# Full wwPDB EM Validation Report ⓘ

Nov 5, 2022 – 10:52 AM EDT

| | | |
|---|---|---|
| PDB ID | : | 5VHZ |
| EMDB ID | : | EMD-8688 |
| Title | : | GluA2-2xGSG1L bound to L-Quisqualate |
| Authors | : | Twomey, E.C.; Yelshanskaya, M.V.; Grassucci, R.A.; Frank, J.; Sobolevsky, A.I. |
| Deposited on | : | 2017-04-13 |
| Resolution | : | 8.40 Å(reported) |

This is a Full wwPDB EM 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/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:

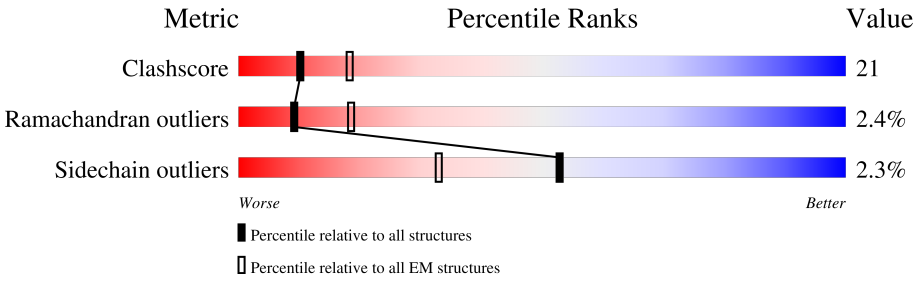
| | | |
|---|---|---|
| EMDB validation analysis | : | 0.0.1.dev43 |
| Mogul | : | 1.8.5 (274361), CSD as541be (2020) |
| MolProbity | : | 4.02b-467 |
| Percentile statistics | : | 20191225.v01 (using entries in the PDB archive December 25th 2019) |
| MapQ | : | 1.9.9 |
| Ideal geometry (proteins) | : | Engh & Huber (2001) |
| Ideal geometry (DNA, RNA) | : | Parkinson et al. (1996) |
| Validation Pipeline (wwPDB-VP) | : | 2.31.2 |

# 1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
*ELECTRON MICROSCOPY*

The reported resolution of this entry is 8.40 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) | EM structures (#Entries) |
|---|---|---|
| Clashscore | 158937 | 4297 |
| Ramachandran outliers | 154571 | 4023 |
| Sidechain outliers | 154315 | 3826 |

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 >=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 EM map (all-atom inclusion < 40%). The numeric value is given above the bar.

| Mol | Chain | Length | Quality of chain |
|---|---|---|---|
| 1 | A | 1057 | 9% 47% 24% · 26% |
| 1 | B | 1057 | 13% 47% 24% · 26% |
| 1 | C | 1057 | 10% 48% 24% · 26% |
| 1 | D | 1057 | 13% 48% 23% · 26% |
| 1 | E | 1057 | 7% 9% 7% · 83% |
| 1 | F | 1057 | 7% 9% 8% 83% |

## 2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 27460 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 Glutamate receptor 2,Germ cell-specific gene 1-like protein.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 1 | A | 783 | Total | C | N | O | S | 0 | 0 |
| | | | 6159 | 3950 | 1023 | 1156 | 30 | | |
| 1 | B | 780 | Total | C | N | O | S | 0 | 0 |
| | | | 6137 | 3938 | 1017 | 1152 | 30 | | |
| 1 | C | 783 | Total | C | N | O | S | 0 | 0 |
| | | | 6159 | 3950 | 1023 | 1156 | 30 | | |
| 1 | D | 780 | Total | C | N | O | S | 0 | 0 |
| | | | 6137 | 3938 | 1017 | 1152 | 30 | | |
| 1 | E | 179 | Total | C | N | O | S | 0 | 0 |
| | | | 1408 | 920 | 231 | 245 | 12 | | |
| 1 | F | 179 | Total | C | N | O | S | 0 | 0 |
| | | | 1408 | 920 | 231 | 245 | 12 | | |

