# Full wwPDB X-ray Structure Validation Report ⓘ

Dec 2, 2023 – 11:12 pm GMT

| | | |
|---|---|---|
| PDB ID | : | 2BHL |
| Title | : | X-RAY STRUCTURE OF HUMAN GLUCOSE-6-PHOSPHATE DEHYDROGENASE (DELETION VARIANT) COMPLEXED WITH GLUCOSE-6-PHOSPHATE |
| Authors | : | Kotaka, M.; Gover, S.; Lam, V.M.S.; Adams, M.J. |
| Deposited on | : | 2005-01-13 |
| Resolution | : | 2.90 Å(reported) |

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
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:

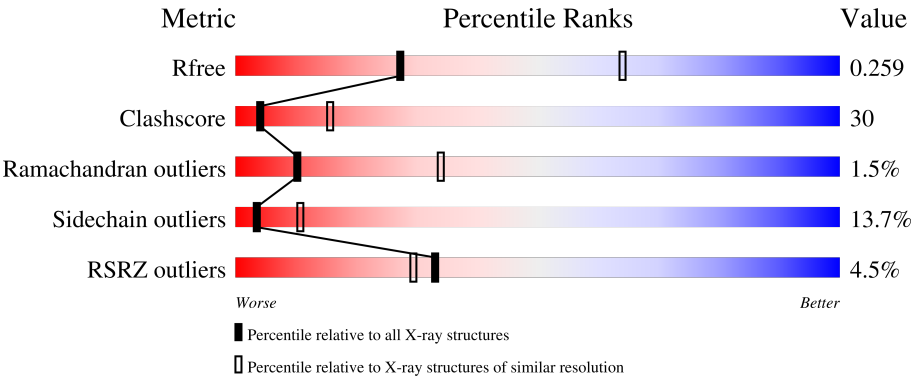
| | | |
|---|---|---|
| MolProbity | : | 4.02b-467 |
| Mogul | : | 1.8.4, CSD as541be (2020) |
| Xtriage (Phenix) | : | 1.13 |
| EDS | : | 2.36 |
| buster-report | : | 1.1.7 (2018) |
| Percentile statistics | : | 20191225.v01 (using entries in the PDB archive December 25th 2019) |
| Refmac | : | 5.8.0158 |
| CCP4 | : | 7.0.044 (Gargrove) |
| Ideal geometry (proteins) | : | Engh & Huber (2001) |
| Ideal geometry (DNA, RNA) | : | Parkinson et al. (1996) |
| Validation Pipeline (wwPDB-VP) | : | 2.36 |

# 1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.90 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 (#Entries) | Similar resolution (#Entries, resolution range(Å)) |
|---|---|---|
| $R_{free}$ | 130704 | 1957 (2.90-2.90) |
| Clashscore | 141614 | 2172 (2.90-2.90) |
| Ramachandran outliers | 138981 | 2115 (2.90-2.90) |
| Sidechain outliers | 138945 | 2117 (2.90-2.90) |
| RSRZ outliers | 127900 | 1906 (2.90-2.90) |

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for >=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 <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

| Mol | Chain | Length | Quality of chain |
|---|---|---|---|
| 1 | A | 489 | 5% 46% 45% 6% · |
| 1 | B | 489 | 4% 48% 44% 5% · |

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

| Mol | Type | Chain | Res | Chirality | Geometry | Clashes | Electron density |
|---|---|---|---|---|---|---|---|
| 2 | GOL | A | 1507 | - | - | X | - |
| 2 | GOL | B | 1506 | - | - | X | - |

## 2 Entry composition (i)

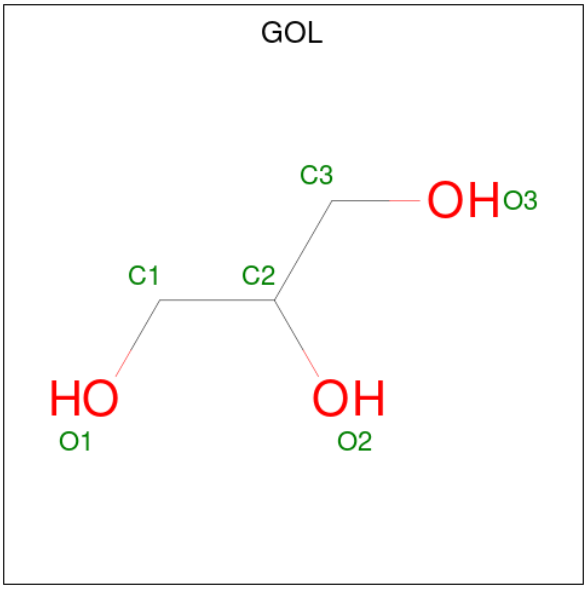
There are 4 unique types of molecules in this entry. The entry contains 7903 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, 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 GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| 1 | A | 479 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 3875 | 2471 | 674 | 710 | 20 | | | |
| 1 | B | 479 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 3879 | 2473 | 674 | 712 | 20 | | | |

- Molecule 2 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



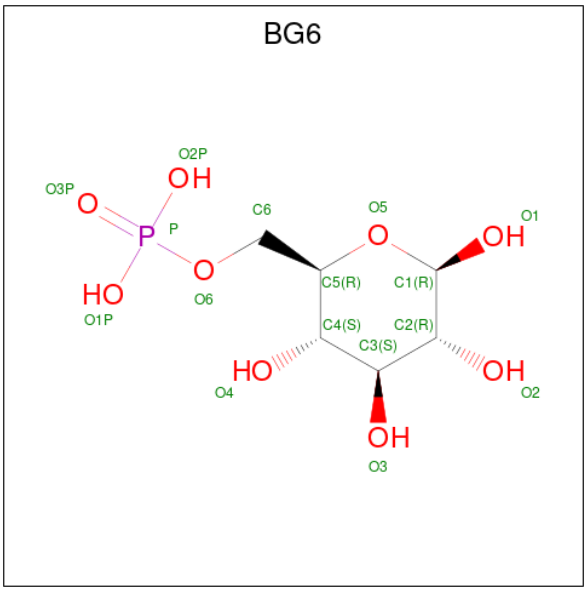

| Mol | Chain | Residues | Atoms | | | ZeroOcc | AltConf |
|---|---|---|---|---|---|---|---|
| 2 | A | 1 | Total | C | O | 0 | 0 |
| | | | 6 | 3 | 3 | | |
| 2 | A | 1 | Total | C | O | 0 | 0 |
| | | | 6 | 3 | 3 | | |
| 2 | A | 1 | Total | C | O | 0 | 0 |
| | | | 6 | 3 | 3 | | |
| 2 | A | 1 | Total | C | O | 0 | 0 |
| | | | 6 | 3 | 3 | | |

*Continued on next page...*

*Continued from previous page...*

| Mol | Chain | Residues | Atoms | ZeroOcc | AltConf |
|---|---|---|---|---|---|
| 2 | B | 1 | Total C O<br>6 3 3 | 0 | 0 |
| 2 | B | 1 | Total C O<br>6 3 3 | 0 | 0 |

- Molecule 3 is 6-O-phosphono-beta-D-glucopyranose (three-letter code: BG6) (formula: $C_6H_{13}O_9P$).




| Mol | Chain | Residues | Atoms | ZeroOcc | AltConf |
|---|---|---|---|---|---|
| 3 | A | 1 | Total C O P<br>16 6 9 1 | 0 | 0 |
| 3 | B | 1 | Total C O P<br>16 6 9 1 | 0 | 0 |

- Molecule 4 is water.

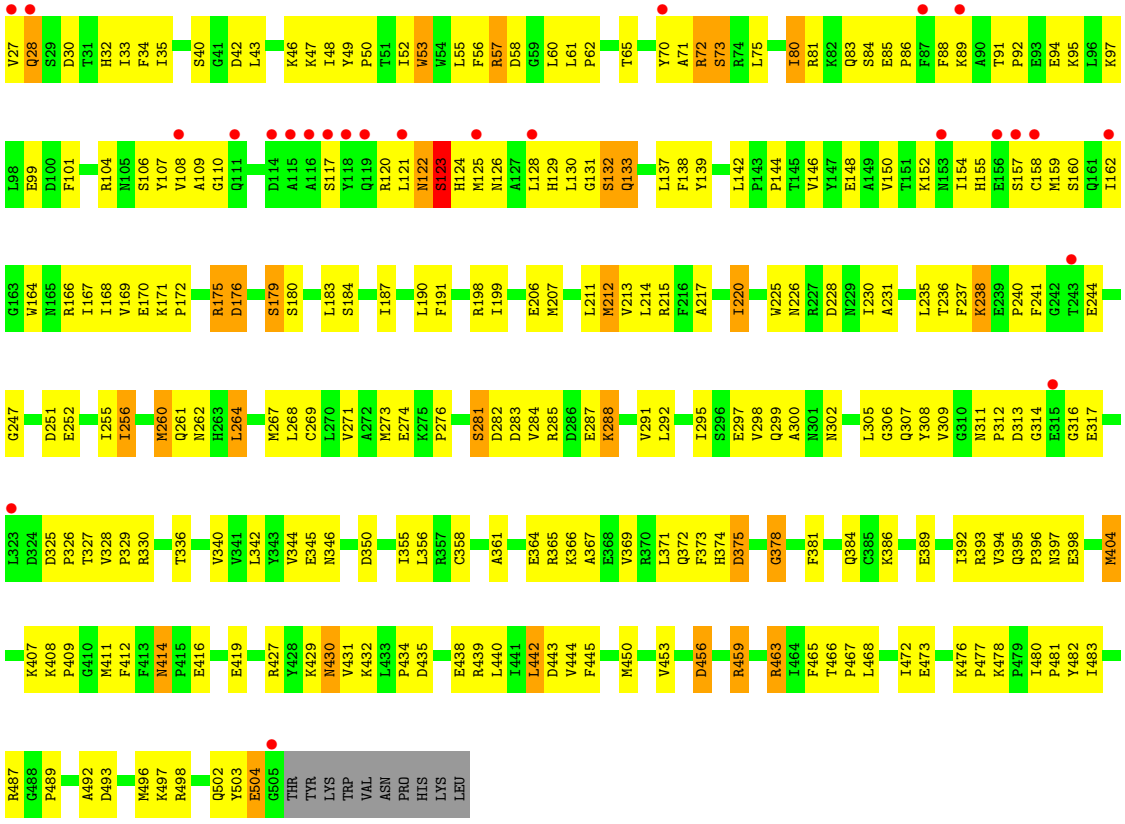
| Mol | Chain | Residues | Atoms | ZeroOcc | AltConf |
|---|---|---|---|---|---|
| 4 | A | 43 | Total O<br>43 43 | 0 | 0 |
| 4 | B | 38 | Total O<br>38 38 | 0 | 0 |

# 3 Residue-property plots (i)

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 electron 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 dot above a residue indicates a poor fit to the electron density (RSRZ > 2). 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.

