 2.21                     | 0.48              |
| 25:8:45:ASP:OD1  | 25:8:46:GLY:N    | 2.46                     | 0.48              |
| 27:A:301:U:C2    | 27:A:338:C:H5'   | 2.47                     | 0.48              |
| 27:A:601:A:H2'   | 27:A:602:A:C8    | 2.48                     | 0.48              |
| 27:A:2170:U:H2'  | 27:A:2171:C:C6   | 2.47                     | 0.48              |
| 27:A:2325:U:H2'  | 27:A:2326:A:H8   | 1.78                     | 0.48              |
| 27:A:2548:U:H5'' | 27:A:2549:G:H5'' | 1.94                     | 0.48              |

*Continued on next page...*

*Continued from previous page...*

| Atom-1           | Atom-2           | Interatomic distance (Å) | Clash overlap (Å) |
|------------------|------------------|--------------------------|-------------------|
| 27:A:2777:G:C2   | 27:A:2807:G:H1'  | 2.47                     | 0.48              |
| 1:E:123:ALA:HB3  | 1:E:131:LEU:HD22 | 1.96                     | 0.48              |
| 17:X:7:ASP:OD2   | 17:X:96:ARG:NH2  | 2.46                     | 0.48              |
| 27:A:997:G:H2'   | 27:A:998:G:H8    | 1.77                     | 0.48              |
| 27:A:1013:U:N3   | 27:A:1014:G:H1'  | 2.28                     | 0.48              |
| 27:A:2253:A:C5   | 27:A:2255:A:H5'  | 2.49                     | 0.48              |
| 28:B:63:U:H2'    | 28:B:64:G:H8     | 1.79                     | 0.48              |
| 16:W:10:ILE:HG22 | 16:W:11:ILE:HD12 | 1.94                     | 0.48              |
| 26:4:12:THR:N    | 26:4:24:THR:O    | 2.34                     | 0.48              |
| 27:A:2094:G:O2'  | 27:A:2095:G:H8   | 1.95                     | 0.48              |
| 27:A:2922:U:H2'  | 27:A:2923:C:C6   | 2.48                     | 0.48              |
| 3:G:137:SER:O    | 3:G:168:SER:OG   | 2.32                     | 0.48              |
| 10:Q:8:PRO:HG2   | 27:A:1870:U:C4   | 2.48                     | 0.48              |
| 11:R:55:LEU:HD12 | 11:R:55:LEU:H    | 1.77                     | 0.48              |
| 13:T:31:LEU:HD22 | 27:A:673:C:H5'   | 1.96                     | 0.48              |
| 27:A:298:G:H2'   | 27:A:299:G:C4    | 2.47                     | 0.48              |
| 27:A:1651:C:H2'  | 27:A:1652:A:C8   | 2.49                     | 0.48              |
| 27:A:1673:A:H5'' | 27:A:1674:G:H5'' | 1.95                     | 0.48              |
| 27:A:1791:A:H2'  | 27:A:1792:A:H8   | 1.79                     | 0.48              |
| 27:A:2145:C:H2'  | 27:A:2146:A:H8   | 1.77                     | 0.48              |
| 27:A:2147:U:H2'  | 27:A:2148:C:C6   | 2.47                     | 0.48              |
| 28:B:4:A:H4'     | 28:B:63:U:H4'    | 1.95                     | 0.48              |
| 14:U:67:HIS:ND1  | 14:U:95:THR:HG22 | 2.29                     | 0.48              |
| 27:A:487:U:H2'   | 27:A:488:G:O4'   | 2.14                     | 0.48              |
| 27:A:672:C:H2'   | 27:A:673:C:H6    | 1.78                     | 0.48              |
| 27:A:1533:U:H5'' | 27:A:1535:C:H42  | 1.77                     | 0.48              |
| 27:A:1679:A:H4'  | 27:A:1679:A:OP1  | 2.14                     | 0.48              |
| 28:B:15:U:OP2    | 28:B:71:C:O2'    | 2.30                     | 0.48              |
| 19:1:2:ALA:HB2   | 27:A:1479:G:OP1  | 2.14                     | 0.48              |
| 20:2:14:THR:OG1  | 20:2:15:ASP:N    | 2.47                     | 0.48              |
| 27:A:2096:G:H2'  | 27:A:2097:G:C8   | 2.48                     | 0.48              |
| 27:A:2248:C:H2'  | 27:A:2249:G:C8   | 2.48                     | 0.48              |
| 27:A:2342:A:H61  | 27:A:2390:U:H1'  | 1.77                     | 0.48              |
| 27:A:2759:G:N3   | 27:A:2760:G:C8   | 2.82                     | 0.48              |
| 27:A:2936:C:OP1  | 27:A:2938:G:H4'  | 2.13                     | 0.48              |
| 25:8:47:ARG:NH2  | 27:A:724:G:OP1   | 2.46                     | 0.48              |
| 27:A:222:A:O2'   | 27:A:508:G:N3    | 2.45                     | 0.48              |
| 27:A:1223:U:H2'  | 27:A:1224:G:H8   | 1.78                     | 0.48              |
| 27:A:1535:C:H2'  | 27:A:1536:A:O4'  | 2.14                     | 0.48              |
| 27:A:1612:U:H2'  | 27:A:1613:G:H8   | 1.79                     | 0.48              |
| 27:A:2467:U:H2'  | 27:A:2468:U:C6   | 2.49                     | 0.48              |

*Continued on next page...*

*Continued from previous page...*

| Atom-1           | Atom-2            | Interatomic distance (Å) | Clash overlap (Å) |
|------------------|-------------------|--------------------------|-------------------|
| 1:E:155:LEU:HD13 | 1:E:177:MET:HE1   | 1.96                     | 0.48              |
| 4:H:155:ARG:HH12 | 4:H:157:ARG:NH1   | 2.12                     | 0.48              |
| 8:N:24:VAL:HG13  | 8:N:33:ALA:HB2    | 1.96                     | 0.48              |
| 12:S:51:GLY:HA2  | 12:S:56:GLU:CD    | 2.39                     | 0.48              |
| 26:4:13:THR:HA   | 26:4:22:PHE:O     | 2.14                     | 0.48              |
| 27:A:772:U:H2'   | 27:A:773:G:C8     | 2.49                     | 0.48              |
| 27:A:1314:C:H2'  | 27:A:1315:C:H6    | 1.78                     | 0.48              |
| 27:A:2738:U:H2'  | 27:A:2739:C:C6    | 2.49                     | 0.48              |
| 27:A:2778:U:H2'  | 27:A:2779:U:C6    | 2.49                     | 0.48              |
| 27:A:2781:G:H2'  | 27:A:2782:C:C6    | 2.49                     | 0.48              |
| 1:E:200:GLU:OE1  | 1:E:200:GLU:N     | 2.38                     | 0.48              |
| 13:T:108:ALA:O   | 13:T:112:VAL:HG13 | 2.12                     | 0.48              |
| 27:A:1012:C:H2'  | 27:A:1013:U:H5'   | 1.95                     | 0.48              |
| 27:A:1996:U:OP2  | 27:A:2001:A:N6    | 2.37                     | 0.48              |
| 27:A:2098:U:H2'  | 27:A:2099:G:O4'   | 2.13                     | 0.48              |
| 4:H:81:ILE:HG22  | 4:H:86:LEU:HB3    | 1.96                     | 0.47              |
| 5:I:68:LEU:HD21  | 27:A:2982:A:C4    | 2.49                     | 0.47              |
| 17:X:88:ASP:OD1  | 17:X:93:LYS:N     | 2.47                     | 0.47              |
| 27:A:356:G:H4'   | 27:A:358:G:C4     | 2.49                     | 0.47              |
| 27:A:1296:G:H2'  | 27:A:1297:G:C8    | 2.49                     | 0.47              |
| 27:A:2279:C:N4   | 27:A:2724:U:H1'   | 2.28                     | 0.47              |
| 27:A:2752:U:O2'  | 27:A:2754:G:OP1   | 2.23                     | 0.47              |
| 1:E:141:VAL:HG13 | 1:E:162:SER:HB2   | 1.96                     | 0.47              |
| 16:W:10:ILE:HD12 | 16:W:37:SER:HB3   | 1.96                     | 0.47              |
| 23:6:16:GLU:OE1  | 23:6:50:PRO:HB2   | 2.14                     | 0.47              |
| 23:6:27:LYS:NZ   | 23:6:32:ASP:O     | 2.47                     | 0.47              |
| 27:A:483:G:H2'   | 27:A:484:C:C6     | 2.49                     | 0.47              |
| 27:A:860:G:O2'   | 27:A:863:G:O2'    | 2.07                     | 0.47              |
| 27:A:974:G:H4'   | 27:A:975:U:O5'    | 2.14                     | 0.47              |
| 27:A:2758:A:H2'  | 27:A:2759:G:O4'   | 2.13                     | 0.47              |
| 27:A:453:U:H2'   | 27:A:454:U:C6     | 2.49                     | 0.47              |
| 27:A:1501:C:H2'  | 27:A:1502:G:C8    | 2.50                     | 0.47              |
| 20:2:6:THR:HG23  | 20:2:9:GLU:OE2    | 2.15                     | 0.47              |
| 27:A:165:U:H2'   | 27:A:166:A:H8     | 1.80                     | 0.47              |
| 27:A:659:U:H3    | 27:A:663:A:H2     | 1.62                     | 0.47              |
| 27:A:1003:A:H2'  | 27:A:1003:A:OP1   | 2.14                     | 0.47              |
| 27:A:1024:A:H2'  | 27:A:1027:C:C5    | 2.50                     | 0.47              |
| 27:A:1337:G:N2   | 27:A:1340:A:OP2   | 2.38                     | 0.47              |
| 27:A:1659:U:H2'  | 27:A:1660:A:H8    | 1.79                     | 0.47              |
| 27:A:2340:A:N6   | 27:A:2394:A:H61   | 2.13                     | 0.47              |
| 27:A:2819:G:N2   | 27:A:2822:A:OP2   | 2.37                     | 0.47              |

*Continued on next page...*

*Continued from previous page...*

| Atom-1           | Atom-2            | Interatomic distance (Å) | Clash overlap (Å) |
|------------------|-------------------|--------------------------|-------------------|
| 14:U:26:LYS:NZ   | 27:A:1282:G:OP1   | 2.48                     | 0.47              |
| 21:3:23:LEU:HD22 | 21:3:28:LEU:HD11  | 1.97                     | 0.47              |
| 27:A:306:U:H2'   | 27:A:307:G:H8     | 1.80                     | 0.47              |
| 27:A:460:G:O2'   | 27:A:488:G:O6     | 2.33                     | 0.47              |
| 27:A:655:G:H22   | 27:A:670:A:H2     | 1.61                     | 0.47              |
| 27:A:2086:U:O4   | 27:A:2096:G:O6    | 2.31                     | 0.47              |
| 4:H:36:PRO:HA    | 4:H:166:THR:HB    | 1.96                     | 0.47              |
| 5:I:132:PHE:HZ   | 5:I:149:ILE:HG21  | 1.79                     | 0.47              |
| 27:A:1234:U:H2'  | 27:A:1235:U:C6    | 2.50                     | 0.47              |
| 27:A:1343:G:H2'  | 27:A:1345:G:C8    | 2.50                     | 0.47              |
| 27:A:1885:G:O2'  | 27:A:2215:U:O4    | 2.25                     | 0.47              |
| 27:A:2375:G:H2'  | 27:A:2376:G:C8    | 2.50                     | 0.47              |
| 1:E:31:LYS:NZ    | 27:A:1647:G:N7    | 2.57                     | 0.47              |
| 3:G:131:VAL:HG12 | 3:G:140:SER:HB2   | 1.95                     | 0.47              |
| 11:R:62:ALA:O    | 11:R:91:ARG:NH1   | 2.48                     | 0.47              |
| 11:R:81:SER:HB2  | 11:R:116:LEU:HB3  | 1.96                     | 0.47              |
| 15:V:23:LYS:NZ   | 27:A:2236:G:N7    | 2.62                     | 0.47              |
| 15:V:52:GLU:HB2  | 15:V:53:PRO:HD3   | 1.96                     | 0.47              |
| 24:7:40:LYS:NZ   | 27:A:557:G:O6     | 2.39                     | 0.47              |
| 27:A:994:A:OP2   | 27:A:1014:G:N2    | 2.41                     | 0.47              |
| 27:A:1614:G:H2'  | 27:A:1615:G:H8    | 1.79                     | 0.47              |
| 28:B:46:A:C4     | 28:B:47:A:C8      | 3.02                     | 0.47              |
| 5:I:59:GLU:OE1   | 5:I:61:ARG:HB2    | 2.15                     | 0.47              |
| 5:I:87:LYS:HZ3   | 5:I:89:GLU:HB3    | 1.80                     | 0.47              |
| 23:6:19:LYS:CG   | 23:6:45:CYS:SG    | 3.02                     | 0.47              |
| 10:Q:95:THR:HG22 | 10:Q:115:LEU:HD23 | 1.97                     | 0.47              |
| 12:S:13:ARG:NH1  | 12:S:80:ILE:O     | 2.44                     | 0.47              |
| 13:T:12:LYS:NZ   | 27:A:1342:C:OP1   | 2.31                     | 0.47              |
| 21:3:39:ASP:OD1  | 21:3:44:ARG:HD3   | 2.15                     | 0.47              |
| 27:A:49:A:H2'    | 27:A:50:A:H8      | 1.77                     | 0.47              |
| 27:A:181:A:H2'   | 27:A:182:C:H6     | 1.80                     | 0.47              |
| 27:A:1554:U:H2'  | 27:A:1555:A:H8    | 1.78                     | 0.47              |
| 27:A:2351:A:H2'  | 27:A:2352:C:C6    | 2.50                     | 0.47              |
| 27:A:2761:U:H2'  | 27:A:2762:C:H6    | 1.78                     | 0.47              |
| 27:A:3030:A:H2'  | 27:A:3031:A:C8    | 2.50                     | 0.47              |
| 3:G:70:GLY:N     | 27:A:2284:A:OP1   | 2.48                     | 0.47              |
| 15:V:8:PRO:HG2   | 15:V:116:SER:HB2  | 1.97                     | 0.47              |
| 27:A:1314:C:H2'  | 27:A:1315:C:C6    | 2.50                     | 0.47              |
| 27:A:2107:G:H4'  | 27:A:2107:G:OP1   | 2.14                     | 0.47              |
| 27:A:2190:A:N3   | 27:A:2816:G:O2'   | 2.46                     | 0.47              |
| 7:M:72:LYS:NZ    | 27:A:1257:G:H5''  | 2.30                     | 0.46              |

*Continued on next page...*

*Continued from previous page...*

| Atom-1           | Atom-2           | Interatomic distance (Å) | Clash overlap (Å) |
|------------------|------------------|--------------------------|-------------------|
| 27:A:9:U:O2      | 27:A:2850:C:H4'  | 2.16                     | 0.46              |
| 27:A:678:A:N1    | 27:A:924:G:O2'   | 2.43                     | 0.46              |
| 27:A:688:A:H2'   | 27:A:689:U:C6    | 2.51                     | 0.46              |
| 27:A:998:G:H22   | 27:A:1010:U:H3   | 1.63                     | 0.46              |
| 27:A:1533:U:O2   | 27:A:1803:A:O2'  | 2.23                     | 0.46              |
| 27:A:2029:A:H2'  | 27:A:2030:C:C6   | 2.50                     | 0.46              |
| 27:A:2288:C:H2'  | 27:A:2289:C:H6   | 1.80                     | 0.46              |
| 27:A:3118:U:H2'  | 27:A:3119:A:C8   | 2.51                     | 0.46              |
| 4:H:145:PHE:CE2  | 4:H:159:MET:HE1  | 2.50                     | 0.46              |
| 5:I:87:LYS:HD2   | 5:I:88:MET:N     | 2.30                     | 0.46              |
| 19:1:36:VAL:HG13 | 19:1:63:ARG:HE   | 1.80                     | 0.46              |
| 23:6:34:ASP:OD1  | 23:6:34:ASP:N    | 2.48                     | 0.46              |
| 27:A:666:A:H1'   | 27:A:2256:G:H8   | 1.79                     | 0.46              |
| 27:A:1002:C:H2'  | 27:A:1003:A:H5'' | 1.96                     | 0.46              |
| 27:A:1259:U:O2   | 27:A:1261:A:N6   | 2.48                     | 0.46              |
| 5:I:77:VAL:HA    | 5:I:80:VAL:HG22  | 1.98                     | 0.46              |
| 27:A:1435:C:C5   | 27:A:1444:U:H5'' | 2.50                     | 0.46              |
| 27:A:1536:A:H2'  | 27:A:1537:U:C6   | 2.50                     | 0.46              |
| 27:A:1537:U:H2'  | 27:A:1538:G:H8   | 1.80                     | 0.46              |
| 27:A:1963:G:H2'  | 27:A:1964:U:C6   | 2.51                     | 0.46              |
| 17:X:45:THR:N    | 17:X:58:GLY:O    | 2.44                     | 0.46              |
| 23:6:20:HIS:CE1  | 27:A:2624:C:H5'' | 2.50                     | 0.46              |
| 27:A:4:G:H2'     | 27:A:5:U:C6      | 2.51                     | 0.46              |
| 27:A:986:G:C2    | 27:A:987:A:H1'   | 2.48                     | 0.46              |
| 27:A:1087:G:H2'  | 27:A:1088:U:C6   | 2.50                     | 0.46              |
| 27:A:1809:U:H2'  | 27:A:1810:A:H8   | 1.79                     | 0.46              |
| 27:A:2532:G:O2'  | 27:A:2534:A:N7   | 2.44                     | 0.46              |
| 27:A:2712:U:H2'  | 27:A:2713:G:C8   | 2.50                     | 0.46              |
| 27:A:2760:G:H2'  | 27:A:2761:U:O4'  | 2.15                     | 0.46              |
| 27:A:289:A:N7    | 27:A:299:G:N1    | 2.63                     | 0.46              |
| 27:A:1650:G:H2'  | 27:A:1651:C:C6   | 2.50                     | 0.46              |
| 27:A:2523:A:H2'  | 27:A:2524:C:H6   | 1.80                     | 0.46              |
| 2:F:60:ARG:HH22  | 27:A:3052:A:P    | 2.37                     | 0.46              |
| 14:U:12:LYS:NZ   | 27:A:1112:C:O2   | 2.47                     | 0.46              |
| 18:Z:41:ARG:NE   | 18:Z:41:ARG:HA   | 2.31                     | 0.46              |
| 23:6:8:ARG:O     | 23:6:26:LYS:HD3  | 2.16                     | 0.46              |
| 27:A:247:G:H4'   | 27:A:474:G:C5    | 2.51                     | 0.46              |
| 27:A:606:U:H2'   | 27:A:607:G:C8    | 2.50                     | 0.46              |
| 27:A:2090:U:H3   | 27:A:2093:G:H1   | 1.64                     | 0.46              |
| 11:R:4:LYS:HD3   | 11:R:5:PRO:O     | 2.16                     | 0.46              |
| 27:A:356:G:H4'   | 27:A:358:G:C5    | 2.50                     | 0.46              |