There are 84 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|---|---|---|---|---|---|
| A | 241 | GLU | ASN | conflict | UNP P19491 |
| A | 382 | LEU | VAL | conflict | UNP P19491 |
| A | ? | - | LEU | deletion | UNP P19491 |
| A | ? | - | THR | deletion | UNP P19491 |
| A | ? | - | GLU | deletion | UNP P19491 |
| A | ? | - | LEU | deletion | UNP P19491 |
| A | ? | - | PRO | deletion | UNP P19491 |
| A | ? | - | SER | deletion | UNP P19491 |
| A | 384 | GLU | GLY | conflict | UNP P19491 |
| A | 385 | ASP | ASN | conflict | UNP P19491 |
| A | 392 | GLN | ASN | conflict | UNP P19491 |
| A | 827 | GLY | - | linker | UNP P19491 |
| A | 828 | THR | - | linker | UNP P19491 |
| A | 829 | GLY | - | linker | UNP P19491 |
| B | 241 | GLU | ASN | conflict | UNP P19491 |
| B | 382 | LEU | VAL | conflict | UNP P19491 |
| B | ? | - | LEU | deletion | UNP P19491 |
| B | ? | - | THR | deletion | UNP P19491 |

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| Chain | Residue | Modelled | Actual | Comment | Reference |
|---|---|---|---|---|---|
| B | ? | - | GLU | deletion | UNP P19491 |
| B | ? | - | LEU | deletion | UNP P19491 |
| B | ? | - | PRO | deletion | UNP P19491 |
| B | ? | - | SER | deletion | UNP P19491 |
| B | 384 | GLU | GLY | conflict | UNP P19491 |
| B | 385 | ASP | ASN | conflict | UNP P19491 |
| B | 392 | GLN | ASN | conflict | UNP P19491 |
| B | 827 | GLY | - | linker | UNP P19491 |
| B | 828 | THR | - | linker | UNP P19491 |
| B | 829 | GLY | - | linker | UNP P19491 |
| C | 241 | GLU | ASN | conflict | UNP P19491 |
| C | 382 | LEU | VAL | conflict | UNP P19491 |
| C | ? | - | LEU | deletion | UNP P19491 |
| C | ? | - | THR | deletion | UNP P19491 |
| C | ? | - | GLU | deletion | UNP P19491 |
| C | ? | - | LEU | deletion | UNP P19491 |
| C | ? | - | PRO | deletion | UNP P19491 |
| C | ? | - | SER | deletion | UNP P19491 |
| C | 384 | GLU | GLY | conflict | UNP P19491 |
| C | 385 | ASP | ASN | conflict | UNP P19491 |
| C | 392 | GLN | ASN | conflict | UNP P19491 |
| C | 827 | GLY | - | linker | UNP P19491 |
| C | 828 | THR | - | linker | UNP P19491 |
| C | 829 | GLY | - | linker | UNP P19491 |
| D | 241 | GLU | ASN | conflict | UNP P19491 |
| D | 382 | LEU | VAL | conflict | UNP P19491 |
| D | ? | - | LEU | deletion | UNP P19491 |
| D | ? | - | THR | deletion | UNP P19491 |
| D | ? | - | GLU | deletion | UNP P19491 |
| D | ? | - | LEU | deletion | UNP P19491 |
| D | ? | - | PRO | deletion | UNP P19491 |
| D | ? | - | SER | deletion | UNP P19491 |
| D | 384 | GLU | GLY | conflict | UNP P19491 |
| D | 385 | ASP | ASN | conflict | UNP P19491 |
| D | 392 | GLN | ASN | conflict | UNP P19491 |
| D | 827 | GLY | - | linker | UNP P19491 |
| D | 828 | THR | - | linker | UNP P19491 |
| D | 829 | GLY | - | linker | UNP P19491 |
| E | -588 | GLU | ASN | conflict | UNP P19491 |
| E | -447 | LEU | VAL | conflict | UNP P19491 |
| E | ? | - | LEU | deletion | UNP P19491 |
| E | ? | - | THR | deletion | UNP P19491 |