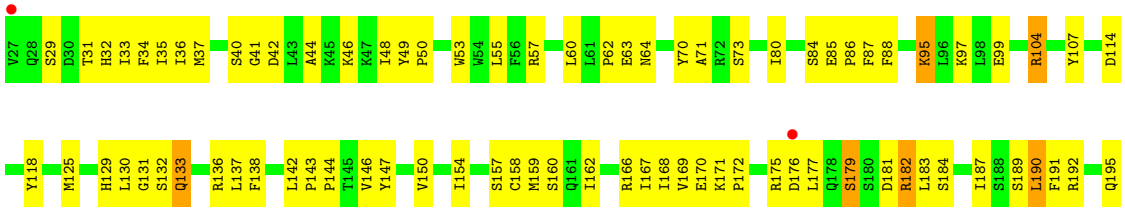
• Molecule 1: GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE

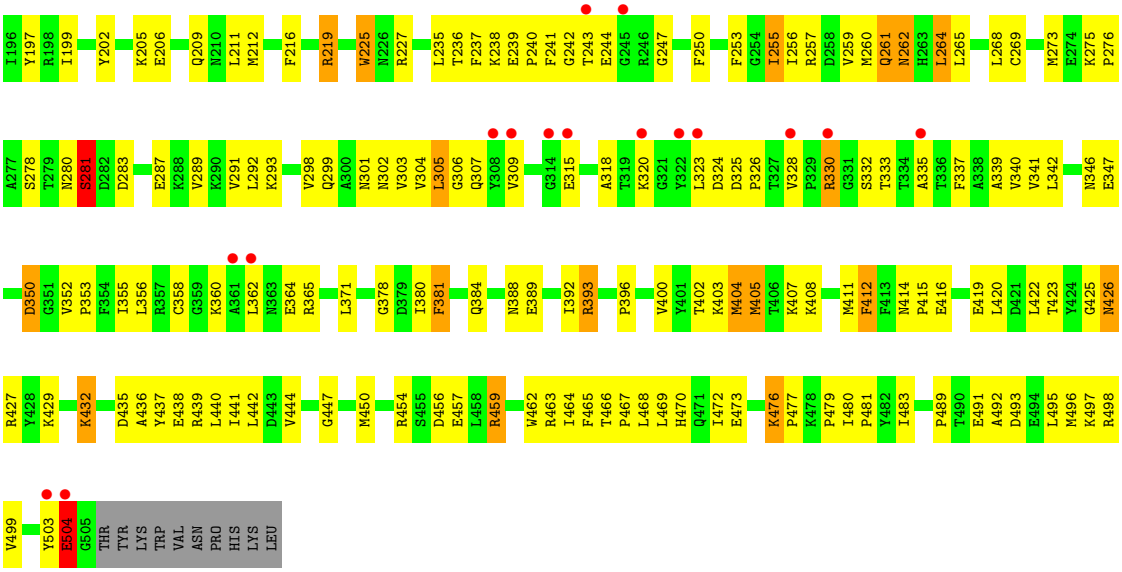
Chain A:


• Molecule 1: GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE

Chain B:


I196 Y197 R198 I199 Y202 K205 E206 Q209 N210 L211 M212 F216 R219 W225 N226 R227 L235 T236 F237 K238 E239 P240 F241 G242 T243 E244 G245 R246 G247 F250 F253 G254 I255 I256 R257 D258 V259 M260 Q261 N262 H263 L264 L265 L268 C269 M273 E274 K275 P276
A277 S278 T279 N280 S281 D282 D283 E287 K288 V289 K290 V291 L292 K293 V298 Q299 A300 N301 N302 V303 V304 L305 G306 Q307 Y308 V309 G314 E315 A318 T319 K320 G321 Y322 L323 D324 D325 P326 T327 V328 P329 R330 G331 S332 T333 T334 A335 T336 F337 A338 A339 V340 V341 L342 N346 E347
D350 G351 V352 P353 F354 I355 L356 R357 C358 G359 K360 A361 L362 N363 E364 R365 L371 G378 D379 I380 F381 Q384 N388 E389 I392 R393 P396 V400 Y401 T402 K403 M404 M405 T406 K407 K408 M411 F412 F413 N414 P415 E416 E419 L420 D421 L422 T423 Y424 G425 N426
R427 Y428 K429 K432 D435 A436 Y437 E438 R439 L440 I441 L442 D443 V444 G447 M450 R454 S455 D456 E457 L458 R459 W462 R463 I464 F465 T466 P467 L468 L469 H470 Q471 I472 E473 K476 P477 K478 P479 I480 P481 Y482 I483 P489 T490 E491 A492 D493 E494 L495 M496 K497 R498
V499 Y503 E504 G505 THR TYR LYS TRP VAL ASN PRO HIS LYS LEU

# 4 Data and refinement statistics (i)

| Property | Value | Source |
|---|---|---|
| Space group | C 2 2 21 | Depositor |
| Cell constants<br>a, b, c, $\alpha$, $\beta$, $\gamma$ | 117.55Å 179.53Å 137.94Å<br>90.00° 90.00° 90.00° | Depositor |
| Resolution (Å) | 69.00 – 2.90<br>68.97 – 2.90 | Depositor<br>EDS |
| % Data completeness<br>(in resolution range) | 98.9 (69.00-2.90)<br>98.7 (68.97-2.90) | Depositor<br>EDS |
| $R_{merge}$ | 0.12 | Depositor |
| $R_{sym}$ | (Not available) | Depositor |
| $< I/\sigma(I) >$ [1] | 2.37 (at 2.91Å) | Xtriage |
| Refinement program | TNT BUSTER/TNT | Depositor |
| R, $R_{free}$ | 0.212 , 0.261<br>0.209 , 0.259 | Depositor<br>DCC |
| $R_{free}$ test set | 1640 reflections (5.08%) | wwPDB-VP |
| Wilson B-factor (Å$^2$) | 53.0 | Xtriage |
| Anisotropy | 0.005 | Xtriage |
| Bulk solvent $k_{sol}$(e/Å$^3$), $B_{sol}$(Å$^2$) | 0.35 , 61.6 | EDS |
| L-test for twinning[2] | $< \|L\| > = 0.49$, $< L^2 > = 0.32$ | Xtriage |
| Estimated twinning fraction | No twinning to report. | Xtriage |
| $F_o$,$F_c$ correlation | 0.92 | EDS |
| Total number of atoms | 7903 | wwPDB-VP |
| Average B, all atoms (Å$^2$) | 50.0 | wwPDB-VP |

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.67% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

# 5 Model quality

## 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: BG6, GOL

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 | A | 0.39 | 0/3966 | 0.63 | 0/5363 |
| 1 | B | 0.40 | 2/3970 (0.1%) | 0.64 | 2/5368 (0.0%) |
| All | All | 0.40 | 2/7936 (0.0%) | 0.64 | 2/10731 (0.0%) |

All (2) bond length outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(Å) | Ideal(Å) |
|---|---|---|---|---|---|---|---|
| 1 | B | 381 | PHE | CG-CD2 | 6.56 | 1.48 | 1.38 |
| 1 | B | 381 | PHE | CE1-CZ | 5.08 | 1.47 | 1.37 |

All (2) bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed($^o$) | Ideal($^o$) |
|---|---|---|---|---|---|---|---|
| 1 | B | 504 | GLU | N-CA-C | 5.89 | 126.89 | 111.00 |
| 1 | B | 381 | PHE | CB-CG-CD2 | -5.79 | 116.75 | 120.80 |

There are no chirality outliers.

There are no planarity outliers.

## 5.2 Too-close contacts

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 | A | 3875 | 0 | 3823 | 242 | 0 |
| 1 | B | 3879 | 0 | 3827 | 241 | 0 |

*Continued on next page...*

*Continued from previous page...*

| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|---|---|---|---|---|---|---|
| 2 | A | 24 | 0 | 32 | 9 | 0 |
| 2 | B | 12 | 0 | 16 | 5 | 0 |
| 3 | A | 16 | 0 | 11 | 0 | 0 |
| 3 | B | 16 | 0 | 11 | 1 | 0 |
| 4 | A | 43 | 0 | 0 | 3 | 0 |
| 4 | B | 38 | 0 | 0 | 1 | 0 |
| All | All | 7903 | 0 | 7720 | 465 | 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 30.

All (465) 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) |
|---|---|---|---|
| 1:B:480:ILE:HD13 | 1:B:491:GLU:HG3 | 1.29 | 1.15 |
| 1:A:238:LYS:HE2 | 1:A:364:GLU:HG2 | 1.32 | 1.08 |
| 1:B:182:ARG:HH11 | 1:B:182:ARG:HG2 | 1.19 | 1.07 |
| 1:B:330:ARG:H | 1:B:330:ARG:HD3 | 1.15 | 1.05 |
| 1:A:442:LEU:HD22 | 1:B:411:MET:HE2 | 1.38 | 1.02 |
| 1:B:330:ARG:H | 1:B:330:ARG:CD | 1.63 | 1.02 |
| 1:B:125:MET:HE2 | 1:B:136:ARG:HG2 | 1.39 | 1.01 |
| 1:B:171:LYS:HB2 | 1:B:172:PRO:HA | 1.51 | 0.89 |
| 1:A:146:VAL:HG12 | 1:A:150:VAL:HG23 | 1.55 | 0.89 |
| 1:B:137:LEU:HD21 | 1:B:168:ILE:HD11 | 1.52 | 0.89 |
| 1:A:171:LYS:HB2 | 1:A:172:PRO:HA | 1.55 | 0.88 |
| 1:B:243:THR:HG21 | 1:B:247:GLY:CA | 2.04 | 0.88 |
| 1:A:138:PHE:HB2 | 1:A:167:ILE:HD12 | 1.56 | 0.88 |
| 1:B:125:MET:CE | 1:B:136:ARG:HG2 | 2.02 | 0.87 |
| 1:B:355:ILE:HG21 | 1:B:496:MET:HE2 | 1.55 | 0.86 |
| 1:A:91:THR:HB | 1:A:92:PRO:HD2 | 1.55 | 0.86 |
| 1:B:355:ILE:HG21 | 1:B:496:MET:CE | 2.07 | 0.85 |
| 1:A:284:VAL:HG21 | 1:A:450:MET:HE3 | 1.56 | 0.85 |
| 1:B:330:ARG:HD3 | 1:B:330:ARG:N | 1.92 | 0.84 |
| 1:A:439:ARG:HA | 1:B:411:MET:HE1 | 1.59 | 0.84 |
| 1:B:138:PHE:HB2 | 1:B:167:ILE:HD12 | 1.59 | 0.84 |
| 1:B:243:THR:HG21 | 1:B:247:GLY:HA2 | 1.60 | 0.84 |
| 1:A:439:ARG:HA | 1:B:411:MET:CE | 2.08 | 0.82 |
| 1:A:260:MET:HE3 | 1:A:340:VAL:HB | 1.61 | 0.82 |
| 1:A:27:VAL:N | 1:A:30:ASP:HB2 | 1.95 | 0.81 |
| 1:B:480:ILE:CD1 | 1:B:491:GLU:HG3 | 2.08 | 0.81 |
| 1:B:407:LYS:HE2 | 1:B:412:PHE:O | 1.82 | 0.80 |

*Continued on next page...*

*Continued from previous page...*

| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|---|---|---|---|
| 1:A:407:LYS:HE2 | 1:A:412:PHE:O | 1.82 | 0.80 |
| 1:B:303:VAL:HG22 | 1:B:340:VAL:HG22 | 1.64 | 0.80 |
| 1:B:146:VAL:HG12 | 1:B:150:VAL:HG23 | 1.63 | 0.79 |
| 1:A:459:ARG:HH11 | 1:A:459:ARG:CG | 1.95 | 0.79 |
| 1:A:292:LEU:HA | 1:A:295:ILE:HD12 | 1.64 | 0.78 |
| 1:B:238:LYS:HE2 | 1:B:364:GLU:HG2 | 1.64 | 0.78 |
| 1:B:287:GLU:O | 1:B:291:VAL:HG23 | 1.84 | 0.78 |
| 1:A:273:MET:HE2 | 1:A:276:PRO:HD3 | 1.66 | 0.78 |
| 1:A:27:VAL:HG12 | 1:A:28:GLN:HG3 | 1.65 | 0.77 |
| 1:B:146:VAL:HG12 | 1:B:150:VAL:CG2 | 2.15 | 0.77 |
| 1:A:463:ARG:HG2 | 1:A:463:ARG:HH11 | 1.49 | 0.76 |
| 1:B:320:LYS:HE2 | 1:B:324:ASP:O | 1.87 | 0.75 |
| 1:B:341:VAL:HG21 | 1:B:499:VAL:HG21 | 1.69 | 0.74 |
| 1:A:411:MET:CE | 1:B:439:ARG:HA | 2.18 | 0.74 |
| 1:A:176:ASP:H | 1:A:179:SER:HB2 | 1.51 | 0.74 |
| 1:B:182:ARG:HH11 | 1:B:182:ARG:CG | 2.00 | 0.74 |
| 1:A:71:ALA:HB3 | 1:A:107:TYR:OH | 1.88 | 0.74 |
| 1:A:264:LEU:HD12 | 1:A:267:MET:CE | 2.18 | 0.73 |
| 1:B:330:ARG:CD | 1:B:330:ARG:N | 2.47 | 0.73 |
| 1:A:459:ARG:HH11 | 1:A:459:ARG:HG3 | 1.51 | 0.73 |
| 1:B:480:ILE:HD13 | 1:B:491:GLU:CG | 2.13 | 0.73 |
| 1:A:138:PHE:HB2 | 1:A:167:ILE:CD1 | 2.19 | 0.73 |
| 1:A:56:PHE:HA | 1:A:61:LEU:HD12 | 1.71 | 0.73 |
| 1:A:56:PHE:CE2 | 1:A:101:PHE:HB2 | 2.24 | 0.72 |
| 1:B:346:ASN:O | 1:B:350:ASP:HB2 | 1.90 | 0.72 |
| 1:B:211:LEU:CD2 | 1:B:392:ILE:HD13 | 2.20 | 0.71 |
| 1:B:273:MET:HA | 1:B:291:VAL:CG2 | 2.19 | 0.71 |
| 1:B:325:ASP:HB3 | 1:B:328:VAL:HG23 | 1.70 | 0.71 |
| 1:B:325:ASP:HB3 | 1:B:328:VAL:CG2 | 2.20 | 0.71 |
| 1:B:405:MET:HE3 | 1:B:416:GLU:O | 1.91 | 0.71 |
| 1:B:281:SER:HA | 1:B:450:MET:HB2 | 1.73 | 0.71 |
| 1:B:459:ARG:HH11 | 1:B:459:ARG:HG2 | 1.54 | 0.71 |
| 1:A:60:LEU:HB3 | 1:A:442:LEU:HD11 | 1.73 | 0.71 |
| 1:B:71:ALA:HB3 | 1:B:107:TYR:OH | 1.90 | 0.70 |
| 1:B:169:VAL:HG12 | 1:B:170:GLU:N | 2.07 | 0.70 |
| 1:A:240:PRO:HD3 | 1:A:365:ARG:HB2 | 1.73 | 0.70 |
| 1:B:480:ILE:HG21 | 1:B:489:PRO:HB3 | 1.74 | 0.69 |
| 1:B:459:ARG:HG2 | 1:B:459:ARG:NH1 | 2.08 | 0.68 |
| 1:B:273:MET:HA | 1:B:291:VAL:HG21 | 1.75 | 0.68 |
| 1:A:48:ILE:N | 1:A:48:ILE:HD13 | 2.08 | 0.68 |
| 1:A:430:ASN:OD1 | 1:A:430:ASN:N | 2.26 | 0.68 |