*Continued on next page...*

*Continued from previous page...*

| Atom-1           | Atom-2           | Interatomic distance (Å) | Clash overlap (Å) |
|------------------|------------------|--------------------------|-------------------|
| 27:A:586:U:H2'   | 27:A:587:G:O4'   | 2.15                     | 0.46              |
| 27:A:977:G:H2'   | 27:A:978:A:O4'   | 2.15                     | 0.46              |
| 27:A:2752:U:H3'  | 27:A:2754:G:C8   | 2.50                     | 0.46              |
| 28:B:107:A:H2'   | 28:B:108:C:C6    | 2.51                     | 0.46              |
| 1:E:210:GLY:HA2  | 27:A:879:A:H5''  | 1.98                     | 0.46              |
| 4:H:41:VAL:HG22  | 4:H:163:VAL:HG22 | 1.97                     | 0.46              |
| 5:I:7:GLN:NE2    | 5:I:8:PRO:O      | 2.48                     | 0.46              |
| 17:X:40:ARG:NH2  | 17:X:61:THR:HG22 | 2.31                     | 0.46              |
| 27:A:341:C:N4    | 27:A:342:C:H41   | 2.13                     | 0.46              |
| 27:A:606:U:H2'   | 27:A:607:G:H8    | 1.80                     | 0.46              |
| 27:A:1074:A:H2   | 27:A:2682:G:H4'  | 1.81                     | 0.46              |
| 27:A:1127:A:N3   | 27:A:1272:C:O2'  | 2.46                     | 0.46              |
| 27:A:1150:A:H2   | 27:A:1240:G:H1   | 1.63                     | 0.46              |
| 27:A:2329:G:N1   | 27:A:2406:U:N3   | 2.59                     | 0.46              |
| 27:A:2873:U:H2'  | 27:A:2874:C:C6   | 2.51                     | 0.46              |
| 27:A:2964:A:H2'  | 27:A:2965:A:C8   | 2.51                     | 0.46              |
| 4:H:112:SER:C    | 4:H:113:ILE:HD12 | 2.40                     | 0.46              |
| 10:Q:74:ASP:N    | 10:Q:74:ASP:OD1  | 2.48                     | 0.46              |
| 12:S:48:ARG:HB2  | 12:S:95:LYS:HG2  | 1.98                     | 0.46              |
| 17:X:40:ARG:HG2  | 17:X:40:ARG:HH11 | 1.81                     | 0.46              |
| 23:6:20:HIS:CD2  | 27:A:2623:A:O3'  | 2.69                     | 0.46              |
| 27:A:666:A:N6    | 27:A:2257:A:H4'  | 2.31                     | 0.46              |
| 27:A:1146:A:H2'  | 27:A:1147:A:C8   | 2.50                     | 0.46              |
| 27:A:1154:G:C6   | 27:A:1238:G:C6   | 3.04                     | 0.46              |
| 27:A:2394:A:H5'  | 27:A:2396:A:N7   | 2.31                     | 0.46              |
| 27:A:2683:A:N1   | 27:A:2718:G:H1'  | 2.31                     | 0.46              |
| 27:A:3118:U:H2'  | 27:A:3119:A:H8   | 1.80                     | 0.46              |
| 1:E:66:ASP:OD2   | 1:E:103:ARG:NH1  | 2.49                     | 0.46              |
| 27:A:1294:U:H2'  | 27:A:1295:U:C6   | 2.50                     | 0.46              |
| 27:A:1559:A:H2'  | 27:A:1560:U:C6   | 2.51                     | 0.46              |
| 27:A:2367:G:N2   | 27:A:2369:C:O2   | 2.49                     | 0.46              |
| 28:B:63:U:H2'    | 28:B:64:G:C8     | 2.51                     | 0.46              |
| 4:H:130:ASP:HB3  | 27:A:2527:G:O4'  | 2.15                     | 0.45              |
| 24:7:13:ARG:NH1  | 27:A:1493:A:OP1  | 2.49                     | 0.45              |
| 27:A:736:G:H1'   | 27:A:740:A:H61   | 1.80                     | 0.45              |
| 27:A:1287:C:H2'  | 27:A:1288:A:H8   | 1.81                     | 0.45              |
| 27:A:1400:G:N2   | 27:A:1443:G:H5'' | 2.32                     | 0.45              |
| 27:A:1530:G:H21  | 27:A:1805:G:N2   | 2.13                     | 0.45              |
| 27:A:2003:A:H1'  | 27:A:2162:A:N6   | 2.31                     | 0.45              |
| 27:A:2613:G:H5'' | 27:A:2614:U:O4'  | 2.16                     | 0.45              |
| 23:6:6:ASP:C     | 23:6:7:VAL:HG13  | 2.22                     | 0.45              |

*Continued on next page...*

*Continued from previous page...*

| Atom-1           | Atom-2           | Interatomic distance (Å) | Clash overlap (Å) |
|------------------|------------------|--------------------------|-------------------|
| 25:8:23:VAL:HG13 | 25:8:47:ARG:HB3  | 1.97                     | 0.45              |
| 27:A:747:A:H2'   | 27:A:748:U:O4'   | 2.16                     | 0.45              |
| 27:A:929:C:H1'   | 27:A:1339:G:N2   | 2.31                     | 0.45              |
| 27:A:2328:G:C6   | 27:A:2408:G:N1   | 2.84                     | 0.45              |
| 5:I:53:VAL:HG12  | 5:I:66:HIS:CD2   | 2.52                     | 0.45              |
| 6:J:5:LEU:HD12   | 6:J:17:ASP:HB2   | 1.99                     | 0.45              |
| 27:A:316:U:O2'   | 27:A:317:G:OP1   | 2.28                     | 0.45              |
| 27:A:643:G:HO2'  | 27:A:644:G:P     | 2.33                     | 0.45              |
| 27:A:2170:U:H2'  | 27:A:2171:C:H6   | 1.80                     | 0.45              |
| 27:A:2342:A:C2   | 27:A:2392:A:H2'  | 2.51                     | 0.45              |
| 27:A:2888:G:O5'  | 27:A:2888:G:H8   | 1.99                     | 0.45              |
| 28:B:49:C:H2'    | 28:B:50:C:C6     | 2.52                     | 0.45              |
| 5:I:89:GLU:OE1   | 5:I:89:GLU:N     | 2.49                     | 0.45              |
| 10:Q:82:GLU:OE1  | 10:Q:82:GLU:N    | 2.49                     | 0.45              |
| 17:X:24:LEU:HD11 | 17:X:34:LEU:HD23 | 1.98                     | 0.45              |
| 27:A:601:A:H2'   | 27:A:602:A:H8    | 1.81                     | 0.45              |
| 27:A:1250:U:H3'  | 27:A:1251:A:H5'' | 1.98                     | 0.45              |
| 27:A:1476:G:H2'  | 27:A:1477:C:H6   | 1.80                     | 0.45              |
| 27:A:2256:G:N2   | 27:A:2678:G:O2'  | 2.47                     | 0.45              |
| 27:A:2415:G:H2'  | 27:A:2416:C:H6   | 1.82                     | 0.45              |
| 27:A:2672:A:H5'  | 27:A:2673:U:H2'  | 1.99                     | 0.45              |
| 10:Q:70:ILE:HD13 | 10:Q:70:ILE:HA   | 1.83                     | 0.45              |
| 16:W:68:ARG:NH2  | 27:A:1449:C:OP1  | 2.49                     | 0.45              |
| 27:A:282:A:C6    | 27:A:305:G:C6    | 3.05                     | 0.45              |
| 27:A:445:U:H1'   | 27:A:446:G:OP2   | 2.17                     | 0.45              |
| 27:A:639:C:O2'   | 27:A:640:G:O5'   | 2.34                     | 0.45              |
| 27:A:1013:U:C4   | 27:A:1014:G:H1'  | 2.52                     | 0.45              |
| 27:A:1656:A:H2'  | 27:A:1657:G:H8   | 1.81                     | 0.45              |
| 27:A:2350:G:H21  | 27:A:2396:A:H1'  | 1.82                     | 0.45              |
| 4:H:40:LYS:HD2   | 4:H:99:ARG:NH2   | 2.31                     | 0.45              |
| 11:R:88:ILE:HD12 | 11:R:88:ILE:HA   | 1.82                     | 0.45              |
| 27:A:764:U:H2'   | 27:A:765:G:C8    | 2.52                     | 0.45              |
| 27:A:1953:C:H2'  | 27:A:1954:C:O4'  | 2.16                     | 0.45              |
| 27:A:2334:U:H4'  | 27:A:2341:U:H1'  | 1.98                     | 0.45              |
| 27:A:2363:A:H2'  | 27:A:2364:C:H6   | 1.80                     | 0.45              |
| 27:A:2366:C:H3'  | 27:A:2367:G:C8   | 2.51                     | 0.45              |
| 27:A:2887:G:H2'  | 27:A:2888:G:O4'  | 2.16                     | 0.45              |
| 1:E:96:HIS:CD2   | 1:E:102:LYS:HG2  | 2.52                     | 0.45              |
| 5:I:30:LYS:HA    | 5:I:30:LYS:HD2   | 1.65                     | 0.45              |
| 27:A:1550:G:HO2' | 27:A:1551:U:H6   | 1.63                     | 0.45              |
| 27:A:2261:U:H2'  | 27:A:2262:C:C6   | 2.51                     | 0.45              |

*Continued on next page...*

*Continued from previous page...*

| Atom-1           | Atom-2           | Interatomic distance (Å) | Clash overlap (Å) |
|------------------|------------------|--------------------------|-------------------|
| 27:A:2356:G:H21  | 27:A:2381:A:N6   | 2.15                     | 0.45              |
| 27:A:3034:C:H2'  | 27:A:3035:C:H6   | 1.81                     | 0.45              |
| 3:G:4:LYS:HD2    | 3:G:17:SER:HB3   | 1.99                     | 0.45              |
| 13:T:120:ASP:OD1 | 13:T:123:ALA:N   | 2.50                     | 0.45              |
| 23:6:18:CYS:C    | 23:6:20:HIS:H    | 2.25                     | 0.45              |
| 27:A:137:G:H2'   | 27:A:138:A:C8    | 2.51                     | 0.45              |
| 27:A:844:G:O2'   | 27:A:878:G:H4'   | 2.16                     | 0.45              |
| 27:A:949:C:C2    | 27:A:950:A:C8    | 3.04                     | 0.45              |
| 27:A:994:A:H5''  | 27:A:1014:G:N2   | 2.32                     | 0.45              |
| 27:A:1140:G:N2   | 27:A:1141:U:O4   | 2.40                     | 0.45              |
| 27:A:2673:U:O2'  | 27:A:2725:C:N4   | 2.49                     | 0.45              |
| 16:W:26:ASP:OD1  | 16:W:26:ASP:O    | 2.35                     | 0.45              |
| 23:6:11:ILE:HD12 | 23:6:11:ILE:C    | 2.41                     | 0.45              |
| 27:A:88:A:H1'    | 27:A:89:A:C8     | 2.52                     | 0.45              |
| 27:A:89:A:HO2'   | 27:A:90:C:P      | 2.38                     | 0.45              |
| 27:A:734:C:H2'   | 27:A:735:U:C6    | 2.52                     | 0.45              |
| 27:A:995:U:H2'   | 27:A:996:G:C8    | 2.52                     | 0.45              |
| 27:A:2285:G:O6   | 27:A:2675:A:C6   | 2.70                     | 0.45              |
| 27:A:2622:C:H2'  | 27:A:2623:A:C8   | 2.52                     | 0.45              |
| 27:A:2703:U:H5'' | 27:A:2761:U:H4'  | 1.98                     | 0.45              |
| 5:I:33:LEU:HB2   | 5:I:76:LEU:HD11  | 1.99                     | 0.45              |
| 27:A:2301:C:H2'  | 27:A:2302:U:C6   | 2.52                     | 0.45              |
| 3:G:201:LEU:O    | 3:G:205:ILE:HG12 | 2.16                     | 0.44              |
| 27:A:1900:C:H2'  | 27:A:1901:C:H6   | 1.81                     | 0.44              |
| 27:A:2189:C:H5'' | 27:A:2190:A:H2'  | 1.99                     | 0.44              |
| 27:A:2746:U:O2'  | 27:A:2871:U:OP1  | 2.31                     | 0.44              |
| 27:A:2758:A:C6   | 27:A:2759:G:C5   | 3.05                     | 0.44              |
| 2:F:166:MET:HE2  | 27:A:2843:C:O2'  | 2.17                     | 0.44              |
| 13:T:54:LYS:NZ   | 27:A:1113:C:OP2  | 2.47                     | 0.44              |
| 27:A:2814:A:H2'  | 27:A:2815:C:H6   | 1.82                     | 0.44              |
| 27:A:2901:G:H2'  | 27:A:2902:A:C8   | 2.52                     | 0.44              |
| 3:G:13:LYS:HB3   | 3:G:13:LYS:HE2   | 1.59                     | 0.44              |
| 6:J:12:LEU:HA    | 6:J:12:LEU:HD23  | 1.76                     | 0.44              |
| 12:S:3:THR:HG23  | 27:A:3096:U:H4'  | 1.99                     | 0.44              |
| 27:A:264:G:H4'   | 27:A:516:G:H22   | 1.81                     | 0.44              |
| 27:A:646:U:H2'   | 27:A:647:G:O4'   | 2.18                     | 0.44              |
| 27:A:1651:C:H2'  | 27:A:1652:A:H8   | 1.82                     | 0.44              |
| 27:A:2385:G:H5'' | 27:A:2394:A:H2'  | 1.99                     | 0.44              |
| 5:I:84:TYR:N     | 5:I:136:GLY:O    | 2.39                     | 0.44              |
| 21:3:58:GLU:OE1  | 21:3:58:GLU:HA   | 2.17                     | 0.44              |
| 27:A:295:U:H2'   | 27:A:296:A:C8    | 2.53                     | 0.44              |

*Continued on next page...*

*Continued from previous page...*

| Atom-1           | Atom-2           | Interatomic distance (Å) | Clash overlap (Å) |
|------------------|------------------|--------------------------|-------------------|
| 27:A:1313:U:H2'  | 27:A:1314:C:H6   | 1.82                     | 0.44              |
| 27:A:1703:G:H2'  | 27:A:1704:U:C6   | 2.52                     | 0.44              |
| 27:A:3019:C:N4   | 27:A:3024:A:N1   | 2.65                     | 0.44              |
| 4:H:171:ALA:O    | 4:H:174:ARG:HG2  | 2.18                     | 0.44              |
| 9:O:80:VAL:HG22  | 9:O:114:GLY:HA2  | 2.00                     | 0.44              |
| 24:7:28:ARG:NH2  | 27:A:210:G:OP1   | 2.33                     | 0.44              |
| 27:A:2375:G:H2'  | 27:A:2376:G:H8   | 1.81                     | 0.44              |
| 4:H:57:ILE:O     | 4:H:61:ILE:HG12  | 2.17                     | 0.44              |
| 7:M:13:ARG:NH2   | 7:M:49:ASP:OD1   | 2.50                     | 0.44              |
| 7:M:93:LEU:HD23  | 7:M:93:LEU:HA    | 1.87                     | 0.44              |
| 25:8:33:LEU:HD22 | 27:A:2643:U:OP2  | 2.18                     | 0.44              |
| 27:A:1398:G:O2'  | 27:A:1400:G:N7   | 2.45                     | 0.44              |
| 27:A:1552:A:N6   | 27:A:1616:A:OP2  | 2.51                     | 0.44              |
| 27:A:2681:U:H2'  | 27:A:2682:G:C8   | 2.52                     | 0.44              |
| 27:A:2738:U:H2'  | 27:A:2739:C:H6   | 1.82                     | 0.44              |
| 27:A:2862:G:HO2' | 27:A:2863:A:H8   | 1.62                     | 0.44              |
| 19:1:48:ARG:HB2  | 19:1:48:ARG:HH11 | 1.83                     | 0.44              |
| 27:A:273:A:H62   | 27:A:313:G:N2    | 2.16                     | 0.44              |
| 27:A:929:C:H2'   | 27:A:930:C:C6    | 2.52                     | 0.44              |
| 27:A:1665:U:H2'  | 27:A:1666:A:H8   | 1.83                     | 0.44              |
| 27:A:2528:G:H22  | 27:A:2536:U:H3   | 1.64                     | 0.44              |
| 27:A:3020:U:O2'  | 27:A:3021:A:O5'  | 2.28                     | 0.44              |
| 22:5:48:ARG:HD3  | 27:A:3106:C:N4   | 2.33                     | 0.44              |
| 27:A:2:A:H2'     | 27:A:3:A:H8      | 1.83                     | 0.44              |
| 27:A:2211:C:H2'  | 27:A:2212:A:H8   | 1.82                     | 0.44              |
| 3:G:210:LYS:HB2  | 3:G:210:LYS:HE2  | 1.73                     | 0.44              |
| 4:H:182:PHE:HA   | 4:H:183:PRO:HD3  | 1.88                     | 0.44              |
| 5:I:151:ARG:HH12 | 27:A:2967:C:HI1' | 1.82                     | 0.44              |
| 13:T:18:LEU:HD23 | 13:T:18:LEU:HA   | 1.87                     | 0.44              |
| 27:A:6:G:H2'     | 27:A:2853:C:H42  | 1.83                     | 0.44              |
| 27:A:151:A:H2'   | 27:A:152:G:C8    | 2.52                     | 0.44              |
| 27:A:290:C:N4    | 27:A:300:G:H21   | 2.16                     | 0.44              |
| 27:A:440:U:H2'   | 27:A:441:G:H8    | 1.83                     | 0.44              |
| 27:A:444:U:H5'   | 27:A:446:G:H4'   | 2.00                     | 0.44              |
| 27:A:2325:U:H3   | 27:A:2410:A:H61  | 1.66                     | 0.44              |
| 27:A:2363:A:C6   | 27:A:2375:G:C6   | 3.06                     | 0.44              |
| 27:A:2394:A:H3'  | 27:A:2396:A:N7   | 2.33                     | 0.44              |
| 27:A:2682:G:H21  | 27:A:2683:A:H61  | 1.64                     | 0.44              |
| 27:A:2862:G:HO2' | 27:A:3002:A:N6   | 2.16                     | 0.44              |
| 2:F:57:ILE:HG23  | 2:F:79:ARG:HB2   | 2.00                     | 0.43              |
| 3:G:69:LYS:HZ1   | 27:A:2284:A:H3'  | 1.83                     | 0.43              |

*Continued on next page...*

*Continued from previous page...*

| Atom-1           | Atom-2           | Interatomic distance (Å) | Clash overlap (Å) |
|------------------|------------------|--------------------------|-------------------|
| 8:N:68:GLU:OE2   | 27:A:2908:U:O2'  | 2.35                     | 0.43              |
| 11:R:90:GLU:HA   | 11:R:93:LYS:HB2  | 1.99                     | 0.43              |
| 27:A:966:U:H2'   | 27:A:967:G:C8    | 2.52                     | 0.43              |
| 27:A:990:G:H1    | 27:A:1018:U:H3   | 0.68                     | 0.43              |
| 27:A:1552:A:N6   | 27:A:1616:A:N7   | 2.65                     | 0.43              |
| 27:A:1859:A:H2'  | 27:A:1860:G:O4'  | 2.17                     | 0.43              |
| 27:A:1921:G:H2'  | 27:A:1922:G:H8   | 1.83                     | 0.43              |
| 27:A:1922:G:H2'  | 27:A:1923:G:C8   | 2.53                     | 0.43              |
| 27:A:2065:A:H2'  | 27:A:2066:G:H8   | 1.83                     | 0.43              |
| 27:A:2883:G:N2   | 27:A:2885:G:H3'  | 2.33                     | 0.43              |
| 2:F:157:PRO:C    | 2:F:159:ARG:H    | 2.26                     | 0.43              |
| 4:H:80:SER:N     | 4:H:88:GLU:OE2   | 2.51                     | 0.43              |
| 4:H:149:ASP:O    | 4:H:153:ILE:HG23 | 2.17                     | 0.43              |
| 13:T:119:GLU:H   | 13:T:119:GLU:CD  | 2.24                     | 0.43              |
| 18:Z:11:ARG:NH2  | 18:Z:12:ASN:OD1  | 2.51                     | 0.43              |
| 23:6:8:ARG:HA    | 23:6:27:LYS:O    | 2.18                     | 0.43              |
| 23:6:24:ILE:HD11 | 25:8:34:GLU:HA   | 2.00                     | 0.43              |
| 27:A:297:G:O2'   | 27:A:298:G:H5'   | 2.18                     | 0.43              |
| 27:A:929:C:H1'   | 27:A:1339:G:H21  | 1.84                     | 0.43              |
| 27:A:1326:G:H1'  | 27:A:1352:A:N6   | 2.34                     | 0.43              |
| 27:A:2457:U:H2'  | 27:A:2458:G:H8   | 1.83                     | 0.43              |
| 27:A:2839:U:H2'  | 27:A:2840:C:H6   | 1.82                     | 0.43              |
| 27:A:2873:U:H2'  | 27:A:2874:C:H6   | 1.82                     | 0.43              |
| 2:F:129:ARG:HD3  | 2:F:130:HIS:NE2  | 2.33                     | 0.43              |
| 4:H:52:ARG:HB2   | 4:H:52:ARG:CZ    | 2.48                     | 0.43              |
| 4:H:126:PRO:HB2  | 4:H:174:ARG:NH1  | 2.33                     | 0.43              |
| 21:3:16:ARG:HD3  | 27:A:1086:C:OP2  | 2.17                     | 0.43              |
| 27:A:992:C:H2'   | 27:A:993:G:O4'   | 2.18                     | 0.43              |
| 27:A:1296:G:H2'  | 27:A:1297:G:H8   | 1.82                     | 0.43              |
| 27:A:1552:A:O5'  | 27:A:1552:A:H8   | 2.01                     | 0.43              |
| 27:A:2011:U:H2'  | 27:A:2012:C:H6   | 1.83                     | 0.43              |
| 5:I:19:ILE:HG12  | 5:I:24:LEU:HG    | 2.00                     | 0.43              |
| 6:J:25:TYR:HE1   | 6:J:29:TYR:CD2   | 2.35                     | 0.43              |
| 27:A:473:C:O2'   | 27:A:476:G:N2    | 2.52                     | 0.43              |
| 27:A:988:U:C5    | 27:A:990:G:C6    | 3.06                     | 0.43              |
| 27:A:2537:C:H2'  | 27:A:2538:A:H8   | 1.83                     | 0.43              |
| 4:H:57:ILE:HD12  | 4:H:57:ILE:HA    | 1.81                     | 0.43              |
| 14:U:51:LYS:HB2  | 14:U:54:ASP:OD1  | 2.19                     | 0.43              |
| 18:Z:29:GLN:OE1  | 27:A:1037:C:O2'  | 2.33                     | 0.43              |
| 27:A:89:A:O2'    | 27:A:90:C:OP1    | 2.29                     | 0.43              |
| 27:A:384:G:H2'   | 27:A:385:G:H8    | 1.83                     | 0.43              |