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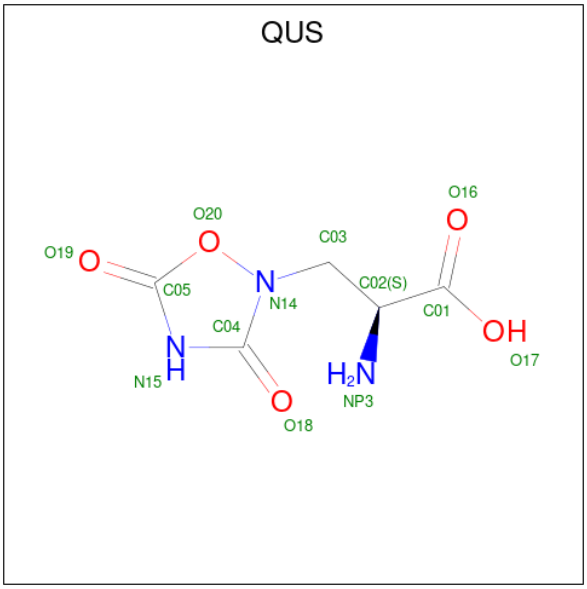
| Chain | Residue | Modelled | Actual | Comment | Reference |
|---|---|---|---|---|---|
| E | ? | - | GLU | deletion | UNP P19491 |
| E | ? | - | LEU | deletion | UNP P19491 |
| E | ? | - | PRO | deletion | UNP P19491 |
| E | ? | - | SER | deletion | UNP P19491 |
| E | -445 | GLU | GLY | conflict | UNP P19491 |
| E | -444 | ASP | ASN | conflict | UNP P19491 |
| E | -437 | GLN | ASN | conflict | UNP P19491 |
| E | -2 | GLY | - | linker | UNP P19491 |
| E | -1 | THR | - | linker | UNP P19491 |
| E | 0 | GLY | - | linker | UNP P19491 |
| F | -588 | GLU | ASN | conflict | UNP P19491 |
| F | -447 | LEU | VAL | conflict | UNP P19491 |
| F | ? | - | LEU | deletion | UNP P19491 |
| F | ? | - | THR | deletion | UNP P19491 |
| F | ? | - | GLU | deletion | UNP P19491 |
| F | ? | - | LEU | deletion | UNP P19491 |
| F | ? | - | PRO | deletion | UNP P19491 |
| F | ? | - | SER | deletion | UNP P19491 |
| F | -445 | GLU | GLY | conflict | UNP P19491 |
| F | -444 | ASP | ASN | conflict | UNP P19491 |
| F | -437 | GLN | ASN | conflict | UNP P19491 |
| F | -2 | GLY | - | linker | UNP P19491 |
| F | -1 | THR | - | linker | UNP P19491 |
| F | 0 | GLY | - | linker | UNP P19491 |

- Molecule 2 is (S)-2-AMINO-3-(3,5-DIOXO-[1,2,4]OXADIAZOLIDIN-2-YL)-PROPIONIC ACID (three-letter code: QUS) (formula: $C_5H_7N_3O_5$).