*Continued on next page...*

*Continued from previous page...*

| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|---|---|---|---|
| 1:B:243:THR:HG21 | 1:B:247:GLY:N | 2.08 | 0.68 |
| 1:B:469:LEU:HA | 1:B:472:ILE:HD12 | 1.75 | 0.68 |
| 1:A:411:MET:HE3 | 1:B:439:ARG:HA | 1.74 | 0.67 |
| 1:A:393:ARG:NH1 | 1:A:397:ASN:O | 2.27 | 0.67 |
| 1:A:456:ASP:N | 1:A:456:ASP:OD1 | 2.27 | 0.67 |
| 1:A:463:ARG:HG2 | 1:A:463:ARG:NH1 | 2.08 | 0.67 |
| 1:B:256:ILE:HA | 1:B:260:MET:HB2 | 1.75 | 0.67 |
| 1:A:56:PHE:CA | 1:A:61:LEU:HD12 | 2.25 | 0.67 |
| 1:A:146:VAL:HG12 | 1:A:150:VAL:CG2 | 2.23 | 0.67 |
| 1:A:273:MET:HA | 1:A:291:VAL:HG21 | 1.76 | 0.67 |
| 1:A:300:ALA:HB1 | 2:A:1507:GOL:H2 | 1.77 | 0.67 |
| 1:B:137:LEU:HD21 | 1:B:168:ILE:CD1 | 2.24 | 0.67 |
| 1:B:144:PRO:HG2 | 1:B:172:PRO:HD2 | 1.74 | 0.67 |
| 1:A:393:ARG:HD2 | 1:A:396:PRO:O | 1.95 | 0.66 |
| 1:B:95:LYS:NZ | 1:B:99:GLU:OE2 | 2.28 | 0.66 |
| 1:B:125:MET:O | 1:B:131:GLY:HA3 | 1.96 | 0.66 |
| 1:B:177:LEU:HB2 | 1:B:462:TRP:HB3 | 1.77 | 0.66 |
| 1:A:355:ILE:HD13 | 1:A:496:MET:HE2 | 1.77 | 0.66 |
| 1:A:81:ARG:O | 1:A:85:GLU:HB2 | 1.95 | 0.66 |
| 1:A:53:TRP:O | 1:A:56:PHE:HB3 | 1.97 | 0.65 |
| 1:A:92:PRO:O | 1:A:95:LYS:HG3 | 1.96 | 0.65 |
| 1:A:473:GLU:O | 1:A:476:LYS:HE2 | 1.96 | 0.65 |
| 1:B:333:THR:OG1 | 1:B:476:LYS:HD3 | 1.95 | 0.65 |
| 1:A:154:ILE:O | 1:A:159:MET:HG2 | 1.95 | 0.65 |
| 1:B:278:SER:OG | 1:B:280:ASN:HB2 | 1.95 | 0.65 |
| 1:A:435:ASP:HB3 | 1:A:438:GLU:HG3 | 1.79 | 0.64 |
| 1:A:342:LEU:HD11 | 1:A:356:LEU:CD1 | 2.27 | 0.64 |
| 1:A:238:LYS:HE2 | 1:A:364:GLU:CG | 2.19 | 0.64 |
| 1:A:309:VAL:CG2 | 1:A:483:ILE:HD13 | 2.27 | 0.64 |
| 1:B:144:PRO:CG | 1:B:172:PRO:HD2 | 2.27 | 0.64 |
| 1:A:231:ALA:HB2 | 1:A:374:HIS:CD2 | 2.33 | 0.64 |
| 1:B:55:LEU:HD23 | 1:B:60:LEU:HD12 | 1.79 | 0.64 |
| 1:A:198:ARG:HG3 | 1:A:198:ARG:HH11 | 1.63 | 0.63 |
| 1:A:260:MET:HE1 | 1:A:340:VAL:HG21 | 1.81 | 0.63 |
| 1:A:213:VAL:O | 1:A:217:ALA:HB3 | 1.99 | 0.63 |
| 1:B:255:ILE:HG12 | 1:B:358:CYS:SG | 2.39 | 0.63 |
| 1:A:271:VAL:HG21 | 1:A:369:VAL:HG11 | 1.81 | 0.62 |
| 1:A:27:VAL:HG12 | 1:A:28:GLN:H | 1.64 | 0.62 |
| 1:A:408:LYS:HD3 | 1:A:412:PHE:CG | 2.34 | 0.62 |
| 1:A:466:THR:HB | 1:A:467:PRO:HD3 | 1.82 | 0.62 |
| 1:A:346:ASN:O | 1:A:350:ASP:HB2 | 2.00 | 0.62 |

*Continued on next page...*

*Continued from previous page...*

| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|---|---|---|---|
| 1:B:211:LEU:HD23 | 1:B:392:ILE:HD13 | 1.80 | 0.62 |
| 1:B:323:LEU:HD23 | 1:B:328:VAL:HG11 | 1.82 | 0.62 |
| 1:B:166:ARG:NH1 | 1:B:444:VAL:O | 2.30 | 0.62 |
| 1:B:183:LEU:HG | 1:B:187:ILE:HD11 | 1.82 | 0.62 |
| 1:A:125:MET:O | 1:A:131:GLY:HA3 | 2.00 | 0.62 |
| 1:A:146:VAL:CG1 | 1:A:150:VAL:HG23 | 2.29 | 0.61 |
| 1:A:166:ARG:NH1 | 1:A:444:VAL:O | 2.34 | 0.61 |
| 1:B:169:VAL:HG12 | 1:B:170:GLU:H | 1.64 | 0.61 |
| 1:A:305:LEU:HD11 | 2:A:1507:GOL:H12 | 1.83 | 0.60 |
| 1:A:342:LEU:HD11 | 1:A:356:LEU:HD11 | 1.82 | 0.60 |
| 1:B:138:PHE:HB2 | 1:B:167:ILE:CD1 | 2.30 | 0.60 |
| 1:A:49:TYR:O | 1:A:52:ILE:HG22 | 2.02 | 0.60 |
| 1:A:264:LEU:HD12 | 1:A:267:MET:HE2 | 1.84 | 0.60 |
| 1:A:468:LEU:O | 1:A:472:ILE:HG13 | 2.01 | 0.60 |
| 1:B:129:HIS:O | 1:B:130:LEU:HB2 | 2.01 | 0.60 |
| 1:A:307:GLN:HA | 1:A:336:THR:OG1 | 2.02 | 0.60 |
| 1:B:171:LYS:CB | 1:B:172:PRO:HA | 2.18 | 0.60 |
| 1:A:287:GLU:O | 1:A:291:VAL:HG23 | 2.02 | 0.60 |
| 1:A:381:PHE:O | 1:A:384:GLN:HG3 | 2.02 | 0.60 |
| 1:B:35:ILE:HD11 | 1:B:125:MET:CE | 2.32 | 0.60 |
| 1:B:381:PHE:O | 1:B:384:GLN:HG3 | 2.01 | 0.60 |
| 1:B:273:MET:CA | 1:B:291:VAL:HG21 | 2.31 | 0.59 |
| 1:B:405:MET:HE3 | 1:B:405:MET:HA | 1.83 | 0.59 |
| 1:A:122:ASN:O | 1:A:125:MET:N | 2.36 | 0.59 |
| 1:A:312:PRO:C | 1:A:314:GLY:H | 2.04 | 0.59 |
| 1:B:44:ALA:HA | 1:B:48:ILE:HB | 1.85 | 0.59 |
| 1:A:99:GLU:OE2 | 1:A:99:GLU:HA | 2.02 | 0.58 |
| 1:A:73:SER:O | 1:A:75:LEU:HG | 2.03 | 0.58 |
| 1:A:144:PRO:HG3 | 1:A:172:PRO:HD2 | 1.86 | 0.58 |
| 1:B:307:GLN:O | 1:B:481:PRO:HA | 2.04 | 0.58 |
| 1:A:170:GLU:HG2 | 4:A:2007:HOH:O | 2.04 | 0.57 |
| 1:A:247:GLY:O | 1:A:328:VAL:HG22 | 2.05 | 0.57 |
| 1:B:202:TYR:HA | 1:B:205:LYS:HD2 | 1.86 | 0.57 |
| 1:A:411:MET:HE2 | 1:B:442:LEU:CD2 | 2.34 | 0.57 |
| 1:B:325:ASP:O | 1:B:328:VAL:HB | 2.04 | 0.57 |
| 1:A:273:MET:HA | 1:A:291:VAL:CG2 | 2.35 | 0.57 |
| 1:B:243:THR:CG2 | 1:B:247:GLY:N | 2.67 | 0.57 |
| 1:A:212:MET:HE1 | 1:A:450:MET:HE3 | 1.87 | 0.57 |
| 1:B:197:TYR:CD2 | 1:B:444:VAL:HG22 | 2.38 | 0.57 |
| 1:B:235:LEU:HD12 | 1:B:356:LEU:HD23 | 1.86 | 0.57 |
| 1:B:456:ASP:OD1 | 1:B:456:ASP:N | 2.36 | 0.57 |

*Continued on next page...*

*Continued from previous page...*

| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|---|---|---|---|
| 1:B:492:ALA:O | 1:B:496:MET:HG3 | 2.05 | 0.57 |
| 1:A:264:LEU:HD12 | 1:A:267:MET:HE3 | 1.86 | 0.57 |
| 1:B:41:GLY:HA3 | 4:B:2002:HOH:O | 2.04 | 0.56 |
| 1:A:171:LYS:CB | 1:A:172:PRO:HA | 2.24 | 0.56 |
| 1:B:114:ASP:O | 1:B:118:TYR:HD1 | 1.87 | 0.56 |
| 1:B:182:ARG:HG2 | 1:B:182:ARG:NH1 | 1.99 | 0.56 |
| 1:B:190:LEU:HB2 | 1:B:191:PHE:CD1 | 2.40 | 0.56 |
| 1:A:35:ILE:HD12 | 1:A:35:ILE:H | 1.70 | 0.56 |
| 1:B:183:LEU:HG | 1:B:187:ILE:CD1 | 2.36 | 0.56 |
| 1:A:240:PRO:HD3 | 1:A:365:ARG:CB | 2.35 | 0.56 |
| 1:A:129:HIS:O | 1:A:130:LEU:HB2 | 2.06 | 0.55 |
| 1:A:298:VAL:HA | 2:A:1506:GOL:O1 | 2.06 | 0.55 |
| 1:A:411:MET:HE2 | 1:B:442:LEU:HD23 | 1.89 | 0.55 |
| 1:B:426:ASN:O | 1:B:429:LYS:HG2 | 2.07 | 0.55 |
| 1:A:88:PHE:O | 1:A:89:LYS:HB3 | 2.07 | 0.55 |
| 1:A:264:LEU:CD2 | 1:A:358:CYS:HB3 | 2.37 | 0.55 |
| 1:B:35:ILE:CG1 | 1:B:125:MET:HE3 | 2.37 | 0.55 |
| 1:A:260:MET:HE1 | 1:A:465:PHE:HE1 | 1.72 | 0.55 |
| 1:A:132:SER:O | 1:A:162:ILE:HD12 | 2.06 | 0.55 |
| 1:A:305:LEU:CD1 | 2:A:1507:GOL:H12 | 2.37 | 0.55 |
| 1:A:342:LEU:CD1 | 1:A:356:LEU:HD11 | 2.36 | 0.55 |
| 1:B:49:TYR:CB | 1:B:50:PRO:HD3 | 2.36 | 0.55 |
| 1:A:307:GLN:O | 1:A:481:PRO:HA | 2.06 | 0.55 |
| 1:B:355:ILE:HG21 | 1:B:496:MET:HE3 | 1.88 | 0.55 |
| 1:A:434:PRO:HD2 | 1:A:439:ARG:NH2 | 2.22 | 0.55 |
| 1:A:273:MET:CE | 1:A:276:PRO:HD3 | 2.37 | 0.54 |
| 1:A:282:ASP:OD1 | 1:A:285:ARG:NH1 | 2.29 | 0.54 |
| 1:B:177:LEU:HD12 | 1:B:177:LEU:O | 2.07 | 0.54 |
| 1:B:262:ASN:OD1 | 1:B:262:ASN:N | 2.35 | 0.54 |
| 1:B:235:LEU:HB2 | 1:B:356:LEU:HD23 | 1.89 | 0.54 |
| 1:B:273:MET:CE | 1:B:276:PRO:HD3 | 2.38 | 0.54 |
| 1:B:206:GLU:OE1 | 1:B:439:ARG:NH2 | 2.39 | 0.54 |
| 1:B:264:LEU:CD2 | 1:B:358:CYS:HB3 | 2.36 | 0.54 |
| 1:B:468:LEU:O | 1:B:472:ILE:HD12 | 2.07 | 0.54 |
| 1:A:284:VAL:HG11 | 1:A:450:MET:HE2 | 1.88 | 0.54 |
| 1:A:442:LEU:HD22 | 1:B:411:MET:CE | 2.24 | 0.54 |
| 1:A:198:ARG:HG3 | 1:A:198:ARG:NH1 | 2.23 | 0.54 |
| 1:B:298:VAL:HG22 | 1:B:342:LEU:CD2 | 2.38 | 0.54 |
| 1:A:260:MET:CE | 1:A:465:PHE:HE1 | 2.22 | 0.53 |
| 1:A:282:ASP:OD1 | 1:A:285:ARG:HD3 | 2.08 | 0.53 |
| 1:A:62:PRO:HD2 | 1:A:65:THR:OG1 | 2.07 | 0.53 |