*Continued on next page...*

*Continued from previous page...*

| Atom-1           | Atom-2           | Interatomic distance (Å) | Clash overlap (Å) |
|------------------|------------------|--------------------------|-------------------|
| 27:A:1639:G:H5'  | 27:A:1640:A:OP1  | 2.19                     | 0.43              |
| 27:A:2603:G:H2'  | 27:A:2604:U:C6   | 2.53                     | 0.43              |
| 14:U:42:VAL:HB   | 14:U:49:THR:HB   | 1.99                     | 0.43              |
| 15:V:104:ARG:NH1 | 27:A:2237:A:H5'  | 2.33                     | 0.43              |
| 27:A:138:A:H61   | 27:A:1813:C:HO2' | 1.66                     | 0.43              |
| 27:A:1640:A:O2'  | 27:A:1641:U:OP1  | 2.36                     | 0.43              |
| 27:A:1705:C:H2'  | 27:A:1706:A:C8   | 2.53                     | 0.43              |
| 27:A:2588:C:H2'  | 27:A:2589:G:O4'  | 2.19                     | 0.43              |
| 27:A:844:G:H5'   | 27:A:845:C:H5''  | 2.00                     | 0.43              |
| 27:A:1430:C:H2'  | 27:A:1431:U:C6   | 2.54                     | 0.43              |
| 27:A:1714:A:H2'  | 27:A:1715:A:C8   | 2.54                     | 0.43              |
| 27:A:2870:C:H2'  | 27:A:2871:U:O4'  | 2.19                     | 0.43              |
| 27:A:2880:U:N3   | 27:A:2889:A:C8   | 2.87                     | 0.43              |
| 25:8:3:LYS:HG3   | 27:A:242:G:C8    | 2.54                     | 0.43              |
| 27:A:166:A:H2'   | 27:A:167:G:O4'   | 2.18                     | 0.43              |
| 27:A:663:A:N3    | 27:A:663:A:H2'   | 2.34                     | 0.43              |
| 27:A:1530:G:N2   | 27:A:1805:G:N1   | 2.64                     | 0.43              |
| 27:A:1557:C:H2'  | 27:A:1558:C:C6   | 2.54                     | 0.43              |
| 27:A:1898:U:H2'  | 27:A:1899:G:O4'  | 2.19                     | 0.43              |
| 27:A:2971:G:O6   | 27:A:2979:C:H5'' | 2.18                     | 0.43              |
| 1:E:217:LYS:HE3  | 1:E:217:LYS:HB3  | 1.73                     | 0.43              |
| 4:H:67:ILE:O     | 4:H:109:ARG:NH2  | 2.52                     | 0.43              |
| 8:N:24:VAL:HG12  | 8:N:30:ARG:HD3   | 2.01                     | 0.43              |
| 23:6:16:GLU:OE1  | 23:6:50:PRO:CB   | 2.66                     | 0.43              |
| 23:6:17:VAL:CG2  | 23:6:49:GLN:HG3  | 2.49                     | 0.43              |
| 27:A:26:U:H2'    | 27:A:27:G:C8     | 2.53                     | 0.43              |
| 27:A:638:U:C2    | 27:A:639:C:C5    | 3.07                     | 0.43              |
| 2:F:130:HIS:CD2  | 2:F:165:ARG:HB3  | 2.54                     | 0.43              |
| 5:I:96:ARG:NH1   | 5:I:98:GLN:HG3   | 2.34                     | 0.43              |
| 23:6:8:ARG:NE    | 27:A:2509:C:OP2  | 2.51                     | 0.43              |
| 27:A:109:U:H2'   | 27:A:110:G:O4'   | 2.19                     | 0.43              |
| 27:A:1696:G:O2'  | 27:A:1736:G:O6   | 2.34                     | 0.43              |
| 27:A:2152:A:H2'  | 27:A:2153:G:O4'  | 2.18                     | 0.43              |
| 27:A:2275:A:H8   | 27:A:2275:A:OP2  | 2.01                     | 0.43              |
| 1:E:149:PRO:HB3  | 1:E:188:ARG:HB3  | 2.00                     | 0.42              |
| 4:H:136:THR:HG21 | 27:A:2527:G:N2   | 2.33                     | 0.42              |
| 17:X:1:MET:SD    | 17:X:28:PRO:HA   | 2.59                     | 0.42              |
| 27:A:296:A:N1    | 27:A:340:A:N6    | 2.66                     | 0.42              |
| 27:A:722:G:H2'   | 27:A:723:C:C6    | 2.54                     | 0.42              |
| 27:A:1005:A:C4   | 27:A:1006:G:C8   | 3.07                     | 0.42              |
| 27:A:2678:G:N3   | 27:A:2678:G:H2'  | 2.34                     | 0.42              |

*Continued on next page...*

*Continued from previous page...*

| Atom-1           | Atom-2            | Interatomic distance (Å) | Clash overlap (Å) |
|------------------|-------------------|--------------------------|-------------------|
| 27:A:2756:G:H4'  | 27:A:2881:A:H2    | 1.84                     | 0.42              |
| 3:G:152:LYS:HE3  | 3:G:152:LYS:HB2   | 1.88                     | 0.42              |
| 4:H:117:ARG:HG3  | 4:H:146:HIS:HE1   | 1.83                     | 0.42              |
| 16:W:52:VAL:HG22 | 16:W:53:LYS:H     | 1.84                     | 0.42              |
| 19:1:36:VAL:HG22 | 19:1:63:ARG:HH21  | 1.84                     | 0.42              |
| 23:6:17:VAL:O    | 23:6:17:VAL:CG1   | 2.58                     | 0.42              |
| 27:A:691:U:H2'   | 27:A:692:C:H6     | 1.84                     | 0.42              |
| 27:A:782:U:H2'   | 27:A:783:G:O4'    | 2.18                     | 0.42              |
| 27:A:1622:G:C2   | 27:A:1623:U:C5    | 3.07                     | 0.42              |
| 27:A:1725:G:H2'  | 27:A:1726:C:O4'   | 2.19                     | 0.42              |
| 27:A:1922:G:H2'  | 27:A:1923:G:H8    | 1.83                     | 0.42              |
| 27:A:2011:U:H2'  | 27:A:2012:C:C6    | 2.53                     | 0.42              |
| 27:A:2400:C:H2'  | 27:A:2401:U:O4'   | 2.19                     | 0.42              |
| 27:A:2753:G:OP2  | 27:A:2754:G:H5''  | 2.19                     | 0.42              |
| 27:A:3045:C:H2'  | 27:A:3046:C:O4'   | 2.19                     | 0.42              |
| 27:A:3057:U:H2'  | 27:A:3058:A:H8    | 1.83                     | 0.42              |
| 2:F:43:GLU:H     | 2:F:43:GLU:CD     | 2.26                     | 0.42              |
| 11:R:25:LEU:HD11 | 11:R:103:ASP:OD1  | 2.19                     | 0.42              |
| 11:R:26:ARG:NH1  | 28:B:9:G:OP1      | 2.47                     | 0.42              |
| 23:6:19:LYS:CD   | 23:6:44:ASN:OD1   | 2.56                     | 0.42              |
| 27:A:193:G:H2'   | 27:A:194:A:O4'    | 2.19                     | 0.42              |
| 27:A:1008:G:C2   | 27:A:1009:U:N3    | 2.87                     | 0.42              |
| 27:A:1065:C:H2'  | 27:A:1066:G:H8    | 1.83                     | 0.42              |
| 27:A:2007:C:H2'  | 27:A:2008:A:C8    | 2.54                     | 0.42              |
| 27:A:2326:A:H2'  | 27:A:2327:C:C6    | 2.54                     | 0.42              |
| 27:A:2388:G:C2   | 27:A:2389:U:H1'   | 2.54                     | 0.42              |
| 27:A:2523:A:H2'  | 27:A:2524:C:C6    | 2.53                     | 0.42              |
| 27:A:2764:C:H2'  | 27:A:2765:A:O4'   | 2.20                     | 0.42              |
| 5:I:84:TYR:CZ    | 5:I:139:LYS:HD2   | 2.55                     | 0.42              |
| 5:I:104:LEU:HD22 | 5:I:124:PHE:CD2   | 2.53                     | 0.42              |
| 11:R:36:PRO:HG2  | 11:R:51:LEU:HD12  | 2.02                     | 0.42              |
| 11:R:37:ARG:HA   | 11:R:101:VAL:HG23 | 2.00                     | 0.42              |
| 13:T:58:ARG:HA   | 13:T:61:TRP:CE3   | 2.54                     | 0.42              |
| 14:U:77:LYS:HE3  | 14:U:86:LYS:HZ3   | 1.85                     | 0.42              |
| 27:A:443:C:H2'   | 27:A:444:U:O4'    | 2.19                     | 0.42              |
| 27:A:754:C:C2    | 27:A:755:A:C8     | 3.08                     | 0.42              |
| 27:A:1015:A:H2'  | 27:A:1016:C:O4'   | 2.18                     | 0.42              |
| 27:A:1090:G:OP2  | 27:A:1091:A:O2'   | 2.37                     | 0.42              |
| 27:A:1804:G:H2'  | 27:A:1805:G:H8    | 1.85                     | 0.42              |
| 27:A:2070:A:H2'  | 27:A:2071:A:H8    | 1.83                     | 0.42              |
| 27:A:2682:G:H21  | 27:A:2683:A:N6    | 2.17                     | 0.42              |

*Continued on next page...*

*Continued from previous page...*

| Atom-1           | Atom-2           | Interatomic distance (Å) | Clash overlap (Å) |
|------------------|------------------|--------------------------|-------------------|
| 27:A:2732:G:O2'  | 27:A:2778:U:O2'  | 2.26                     | 0.42              |
| 27:A:2861:U:H2'  | 27:A:2862:G:O4'  | 2.19                     | 0.42              |
| 27:A:2969:C:H2'  | 27:A:2970:U:C6   | 2.54                     | 0.42              |
| 3:G:143:THR:O    | 3:G:147:THR:HG23 | 2.20                     | 0.42              |
| 6:J:8:GLU:OE1    | 6:J:14:ALA:HA    | 2.19                     | 0.42              |
| 22:5:38:LYS:HA   | 22:5:38:LYS:HD3  | 1.80                     | 0.42              |
| 27:A:180:A:H2'   | 27:A:181:A:H8    | 1.84                     | 0.42              |
| 27:A:290:C:N4    | 27:A:299:G:H22   | 2.17                     | 0.42              |
| 27:A:971:G:H2'   | 27:A:972:A:C8    | 2.55                     | 0.42              |
| 27:A:1003:A:N3   | 27:A:1004:C:O2'  | 2.52                     | 0.42              |
| 27:A:1876:A:H2'  | 27:A:1877:U:C6   | 2.55                     | 0.42              |
| 27:A:2327:C:H2'  | 27:A:2328:G:C8   | 2.54                     | 0.42              |
| 27:A:2551:A:H2'  | 27:A:2552:A:C8   | 2.54                     | 0.42              |
| 27:A:2671:G:C8   | 27:A:2724:U:H3'  | 2.54                     | 0.42              |
| 28:B:40:A:H2'    | 28:B:41:U:C6     | 2.54                     | 0.42              |
| 5:I:30:LYS:HG2   | 5:I:81:THR:O     | 2.19                     | 0.42              |
| 5:I:68:LEU:HD22  | 27:A:2981:A:N1   | 2.35                     | 0.42              |
| 14:U:39:VAL:HG12 | 14:U:55:LEU:HD22 | 2.02                     | 0.42              |
| 20:2:10:LEU:HD23 | 20:2:10:LEU:HA   | 1.88                     | 0.42              |
| 27:A:81:A:C2     | 27:A:100:A:C5    | 3.07                     | 0.42              |
| 27:A:298:G:O2'   | 27:A:299:G:O4'   | 2.27                     | 0.42              |
| 27:A:724:G:N2    | 27:A:727:A:OP2   | 2.40                     | 0.42              |
| 27:A:943:U:H4'   | 27:A:946:G:N1    | 2.34                     | 0.42              |
| 27:A:1064:A:H2'  | 27:A:1065:C:C6   | 2.55                     | 0.42              |
| 27:A:1556:A:H2   | 27:A:1615:G:N1   | 2.18                     | 0.42              |
| 27:A:1678:U:H5'  | 27:A:1679:A:OP2  | 2.19                     | 0.42              |
| 27:A:2085:C:O2'  | 27:A:2086:U:O4'  | 2.37                     | 0.42              |
| 27:A:2086:U:H2'  | 27:A:2087:C:H6   | 1.84                     | 0.42              |
| 27:A:2729:G:O2'  | 27:A:2730:U:O5'  | 2.36                     | 0.42              |
| 2:F:96:GLU:OE1   | 2:F:96:GLU:N     | 2.52                     | 0.42              |
| 4:H:148:ILE:HD13 | 4:H:153:ILE:HG21 | 2.00                     | 0.42              |
| 12:S:81:ASP:OD1  | 12:S:82:HIS:N    | 2.53                     | 0.42              |
| 24:7:37:ARG:NH1  | 24:7:44:ALA:O    | 2.52                     | 0.42              |
| 27:A:735:U:H2'   | 27:A:736:G:O4'   | 2.19                     | 0.42              |
| 27:A:990:G:N2    | 27:A:1018:U:O2   | 2.25                     | 0.42              |
| 27:A:1016:C:H3'  | 27:A:1017:G:H8   | 1.84                     | 0.42              |
| 27:A:2883:G:H2'  | 27:A:2885:G:OP2  | 2.20                     | 0.42              |
| 3:G:6:ASP:OD1    | 3:G:6:ASP:N      | 2.35                     | 0.42              |
| 4:H:64:LEU:HD23  | 4:H:64:LEU:HA    | 1.81                     | 0.42              |
| 9:O:55:MET:HE2   | 9:O:55:MET:HB2   | 1.92                     | 0.42              |
| 11:R:93:LYS:NZ   | 11:R:124:GLY:HA3 | 2.35                     | 0.42              |

*Continued on next page...*

*Continued from previous page...*

| Atom-1           | Atom-2           | Interatomic distance (Å) | Clash overlap (Å) |
|------------------|------------------|--------------------------|-------------------|
| 27:A:422:A:H2'   | 27:A:423:C:O4'   | 2.19                     | 0.42              |
| 27:A:637:G:C4    | 27:A:638:U:C5    | 3.08                     | 0.42              |
| 27:A:994:A:H3'   | 27:A:995:U:C6    | 2.55                     | 0.42              |
| 27:A:1485:C:H2'  | 27:A:1486:G:O4'  | 2.19                     | 0.42              |
| 27:A:1947:U:H1'  | 27:A:1948:A:C2   | 2.55                     | 0.42              |
| 27:A:2253:A:C6   | 27:A:2255:A:H5'  | 2.55                     | 0.42              |
| 27:A:2460:U:H2'  | 27:A:2461:G:O4'  | 2.20                     | 0.42              |
| 27:A:2723:C:H2'  | 27:A:2724:U:C2   | 2.54                     | 0.42              |
| 27:A:2872:G:H2'  | 27:A:2873:U:H6   | 1.82                     | 0.42              |
| 1:E:273:ARG:HD2  | 1:E:276:LYS:HD2  | 2.01                     | 0.42              |
| 10:Q:67:MET:HE1  | 27:A:1675:U:C4   | 2.54                     | 0.42              |
| 18:Z:12:ASN:ND2  | 27:A:2501:G:O5'  | 2.53                     | 0.42              |
| 19:1:63:ARG:NH1  | 27:A:2315:U:OP2  | 2.52                     | 0.42              |
| 27:A:459:A:H61   | 27:A:489:A:H3'   | 1.83                     | 0.42              |
| 27:A:1000:C:H3'  | 27:A:1001:C:H5'' | 2.02                     | 0.42              |
| 27:A:1654:G:H2'  | 27:A:1655:A:C8   | 2.55                     | 0.42              |
| 3:G:101:ARG:HE   | 3:G:101:ARG:HB3  | 1.47                     | 0.42              |
| 5:I:104:LEU:HD12 | 5:I:104:LEU:HA   | 1.87                     | 0.42              |
| 26:4:36:GLU:HG2  | 26:4:37:VAL:N    | 2.35                     | 0.42              |
| 27:A:150:C:H2'   | 27:A:151:A:C8    | 2.54                     | 0.42              |
| 27:A:337:U:O2    | 27:A:344:G:C2    | 2.72                     | 0.42              |
| 27:A:824:G:H2'   | 27:A:825:C:C6    | 2.55                     | 0.42              |
| 27:A:1729:A:H2'  | 27:A:1731:A:C8   | 2.54                     | 0.42              |
| 27:A:2416:C:H2'  | 27:A:2417:C:H6   | 1.85                     | 0.42              |
| 5:I:22:GLN:NE2   | 5:I:38:ALA:O     | 2.53                     | 0.41              |
| 9:O:49:MET:HE3   | 9:O:49:MET:HB3   | 1.90                     | 0.41              |
| 24:7:45:LEU:HD12 | 24:7:45:LEU:HA   | 1.86                     | 0.41              |
| 27:A:279:U:H2'   | 27:A:280:G:C8    | 2.52                     | 0.41              |
| 27:A:1079:C:H4'  | 27:A:2720:C:O2'  | 2.20                     | 0.41              |
| 27:A:1288:A:H2'  | 27:A:1289:A:H8   | 1.85                     | 0.41              |
| 27:A:2074:G:O6   | 27:A:2075:G:N1   | 2.52                     | 0.41              |
| 27:A:2243:C:H2'  | 27:A:2244:A:C8   | 2.55                     | 0.41              |
| 28:B:50:C:H2'    | 28:B:51:G:C8     | 2.54                     | 0.41              |
| 5:I:35:LEU:HD22  | 5:I:36:ASP:H     | 1.83                     | 0.41              |
| 11:R:125:LEU:C   | 11:R:126:LYS:HE2 | 2.46                     | 0.41              |
| 25:8:43:ARG:HH22 | 27:A:2586:G:H3'  | 1.85                     | 0.41              |
| 27:A:149:C:H2'   | 27:A:150:C:C6    | 2.54                     | 0.41              |
| 27:A:180:A:H2'   | 27:A:181:A:C8    | 2.55                     | 0.41              |
| 27:A:1479:G:H4'  | 27:A:2025:C:H5   | 1.86                     | 0.41              |
| 27:A:2181:C:H2'  | 27:A:2182:C:H6   | 1.84                     | 0.41              |
| 27:A:2255:A:O2'  | 27:A:2256:G:OP1  | 2.34                     | 0.41              |