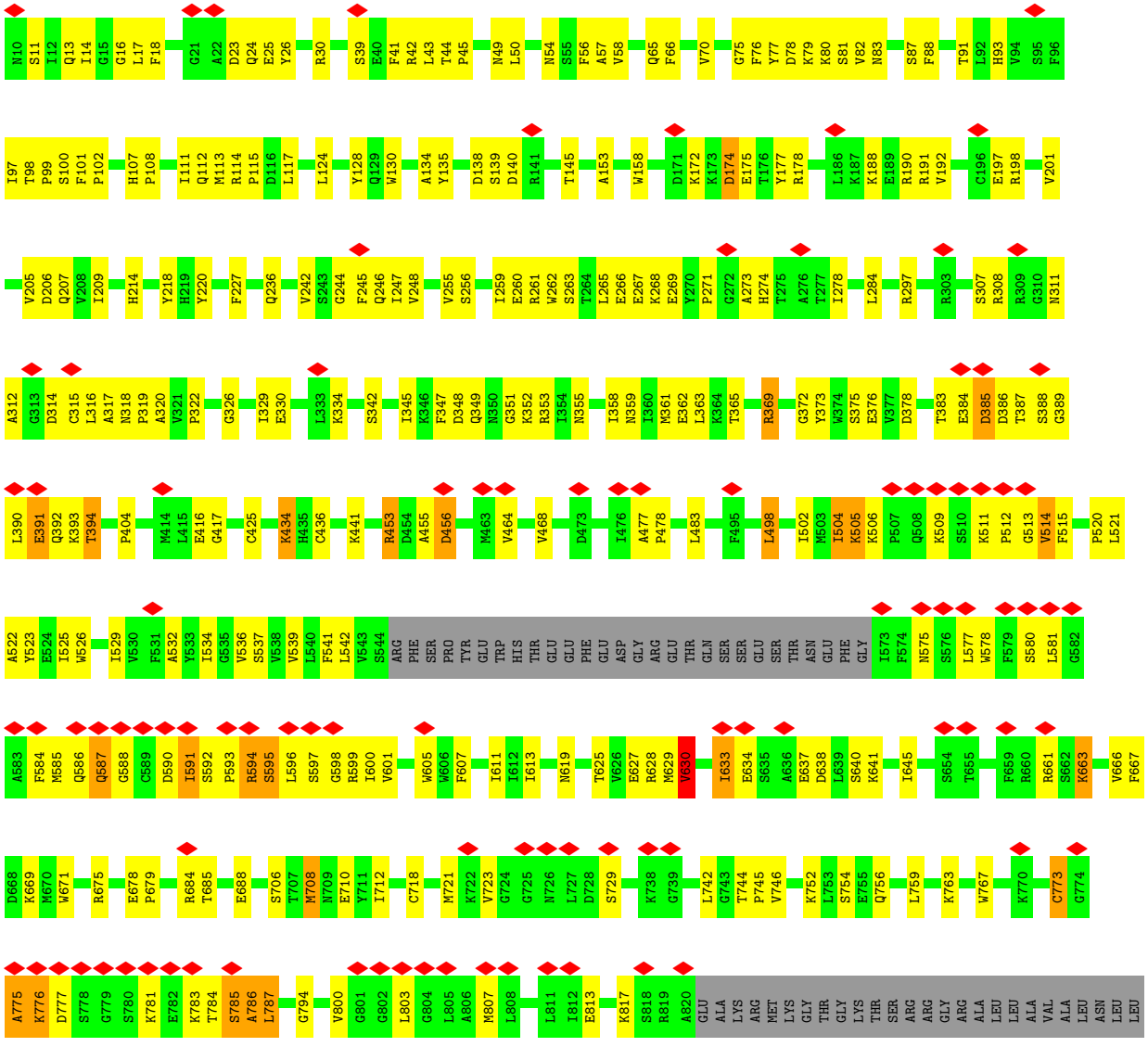
| Mol | Chain | Residues | Atoms | | | | AltConf |
|---|---|---|---|---|---|---|---|
| 2 | A | 1 | Total | C | N | O | 0 |
| | | | 13 | 5 | 3 | 5 | |
| 2 | B | 1 | Total | C | N | O | 0 |
| | | | 13 | 5 | 3 | 5 | |
| 2 | C | 1 | Total | C | N | O | 0 |
| | | | 13 | 5 | 3 | 5 | |
| 2 | D | 1 | Total | C | N | O | 0 |
| | | | 13 | 5 | 3 | 5 | |