*Continued on next page...*

*Continued from previous page...*

| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|---|---|---|---|
| 1:A:121:LEU:O | 1:A:124:HIS:HB3 | 2.09 | 0.53 |
| 1:A:260:MET:HE2 | 1:A:465:PHE:CE1 | 2.44 | 0.53 |
| 1:B:34:PHE:CE1 | 1:B:137:LEU:HD22 | 2.43 | 0.53 |
| 1:B:298:VAL:HG22 | 1:B:342:LEU:HD21 | 1.89 | 0.53 |
| 1:A:268:LEU:HD23 | 1:A:268:LEU:C | 2.29 | 0.53 |
| 1:A:133:GLN:HA | 1:A:162:ILE:HD12 | 1.90 | 0.53 |
| 1:A:211:LEU:HD23 | 1:A:392:ILE:HD13 | 1.91 | 0.53 |
| 1:B:225:TRP:CZ2 | 1:B:371:LEU:HD11 | 2.43 | 0.53 |
| 1:A:138:PHE:CD1 | 1:A:167:ILE:CD1 | 2.92 | 0.53 |
| 1:B:432:LYS:NZ | 2:B:1506:GOL:H11 | 2.24 | 0.53 |
| 1:B:216:PHE:HB3 | 1:B:275:LYS:HE3 | 1.90 | 0.52 |
| 1:A:27:VAL:HG12 | 1:A:28:GLN:CG | 2.38 | 0.52 |
| 1:A:308:TYR:HB3 | 1:A:482:TYR:CZ | 2.45 | 0.52 |
| 1:B:95:LYS:O | 1:B:99:GLU:HG2 | 2.09 | 0.52 |
| 1:B:211:LEU:HD21 | 1:B:392:ILE:HD13 | 1.89 | 0.52 |
| 1:B:325:ASP:OD1 | 1:B:326:PRO:HD2 | 2.10 | 0.52 |
| 1:A:367:ALA:HB3 | 1:A:395:GLN:HG2 | 1.91 | 0.52 |
| 1:A:85:GLU:N | 1:A:86:PRO:CD | 2.73 | 0.52 |
| 1:A:206:GLU:OE2 | 1:B:407:LYS:NZ | 2.42 | 0.52 |
| 1:B:239:GLU:HG2 | 1:B:241:PHE:CZ | 2.44 | 0.52 |
| 1:B:309:VAL:CG2 | 1:B:483:ILE:HD13 | 2.39 | 0.52 |
| 1:B:260:MET:HG3 | 1:B:358:CYS:SG | 2.50 | 0.52 |
| 1:A:117:SER:HA | 1:A:120:ARG:CZ | 2.40 | 0.52 |
| 1:A:117:SER:O | 1:A:120:ARG:HB2 | 2.10 | 0.52 |
| 1:B:242:GLY:O | 1:B:244:GLU:HG3 | 2.10 | 0.52 |
| 1:B:260:MET:CE | 1:B:465:PHE:CE1 | 2.93 | 0.52 |
| 1:A:137:LEU:CD1 | 1:A:164:TRP:CZ3 | 2.93 | 0.51 |
| 1:A:375:ASP:OD1 | 1:A:375:ASP:N | 2.43 | 0.51 |
| 1:B:269:CYS:SG | 1:B:292:LEU:HD21 | 2.50 | 0.51 |
| 1:B:389:GLU:OE1 | 1:B:403:LYS:HE2 | 2.11 | 0.51 |
| 1:B:170:GLU:HG3 | 1:B:199:ILE:HB | 1.92 | 0.51 |
| 1:A:271:VAL:CG2 | 1:A:369:VAL:HG11 | 2.40 | 0.51 |
| 1:B:468:LEU:HG | 1:B:472:ILE:HD11 | 1.92 | 0.51 |
| 1:A:439:ARG:HA | 1:B:411:MET:HE3 | 1.89 | 0.51 |
| 1:A:480:ILE:HG21 | 1:A:489:PRO:HB3 | 1.92 | 0.51 |
| 1:B:49:TYR:HB2 | 1:B:50:PRO:HD3 | 1.93 | 0.51 |
| 1:A:309:VAL:HG23 | 1:A:483:ILE:HD13 | 1.92 | 0.51 |
| 1:A:207:MET:HB2 | 1:A:394:VAL:HA | 1.91 | 0.51 |
| 1:A:175:ARG:NH2 | 1:A:252:GLU:O | 2.33 | 0.51 |
| 1:B:169:VAL:CG1 | 1:B:170:GLU:N | 2.74 | 0.51 |
| 1:A:110:GLY:HA3 | 1:A:117:SER:HB3 | 1.93 | 0.50 |

*Continued on next page...*

*Continued from previous page...*

| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|---|---|---|---|
| 1:A:42:ASP:O | 1:A:46:LYS:HB2 | 2.10 | 0.50 |
| 1:B:412:PHE:N | 1:B:412:PHE:CD2 | 2.79 | 0.50 |
| 1:A:108:VAL:HG11 | 1:A:121:LEU:HA | 1.92 | 0.50 |
| 1:A:300:ALA:HB1 | 2:A:1507:GOL:C2 | 2.42 | 0.50 |
| 1:A:411:MET:HE1 | 1:B:439:ARG:HA | 1.93 | 0.50 |
| 1:A:49:TYR:CB | 1:A:50:PRO:HD3 | 2.42 | 0.50 |
| 1:A:235:LEU:CD1 | 1:A:268:LEU:HB2 | 2.42 | 0.50 |
| 1:A:302:ASN:OD1 | 1:A:498:ARG:NH2 | 2.40 | 0.50 |
| 1:B:35:ILE:HD12 | 1:B:35:ILE:H | 1.76 | 0.50 |
| 1:B:323:LEU:HD23 | 1:B:328:VAL:CG1 | 2.42 | 0.50 |
| 1:B:405:MET:CE | 1:B:416:GLU:C | 2.80 | 0.50 |
| 1:A:144:PRO:CG | 1:A:172:PRO:HD2 | 2.41 | 0.50 |
| 1:A:393:ARG:CD | 1:A:396:PRO:O | 2.60 | 0.50 |
| 1:A:260:MET:CE | 1:A:465:PHE:CE1 | 2.94 | 0.50 |
| 1:A:372:GLN:HA | 1:A:389:GLU:HG2 | 1.93 | 0.50 |
| 1:B:304:VAL:HB | 1:B:339:ALA:HB3 | 1.93 | 0.50 |
| 1:A:133:GLN:HA | 1:A:162:ILE:HB | 1.93 | 0.50 |
| 1:A:300:ALA:CB | 2:A:1507:GOL:H2 | 2.42 | 0.50 |
| 1:A:440:LEU:O | 1:A:443:ASP:HB2 | 2.12 | 0.50 |
| 1:B:57:ARG:HA | 1:B:97:LYS:HD3 | 1.93 | 0.49 |
| 1:B:37:MET:HE1 | 1:B:70:TYR:CD1 | 2.47 | 0.49 |
| 1:B:333:THR:HB | 1:B:477:PRO:O | 2.12 | 0.49 |
| 1:B:438:GLU:O | 1:B:442:LEU:HB2 | 2.12 | 0.49 |
| 1:A:231:ALA:HB2 | 1:A:374:HIS:HD2 | 1.75 | 0.49 |
| 1:A:393:ARG:NH1 | 1:A:397:ASN:HB3 | 2.28 | 0.49 |
| 1:B:466:THR:HB | 1:B:467:PRO:HD3 | 1.95 | 0.49 |
| 1:A:190:LEU:HB2 | 1:A:191:PHE:CD1 | 2.48 | 0.49 |
| 1:A:241:PHE:O | 1:A:361:ALA:N | 2.45 | 0.49 |
| 1:B:181:ASP:OD2 | 1:B:459:ARG:NH1 | 2.46 | 0.49 |
| 1:B:381:PHE:CD1 | 1:B:415:PRO:HG3 | 2.48 | 0.49 |
| 1:B:37:MET:CE | 1:B:70:TYR:CD1 | 2.95 | 0.49 |
| 1:B:250:PHE:O | 1:B:253:PHE:N | 2.39 | 0.49 |
| 1:A:91:THR:CB | 1:A:92:PRO:HD2 | 2.33 | 0.49 |
| 1:A:492:ALA:O | 1:A:496:MET:HG3 | 2.13 | 0.49 |
| 1:B:197:TYR:OH | 1:B:447:GLY:HA2 | 2.12 | 0.49 |
| 1:B:260:MET:CE | 1:B:465:PHE:CZ | 2.95 | 0.49 |
| 1:B:273:MET:HA | 1:B:291:VAL:HG22 | 1.94 | 0.49 |
| 1:B:476:LYS:N | 1:B:477:PRO:HD3 | 2.27 | 0.49 |
| 1:B:393:ARG:HD2 | 1:B:396:PRO:O | 2.13 | 0.49 |
| 1:A:311:ASN:O | 1:A:314:GLY:HA3 | 2.13 | 0.49 |
| 1:A:137:LEU:HD22 | 1:A:445:PHE:CZ | 2.48 | 0.48 |