*Continued on next page...*

*Continued from previous page...*

| Atom-1           | Atom-2           | Interatomic distance (Å) | Clash overlap (Å) |
|------------------|------------------|--------------------------|-------------------|
| 27:A:2288:C:H2'  | 27:A:2289:C:C6   | 2.55                     | 0.41              |
| 27:A:2901:G:H2'  | 27:A:2902:A:H8   | 1.85                     | 0.41              |
| 2:F:166:MET:HE1  | 27:A:2843:C:O2   | 2.19                     | 0.41              |
| 4:H:110:LEU:HD12 | 4:H:114:ALA:HB3  | 2.01                     | 0.41              |
| 9:O:31:LYS:O     | 9:O:31:LYS:HG2   | 2.20                     | 0.41              |
| 10:Q:42:ARG:NH2  | 27:A:3038:C:OP1  | 2.53                     | 0.41              |
| 22:5:7:ARG:NH1   | 27:A:671:G:O2'   | 2.53                     | 0.41              |
| 25:8:24:ARG:NH2  | 27:A:2585:U:OP1  | 2.53                     | 0.41              |
| 27:A:248:G:H5'   | 27:A:250:G:N7    | 2.36                     | 0.41              |
| 27:A:278:A:H2'   | 27:A:279:U:C6    | 2.55                     | 0.41              |
| 27:A:935:A:H4'   | 27:A:951:G:N2    | 2.35                     | 0.41              |
| 27:A:1018:U:H1'  | 27:A:1019:C:H41  | 1.85                     | 0.41              |
| 27:A:1313:U:H2'  | 27:A:1314:C:C6   | 2.54                     | 0.41              |
| 27:A:1544:U:C4   | 27:A:1626:G:O6   | 2.74                     | 0.41              |
| 27:A:1648:A:H4'  | 27:A:1649:C:O5'  | 2.18                     | 0.41              |
| 27:A:2019:A:H2'  | 27:A:2020:A:H8   | 1.81                     | 0.41              |
| 27:A:2332:U:N3   | 27:A:2333:G:O6   | 2.54                     | 0.41              |
| 27:A:2491:A:H5'' | 27:A:2492:A:H5'  | 2.02                     | 0.41              |
| 27:A:2581:G:H2'  | 27:A:2583:C:OP2  | 2.20                     | 0.41              |
| 27:A:2601:A:H2'  | 27:A:2602:A:C8   | 2.55                     | 0.41              |
| 27:A:2878:A:N1   | 27:A:2889:A:H5'' | 2.34                     | 0.41              |
| 2:F:10:LYS:HB2   | 2:F:198:ILE:HD11 | 2.02                     | 0.41              |
| 17:X:41:ILE:HD12 | 27:A:568:A:H5''  | 2.03                     | 0.41              |
| 27:A:362:A:H2'   | 27:A:363:A:C8    | 2.55                     | 0.41              |
| 27:A:1659:U:H2'  | 27:A:1660:A:C8   | 2.54                     | 0.41              |
| 27:A:1907:A:H2'  | 27:A:1908:A:C8   | 2.55                     | 0.41              |
| 27:A:2255:A:N6   | 27:A:2722:C:H1'  | 2.34                     | 0.41              |
| 27:A:2297:U:H2'  | 27:A:2298:U:H6   | 1.85                     | 0.41              |
| 27:A:2366:C:H3'  | 27:A:2367:G:H8   | 1.85                     | 0.41              |
| 3:G:3:LEU:HD12   | 3:G:4:LYS:H      | 1.85                     | 0.41              |
| 3:G:28:GLU:OE1   | 3:G:29:PRO:HD2   | 2.20                     | 0.41              |
| 5:I:3:ARG:O      | 5:I:6:LYS:HG2    | 2.21                     | 0.41              |
| 10:Q:63:ARG:HA   | 10:Q:80:PHE:CZ   | 2.55                     | 0.41              |
| 18:Z:18:ALA:HB1  | 27:A:2495:G:OP1  | 2.21                     | 0.41              |
| 20:2:7:PRO:HA    | 20:2:10:LEU:HB2  | 2.03                     | 0.41              |
| 23:6:7:VAL:O     | 23:6:8:ARG:C     | 2.63                     | 0.41              |
| 27:A:158:G:O2'   | 27:A:165:U:O4    | 2.37                     | 0.41              |
| 27:A:191:G:OP2   | 27:A:191:G:N2    | 2.49                     | 0.41              |
| 27:A:579:A:H2'   | 27:A:580:G:O4'   | 2.20                     | 0.41              |
| 27:A:669:G:H2'   | 27:A:670:A:C8    | 2.55                     | 0.41              |
| 27:A:2416:C:H2'  | 27:A:2417:C:C6   | 2.56                     | 0.41              |

*Continued on next page...*

*Continued from previous page...*

| Atom-1           | Atom-2           | Interatomic distance (Å) | Clash overlap (Å) |
|------------------|------------------|--------------------------|-------------------|
| 28:B:44:C:H2'    | 28:B:46:A:N7     | 2.35                     | 0.41              |
| 6:J:21:VAL:HG22  | 6:J:25:TYR:HB3   | 2.02                     | 0.41              |
| 15:V:32:ARG:NH2  | 27:A:606:U:H5''  | 2.36                     | 0.41              |
| 26:4:1:MET:N     | 28:B:41:U:O4     | 2.37                     | 0.41              |
| 27:A:567:A:N3    | 27:A:569:G:H5''  | 2.35                     | 0.41              |
| 27:A:1407:G:H2'  | 27:A:1408:C:C6   | 2.56                     | 0.41              |
| 27:A:1487:U:O2'  | 27:A:2436:A:N3   | 2.43                     | 0.41              |
| 27:A:2147:U:H2'  | 27:A:2148:C:H6   | 1.84                     | 0.41              |
| 27:A:2338:G:H4'  | 27:A:2388:G:N2   | 2.36                     | 0.41              |
| 27:A:2739:C:H2'  | 27:A:2740:G:H8   | 1.85                     | 0.41              |
| 27:A:2777:G:H2'  | 27:A:2778:U:O4'  | 2.20                     | 0.41              |
| 27:A:3017:C:C2   | 27:A:3018:U:C5   | 3.09                     | 0.41              |
| 4:H:180:LEU:HD23 | 4:H:180:LEU:HA   | 1.93                     | 0.41              |
| 13:T:7:ALA:O     | 13:T:11:GLN:HG2  | 2.21                     | 0.41              |
| 20:2:36:MET:HE2  | 20:2:41:LEU:HD21 | 2.03                     | 0.41              |
| 23:6:35:ARG:HD3  | 23:6:52:LYS:HG2  | 2.02                     | 0.41              |
| 27:A:365:U:O2    | 27:A:437:G:N2    | 2.44                     | 0.41              |
| 27:A:2087:C:H2'  | 27:A:2088:C:O4'  | 2.21                     | 0.41              |
| 27:A:2256:G:H22  | 27:A:2678:G:H1'  | 1.86                     | 0.41              |
| 28:B:52:G:H2'    | 28:B:53:A:C8     | 2.55                     | 0.41              |
| 2:F:160:VAL:HG21 | 27:A:2842:G:H21  | 1.86                     | 0.41              |
| 4:H:87:ARG:HG2   | 4:H:90:MET:HE2   | 2.02                     | 0.41              |
| 5:I:55:ARG:HD3   | 5:I:66:HIS:HB2   | 2.01                     | 0.41              |
| 11:R:76:ASP:OD1  | 11:R:77:LYS:N    | 2.49                     | 0.41              |
| 27:A:350:A:C6    | 27:A:351:G:C2    | 3.08                     | 0.41              |
| 27:A:1287:C:H2'  | 27:A:1288:A:C8   | 2.56                     | 0.41              |
| 27:A:2376:G:H2'  | 27:A:2377:G:H8   | 1.86                     | 0.41              |
| 27:A:2642:G:H2'  | 27:A:2643:U:O4'  | 2.20                     | 0.41              |
| 27:A:2851:G:O2'  | 27:A:3005:A:N1   | 2.51                     | 0.41              |
| 27:A:3043:G:O2'  | 27:A:3045:C:OP2  | 2.34                     | 0.41              |
| 28:B:95:G:H2'    | 28:B:96:A:O4'    | 2.20                     | 0.41              |
| 2:F:94:GLU:N     | 2:F:94:GLU:CD    | 2.79                     | 0.41              |
| 5:I:92:GLY:HA3   | 5:I:95:TYR:HE2   | 1.85                     | 0.41              |
| 5:I:144:GLN:CD   | 27:A:2968:G:H21  | 2.27                     | 0.41              |
| 7:M:102:GLU:OE1  | 27:A:3004:C:N4   | 2.53                     | 0.41              |
| 11:R:9:ASN:OD1   | 11:R:10:ILE:N    | 2.53                     | 0.41              |
| 17:X:34:LEU:HD12 | 17:X:34:LEU:HA   | 1.92                     | 0.41              |
| 23:6:16:GLU:CD   | 23:6:50:PRO:HB2  | 2.45                     | 0.41              |
| 23:6:36:LEU:HD12 | 23:6:36:LEU:HA   | 1.92                     | 0.41              |
| 27:A:113:C:O2'   | 27:A:123:A:N3    | 2.49                     | 0.41              |
| 27:A:324:C:O2    | 27:A:452:G:N2    | 2.53                     | 0.41              |

*Continued on next page...*

*Continued from previous page...*

| Atom-1           | Atom-2           | Interatomic distance (Å) | Clash overlap (Å) |
|------------------|------------------|--------------------------|-------------------|
| 27:A:621:U:H2'   | 27:A:622:C:H6    | 1.83                     | 0.41              |
| 27:A:733:U:H2'   | 27:A:734:C:C6    | 2.55                     | 0.41              |
| 27:A:756:A:H3'   | 27:A:757:G:N2    | 2.35                     | 0.41              |
| 27:A:864:A:H4'   | 27:A:1386:G:N3   | 2.35                     | 0.41              |
| 27:A:973:G:H3'   | 27:A:974:G:C8    | 2.56                     | 0.41              |
| 27:A:1062:A:C4   | 27:A:2672:A:C2   | 3.09                     | 0.41              |
| 27:A:1665:U:H2'  | 27:A:1666:A:C8   | 2.56                     | 0.41              |
| 27:A:1715:A:H2'  | 27:A:1716:A:C8   | 2.56                     | 0.41              |
| 27:A:1901:C:H2'  | 27:A:1902:C:C6   | 2.56                     | 0.41              |
| 27:A:2181:C:H2'  | 27:A:2182:C:C6   | 2.56                     | 0.41              |
| 27:A:2671:G:O4'  | 27:A:2725:C:N4   | 2.54                     | 0.41              |
| 27:A:2801:A:O4'  | 27:A:2836:C:N4   | 2.54                     | 0.41              |
| 27:A:2902:A:H2'  | 27:A:2903:A:H8   | 1.82                     | 0.41              |
| 10:Q:65:GLU:O    | 10:Q:68:LYS:HG2  | 2.21                     | 0.41              |
| 11:R:18:ARG:HD2  | 11:R:107:TYR:CZ  | 2.55                     | 0.41              |
| 14:U:84:TYR:CE1  | 27:A:1302:G:H5'' | 2.56                     | 0.41              |
| 16:W:4:ILE:O     | 20:2:26:LYS:NZ   | 2.54                     | 0.41              |
| 27:A:673:C:H2'   | 27:A:674:U:H6    | 1.84                     | 0.41              |
| 27:A:812:C:H2'   | 27:A:813:C:C6    | 2.56                     | 0.41              |
| 27:A:965:U:H2'   | 27:A:966:U:C6    | 2.56                     | 0.41              |
| 27:A:2189:C:OP1  | 27:A:2190:A:O2'  | 2.30                     | 0.41              |
| 27:A:2359:G:N1   | 27:A:2379:G:H1'  | 2.36                     | 0.41              |
| 27:A:2760:G:C5   | 27:A:2761:U:C4   | 3.09                     | 0.41              |
| 1:E:226:MET:SD   | 1:E:231:HIS:HB2  | 2.61                     | 0.40              |
| 3:G:154:VAL:HG23 | 3:G:193:ASP:HB2  | 2.02                     | 0.40              |
| 3:G:178:ILE:HG13 | 3:G:179:SER:N    | 2.35                     | 0.40              |
| 8:N:16:ALA:HB2   | 8:N:52:VAL:HG21  | 2.03                     | 0.40              |
| 16:W:69:THR:OG1  | 16:W:72:GLY:O    | 2.34                     | 0.40              |
| 27:A:620:G:H2'   | 27:A:621:U:C6    | 2.55                     | 0.40              |
| 27:A:772:U:H2'   | 27:A:773:G:H8    | 1.85                     | 0.40              |
| 27:A:825:C:H2'   | 27:A:826:G:C8    | 2.56                     | 0.40              |
| 27:A:1069:G:C6   | 27:A:1083:G:C6   | 3.09                     | 0.40              |
| 27:A:1077:A:H5'' | 27:A:1078:G:OP1  | 2.21                     | 0.40              |
| 27:A:1523:U:H2'  | 27:A:1524:G:C8   | 2.56                     | 0.40              |
| 27:A:2425:U:O2'  | 27:A:2427:G:OP1  | 2.39                     | 0.40              |
| 27:A:2683:A:C2   | 27:A:2718:G:H1'  | 2.56                     | 0.40              |
| 28:B:110:G:H2'   | 28:B:111:C:C6    | 2.57                     | 0.40              |
| 3:G:19:GLU:OE2   | 3:G:19:GLU:C     | 2.64                     | 0.40              |
| 4:H:105:GLU:OE1  | 26:4:25:ARG:HG2  | 2.21                     | 0.40              |
| 10:Q:5:THR:HG23  | 27:A:2914:A:H62  | 1.86                     | 0.40              |
| 11:R:73:ILE:HG23 | 11:R:80:HIS:HD2  | 1.86                     | 0.40              |

*Continued on next page...*

*Continued from previous page...*

| Atom-1           | Atom-2           | Interatomic distance (Å) | Clash overlap (Å) |
|------------------|------------------|--------------------------|-------------------|
| 18:Z:12:ASN:HD21 | 27:A:2501:G:H3'  | 1.86                     | 0.40              |
| 23:6:35:ARG:HA   | 23:6:53:GLU:OE2  | 2.21                     | 0.40              |
| 27:A:206:A:H2'   | 27:A:207:C:O4'   | 2.21                     | 0.40              |
| 27:A:284:G:H1'   | 27:A:303:G:N1    | 2.36                     | 0.40              |
| 27:A:356:G:N2    | 27:A:357:U:O4    | 2.54                     | 0.40              |
| 27:A:1259:U:H1'  | 27:A:1261:A:C6   | 2.56                     | 0.40              |
| 27:A:1530:G:H22  | 27:A:1805:G:H1   | 1.65                     | 0.40              |
| 27:A:1706:A:H2'  | 27:A:1707:G:H8   | 1.86                     | 0.40              |
| 27:A:1781:C:H2'  | 27:A:1782:U:C6   | 2.57                     | 0.40              |
| 27:A:2516:U:H2'  | 27:A:2517:C:C6   | 2.57                     | 0.40              |
| 27:A:2780:C:H2'  | 27:A:2781:G:O4'  | 2.21                     | 0.40              |
| 2:F:139:HIS:NE2  | 27:A:1888:C:O2   | 2.53                     | 0.40              |
| 3:G:115:LEU:HD23 | 3:G:115:LEU:HA   | 1.84                     | 0.40              |
| 9:O:125:THR:HA   | 9:O:145:THR:O    | 2.22                     | 0.40              |
| 20:2:56:ARG:NH1  | 27:A:74:C:OP1    | 2.50                     | 0.40              |
| 26:4:38:CYS:SG   | 26:4:39:SER:N    | 2.94                     | 0.40              |
| 27:A:954:U:H2'   | 27:A:955:C:C6    | 2.55                     | 0.40              |
| 27:A:973:G:N3    | 27:A:2492:A:H2'  | 2.36                     | 0.40              |
| 27:A:1560:U:H2'  | 27:A:1561:C:C6   | 2.57                     | 0.40              |
| 27:A:2331:U:H2'  | 27:A:2332:U:C2   | 2.56                     | 0.40              |
| 27:A:2490:A:H4'  | 27:A:2491:A:N3   | 2.36                     | 0.40              |
| 3:G:206:SER:O    | 3:G:210:LYS:HB3  | 2.21                     | 0.40              |
| 8:N:63:VAL:HG23  | 8:N:64:ARG:HG3   | 2.02                     | 0.40              |
| 11:R:121:ARG:HG3 | 11:R:127:PHE:CE2 | 2.57                     | 0.40              |
| 21:3:44:ARG:O    | 21:3:47:ILE:HG13 | 2.21                     | 0.40              |
| 27:A:181:A:H2'   | 27:A:182:C:C6    | 2.55                     | 0.40              |
| 27:A:609:G:H2'   | 27:A:610:C:C6    | 2.56                     | 0.40              |
| 27:A:1771:U:H2'  | 27:A:1772:G:O4'  | 2.22                     | 0.40              |
| 27:A:2331:U:H1'  | 27:A:2405:A:N1   | 2.36                     | 0.40              |
| 27:A:2675:A:OP1  | 27:A:2721:A:N6   | 2.54                     | 0.40              |
| 1:E:256:ARG:HG2  | 27:A:2061:U:H5'' | 2.01                     | 0.40              |
| 1:E:270:ARG:HD3  | 1:E:273:ARG:NH2  | 2.32                     | 0.40              |
| 3:G:108:ALA:HB1  | 3:G:112:ARG:NH1  | 2.36                     | 0.40              |
| 4:H:139:LEU:HD13 | 4:H:144:MET:SD   | 2.61                     | 0.40              |
| 27:A:287:A:C6    | 27:A:300:G:C5    | 3.10                     | 0.40              |
| 27:A:390:G:H2'   | 27:A:391:G:C8    | 2.57                     | 0.40              |
| 27:A:667:A:H4'   | 27:A:2724:U:H5'  | 2.04                     | 0.40              |
| 27:A:2074:G:H21  | 27:A:2109:A:H62  | 1.69                     | 0.40              |
| 27:A:2219:U:H3'  | 27:A:2220:C:H2'  | 2.03                     | 0.40              |
| 27:A:2222:A:H4'  | 27:A:2948:C:O2'  | 2.21                     | 0.40              |
| 27:A:2331:U:H1'  | 27:A:2405:A:C2   | 2.57                     | 0.40              |

*Continued on next page...*

*Continued from previous page...*

| Atom-1          | Atom-2          | Interatomic distance (Å) | Clash overlap (Å) |
|-----------------|-----------------|--------------------------|-------------------|
| 27:A:2745:C:H2' | 27:A:2746:U:C6  | 2.57                     | 0.40              |
| 27:A:2751:C:H2' | 27:A:2752:U:O4' | 2.22                     | 0.40              |