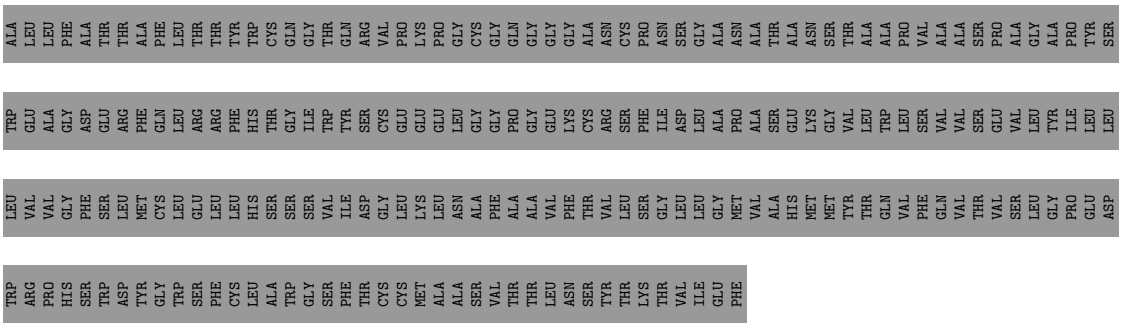
# 3 Residue-property plots (i)

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 