*Continued on next page...*

*Continued from previous page...*

| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|---|---|---|---|
| 1:A:150:VAL:O | 1:A:154:ILE:HG13 | 2.12 | 0.48 |
| 1:A:247:GLY:O | 1:A:251:ASP:HB2 | 2.13 | 0.48 |
| 1:A:411:MET:CE | 1:B:442:LEU:HD23 | 2.42 | 0.48 |
| 1:A:375:ASP:O | 1:B:219:ARG:NH1 | 2.47 | 0.48 |
| 1:B:237:PHE:CG | 1:B:259:VAL:HG11 | 2.48 | 0.48 |
| 1:A:235:LEU:HD11 | 1:A:268:LEU:HB2 | 1.95 | 0.48 |
| 1:B:454:ARG:O | 1:B:457:GLU:HB2 | 2.13 | 0.48 |
| 1:A:264:LEU:HD21 | 1:A:358:CYS:HB3 | 1.95 | 0.48 |
| 1:A:459:ARG:HG3 | 1:A:459:ARG:NH1 | 2.25 | 0.48 |
| 1:A:168:ILE:HD11 | 1:A:444:VAL:HG21 | 1.95 | 0.48 |
| 1:A:477:PRO:HG3 | 2:A:1507:GOL:C3 | 2.43 | 0.48 |
| 1:A:27:VAL:HG12 | 1:A:28:GLN:N | 2.28 | 0.47 |
| 1:A:260:MET:HE2 | 1:A:465:PHE:CZ | 2.49 | 0.47 |
| 1:A:342:LEU:HD12 | 1:A:356:LEU:HG | 1.96 | 0.47 |
| 1:B:42:ASP:O | 1:B:46:LYS:HG3 | 2.14 | 0.47 |
| 1:B:235:LEU:CD1 | 1:B:356:LEU:HD23 | 2.44 | 0.47 |
| 1:A:271:VAL:HG21 | 1:A:369:VAL:CG1 | 2.44 | 0.47 |
| 1:B:306:GLY:HA2 | 1:B:480:ILE:O | 2.13 | 0.47 |
| 1:B:400:VAL:HG13 | 1:B:422:LEU:HB3 | 1.95 | 0.47 |
| 1:A:342:LEU:CD1 | 1:A:356:LEU:CD1 | 2.92 | 0.47 |
| 1:B:333:THR:CG2 | 1:B:476:LYS:HD3 | 2.44 | 0.47 |
| 1:A:27:VAL:CG1 | 1:A:28:GLN:H | 2.24 | 0.47 |
| 1:A:49:TYR:HB2 | 1:A:50:PRO:HD3 | 1.96 | 0.47 |
| 1:A:183:LEU:O | 1:A:187:ILE:HG13 | 2.14 | 0.47 |
| 1:B:85:GLU:N | 1:B:86:PRO:CD | 2.77 | 0.47 |
| 1:B:298:VAL:HG23 | 1:B:464:ILE:HG22 | 1.95 | 0.47 |
| 1:A:132:SER:C | 1:A:162:ILE:HD12 | 2.35 | 0.47 |
| 1:B:137:LEU:CD2 | 1:B:168:ILE:CD1 | 2.91 | 0.47 |
| 1:B:235:LEU:HD12 | 1:B:356:LEU:CD2 | 2.45 | 0.47 |
| 1:B:302:ASN:O | 1:B:495:LEU:HD21 | 2.14 | 0.47 |
| 1:B:353:PRO:CB | 1:B:499:VAL:CG1 | 2.93 | 0.47 |
| 1:A:137:LEU:CD1 | 1:A:164:TRP:HZ3 | 2.26 | 0.47 |
| 1:A:138:PHE:CD1 | 1:A:167:ILE:HD11 | 2.49 | 0.47 |
| 1:B:169:VAL:CG1 | 1:B:170:GLU:H | 2.27 | 0.47 |
| 1:B:408:LYS:HE2 | 1:B:412:PHE:CD1 | 2.50 | 0.47 |
| 1:A:409:PRO:HA | 1:B:206:GLU:OE2 | 2.15 | 0.47 |
| 1:B:175:ARG:O | 1:B:462:TRP:CZ3 | 2.67 | 0.47 |
| 1:B:495:LEU:O | 1:B:499:VAL:HG23 | 2.14 | 0.47 |
| 1:A:260:MET:HA | 1:A:264:LEU:HB2 | 1.97 | 0.47 |
| 1:A:463:ARG:HH11 | 1:A:463:ARG:CG | 2.20 | 0.47 |
| 1:B:360:LYS:NZ | 3:B:1508:BG6:O3 | 2.48 | 0.47 |

*Continued on next page...*

*Continued from previous page...*

| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|---|---|---|---|
| 1:A:70:TYR:HD2 | 1:A:121:LEU:HD13 | 1.80 | 0.47 |
| 1:B:84:SER:C | 1:B:86:PRO:HD2 | 2.35 | 0.47 |
| 1:B:182:ARG:CG | 1:B:182:ARG:NH1 | 2.66 | 0.46 |
| 1:A:123:SER:HA | 1:A:126:ASN:HB2 | 1.97 | 0.46 |
| 1:B:289:VAL:O | 1:B:293:LYS:HG3 | 2.15 | 0.46 |
| 1:A:176:ASP:OD2 | 1:A:179:SER:HB2 | 2.15 | 0.46 |
| 1:A:298:VAL:HG12 | 1:A:299:GLN:N | 2.30 | 0.46 |
| 1:A:408:LYS:HD2 | 1:A:414:ASN:HD21 | 1.80 | 0.46 |
| 1:B:304:VAL:HG23 | 1:B:495:LEU:HD22 | 1.96 | 0.46 |
| 1:B:273:MET:HE2 | 1:B:276:PRO:HD3 | 1.98 | 0.46 |
| 1:A:238:LYS:CE | 1:A:364:GLU:HG2 | 2.24 | 0.46 |
| 1:A:355:ILE:HD13 | 1:A:496:MET:CE | 2.45 | 0.46 |
| 1:B:46:LYS:HD3 | 1:B:87:PHE:CE2 | 2.51 | 0.46 |
| 1:B:227:ARG:HA | 1:B:352:VAL:HG21 | 1.97 | 0.46 |
| 1:B:432:LYS:HZ2 | 2:B:1506:GOL:H11 | 1.80 | 0.46 |
| 1:A:295:ILE:HG12 | 1:A:344:VAL:HG22 | 1.98 | 0.46 |
| 1:B:35:ILE:HD12 | 1:B:35:ILE:N | 2.31 | 0.46 |
| 1:B:209:GLN:NE2 | 1:B:439:ARG:HD2 | 2.31 | 0.46 |
| 1:A:235:LEU:CD2 | 1:A:369:VAL:HG13 | 2.46 | 0.45 |
| 1:B:35:ILE:HD12 | 1:B:137:LEU:O | 2.16 | 0.45 |
| 1:A:72:ARG:HH11 | 1:A:72:ARG:CG | 2.30 | 0.45 |
| 1:A:80:ILE:HG22 | 1:A:81:ARG:N | 2.32 | 0.45 |
| 1:A:212:MET:CE | 1:A:450:MET:HE3 | 2.46 | 0.45 |
| 1:A:212:MET:HE2 | 1:A:450:MET:HE1 | 1.98 | 0.45 |
| 1:B:35:ILE:HD11 | 1:B:125:MET:HE3 | 1.96 | 0.45 |
| 1:A:231:ALA:CB | 1:A:374:HIS:CD2 | 3.00 | 0.45 |
| 1:A:284:VAL:HG21 | 1:A:450:MET:CE | 2.38 | 0.45 |
| 1:B:144:PRO:HA | 1:B:147:TYR:CG | 2.52 | 0.45 |
| 1:B:337:PHE:CE2 | 1:B:489:PRO:HD2 | 2.52 | 0.45 |
| 1:B:400:VAL:HG13 | 1:B:400:VAL:O | 2.16 | 0.45 |
| 1:A:220:ILE:HB | 1:B:388:ASN:OD1 | 2.16 | 0.45 |
| 1:B:238:LYS:HG2 | 1:B:362:LEU:HD12 | 1.99 | 0.45 |
| 1:B:292:LEU:O | 1:B:463:ARG:NH2 | 2.49 | 0.45 |
| 1:A:269:CYS:O | 1:A:273:MET:HB3 | 2.17 | 0.45 |
| 1:A:273:MET:HE3 | 1:A:287:GLU:HB3 | 1.99 | 0.45 |
| 1:A:477:PRO:HG3 | 2:A:1507:GOL:H32 | 1.99 | 0.45 |
| 1:B:57:ARG:NH2 | 2:B:1506:GOL:O1 | 2.49 | 0.45 |
| 1:A:109:ALA:O | 1:A:120:ARG:NH1 | 2.50 | 0.44 |
| 1:A:408:LYS:HB3 | 1:A:412:PHE:HB2 | 1.98 | 0.44 |
| 1:B:436:ALA:O | 1:B:440:LEU:HB2 | 2.17 | 0.44 |
| 1:B:423:THR:HG22 | 1:B:425:GLY:H | 1.81 | 0.44 |

*Continued on next page...*

*Continued from previous page...*

| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|---|---|---|---|
| 1:B:432:LYS:NZ | 2:B:1506:GOL:C1 | 2.79 | 0.44 |
| 1:A:273:MET:HE3 | 1:A:274:GLU:O | 2.18 | 0.44 |
| 1:A:260:MET:HE3 | 1:A:340:VAL:CB | 2.40 | 0.44 |
| 1:A:312:PRO:C | 1:A:314:GLY:N | 2.70 | 0.44 |
| 1:A:198:ARG:HB2 | 1:A:453:VAL:O | 2.18 | 0.44 |
| 1:A:297:GLU:O | 2:A:1506:GOL:H2 | 2.17 | 0.44 |
| 1:A:125:MET:HA | 1:A:128:LEU:HG | 1.99 | 0.44 |
| 1:A:230:ILE:HG12 | 1:A:373:PHE:CE1 | 2.53 | 0.44 |
| 1:B:176:ASP:HB2 | 1:B:179:SER:OG | 2.18 | 0.44 |
| 1:B:315:GLU:O | 1:B:318:ALA:HB3 | 2.17 | 0.44 |
| 1:A:55:LEU:HD22 | 1:A:442:LEU:CD1 | 2.48 | 0.44 |
| 1:A:306:GLY:HA2 | 1:A:480:ILE:O | 2.18 | 0.44 |
| 1:A:84:SER:C | 1:A:86:PRO:HD2 | 2.38 | 0.43 |
| 1:A:260:MET:CE | 1:A:340:VAL:HG21 | 2.47 | 0.43 |
| 1:B:36:ILE:CD1 | 1:B:48:ILE:HG22 | 2.48 | 0.43 |
| 1:B:172:PRO:HG3 | 1:B:253:PHE:CZ | 2.53 | 0.43 |
| 1:B:305:LEU:HB3 | 1:B:335:ALA:HB2 | 1.98 | 0.43 |
| 1:A:273:MET:CA | 1:A:291:VAL:HG21 | 2.45 | 0.43 |
| 1:A:480:ILE:CG2 | 1:A:489:PRO:HB3 | 2.48 | 0.43 |
| 1:B:261:GLN:HE21 | 1:B:261:GLN:HB3 | 1.66 | 0.43 |
| 1:B:380:ILE:HG12 | 1:B:381:PHE:CE2 | 2.54 | 0.43 |
| 1:B:432:LYS:HZ2 | 2:B:1506:GOL:C1 | 2.32 | 0.43 |
| 1:B:142:LEU:HB3 | 1:B:143:PRO:HD2 | 2.00 | 0.43 |
| 1:A:88:PHE:HD2 | 1:A:88:PHE:N | 2.17 | 0.43 |
| 1:B:36:ILE:HD13 | 1:B:48:ILE:HG22 | 1.99 | 0.43 |
| 1:B:172:PRO:HG3 | 1:B:253:PHE:HZ | 1.84 | 0.43 |
| 1:B:235:LEU:CD1 | 1:B:356:LEU:CD2 | 2.97 | 0.43 |
| 1:A:30:ASP:O | 1:A:32:HIS:HD2 | 2.01 | 0.43 |
| 1:B:53:TRP:CD1 | 1:B:88:PHE:HB3 | 2.54 | 0.43 |
| 1:B:260:MET:HE2 | 1:B:465:PHE:CE1 | 2.54 | 0.43 |
| 1:A:57:ARG:HG2 | 1:A:58:ASP:N | 2.33 | 0.43 |
| 1:A:281:SER:OG | 1:A:450:MET:N | 2.52 | 0.43 |
| 1:A:308:TYR:HB3 | 1:A:482:TYR:CE2 | 2.53 | 0.42 |
| 1:A:146:VAL:HG12 | 1:A:146:VAL:O | 2.18 | 0.42 |
| 1:B:268:LEU:C | 1:B:268:LEU:HD23 | 2.39 | 0.42 |
| 1:B:309:VAL:HG23 | 1:B:483:ILE:HD13 | 2.01 | 0.42 |
| 1:A:34:PHE:CE1 | 1:A:137:LEU:HD23 | 2.53 | 0.42 |
| 1:A:431:VAL:HG12 | 1:A:432:LYS:N | 2.35 | 0.42 |
| 1:B:35:ILE:HG12 | 1:B:125:MET:CE | 2.49 | 0.42 |
| 1:A:139:TYR:CE1 | 1:A:168:ILE:HG21 | 2.53 | 0.42 |
| 1:A:237:PHE:CD1 | 1:A:237:PHE:C | 2.93 | 0.42 |