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

| Mol | Chain | Analysed      | Favoured  | Allowed | Outliers | Percentiles |     |
|-----|-------|---------------|-----------|---------|----------|-------------|-----|
| 1   | E     | 273/278 (98%) | 262 (96%) | 11 (4%) | 0        | 100         | 100 |
| 2   | F     | 212/217 (98%) | 202 (95%) | 10 (5%) | 0        | 100         | 100 |
| 3   | G     | 207/215 (96%) | 201 (97%) | 6 (3%)  | 0        | 100         | 100 |
| 4   | H     | 179/187 (96%) | 167 (93%) | 12 (7%) | 0        | 100         | 100 |
| 5   | I     | 163/179 (91%) | 161 (99%) | 2 (1%)  | 0        | 100         | 100 |
| 6   | J     | 39/151 (26%)  | 39 (100%) | 0       | 0        | 100         | 100 |
| 7   | M     | 144/147 (98%) | 137 (95%) | 7 (5%)  | 0        | 100         | 100 |
| 8   | N     | 120/122 (98%) | 116 (97%) | 4 (3%)  | 0        | 100         | 100 |
| 9   | O     | 143/147 (97%) | 131 (92%) | 12 (8%) | 0        | 100         | 100 |
| 10  | Q     | 116/199 (58%) | 112 (97%) | 4 (3%)  | 0        | 100         | 100 |
| 11  | R     | 122/127 (96%) | 121 (99%) | 1 (1%)  | 0        | 100         | 100 |
| 12  | S     | 111/113 (98%) | 103 (93%) | 8 (7%)  | 0        | 100         | 100 |
| 13  | T     | 122/129 (95%) | 119 (98%) | 3 (2%)  | 0        | 100         | 100 |
| 14  | U     | 98/103 (95%)  | 94 (96%)  | 4 (4%)  | 0        | 100         | 100 |
| 15  | V     | 111/153 (72%) | 108 (97%) | 3 (3%)  | 0        | 100         | 100 |
| 16  | W     | 95/100 (95%)  | 93 (98%)  | 2 (2%)  | 0        | 100         | 100 |
| 17  | X     | 89/105 (85%)  | 86 (97%)  | 3 (3%)  | 0        | 100         | 100 |
| 18  | Z     | 75/88 (85%)   | 69 (92%)  | 6 (8%)  | 0        | 100         | 100 |

*Continued on next page...*

Continued from previous page...

| Mol | Chain | Analysed        | Favoured   | Allowed  | Outliers | Percentiles |     |
|-----|-------|-----------------|------------|----------|----------|-------------|-----|
| 19  | 1     | 61/64 (95%)     | 60 (98%)   | 1 (2%)   | 0        | 100         | 100 |
| 20  | 2     | 61/77 (79%)     | 59 (97%)   | 2 (3%)   | 0        | 100         | 100 |
| 21  | 3     | 56/61 (92%)     | 55 (98%)   | 1 (2%)   | 0        | 100         | 100 |
| 22  | 5     | 52/57 (91%)     | 52 (100%)  | 0        | 0        | 100         | 100 |
| 23  | 6     | 47/55 (86%)     | 42 (89%)   | 4 (8%)   | 1 (2%)   | 5           | 15  |
| 24  | 7     | 43/47 (92%)     | 43 (100%)  | 0        | 0        | 100         | 100 |
| 25  | 8     | 61/64 (95%)     | 60 (98%)   | 1 (2%)   | 0        | 100         | 100 |
| 26  | 4     | 46/75 (61%)     | 44 (96%)   | 2 (4%)   | 0        | 100         | 100 |
| All | All   | 2846/3260 (87%) | 2736 (96%) | 109 (4%) | 1 (0%)   | 100         | 100 |

All (1) Ramachandran outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 23  | 6     | 7   | VAL  |

### 5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

| Mol | Chain | Analysed       | Rotameric | Outliers | Percentiles |    |
|-----|-------|----------------|-----------|----------|-------------|----|
| 1   | E     | 215/218 (99%)  | 206 (96%) | 9 (4%)   | 26          | 55 |
| 2   | F     | 160/163 (98%)  | 154 (96%) | 6 (4%)   | 29          | 58 |
| 3   | G     | 169/173 (98%)  | 161 (95%) | 8 (5%)   | 23          | 51 |
| 4   | H     | 150/156 (96%)  | 145 (97%) | 5 (3%)   | 33          | 63 |
| 5   | I     | 139/150 (93%)  | 132 (95%) | 7 (5%)   | 22          | 48 |
| 6   | J     | 31/116 (27%)   | 28 (90%)  | 3 (10%)  | 8           | 20 |
| 7   | M     | 119/120 (99%)  | 115 (97%) | 4 (3%)   | 32          | 62 |
| 8   | N     | 100/100 (100%) | 98 (98%)  | 2 (2%)   | 48          | 76 |
| 9   | O     | 112/114 (98%)  | 109 (97%) | 3 (3%)   | 39          | 69 |
| 10  | Q     | 97/158 (61%)   | 96 (99%)  | 1 (1%)   | 68          | 86 |

Continued on next page...

*Continued from previous page...*

| Mol | Chain | Analysed        | Rotameric  | Outliers | Percentiles |     |
|-----|-------|-----------------|------------|----------|-------------|-----|
| 11  | R     | 92/94 (98%)     | 85 (92%)   | 7 (8%)   | 12          | 30  |
| 12  | S     | 100/100 (100%)  | 93 (93%)   | 7 (7%)   | 14          | 34  |
| 13  | T     | 97/99 (98%)     | 94 (97%)   | 3 (3%)   | 35          | 65  |
| 14  | U     | 81/83 (98%)     | 71 (88%)   | 10 (12%) | 4           | 12  |
| 15  | V     | 89/117 (76%)    | 87 (98%)   | 2 (2%)   | 45          | 74  |
| 16  | W     | 83/85 (98%)     | 79 (95%)   | 4 (5%)   | 23          | 50  |
| 17  | X     | 79/86 (92%)     | 72 (91%)   | 7 (9%)   | 9           | 23  |
| 18  | Z     | 56/63 (89%)     | 50 (89%)   | 6 (11%)  | 6           | 16  |
| 19  | 1     | 50/51 (98%)     | 49 (98%)   | 1 (2%)   | 48          | 76  |
| 20  | 2     | 58/66 (88%)     | 55 (95%)   | 3 (5%)   | 21          | 47  |
| 21  | 3     | 52/54 (96%)     | 49 (94%)   | 3 (6%)   | 18          | 42  |
| 22  | 5     | 43/46 (94%)     | 41 (95%)   | 2 (5%)   | 23          | 51  |
| 23  | 6     | 47/52 (90%)     | 47 (100%)  | 0        | 100         | 100 |
| 24  | 7     | 35/36 (97%)     | 34 (97%)   | 1 (3%)   | 37          | 67  |
| 25  | 8     | 53/54 (98%)     | 49 (92%)   | 4 (8%)   | 12          | 31  |
| 26  | 4     | 43/63 (68%)     | 42 (98%)   | 1 (2%)   | 44          | 73  |
| All | All   | 2350/2617 (90%) | 2241 (95%) | 109 (5%) | 25          | 51  |

All (109) residues with a non-rotameric sidechain are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1   | E     | 71  | ASP  |
| 1   | E     | 89  | THR  |
| 1   | E     | 118 | GLU  |
| 1   | E     | 131 | LEU  |
| 1   | E     | 158 | SER  |
| 1   | E     | 161 | VAL  |
| 1   | E     | 211 | ARG  |
| 1   | E     | 244 | ARG  |
| 1   | E     | 257 | THR  |
| 2   | F     | 41  | THR  |
| 2   | F     | 92  | VAL  |
| 2   | F     | 101 | LEU  |
| 2   | F     | 151 | ILE  |
| 2   | F     | 167 | SER  |
| 2   | F     | 192 | LEU  |

*Continued on next page...*

*Continued from previous page...*

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 3   | G     | 3   | LEU  |
| 3   | G     | 27  | VAL  |
| 3   | G     | 39  | THR  |
| 3   | G     | 55  | ARG  |
| 3   | G     | 63  | LYS  |
| 3   | G     | 85  | THR  |
| 3   | G     | 140 | SER  |
| 3   | G     | 178 | ILE  |
| 4   | H     | 57  | ILE  |
| 4   | H     | 96  | VAL  |
| 4   | H     | 159 | MET  |
| 4   | H     | 164 | VAL  |
| 4   | H     | 176 | LEU  |
| 5   | I     | 9   | VAL  |
| 5   | I     | 32  | THR  |
| 5   | I     | 54  | THR  |
| 5   | I     | 57  | ASP  |
| 5   | I     | 90  | ILE  |
| 5   | I     | 93  | VAL  |
| 5   | I     | 112 | HIS  |
| 6   | J     | 18  | THR  |
| 6   | J     | 30  | LEU  |
| 6   | J     | 38  | VAL  |
| 7   | M     | 14  | SER  |
| 7   | M     | 21  | SER  |
| 7   | M     | 109 | LEU  |
| 7   | M     | 112 | ASN  |
| 8   | N     | 61  | VAL  |
| 8   | N     | 81  | GLU  |
| 9   | O     | 73  | THR  |
| 9   | O     | 132 | SER  |
| 9   | O     | 145 | THR  |
| 10  | Q     | 15  | SER  |
| 11  | R     | 24  | ARG  |
| 11  | R     | 25  | LEU  |
| 11  | R     | 32  | THR  |
| 11  | R     | 58  | THR  |
| 11  | R     | 108 | THR  |
| 11  | R     | 113 | ILE  |
| 11  | R     | 116 | LEU  |
| 12  | S     | 1   | MET  |
| 12  | S     | 26  | ASN  |

*Continued on next page...*

*Continued from previous page...*

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 12  | S     | 69  | VAL  |
| 12  | S     | 82  | HIS  |
| 12  | S     | 84  | ASP  |
| 12  | S     | 87  | THR  |
| 12  | S     | 101 | GLU  |
| 13  | T     | 16  | THR  |
| 13  | T     | 88  | VAL  |
| 13  | T     | 112 | VAL  |
| 14  | U     | 3   | THR  |
| 14  | U     | 7   | VAL  |
| 14  | U     | 9   | THR  |
| 14  | U     | 22  | VAL  |
| 14  | U     | 24  | VAL  |
| 14  | U     | 36  | SER  |
| 14  | U     | 39  | VAL  |
| 14  | U     | 51  | LYS  |
| 14  | U     | 53  | ASP  |
| 14  | U     | 73  | ILE  |
| 15  | V     | 11  | THR  |
| 15  | V     | 51  | SER  |
| 16  | W     | 40  | THR  |
| 16  | W     | 69  | THR  |
| 16  | W     | 71  | THR  |
| 16  | W     | 96  | PHE  |
| 17  | X     | 3   | VAL  |
| 17  | X     | 20  | LYS  |
| 17  | X     | 29  | ASP  |
| 17  | X     | 38  | VAL  |
| 17  | X     | 61  | THR  |
| 17  | X     | 83  | VAL  |
| 17  | X     | 100 | THR  |
| 18  | Z     | 10  | SER  |
| 18  | Z     | 12  | ASN  |
| 18  | Z     | 38  | VAL  |
| 18  | Z     | 49  | VAL  |
| 18  | Z     | 72  | LYS  |
| 18  | Z     | 76  | LYS  |
| 19  | 1     | 45  | ASN  |
| 20  | 2     | 5   | THR  |
| 20  | 2     | 6   | THR  |
| 20  | 2     | 53  | GLU  |
| 21  | 3     | 12  | THR  |

*Continued on next page...*

*Continued from previous page...*

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 21  | 3     | 28  | LEU  |
| 21  | 3     | 35  | VAL  |
| 22  | 5     | 13  | THR  |
| 22  | 5     | 39  | VAL  |
| 24  | 7     | 46  | THR  |
| 25  | 8     | 6   | THR  |
| 25  | 8     | 23  | VAL  |
| 25  | 8     | 25  | GLN  |
| 25  | 8     | 50  | VAL  |
| 26  | 4     | 22  | PHE  |

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 2   | F     | 178 | GLN  |
| 3   | G     | 41  | GLN  |
| 3   | G     | 91  | HIS  |
| 3   | G     | 100 | GLN  |
| 3   | G     | 184 | ASN  |
| 4   | H     | 146 | HIS  |
| 5   | I     | 103 | ASN  |
| 8   | N     | 3   | GLN  |
| 13  | T     | 39  | GLN  |
| 19  | 1     | 47  | GLN  |
| 20  | 2     | 35  | GLN  |
| 23  | 6     | 22  | ASN  |
| 25  | 8     | 25  | GLN  |
| 25  | 8     | 63  | ASN  |

### 5.3.3 RNA ⓘ

| Mol | Chain | Analysed        | Backbone Outliers | Pucker Outliers |
|-----|-------|-----------------|-------------------|-----------------|
| 27  | A     | 3013/3119 (96%) | 568 (18%)         | 15 (0%)         |
| 28  | B     | 116/118 (98%)   | 17 (14%)          | 1 (0%)          |
| All | All   | 3129/3237 (96%) | 585 (18%)         | 16 (0%)         |

All (585) RNA backbone outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 27  | A     | 7   | U    |

*Continued on next page...*

*Continued from previous page...*

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 27  | A     | 9   | U    |
| 27  | A     | 12  | G    |
| 27  | A     | 20  | G    |
| 27  | A     | 24  | G    |
| 27  | A     | 29  | C    |
| 27  | A     | 33  | G    |
| 27  | A     | 47  | U    |
| 27  | A     | 55  | G    |
| 27  | A     | 60  | A    |
| 27  | A     | 68  | A    |
| 27  | A     | 71  | A    |
| 27  | A     | 72  | G    |
| 27  | A     | 81  | A    |
| 27  | A     | 82  | G    |
| 27  | A     | 89  | A    |
| 27  | A     | 90  | C    |
| 27  | A     | 91  | C    |
| 27  | A     | 94  | G    |
| 27  | A     | 95  | C    |
| 27  | A     | 98  | U    |
| 27  | A     | 99  | G    |
| 27  | A     | 115 | A    |
| 27  | A     | 116 | A    |
| 27  | A     | 117 | U    |
| 27  | A     | 125 | C    |
| 27  | A     | 148 | A    |
| 27  | A     | 164 | A    |
| 27  | A     | 172 | C    |
| 27  | A     | 180 | A    |
| 27  | A     | 195 | A    |
| 27  | A     | 198 | A    |
| 27  | A     | 212 | A    |
| 27  | A     | 214 | G    |
| 27  | A     | 215 | A    |
| 27  | A     | 221 | A    |
| 27  | A     | 227 | A    |
| 27  | A     | 229 | U    |
| 27  | A     | 230 | G    |
| 27  | A     | 248 | G    |
| 27  | A     | 250 | G    |
| 27  | A     | 265 | A    |
| 27  | A     | 267 | G    |

*Continued on next page...*

*Continued from previous page...*

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 27  | A     | 270 | U    |
| 27  | A     | 271 | A    |
| 27  | A     | 272 | A    |
| 27  | A     | 275 | C    |
| 27  | A     | 283 | U    |
| 27  | A     | 285 | U    |
| 27  | A     | 286 | G    |
| 27  | A     | 290 | C    |
| 27  | A     | 297 | G    |
| 27  | A     | 298 | G    |
| 27  | A     | 299 | G    |
| 27  | A     | 300 | G    |
| 27  | A     | 301 | U    |
| 27  | A     | 302 | U    |
| 27  | A     | 303 | G    |
| 27  | A     | 305 | G    |
| 27  | A     | 313 | G    |
| 27  | A     | 314 | G    |
| 27  | A     | 315 | U    |
| 27  | A     | 317 | G    |
| 27  | A     | 318 | U    |
| 27  | A     | 319 | G    |
| 27  | A     | 322 | A    |
| 27  | A     | 324 | C    |
| 27  | A     | 330 | U    |
| 27  | A     | 331 | U    |
| 27  | A     | 332 | C    |
| 27  | A     | 336 | C    |
| 27  | A     | 337 | U    |
| 27  | A     | 338 | C    |
| 27  | A     | 344 | G    |
| 27  | A     | 346 | C    |
| 27  | A     | 350 | A    |
| 27  | A     | 351 | G    |
| 27  | A     | 352 | G    |
| 27  | A     | 353 | G    |
| 27  | A     | 357 | U    |
| 27  | A     | 358 | G    |
| 27  | A     | 359 | A    |
| 27  | A     | 361 | A    |
| 27  | A     | 364 | A    |
| 27  | A     | 370 | U    |

*Continued on next page...*

*Continued from previous page...*

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 27  | A     | 371 | G    |
| 27  | A     | 384 | G    |
| 27  | A     | 393 | U    |
| 27  | A     | 399 | G    |
| 27  | A     | 412 | A    |
| 27  | A     | 413 | G    |
| 27  | A     | 424 | G    |
| 27  | A     | 434 | G    |
| 27  | A     | 437 | G    |
| 27  | A     | 444 | U    |
| 27  | A     | 445 | U    |
| 27  | A     | 446 | G    |
| 27  | A     | 450 | G    |
| 27  | A     | 452 | G    |
| 27  | A     | 454 | U    |
| 27  | A     | 460 | G    |
| 27  | A     | 474 | G    |
| 27  | A     | 489 | A    |
| 27  | A     | 490 | A    |
| 27  | A     | 493 | U    |
| 27  | A     | 494 | G    |
| 27  | A     | 509 | U    |
| 27  | A     | 512 | G    |
| 27  | A     | 514 | C    |
| 27  | A     | 523 | U    |
| 27  | A     | 543 | U    |
| 27  | A     | 544 | U    |
| 27  | A     | 566 | A    |
| 27  | A     | 568 | A    |
| 27  | A     | 569 | G    |
| 27  | A     | 589 | A    |
| 27  | A     | 591 | G    |
| 27  | A     | 592 | A    |
| 27  | A     | 594 | U    |
| 27  | A     | 595 | A    |
| 27  | A     | 596 | C    |
| 27  | A     | 617 | U    |
| 27  | A     | 618 | C    |
| 27  | A     | 619 | C    |
| 27  | A     | 620 | G    |
| 27  | A     | 623 | A    |
| 27  | A     | 635 | G    |

*Continued on next page...*

*Continued from previous page...*

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 27  | A     | 636 | U    |
| 27  | A     | 637 | G    |
| 27  | A     | 638 | U    |
| 27  | A     | 639 | C    |
| 27  | A     | 640 | G    |
| 27  | A     | 642 | G    |
| 27  | A     | 644 | G    |
| 27  | A     | 655 | G    |
| 27  | A     | 664 | A    |
| 27  | A     | 665 | G    |
| 27  | A     | 667 | A    |
| 27  | A     | 679 | G    |
| 27  | A     | 684 | G    |
| 27  | A     | 685 | G    |
| 27  | A     | 696 | A    |
| 27  | A     | 706 | G    |
| 27  | A     | 707 | G    |
| 27  | A     | 708 | G    |
| 27  | A     | 709 | U    |
| 27  | A     | 721 | A    |
| 27  | A     | 728 | G    |
| 27  | A     | 731 | A    |
| 27  | A     | 738 | A    |
| 27  | A     | 740 | A    |
| 27  | A     | 747 | A    |
| 27  | A     | 754 | C    |
| 27  | A     | 756 | A    |
| 27  | A     | 758 | A    |
| 27  | A     | 759 | G    |
| 27  | A     | 760 | U    |
| 27  | A     | 764 | U    |
| 27  | A     | 766 | G    |
| 27  | A     | 768 | G    |
| 27  | A     | 784 | G    |
| 27  | A     | 785 | A    |
| 27  | A     | 794 | G    |
| 27  | A     | 801 | U    |
| 27  | A     | 832 | G    |
| 27  | A     | 838 | G    |
| 27  | A     | 839 | U    |
| 27  | A     | 845 | C    |
| 27  | A     | 862 | U    |

*Continued on next page...*

*Continued from previous page...*

| Mol | Chain | Res  | Type |
|-----|-------|------|------|
| 27  | A     | 863  | G    |
| 27  | A     | 868  | C    |
| 27  | A     | 872  | G    |
| 27  | A     | 878  | G    |
| 27  | A     | 879  | A    |
| 27  | A     | 880  | G    |
| 27  | A     | 890  | G    |
| 27  | A     | 891  | G    |
| 27  | A     | 897  | A    |
| 27  | A     | 899  | G    |
| 27  | A     | 900  | G    |
| 27  | A     | 907  | A    |
| 27  | A     | 920  | G    |
| 27  | A     | 927  | C    |
| 27  | A     | 942  | U    |
| 27  | A     | 960  | G    |
| 27  | A     | 961  | U    |
| 27  | A     | 972  | A    |
| 27  | A     | 975  | U    |
| 27  | A     | 981  | U    |
| 27  | A     | 982  | A    |
| 27  | A     | 987  | A    |
| 27  | A     | 988  | U    |
| 27  | A     | 989  | G    |
| 27  | A     | 990  | G    |
| 27  | A     | 991  | C    |
| 27  | A     | 994  | A    |
| 27  | A     | 995  | U    |
| 27  | A     | 1001 | C    |
| 27  | A     | 1002 | C    |
| 27  | A     | 1003 | A    |
| 27  | A     | 1004 | C    |
| 27  | A     | 1005 | A    |
| 27  | A     | 1007 | G    |
| 27  | A     | 1008 | G    |
| 27  | A     | 1009 | U    |
| 27  | A     | 1010 | U    |
| 27  | A     | 1012 | C    |
| 27  | A     | 1013 | U    |
| 27  | A     | 1014 | G    |
| 27  | A     | 1018 | U    |
| 27  | A     | 1019 | C    |

*Continued on next page...*

*Continued from previous page...*

| Mol | Chain | Res  | Type |
|-----|-------|------|------|
| 27  | A     | 1022 | C    |
| 27  | A     | 1025 | A    |
| 27  | A     | 1030 | C    |
| 27  | A     | 1047 | A    |
| 27  | A     | 1048 | A    |
| 27  | A     | 1049 | G    |
| 27  | A     | 1058 | A    |
| 27  | A     | 1063 | G    |
| 27  | A     | 1076 | A    |
| 27  | A     | 1078 | G    |
| 27  | A     | 1085 | G    |
| 27  | A     | 1092 | G    |
| 27  | A     | 1101 | A    |
| 27  | A     | 1114 | G    |
| 27  | A     | 1127 | A    |
| 27  | A     | 1130 | C    |
| 27  | A     | 1131 | G    |
| 27  | A     | 1144 | A    |
| 27  | A     | 1151 | U    |
| 27  | A     | 1158 | U    |
| 27  | A     | 1164 | A    |
| 27  | A     | 1165 | G    |
| 27  | A     | 1230 | G    |
| 27  | A     | 1232 | G    |
| 27  | A     | 1235 | U    |
| 27  | A     | 1238 | G    |
| 27  | A     | 1240 | G    |
| 27  | A     | 1242 | C    |
| 27  | A     | 1245 | U    |
| 27  | A     | 1248 | U    |
| 27  | A     | 1250 | U    |
| 27  | A     | 1251 | A    |
| 27  | A     | 1252 | G    |
| 27  | A     | 1253 | C    |
| 27  | A     | 1254 | G    |
| 27  | A     | 1260 | C    |
| 27  | A     | 1261 | A    |
| 27  | A     | 1292 | U    |
| 27  | A     | 1293 | G    |
| 27  | A     | 1298 | C    |
| 27  | A     | 1335 | G    |
| 27  | A     | 1344 | A    |

*Continued on next page...*

*Continued from previous page...*

| Mol | Chain | Res  | Type |
|-----|-------|------|------|
| 27  | A     | 1352 | A    |
| 27  | A     | 1353 | G    |
| 27  | A     | 1359 | G    |
| 27  | A     | 1365 | G    |
| 27  | A     | 1371 | G    |
| 27  | A     | 1386 | G    |
| 27  | A     | 1387 | A    |
| 27  | A     | 1389 | U    |
| 27  | A     | 1404 | C    |
| 27  | A     | 1415 | A    |
| 27  | A     | 1416 | A    |
| 27  | A     | 1427 | U    |
| 27  | A     | 1436 | C    |
| 27  | A     | 1456 | G    |
| 27  | A     | 1459 | U    |
| 27  | A     | 1465 | C    |
| 27  | A     | 1467 | U    |
| 27  | A     | 1480 | A    |
| 27  | A     | 1493 | A    |
| 27  | A     | 1494 | U    |
| 27  | A     | 1499 | A    |
| 27  | A     | 1507 | G    |
| 27  | A     | 1508 | A    |
| 27  | A     | 1510 | A    |
| 27  | A     | 1511 | U    |
| 27  | A     | 1522 | G    |
| 27  | A     | 1531 | C    |
| 27  | A     | 1533 | U    |
| 27  | A     | 1534 | C    |
| 27  | A     | 1539 | A    |
| 27  | A     | 1540 | U    |
| 27  | A     | 1543 | A    |
| 27  | A     | 1550 | G    |
| 27  | A     | 1551 | U    |
| 27  | A     | 1552 | A    |
| 27  | A     | 1553 | C    |
| 27  | A     | 1554 | U    |
| 27  | A     | 1609 | G    |
| 27  | A     | 1625 | G    |
| 27  | A     | 1627 | U    |
| 27  | A     | 1628 | A    |
| 27  | A     | 1629 | G    |

*Continued on next page...*

*Continued from previous page...*

| Mol | Chain | Res  | Type |
|-----|-------|------|------|
| 27  | A     | 1630 | U    |
| 27  | A     | 1632 | G    |
| 27  | A     | 1633 | U    |
| 27  | A     | 1639 | G    |
| 27  | A     | 1640 | A    |
| 27  | A     | 1641 | U    |
| 27  | A     | 1648 | A    |
| 27  | A     | 1649 | C    |
| 27  | A     | 1670 | G    |
| 27  | A     | 1676 | G    |
| 27  | A     | 1679 | A    |
| 27  | A     | 1680 | A    |
| 27  | A     | 1681 | U    |
| 27  | A     | 1703 | G    |
| 27  | A     | 1710 | A    |
| 27  | A     | 1711 | G    |
| 27  | A     | 1714 | A    |
| 27  | A     | 1716 | A    |
| 27  | A     | 1717 | U    |
| 27  | A     | 1724 | G    |
| 27  | A     | 1728 | U    |
| 27  | A     | 1731 | A    |
| 27  | A     | 1737 | A    |
| 27  | A     | 1738 | G    |
| 27  | A     | 1754 | G    |
| 27  | A     | 1755 | A    |
| 27  | A     | 1756 | G    |
| 27  | A     | 1757 | U    |
| 27  | A     | 1767 | U    |
| 27  | A     | 1786 | G    |
| 27  | A     | 1789 | A    |
| 27  | A     | 1798 | U    |
| 27  | A     | 1826 | A    |
| 27  | A     | 1864 | U    |
| 27  | A     | 1866 | C    |
| 27  | A     | 1867 | G    |
| 27  | A     | 1871 | G    |
| 27  | A     | 1872 | A    |
| 27  | A     | 1892 | G    |
| 27  | A     | 1895 | A    |
| 27  | A     | 1933 | G    |
| 27  | A     | 1946 | U    |

*Continued on next page...*

*Continued from previous page...*

| Mol | Chain | Res  | Type |
|-----|-------|------|------|
| 27  | A     | 1947 | U    |
| 27  | A     | 1949 | C    |
| 27  | A     | 1955 | A    |
| 27  | A     | 1961 | G    |
| 27  | A     | 1973 | C    |
| 27  | A     | 1975 | A    |
| 27  | A     | 1981 | U    |
| 27  | A     | 1990 | A    |
| 27  | A     | 1999 | U    |
| 27  | A     | 2003 | A    |
| 27  | A     | 2004 | A    |
| 27  | A     | 2017 | C    |
| 27  | A     | 2018 | G    |
| 27  | A     | 2026 | A    |
| 27  | A     | 2033 | U    |
| 27  | A     | 2046 | A    |
| 27  | A     | 2064 | A    |
| 27  | A     | 2065 | A    |
| 27  | A     | 2074 | G    |
| 27  | A     | 2075 | G    |
| 27  | A     | 2085 | C    |
| 27  | A     | 2086 | U    |
| 27  | A     | 2087 | C    |
| 27  | A     | 2088 | C    |
| 27  | A     | 2089 | C    |
| 27  | A     | 2090 | U    |
| 27  | A     | 2091 | U    |
| 27  | A     | 2092 | U    |
| 27  | A     | 2093 | G    |
| 27  | A     | 2094 | G    |
| 27  | A     | 2095 | G    |
| 27  | A     | 2096 | G    |
| 27  | A     | 2105 | G    |
| 27  | A     | 2106 | A    |
| 27  | A     | 2107 | G    |
| 27  | A     | 2130 | G    |
| 27  | A     | 2137 | A    |
| 27  | A     | 2141 | U    |
| 27  | A     | 2153 | G    |
| 27  | A     | 2154 | G    |
| 27  | A     | 2160 | A    |
| 27  | A     | 2161 | A    |

*Continued on next page...*

*Continued from previous page...*

| Mol | Chain | Res  | Type |
|-----|-------|------|------|
| 27  | A     | 2162 | A    |
| 27  | A     | 2163 | U    |
| 27  | A     | 2179 | U    |
| 27  | A     | 2191 | C    |
| 27  | A     | 2194 | A    |
| 27  | A     | 2195 | U    |
| 27  | A     | 2196 | G    |
| 27  | A     | 2215 | U    |
| 27  | A     | 2217 | U    |
| 27  | A     | 2221 | A    |
| 27  | A     | 2244 | A    |
| 27  | A     | 2247 | A    |
| 27  | A     | 2251 | G    |
| 27  | A     | 2254 | A    |
| 27  | A     | 2255 | A    |
| 27  | A     | 2256 | G    |
| 27  | A     | 2257 | A    |
| 27  | A     | 2263 | G    |
| 27  | A     | 2267 | C    |
| 27  | A     | 2279 | C    |
| 27  | A     | 2280 | G    |
| 27  | A     | 2284 | A    |
| 27  | A     | 2285 | G    |
| 27  | A     | 2286 | A    |
| 27  | A     | 2287 | C    |
| 27  | A     | 2316 | G    |
| 27  | A     | 2320 | C    |
| 27  | A     | 2322 | C    |
| 27  | A     | 2324 | A    |
| 27  | A     | 2325 | U    |
| 27  | A     | 2328 | G    |
| 27  | A     | 2329 | G    |
| 27  | A     | 2330 | U    |
| 27  | A     | 2331 | U    |
| 27  | A     | 2334 | U    |
| 27  | A     | 2335 | G    |
| 27  | A     | 2338 | G    |
| 27  | A     | 2339 | G    |
| 27  | A     | 2340 | A    |
| 27  | A     | 2341 | U    |
| 27  | A     | 2342 | A    |
| 27  | A     | 2343 | G    |

*Continued on next page...*

*Continued from previous page...*

| Mol | Chain | Res  | Type |
|-----|-------|------|------|
| 27  | A     | 2345 | U    |
| 27  | A     | 2346 | G    |
| 27  | A     | 2347 | G    |
| 27  | A     | 2351 | A    |
| 27  | A     | 2353 | U    |
| 27  | A     | 2354 | G    |
| 27  | A     | 2355 | U    |
| 27  | A     | 2356 | G    |
| 27  | A     | 2357 | A    |
| 27  | A     | 2368 | C    |
| 27  | A     | 2370 | A    |
| 27  | A     | 2371 | G    |
| 27  | A     | 2372 | U    |
| 27  | A     | 2380 | G    |
| 27  | A     | 2382 | G    |
| 27  | A     | 2384 | C    |
| 27  | A     | 2386 | U    |
| 27  | A     | 2387 | U    |
| 27  | A     | 2388 | G    |
| 27  | A     | 2389 | U    |
| 27  | A     | 2390 | U    |
| 27  | A     | 2393 | A    |
| 27  | A     | 2394 | A    |
| 27  | A     | 2395 | U    |
| 27  | A     | 2396 | A    |
| 27  | A     | 2399 | A    |
| 27  | A     | 2401 | U    |
| 27  | A     | 2402 | C    |
| 27  | A     | 2403 | U    |
| 27  | A     | 2404 | G    |
| 27  | A     | 2407 | C    |
| 27  | A     | 2408 | G    |
| 27  | A     | 2410 | A    |
| 27  | A     | 2413 | G    |
| 27  | A     | 2421 | A    |
| 27  | A     | 2422 | A    |
| 27  | A     | 2427 | G    |
| 27  | A     | 2434 | A    |
| 27  | A     | 2436 | A    |
| 27  | A     | 2447 | G    |
| 27  | A     | 2449 | A    |
| 27  | A     | 2462 | G    |

*Continued on next page...*

*Continued from previous page...*

| Mol | Chain | Res  | Type |
|-----|-------|------|------|
| 27  | A     | 2463 | G    |
| 27  | A     | 2467 | U    |
| 27  | A     | 2503 | G    |
| 27  | A     | 2504 | G    |
| 27  | A     | 2507 | C    |
| 27  | A     | 2511 | A    |
| 27  | A     | 2512 | A    |
| 27  | A     | 2529 | A    |
| 27  | A     | 2532 | G    |
| 27  | A     | 2544 | U    |
| 27  | A     | 2545 | G    |
| 27  | A     | 2548 | U    |
| 27  | A     | 2549 | G    |
| 27  | A     | 2558 | C    |
| 27  | A     | 2559 | A    |
| 27  | A     | 2560 | A    |
| 27  | A     | 2571 | C    |
| 27  | A     | 2574 | C    |
| 27  | A     | 2607 | G    |
| 27  | A     | 2609 | A    |
| 27  | A     | 2626 | U    |
| 27  | A     | 2627 | C    |
| 27  | A     | 2630 | A    |
| 27  | A     | 2647 | U    |
| 27  | A     | 2649 | A    |
| 27  | A     | 2653 | G    |
| 27  | A     | 2654 | A    |
| 27  | A     | 2655 | U    |
| 27  | A     | 2659 | A    |
| 27  | A     | 2665 | C    |
| 27  | A     | 2672 | A    |
| 27  | A     | 2673 | U    |
| 27  | A     | 2677 | A    |
| 27  | A     | 2678 | G    |
| 27  | A     | 2679 | G    |
| 27  | A     | 2688 | C    |
| 27  | A     | 2693 | A    |
| 27  | A     | 2694 | G    |
| 27  | A     | 2704 | C    |
| 27  | A     | 2705 | G    |
| 27  | A     | 2714 | G    |
| 27  | A     | 2715 | U    |

*Continued on next page...*

*Continued from previous page...*

| Mol | Chain | Res  | Type |
|-----|-------|------|------|
| 27  | A     | 2718 | G    |
| 27  | A     | 2722 | C    |
| 27  | A     | 2726 | G    |
| 27  | A     | 2727 | A    |
| 27  | A     | 2729 | G    |
| 27  | A     | 2730 | U    |
| 27  | A     | 2731 | C    |
| 27  | A     | 2742 | A    |
| 27  | A     | 2744 | C    |
| 27  | A     | 2749 | G    |
| 27  | A     | 2753 | G    |
| 27  | A     | 2754 | G    |
| 27  | A     | 2759 | G    |
| 27  | A     | 2761 | U    |
| 27  | A     | 2766 | A    |
| 27  | A     | 2786 | U    |
| 27  | A     | 2790 | A    |
| 27  | A     | 2791 | G    |
| 27  | A     | 2796 | A    |
| 27  | A     | 2797 | C    |
| 27  | A     | 2826 | A    |
| 27  | A     | 2827 | G    |
| 27  | A     | 2833 | U    |
| 27  | A     | 2837 | U    |
| 27  | A     | 2853 | C    |
| 27  | A     | 2854 | A    |
| 27  | A     | 2862 | G    |
| 27  | A     | 2865 | G    |
| 27  | A     | 2870 | C    |
| 27  | A     | 2876 | C    |
| 27  | A     | 2913 | U    |
| 27  | A     | 2915 | C    |
| 27  | A     | 2926 | A    |
| 27  | A     | 2936 | C    |
| 27  | A     | 2938 | G    |
| 27  | A     | 2948 | C    |
| 27  | A     | 2950 | C    |
| 27  | A     | 2957 | A    |
| 27  | A     | 2968 | G    |
| 27  | A     | 2974 | A    |
| 27  | A     | 2981 | A    |
| 27  | A     | 2982 | A    |

*Continued on next page...*

*Continued from previous page...*

| Mol | Chain | Res  | Type |
|-----|-------|------|------|
| 27  | A     | 2985 | G    |
| 27  | A     | 2989 | A    |
| 27  | A     | 3002 | A    |
| 27  | A     | 3009 | U    |
| 27  | A     | 3013 | C    |
| 27  | A     | 3014 | A    |
| 27  | A     | 3020 | U    |
| 27  | A     | 3021 | A    |
| 27  | A     | 3022 | G    |
| 27  | A     | 3029 | U    |
| 27  | A     | 3039 | C    |
| 27  | A     | 3042 | A    |
| 27  | A     | 3056 | A    |
| 27  | A     | 3082 | U    |
| 27  | A     | 3088 | C    |
| 27  | A     | 3093 | A    |
| 27  | A     | 3105 | C    |
| 27  | A     | 3106 | C    |
| 27  | A     | 3107 | G    |
| 27  | A     | 3114 | A    |
| 27  | A     | 3115 | A    |
| 28  | B     | 3    | U    |
| 28  | B     | 4    | A    |
| 28  | B     | 9    | G    |
| 28  | B     | 11   | U    |
| 28  | B     | 12   | C    |
| 28  | B     | 13   | C    |
| 28  | B     | 30   | G    |
| 28  | B     | 36   | U    |
| 28  | B     | 42   | C    |
| 28  | B     | 54   | A    |
| 28  | B     | 57   | U    |
| 28  | B     | 68   | G    |
| 28  | B     | 87   | U    |
| 28  | B     | 88   | C    |
| 28  | B     | 89   | C    |
| 28  | B     | 107  | A    |
| 28  | B     | 115  | A    |

All (16) RNA pucker outliers are listed below:

*Continued on next page...*

*Continued from previous page...*

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
|-----|-------|-----|------|

| Mol | Chain | Res  | Type |
|-----|-------|------|------|
| 27  | A     | 89   | A    |
| 27  | A     | 97   | U    |
| 27  | A     | 316  | U    |
| 27  | A     | 357  | U    |
| 27  | A     | 445  | U    |
| 27  | A     | 643  | G    |
| 27  | A     | 919  | A    |
| 27  | A     | 974  | G    |
| 27  | A     | 1002 | C    |
| 27  | A     | 1004 | C    |
| 27  | A     | 1084 | U    |
| 27  | A     | 2094 | G    |
| 27  | A     | 2350 | G    |
| 27  | A     | 2381 | A    |
| 27  | A     | 2729 | G    |
| 28  | B     | 10   | G    |

## 5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

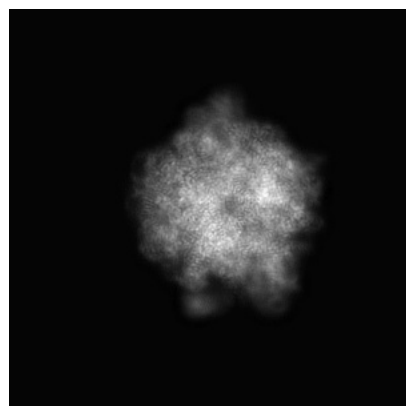
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-37552. These allow visual inspection of the internal detail of the map and identification of artifacts.