*Continued on next page...*

*Continued from previous page...*

| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|---|---|---|---|
| 1:B:150:VAL:HG12 | 1:B:154:ILE:HD12 | 2.00 | 0.42 |
| 1:B:405:MET:HE3 | 1:B:416:GLU:C | 2.39 | 0.42 |
| 1:B:459:ARG:HH11 | 1:B:459:ARG:CG | 2.23 | 0.42 |
| 1:B:303:VAL:CG1 | 1:B:304:VAL:N | 2.82 | 0.42 |
| 1:A:487:ARG:NH2 | 1:A:493:ASP:OD1 | 2.53 | 0.42 |
| 1:B:304:VAL:O | 1:B:304:VAL:HG12 | 2.19 | 0.42 |
| 1:A:404:MET:HE2 | 1:A:404:MET:HB2 | 1.82 | 0.42 |
| 1:A:91:THR:HB | 1:A:92:PRO:CD | 2.38 | 0.42 |
| 1:A:199:ILE:HG22 | 4:A:2007:HOH:O | 2.19 | 0.42 |
| 1:A:407:LYS:NZ | 1:B:206:GLU:OE2 | 2.53 | 0.42 |
| 1:B:166:ARG:C | 1:B:167:ILE:HD13 | 2.40 | 0.42 |
| 1:B:404:MET:HE3 | 1:B:420:LEU:HD12 | 2.02 | 0.42 |
| 1:B:35:ILE:CD1 | 1:B:125:MET:CE | 2.98 | 0.42 |
| 1:B:298:VAL:HG23 | 1:B:464:ILE:CG2 | 2.50 | 0.42 |
| 1:A:34:PHE:CD1 | 1:A:137:LEU:HD23 | 2.55 | 0.42 |
| 1:B:493:ASP:O | 1:B:496:MET:HB2 | 2.19 | 0.42 |
| 1:B:307:GLN:HB2 | 1:B:479:PRO:HB2 | 2.01 | 0.41 |
| 1:B:325:ASP:HA | 1:B:326:PRO:HD3 | 1.89 | 0.41 |
| 1:A:155:HIS:CD2 | 1:A:190:LEU:HB3 | 2.55 | 0.41 |
| 1:B:49:TYR:CB | 1:B:50:PRO:CD | 2.98 | 0.41 |
| 1:B:250:PHE:O | 1:B:253:PHE:HB2 | 2.19 | 0.41 |
| 1:B:466:THR:CB | 1:B:467:PRO:HD3 | 2.51 | 0.41 |
| 1:A:72:ARG:HH11 | 1:A:72:ARG:HG2 | 1.85 | 0.41 |
| 1:A:85:GLU:N | 1:A:86:PRO:HD2 | 2.36 | 0.41 |
| 1:A:325:ASP:HA | 1:A:326:PRO:HD3 | 1.80 | 0.41 |
| 1:A:212:MET:CE | 1:A:450:MET:CE | 2.98 | 0.41 |
| 1:A:260:MET:CE | 1:A:340:VAL:CG2 | 2.99 | 0.41 |
| 1:B:55:LEU:CD2 | 1:B:60:LEU:HD12 | 2.48 | 0.41 |
| 1:B:265:LEU:O | 1:B:268:LEU:HB3 | 2.20 | 0.41 |
| 1:B:425:GLY:O | 1:B:429:LYS:HD3 | 2.20 | 0.41 |
| 1:B:435:ASP:OD2 | 1:B:437:TYR:HB2 | 2.20 | 0.41 |
| 1:B:480:ILE:CG2 | 1:B:489:PRO:HB3 | 2.46 | 0.41 |
| 1:B:31:THR:HA | 1:B:64:ASN:HB2 | 2.03 | 0.41 |
| 1:B:33:ILE:HD13 | 1:B:125:MET:HG2 | 2.02 | 0.41 |
| 1:A:137:LEU:HD13 | 1:A:164:TRP:CZ3 | 2.54 | 0.41 |
| 1:A:325:ASP:OD2 | 1:A:327:THR:HG23 | 2.19 | 0.41 |
| 1:A:398:GLU:H | 1:A:398:GLU:CD | 2.23 | 0.41 |
| 1:B:408:LYS:HG2 | 1:B:412:PHE:CG | 2.55 | 0.41 |
| 1:A:33:ILE:HD13 | 1:A:125:MET:HB3 | 2.02 | 0.41 |
| 1:A:238:LYS:HB3 | 1:A:238:LYS:HE3 | 1.95 | 0.41 |
| 1:A:81:ARG:HH12 | 1:A:99:GLU:CD | 2.23 | 0.41 |

*Continued on next page...*

*Continued from previous page...*

| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|---|---|---|---|
| 1:B:36:ILE:HD13 | 1:B:48:ILE:CG2 | 2.51 | 0.41 |
| 1:B:400:VAL:CG1 | 1:B:422:LEU:HB3 | 2.51 | 0.41 |
| 1:B:466:THR:CB | 1:B:467:PRO:CD | 2.99 | 0.41 |
| 1:A:226:ASN:OD1 | 1:A:228:ASP:HB2 | 2.21 | 0.41 |
| 1:A:255:ILE:HG23 | 1:A:256:ILE:N | 2.36 | 0.41 |
| 1:A:355:ILE:HG21 | 1:A:496:MET:CE | 2.51 | 0.41 |
| 1:A:411:MET:CE | 1:B:442:LEU:CD2 | 2.98 | 0.41 |
| 1:A:503:TYR:CD2 | 1:A:504:GLU:N | 2.89 | 0.41 |
| 1:B:133:GLN:HA | 1:B:162:ILE:HB | 2.03 | 0.41 |
| 1:B:137:LEU:CD2 | 1:B:168:ILE:HD11 | 2.37 | 0.41 |
| 1:A:264:LEU:CD1 | 1:A:267:MET:HE2 | 2.49 | 0.41 |
| 1:B:493:ASP:O | 1:B:497:LYS:HG3 | 2.21 | 0.41 |
| 1:A:88:PHE:N | 1:A:88:PHE:CD2 | 2.87 | 0.40 |
| 1:B:32:HIS:CD2 | 1:B:62:PRO:HG2 | 2.56 | 0.40 |
| 1:A:211:LEU:CD2 | 1:A:392:ILE:CD1 | 2.99 | 0.40 |
| 1:A:273:MET:HE3 | 1:A:287:GLU:CB | 2.51 | 0.40 |
| 1:A:378:GLY:O | 1:B:275:LYS:NZ | 2.41 | 0.40 |
| 1:B:240:PRO:HA | 1:B:362:LEU:O | 2.21 | 0.40 |
| 1:B:477:PRO:O | 1:B:479:PRO:HD3 | 2.22 | 0.40 |
| 1:B:192:ARG:HG3 | 1:B:195:GLN:OE1 | 2.21 | 0.40 |
| 1:A:214:LEU:HD23 | 1:A:214:LEU:HA | 1.84 | 0.40 |
| 1:B:307:GLN:N | 1:B:480:ILE:O | 2.50 | 0.40 |
| 1:B:404:MET:CE | 1:B:420:LEU:CD1 | 2.99 | 0.40 |
| 1:B:405:MET:CE | 1:B:416:GLU:O | 2.67 | 0.40 |
| 1:A:288:LYS:NZ | 4:A:2020:HOH:O | 2.46 | 0.40 |
| 1:B:63:GLU:O | 1:B:104:ARG:NH2 | 2.55 | 0.40 |
| 1:B:176:ASP:N | 1:B:179:SER:OG | 2.49 | 0.40 |
| 1:B:275:LYS:HA | 1:B:276:PRO:HD2 | 1.88 | 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 X-ray entries followed by that with respect to entries of similar resolution.

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 | A | 477/489 (98%) | 417 (87%) | 51 (11%) | 9 (2%) | 8 28 |
| 1 | B | 477/489 (98%) | 437 (92%) | 35 (7%) | 5 (1%) | 15 45 |
| All | All | 954/978 (98%) | 854 (90%) | 86 (9%) | 14 (2%) | 10 34 |

All (14) Ramachandran outliers are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 1 | A | 122 | ASN |
| 1 | B | 158 | CYS |
| 1 | B | 504 | GLU |
| 1 | A | 73 | SER |
| 1 | A | 158 | CYS |
| 1 | B | 281 | SER |
| 1 | A | 123 | SER |
| 1 | A | 244 | GLU |
| 1 | A | 504 | GLU |
| 1 | B | 350 | ASP |
| 1 | B | 378 | GLY |
| 1 | A | 378 | GLY |
| 1 | A | 329 | PRO |
| 1 | A | 316 | GLY |

### 5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

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 | A | 418/429 (97%) | 355 (85%) | 63 (15%) | 3 9 |
| 1 | B | 419/429 (98%) | 367 (88%) | 52 (12%) | 4 14 |
| All | All | 837/858 (98%) | 722 (86%) | 115 (14%) | 3 11 |

All (115) residues with a non-rotameric sidechain are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 1 | A | 28 | GLN |
| 1 | A | 40 | SER |

*Continued on next page...*

*Continued from previous page...*

| Mol | Chain | Res | Type |
|---|---|---|---|
| 1 | A | 43 | LEU |
| 1 | A | 47 | LYS |
| 1 | A | 53 | TRP |
| 1 | A | 57 | ARG |
| 1 | A | 72 | ARG |
| 1 | A | 80 | ILE |
| 1 | A | 83 | GLN |
| 1 | A | 94 | GLU |
| 1 | A | 97 | LYS |
| 1 | A | 104 | ARG |
| 1 | A | 106 | SER |
| 1 | A | 123 | SER |
| 1 | A | 132 | SER |
| 1 | A | 133 | GLN |
| 1 | A | 142 | LEU |
| 1 | A | 148 | GLU |
| 1 | A | 152 | LYS |
| 1 | A | 157 | SER |
| 1 | A | 160 | SER |
| 1 | A | 169 | VAL |
| 1 | A | 175 | ARG |
| 1 | A | 176 | ASP |
| 1 | A | 179 | SER |
| 1 | A | 180 | SER |
| 1 | A | 184 | SER |
| 1 | A | 212 | MET |
| 1 | A | 215 | ARG |
| 1 | A | 220 | ILE |
| 1 | A | 225 | TRP |
| 1 | A | 236 | THR |
| 1 | A | 238 | LYS |
| 1 | A | 256 | ILE |
| 1 | A | 260 | MET |
| 1 | A | 261 | GLN |
| 1 | A | 262 | ASN |
| 1 | A | 264 | LEU |
| 1 | A | 281 | SER |
| 1 | A | 283 | ASP |
| 1 | A | 288 | LYS |
| 1 | A | 313 | ASP |
| 1 | A | 317 | GLU |
| 1 | A | 330 | ARG |

*Continued on next page...*

*Continued from previous page...*

| Mol | Chain | Res | Type |
|---|---|---|---|
| 1 | A | 345 | GLU |
| 1 | A | 366 | LYS |
| 1 | A | 371 | LEU |
| 1 | A | 375 | ASP |
| 1 | A | 386 | LYS |
| 1 | A | 404 | MET |
| 1 | A | 414 | ASN |
| 1 | A | 416 | GLU |
| 1 | A | 419 | GLU |
| 1 | A | 427 | ARG |
| 1 | A | 429 | LYS |
| 1 | A | 430 | ASN |
| 1 | A | 442 | LEU |
| 1 | A | 456 | ASP |
| 1 | A | 459 | ARG |
| 1 | A | 463 | ARG |
| 1 | A | 478 | LYS |
| 1 | A | 497 | LYS |
| 1 | A | 502 | GLN |
| 1 | B | 29 | SER |
| 1 | B | 40 | SER |
| 1 | B | 73 | SER |
| 1 | B | 80 | ILE |
| 1 | B | 95 | LYS |
| 1 | B | 104 | ARG |
| 1 | B | 132 | SER |
| 1 | B | 133 | GLN |
| 1 | B | 157 | SER |
| 1 | B | 159 | MET |
| 1 | B | 160 | SER |
| 1 | B | 179 | SER |
| 1 | B | 182 | ARG |
| 1 | B | 184 | SER |
| 1 | B | 189 | SER |
| 1 | B | 190 | LEU |
| 1 | B | 212 | MET |
| 1 | B | 219 | ARG |
| 1 | B | 225 | TRP |
| 1 | B | 236 | THR |
| 1 | B | 255 | ILE |
| 1 | B | 257 | ARG |
| 1 | B | 261 | GLN |

*Continued on next page...*

*Continued from previous page...*

| Mol | Chain | Res | Type |
|---|---|---|---|
| 1 | B | 262 | ASN |
| 1 | B | 264 | LEU |
| 1 | B | 281 | SER |
| 1 | B | 283 | ASP |
| 1 | B | 299 | GLN |
| 1 | B | 301 | ASN |
| 1 | B | 305 | LEU |
| 1 | B | 330 | ARG |
| 1 | B | 332 | SER |
| 1 | B | 347 | GLU |
| 1 | B | 365 | ARG |
| 1 | B | 393 | ARG |
| 1 | B | 402 | THR |
| 1 | B | 404 | MET |
| 1 | B | 405 | MET |
| 1 | B | 412 | PHE |
| 1 | B | 414 | ASN |
| 1 | B | 419 | GLU |
| 1 | B | 426 | ASN |
| 1 | B | 427 | ARG |
| 1 | B | 432 | LYS |
| 1 | B | 441 | ILE |
| 1 | B | 459 | ARG |
| 1 | B | 470 | HIS |
| 1 | B | 473 | GLU |
| 1 | B | 476 | LYS |
| 1 | B | 498 | ARG |
| 1 | B | 503 | TYR |
| 1 | B | 504 | GLU |

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 1 | A | 32 | HIS |
| 1 | A | 261 | GLN |
| 1 | A | 311 | ASN |
| 1 | A | 374 | HIS |
| 1 | B | 32 | HIS |
| 1 | B | 261 | GLN |
| 1 | B | 299 | GLN |
| 1 | B | 451 | HIS |
| 1 | B | 471 | GLN |

### 5.3.3 RNA (i)

There are no RNA molecules in this entry.