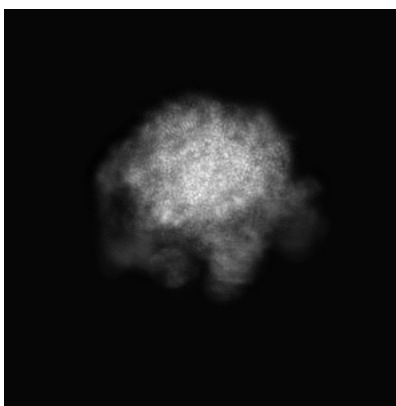
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

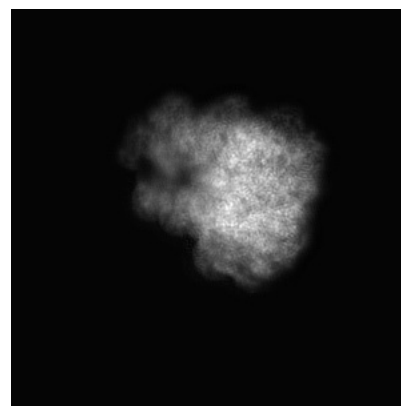
#### 6.1.1 Primary map



X

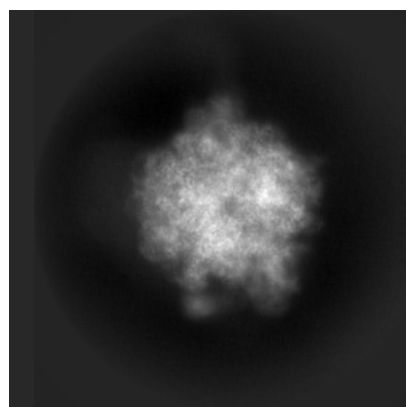


Y

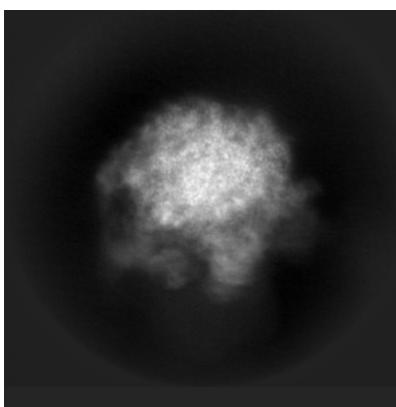


Z

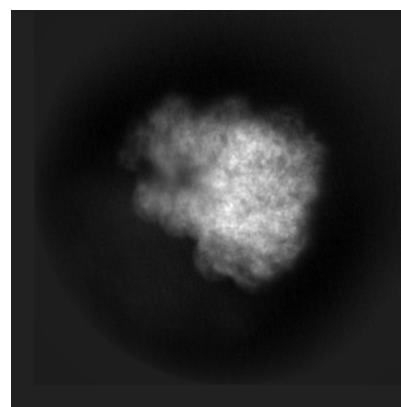
#### 6.1.2 Raw map



X



Y

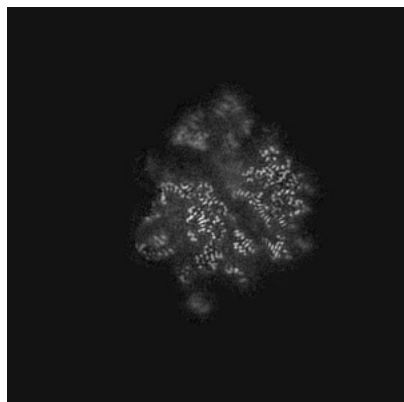


Z

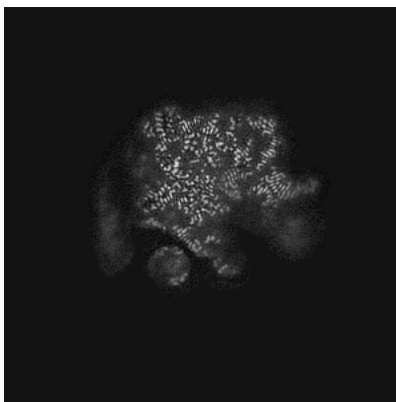
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

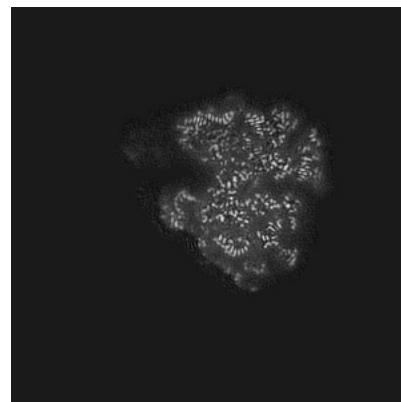
### 6.2.1 Primary map



X Index: 190

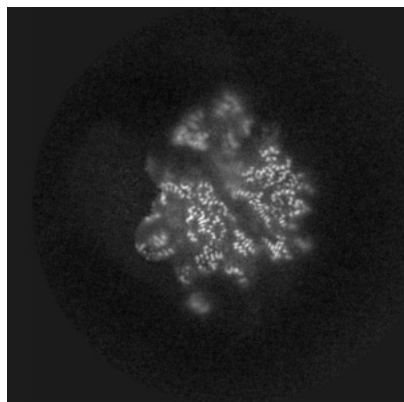


Y Index: 190

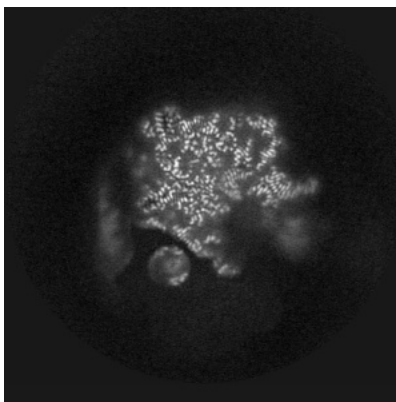


Z Index: 190

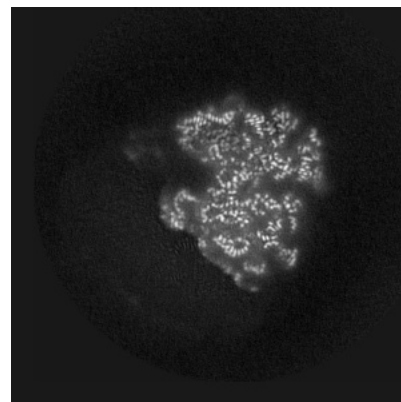
### 6.2.2 Raw map



X Index: 190



Y Index: 190

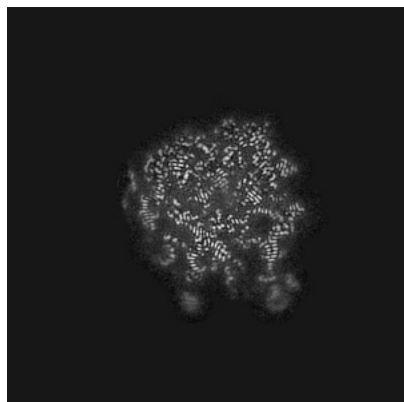


Z Index: 190

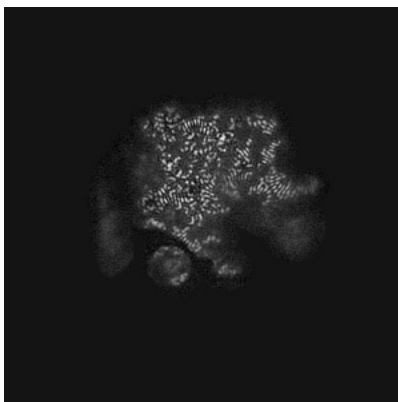
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

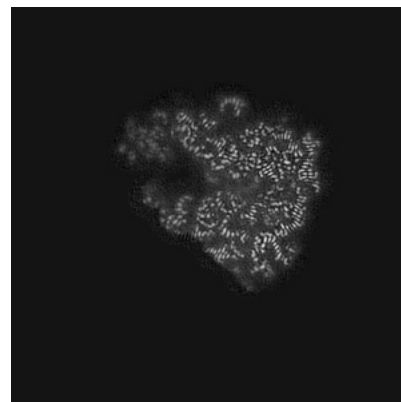
### 6.3.1 Primary map



X Index: 230

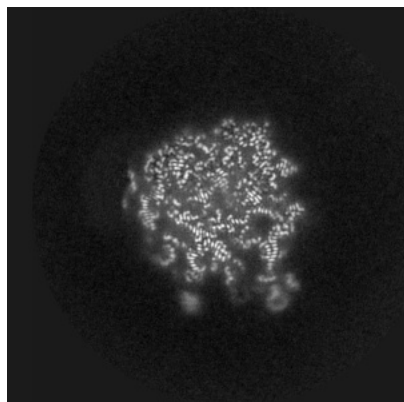


Y Index: 191

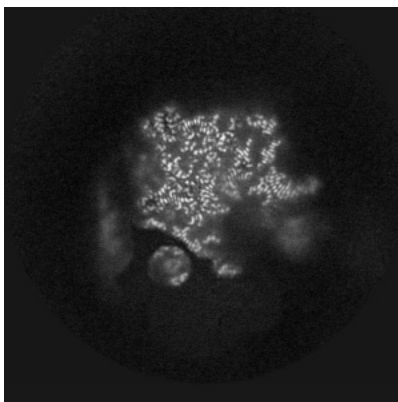


Z Index: 199

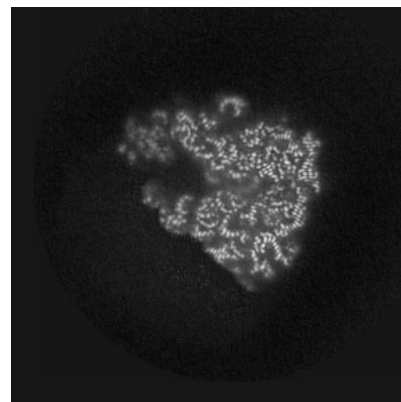
### 6.3.2 Raw map



X Index: 230



Y Index: 191

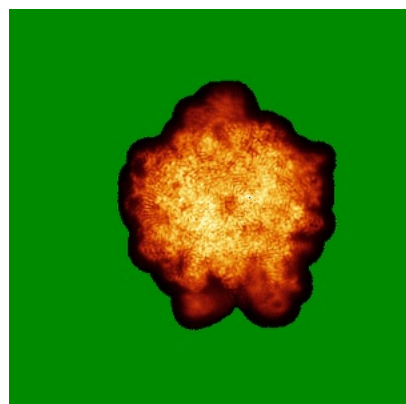


Z Index: 199

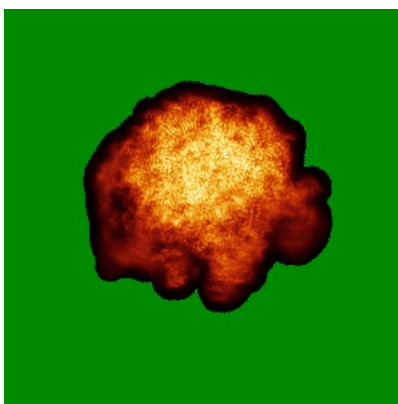
The images above show the largest variance slices of the map in three orthogonal directions.

## 6.4 Orthogonal standard-deviation projections (False-color) [i](#)

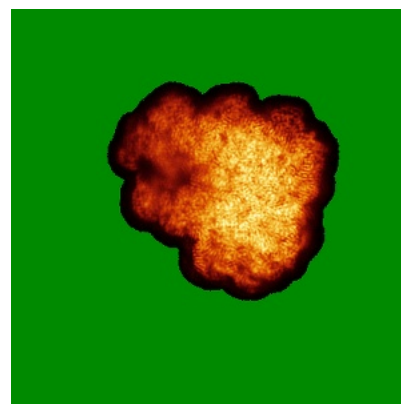
### 6.4.1 Primary map



X

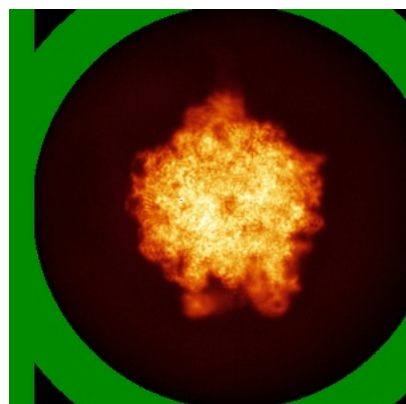


Y

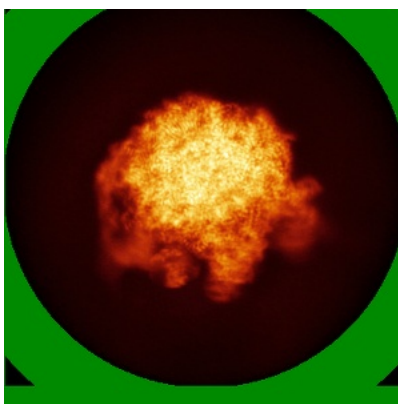


Z

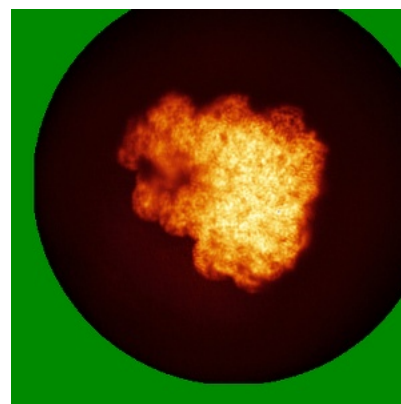
### 6.4.2 Raw map



X



Y

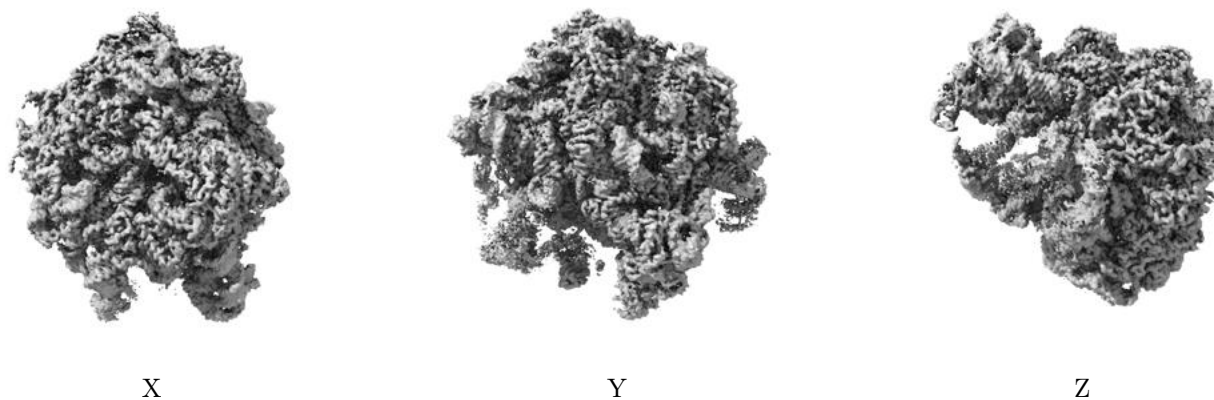


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

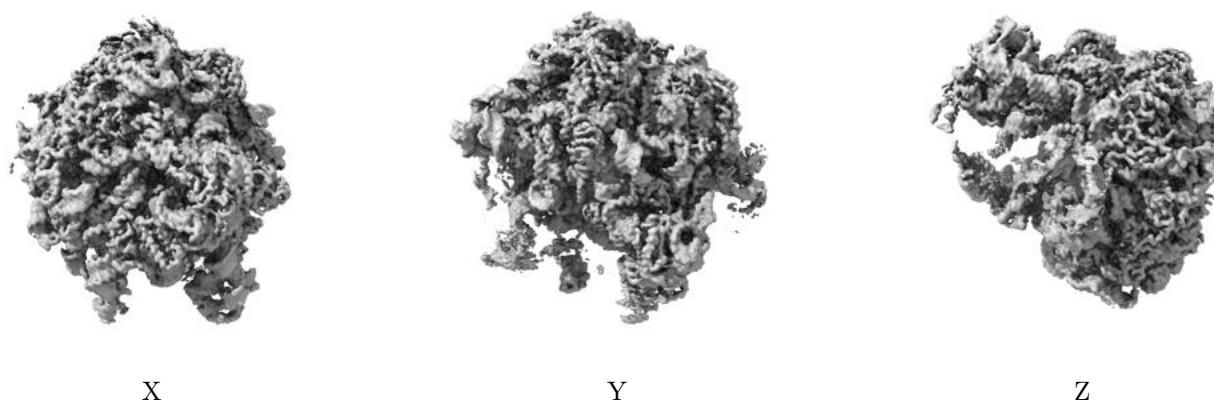
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.045. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

### 6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

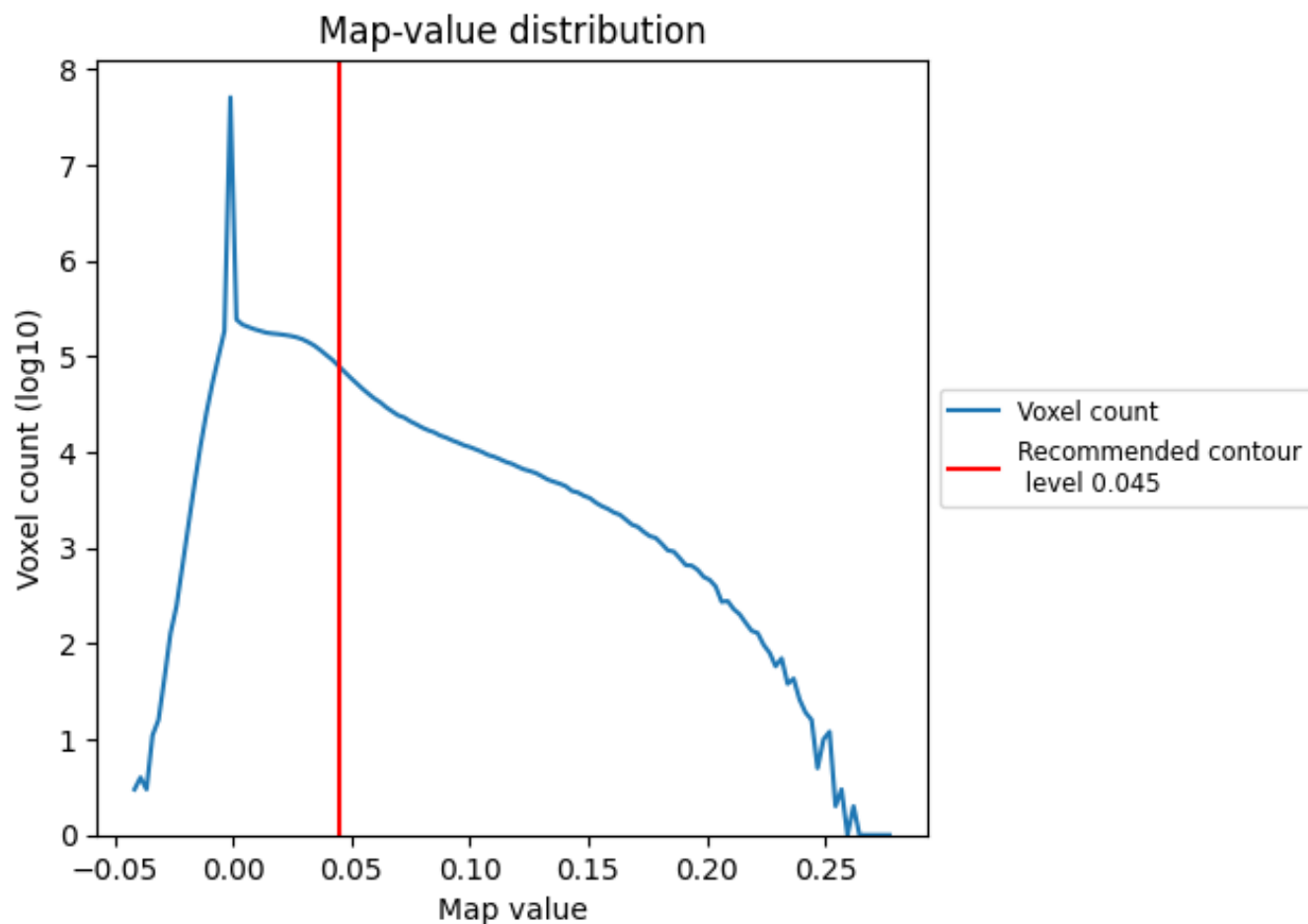
## 6.6 Mask visualisation [i](#)

This section was not generated. No masks/segmentation were deposited.