## 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 monosaccharides in this entry.

## 5.6 Ligand geometry (i)

8 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

| Mol | Type | Chain | Res | Link | Bond lengths | | | Bond angles | | |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | Counts | RMSZ | $\#\|Z\| > 2$ | Counts | RMSZ | $\#\|Z\| > 2$ |
| 2 | GOL | A | 1506 | - | 5,5,5 | 0.50 | 0 | 5,5,5 | 0.66 | 0 |
| 3 | BG6 | A | 1510 | - | 16,16,16 | 0.68 | 0 | 24,24,24 | 1.10 | 3 (12%) |
| 2 | GOL | A | 1509 | - | 5,5,5 | 0.35 | 0 | 5,5,5 | 0.40 | 0 |
| 2 | GOL | A | 1508 | - | 5,5,5 | 0.46 | 0 | 5,5,5 | 0.41 | 0 |
| 2 | GOL | B | 1507 | - | 5,5,5 | 0.43 | 0 | 5,5,5 | 0.47 | 0 |
| 2 | GOL | A | 1507 | - | 5,5,5 | 0.37 | 0 | 5,5,5 | 0.31 | 0 |
| 2 | GOL | B | 1506 | - | 5,5,5 | 0.34 | 0 | 5,5,5 | 0.45 | 0 |
| 3 | BG6 | B | 1508 | - | 16,16,16 | 0.71 | 0 | 24,24,24 | 1.13 | 3 (12%) |

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

| Mol | Type | Chain | Res | Link | Chirals | Torsions | Rings |
|---|---|---|---|---|---|---|---|
| 2 | GOL | A | 1506 | - | - | 1/4/4/4 | - |
| 3 | BG6 | A | 1510 | - | - | 1/6/26/26 | 0/1/1/1 |

*Continued on next page...*

*Continued from previous page...*

| Mol | Type | Chain | Res | Link | Chirals | Torsions | Rings |
|---|---|---|---|---|---|---|---|
| 2 | GOL | A | 1509 | - | - | 4/4/4/4 | - |
| 2 | GOL | A | 1508 | - | - | 1/4/4/4 | - |
| 2 | GOL | B | 1507 | - | - | 3/4/4/4 | - |
| 2 | GOL | A | 1507 | - | - | 2/4/4/4 | - |
| 2 | GOL | B | 1506 | - | - | 3/4/4/4 | - |
| 3 | BG6 | B | 1508 | - | - | 0/6/26/26 | 0/1/1/1 |

There are no bond length outliers.

All (6) bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed($^o$) | Ideal($^o$) |
|---|---|---|---|---|---|---|---|
| 3 | B | 1508 | BG6 | O2P-P-O6 | -2.87 | 99.09 | 106.73 |
| 3 | A | 1510 | BG6 | O2P-P-O1P | 2.72 | 118.02 | 107.64 |
| 3 | B | 1508 | BG6 | O2P-P-O1P | 2.67 | 117.86 | 107.64 |
| 3 | A | 1510 | BG6 | O2P-P-O6 | -2.62 | 99.75 | 106.73 |
| 3 | A | 1510 | BG6 | O1P-P-O6 | -2.34 | 100.49 | 106.73 |
| 3 | B | 1508 | BG6 | O1P-P-O6 | -2.18 | 100.94 | 106.73 |

There are no chirality outliers.

All (15) torsion outliers are listed below:

| Mol | Chain | Res | Type | Atoms |
|---|---|---|---|---|
| 2 | A | 1509 | GOL | O1-C1-C2-C3 |
| 2 | A | 1509 | GOL | C1-C2-C3-O3 |
| 2 | B | 1506 | GOL | O1-C1-C2-C3 |
| 2 | B | 1506 | GOL | C1-C2-C3-O3 |
| 2 | B | 1507 | GOL | O1-C1-C2-C3 |
| 2 | B | 1507 | GOL | C1-C2-C3-O3 |
| 2 | A | 1509 | GOL | O2-C2-C3-O3 |
| 2 | A | 1507 | GOL | O1-C1-C2-C3 |
| 2 | A | 1509 | GOL | O1-C1-C2-O2 |
| 2 | B | 1506 | GOL | O1-C1-C2-O2 |
| 2 | B | 1507 | GOL | O1-C1-C2-O2 |
| 2 | A | 1507 | GOL | O1-C1-C2-O2 |
| 3 | A | 1510 | BG6 | O5-C5-C6-O6 |
| 2 | A | 1506 | GOL | O2-C2-C3-O3 |
| 2 | A | 1508 | GOL | C1-C2-C3-O3 |

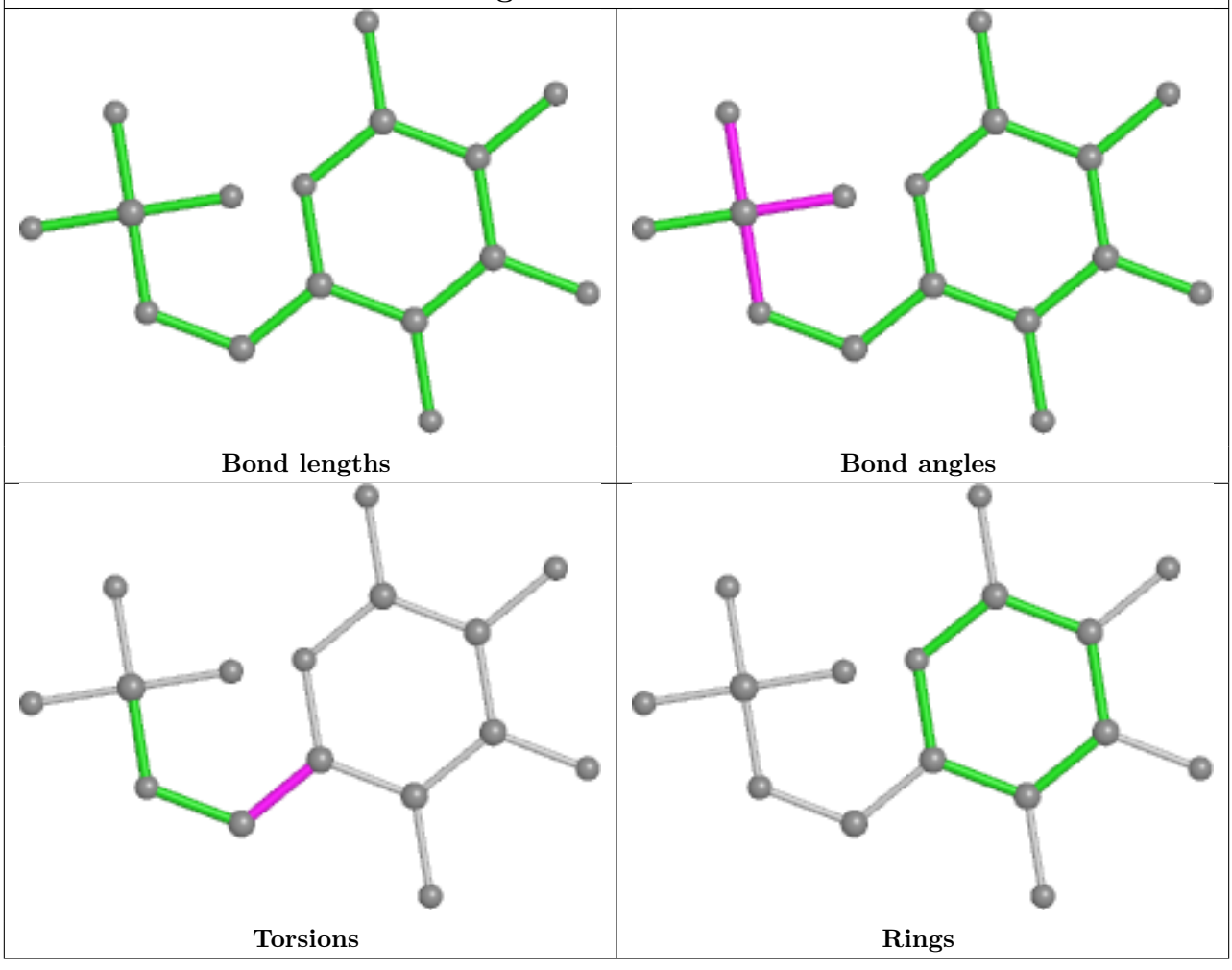
There are no ring outliers.

4 monomers are involved in 15 short contacts:

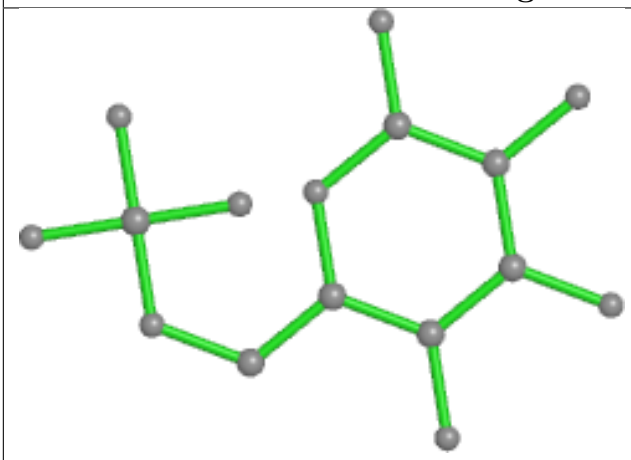
| Mol | Chain | Res | Type | Clashes | Symm-Clashes |
|---|---|---|---|---|---|
| 2 | A | 1506 | GOL | 2 | 0 |
| 2 | A | 1507 | GOL | 7 | 0 |
| 2 | B | 1506 | GOL | 5 | 0 |
| 3 | B | 1508 | BG6 | 1 | 0 |

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

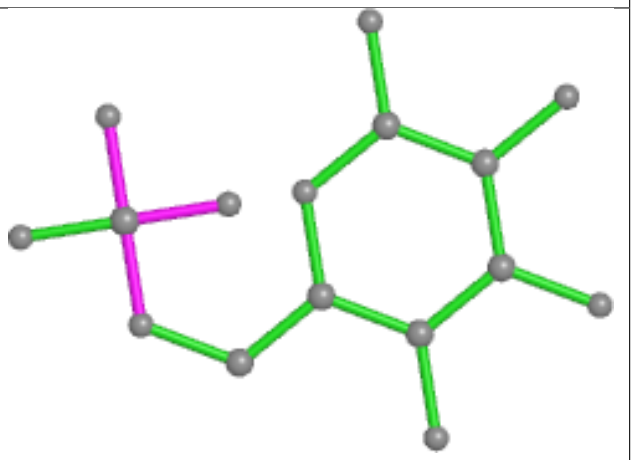
**Ligand BG6 A 1510**



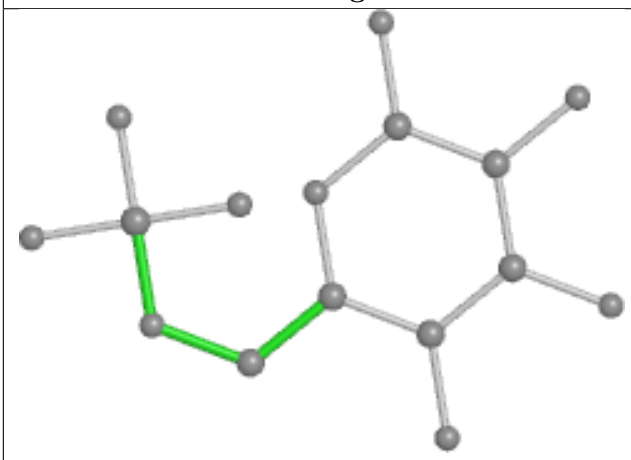
**Ligand BG6 B 1508**



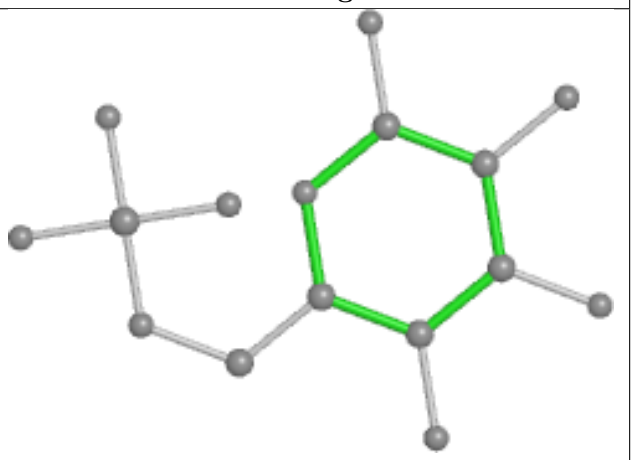
Bond lengths



Bond angles



Torsions



Rings

## 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 Fit of model and data

## 6.1 Protein, DNA and RNA chains

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, $95^{th}$ percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

| Mol | Chain | Analysed | <RSRZ> | #RSRZ>2 | | | OWAB(Å$^2$) | Q<0.9 |
|---|---|---|---|---|---|---|---|---|
| 1 | A | 479/489 (97%) | 0.46 | 25 (5%) | 27 | 23 | 25, 47, 72, 94 | 1 (0%) |
| 1 | B | 479/489 (97%) | 0.35 | 18 (3%) | 40 | 36 | 30, 51, 76, 94 | 0 |
| All | All | 958/978 (97%) | 0.40 | 43 (4%) | 33 | 29 | 25, 49, 74, 94 | 1 (0%) |

All (43) RSRZ outliers are listed below:

| Mol | Chain | Res | Type | RSRZ |
|---|---|---|---|---|
| 1 | A | 118 | TYR | 4.9 |
| 1 | B | 503 | TYR | 4.0 |
| 1 | B | 27 | VAL | 3.9 |
| 1 | A | 111 | GLN | 3.8 |
| 1 | A | 27 | VAL | 3.6 |
| 1 | B | 243 | THR | 3.6 |
| 1 | A | 117 | SER | 3.4 |
| 1 | B | 315 | GLU | 3.3 |
| 1 | B | 361 | ALA | 3.2 |
| 1 | A | 156 | GLU | 3.2 |
| 1 | A | 125 | MET | 3.1 |
| 1 | A | 157 | SER | 3.1 |
| 1 | B | 245 | GLY | 3.1 |
| 1 | B | 320 | LYS | 3.0 |
| 1 | B | 328 | VAL | 3.0 |
| 1 | A | 121 | LEU | 3.0 |
| 1 | B | 314 | GLY | 3.0 |
| 1 | A | 158 | CYS | 2.8 |
| 1 | A | 108 | VAL | 2.7 |
| 1 | A | 28 | GLN | 2.7 |
| 1 | A | 315 | GLU | 2.6 |
| 1 | A | 114 | ASP | 2.6 |
| 1 | A | 243 | THR | 2.5 |
| 1 | A | 70 | TYR | 2.5 |

*Continued on next page...*

*Continued from previous page...*

| Mol | Chain | Res | Type | RSRZ |
|---|---|---|---|---|
| 1 | A | 116 | ALA | 2.5 |
| 1 | A | 323 | LEU | 2.4 |
| 1 | B | 323 | LEU | 2.4 |
| 1 | A | 505 | GLY | 2.4 |
| 1 | A | 119 | GLN | 2.4 |
| 1 | A | 115 | ALA | 2.4 |
| 1 | B | 308 | TYR | 2.3 |
| 1 | B | 322 | TYR | 2.3 |
| 1 | B | 335 | ALA | 2.3 |
| 1 | A | 87 | PHE | 2.2 |
| 1 | B | 330 | ARG | 2.2 |
| 1 | B | 362 | LEU | 2.2 |
| 1 | B | 504 | GLU | 2.1 |
| 1 | A | 153 | ASN | 2.1 |
| 1 | A | 128 | LEU | 2.1 |
| 1 | A | 162 | ILE | 2.1 |
| 1 | A | 89 | LYS | 2.1 |
| 1 | B | 309 | VAL | 2.1 |
| 1 | B | 176 | ASP | 2.0 |

## 6.2 Non-standard residues in protein, DNA, RNA chains (i)

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

## 6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

## 6.4 Ligands (i)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, $95^{th}$ percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

| Mol | Type | Chain | Res | Atoms | RSCC | RSR | B-factors(Å$^2$) | Q<0.9 |
|---|---|---|---|---|---|---|---|---|
| 2 | GOL | B | 1507 | 6/6 | 0.73 | 0.38 | 53,53,53,53 | 0 |
| 2 | GOL | B | 1506 | 6/6 | 0.82 | 0.38 | 58,58,59,59 | 0 |
| 2 | GOL | A | 1506 | 6/6 | 0.84 | 0.41 | 50,51,52,53 | 0 |
| 2 | GOL | A | 1509 | 6/6 | 0.86 | 0.29 | 59,59,59,60 | 0 |

*Continued on next page...*

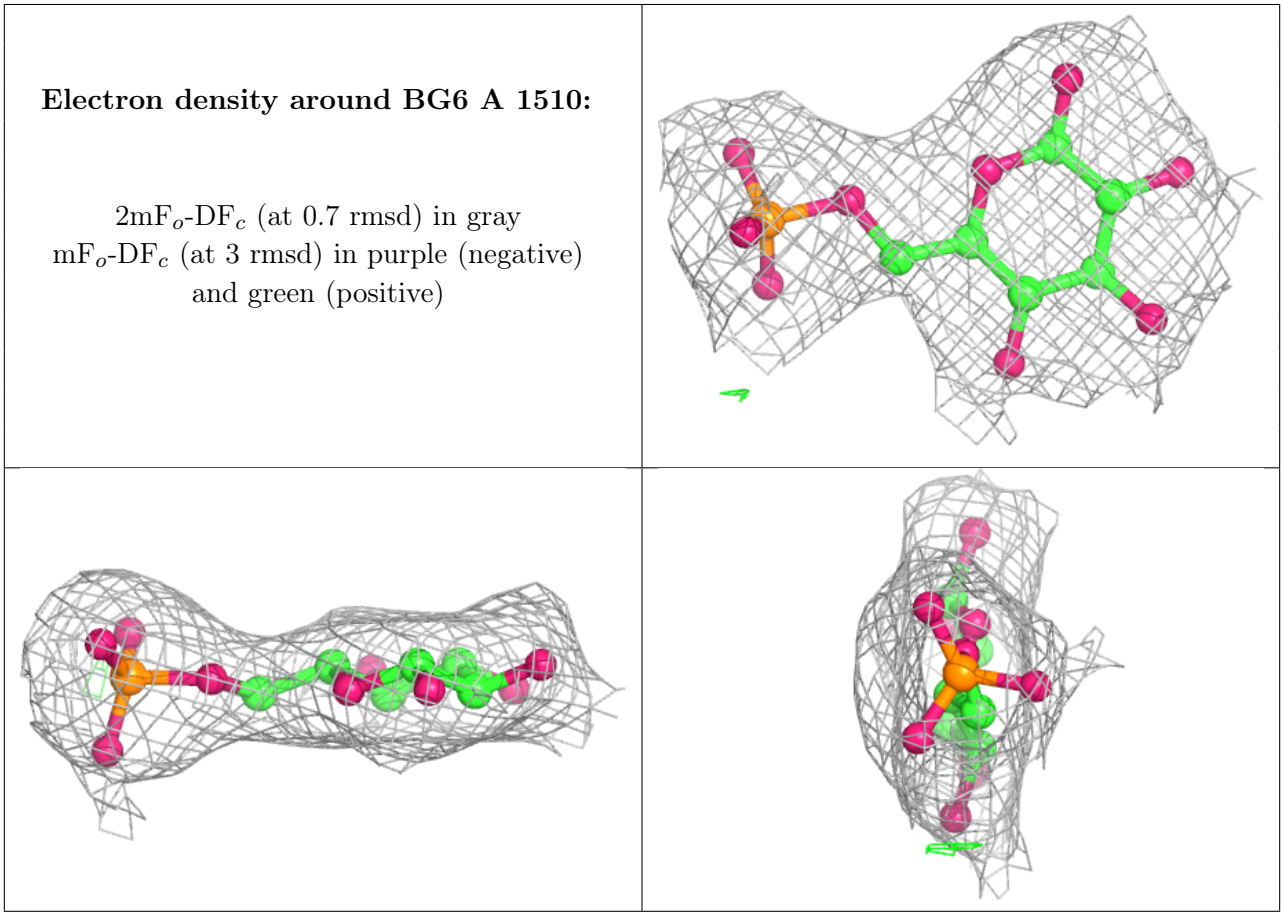
*Continued from previous page...*

| Mol | Type | Chain | Res | Atoms | RSCC | RSR | B-factors(Å$^2$) | Q<0.9 |
|---|---|---|---|---|---|---|---|---|
| 2 | GOL | A | 1507 | 6/6 | 0.89 | 0.37 | 52,52,52,53 | 0 |
| 2 | GOL | A | 1508 | 6/6 | 0.93 | 0.19 | 50,51,52,52 | 0 |
| 3 | BG6 | A | 1510 | 16/16 | 0.97 | 0.14 | 45,46,48,48 | 0 |
| 3 | BG6 | B | 1508 | 16/16 | 0.97 | 0.15 | 50,50,51,51 | 0 |

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

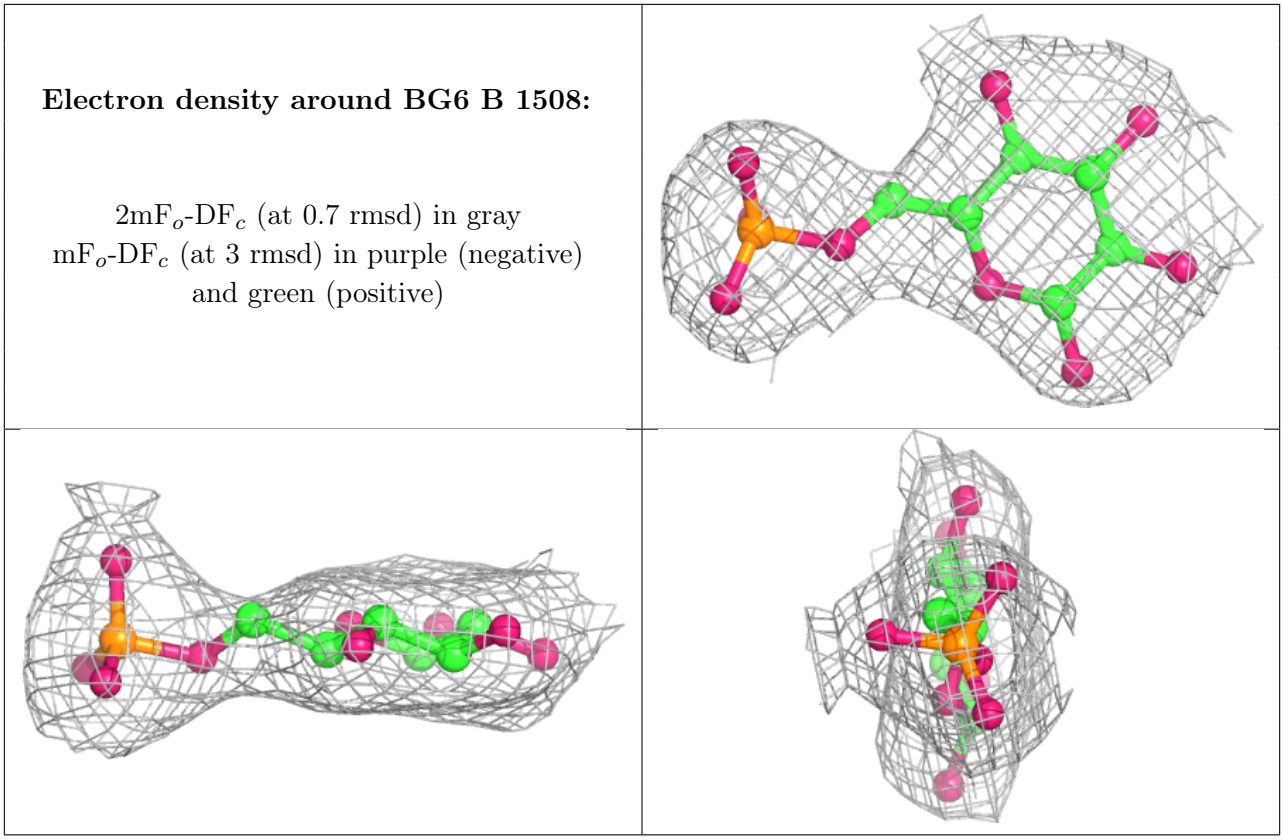
**Electron density around BG6 A 1510:**

$2mF_o$-$DF_c$ (at 0.7 rmsd) in gray
$mF_o$-$DF_c$ (at 3 rmsd) in purple (negative) and green (positive)



**Electron density around BG6 B 1508:**

$2mF_o$-$DF_c$ (at 0.7 rmsd) in gray
$mF_o$-$DF_c$ (at 3 rmsd) in purple (negative) and green (positive)



## 6.5 Other polymers (i)

There are no such residues in this entry.