## 7 Map analysis [i](#)

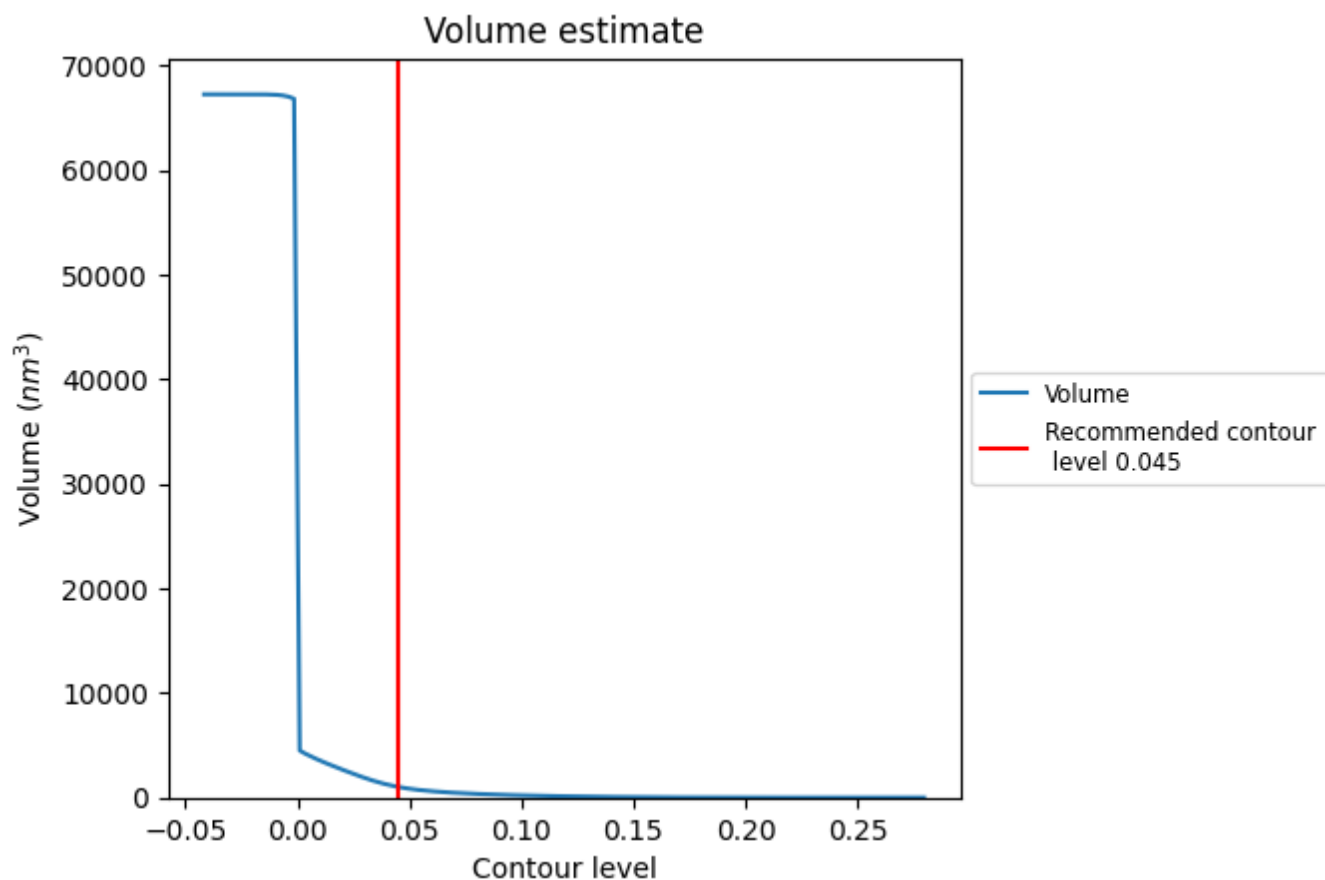
This section contains the results of statistical analysis of the map.

### 7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

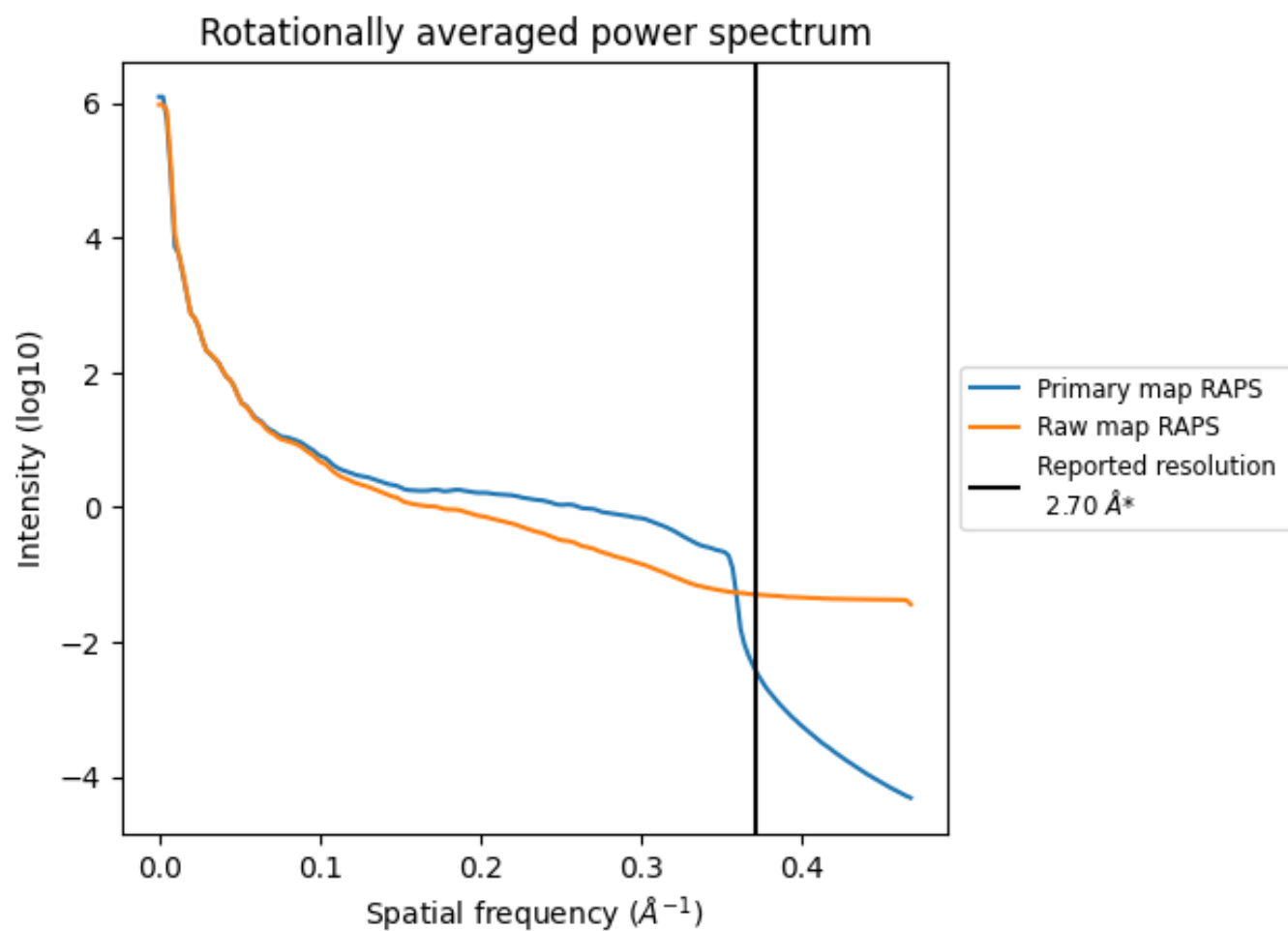
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1020 nm<sup>3</sup>; this corresponds to an approximate mass of 922 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

### 7.3 Rotationally averaged power spectrum ⓘ

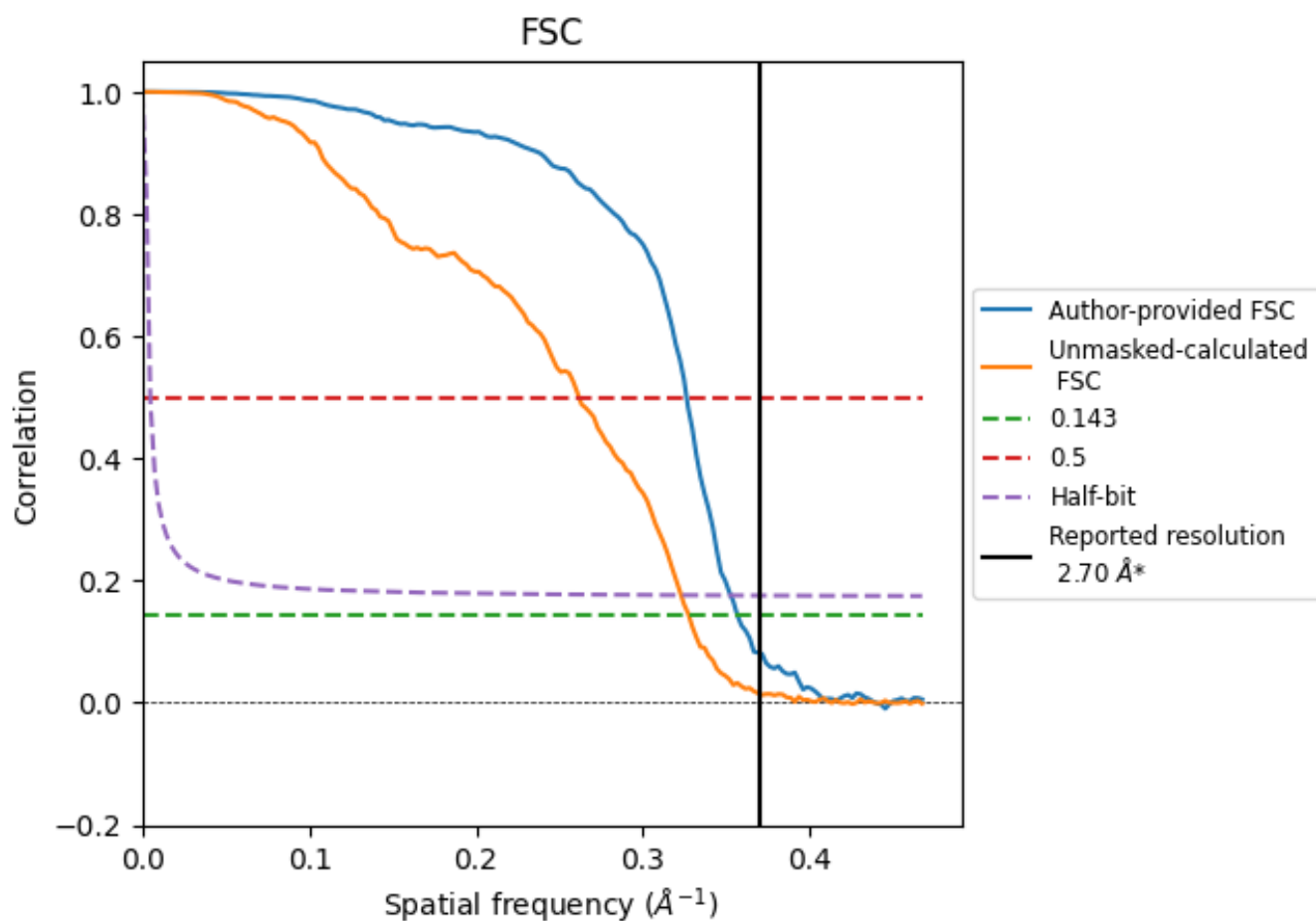


\*Reported resolution corresponds to spatial frequency of 0.370  $\text{\AA}^{-1}$

## 8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

### 8.1 FSC [i](#)



\*Reported resolution corresponds to spatial frequency of  $0.370 \text{ \AA}^{-1}$

## 8.2 Resolution estimates [i](#)

| Resolution estimate (Å)   | Estimation criterion (FSC cut-off) |      |          |
|---------------------------|------------------------------------|------|----------|
|                           | 0.143                              | 0.5  | Half-bit |
| Reported by author        | 2.70                               | -    | -        |
| Author-provided FSC curve | 2.80                               | 3.07 | 2.84     |
| Unmasked-calculated*      | 3.05                               | 3.82 | 3.10     |

\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.05 differs from the reported value 2.7 by more than 10 %

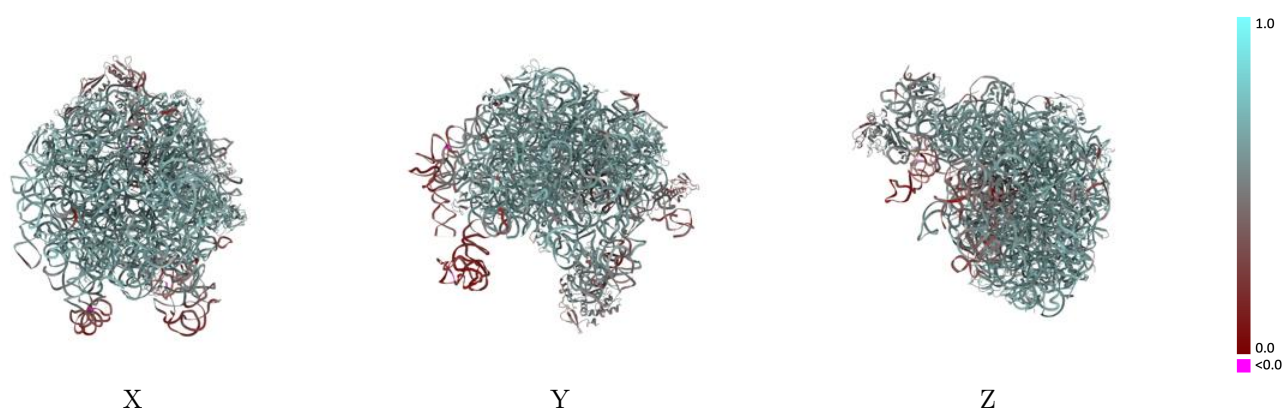
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-37552 and PDB model 8WHY. Per-residue inclusion information can be found in section 3 on page 9.

### 9.1 Map-model overlay [i](#)

This section was not generated.

### 9.2 Q-score mapped to coordinate model [i](#)

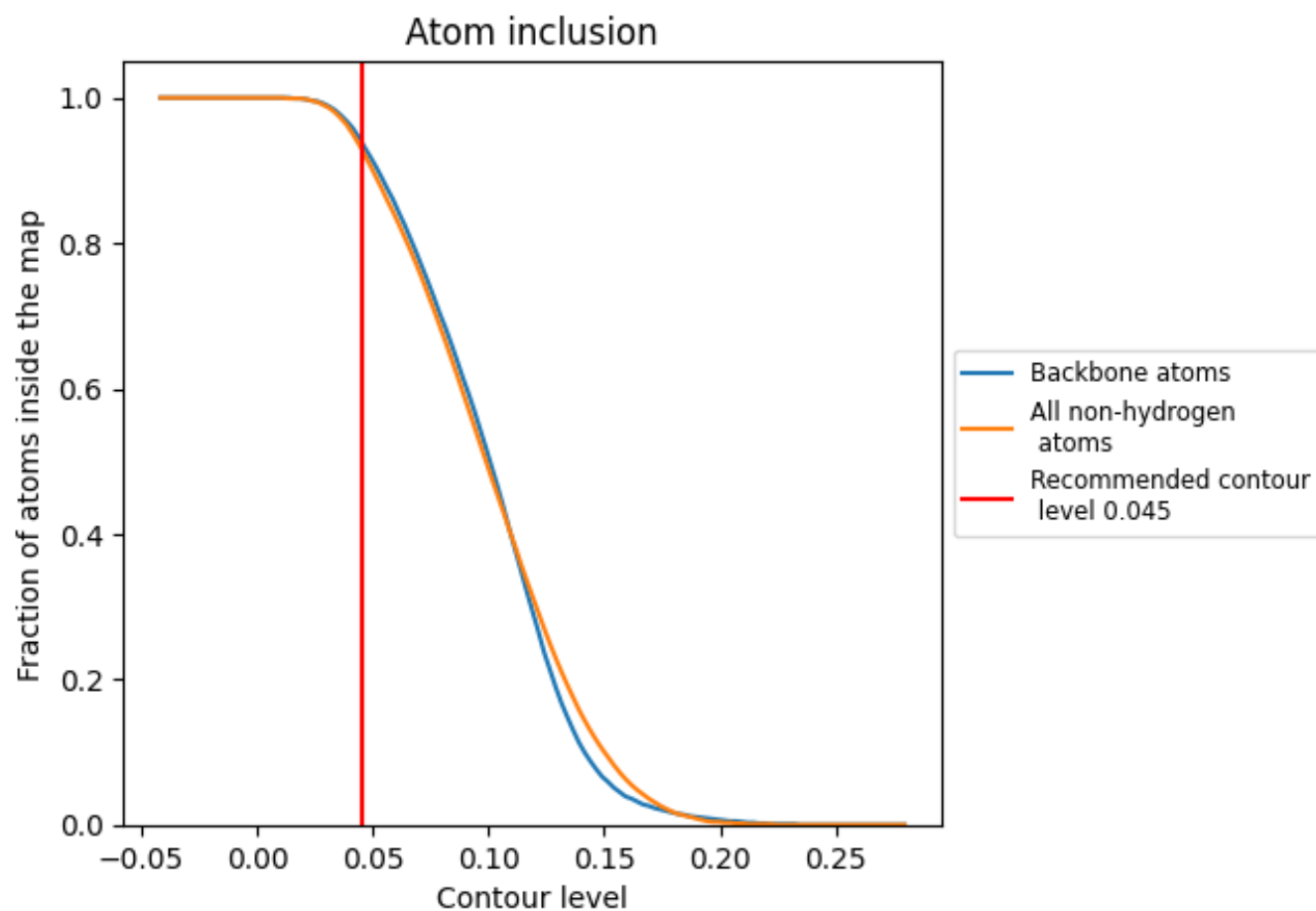


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

### 9.3 Atom inclusion mapped to coordinate model [i](#)

This section was not generated.

## 9.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 93% of all non-hydrogen atoms, are inside the map.

## 9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.045) and Q-score for the entire model and for each chain.

| Chain | Atom inclusion                                                                             | Q-score                                                                                    |
|-------|--------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------|
| All   |  0.9310   |  0.5670   |
| 1     |  0.9120   |  0.5730   |
| 2     |  0.9230   |  0.5780   |
| 3     |  0.9470   |  0.6130   |
| 4     |  0.5250   |  0.3830   |
| 5     |  0.9030   |  0.6140   |
| 6     |  0.8050   |  0.5260   |
| 7     |  1.0000   |  0.6400   |
| 8     |  0.9630   |  0.6210   |
| A     |  0.9370   |  0.5640   |
| B     |  0.9700   |  0.5290   |
| E     |  0.9840   |  0.6320   |
| F     |  0.9520   |  0.6110   |
| G     |  0.9210   |  0.5910   |
| H     |  0.8120  |  0.4940  |
| I     |  0.6060 |  0.3740 |
| J     |  0.6900 |  0.5240 |
| M     |  0.9600 |  0.6130 |
| N     |  0.9660 |  0.6130 |
| O     |  0.9370 |  0.6040 |
| Q     |  0.9800 |  0.6250 |
| R     |  0.8810 |  0.5310 |
| S     |  0.9590 |  0.5980 |
| T     |  0.9720 |  0.6180 |
| U     |  0.9380 |  0.6220 |
| V     |  0.9780 |  0.6230 |
| W     |  0.9310 |  0.6040 |
| X     |  0.8750 |  0.5790 |
| Z     |  0.9660 |  0.6050 |