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: Glutamate receptor 2,Germ cell-specific gene 1-like protein

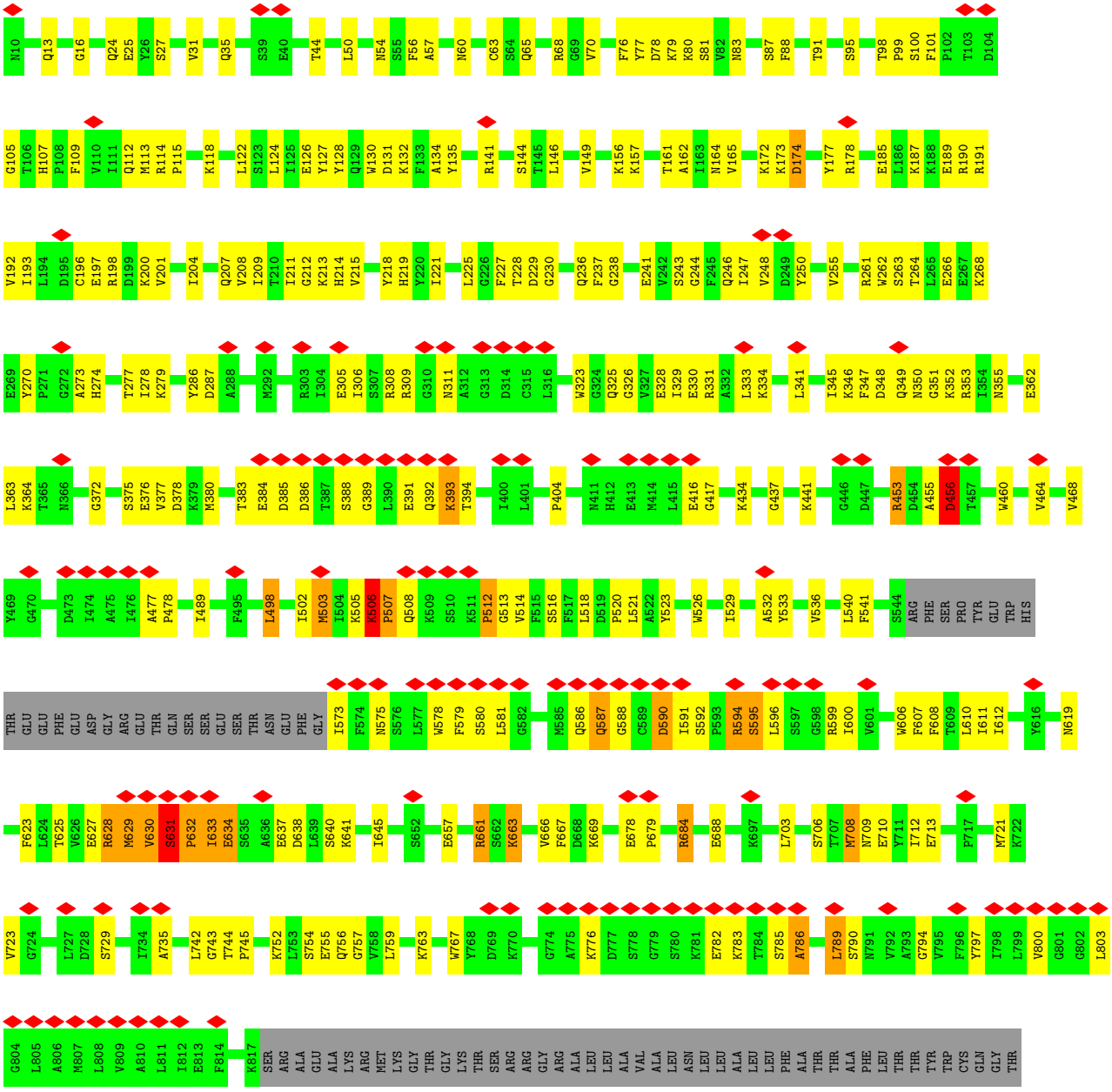
Chain A:



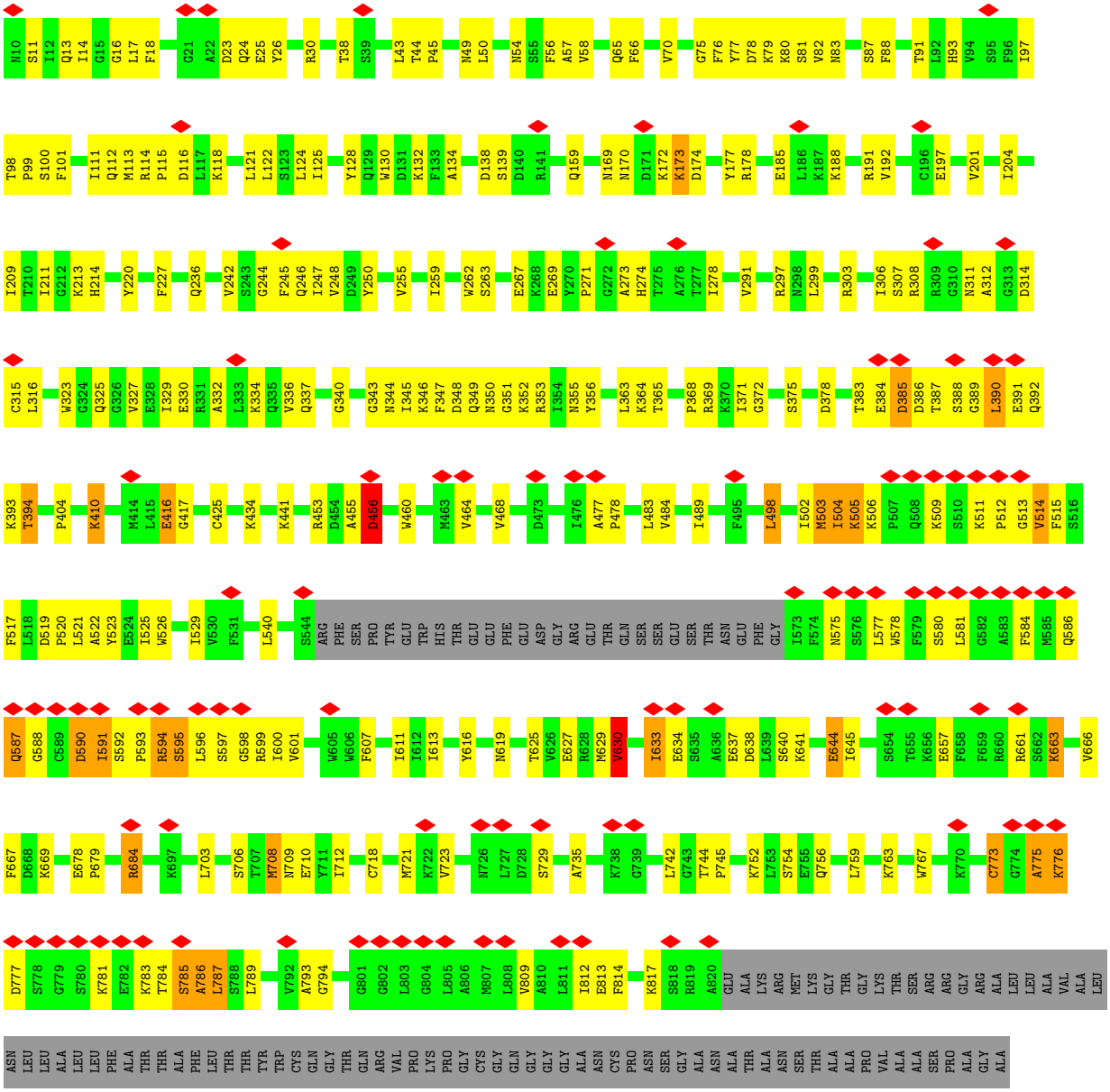

• Molecule 1: Glutamate receptor 2,Germ cell-specific gene 1-like protein

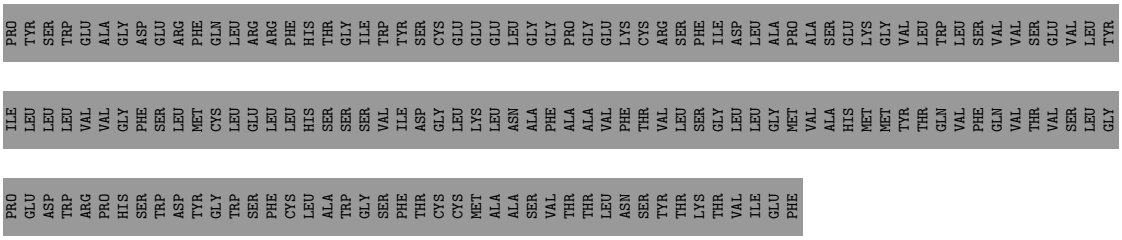
Chain B:

• Molecule 1: Glutamate receptor 2,Germ cell-specific gene 1-like protein

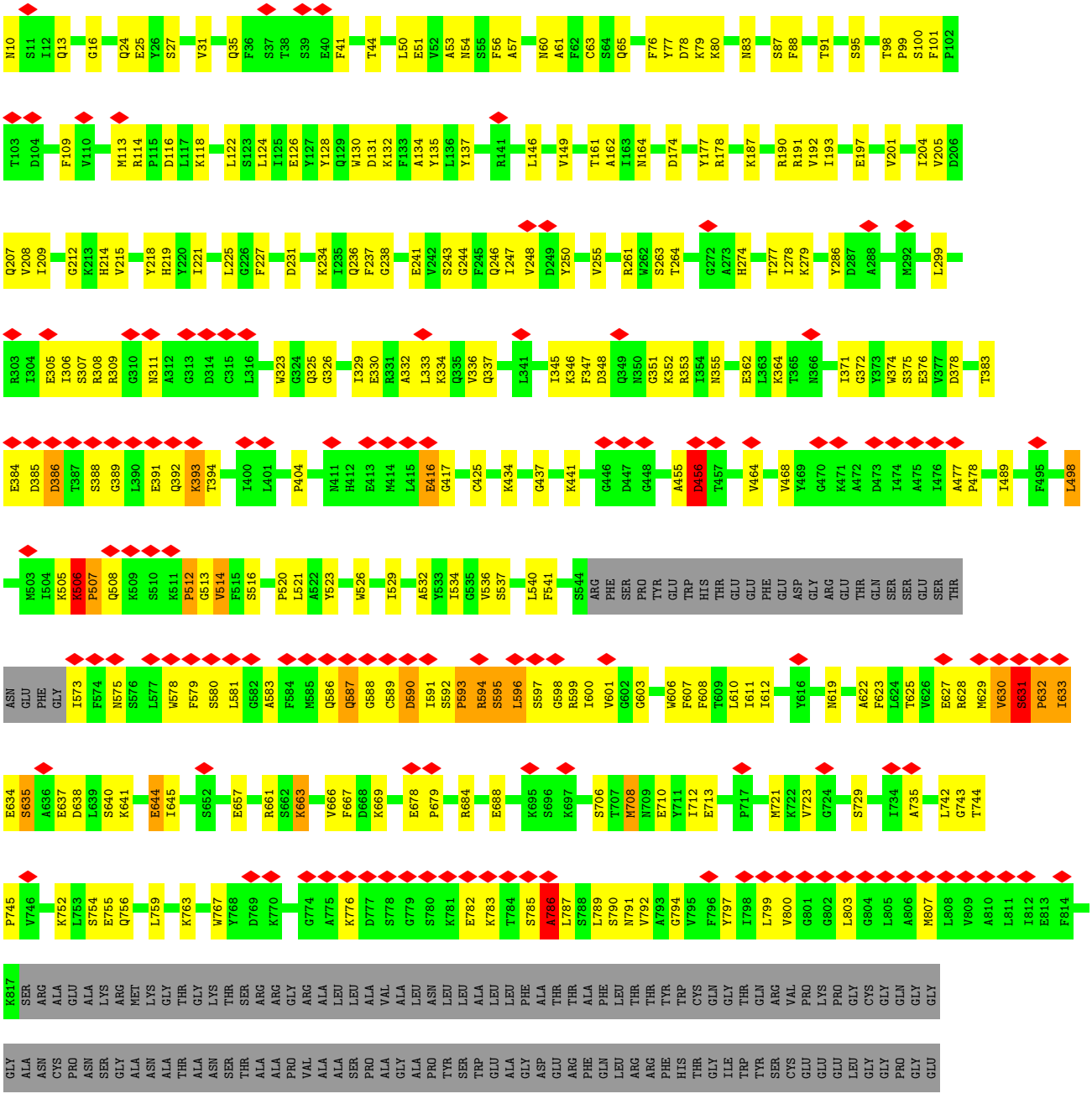
Chain C:

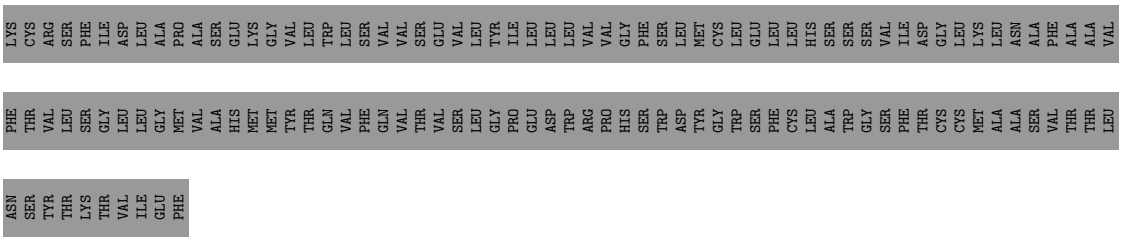






• Molecule 1: Glutamate receptor 2,Germ cell-specific gene 1-like protein

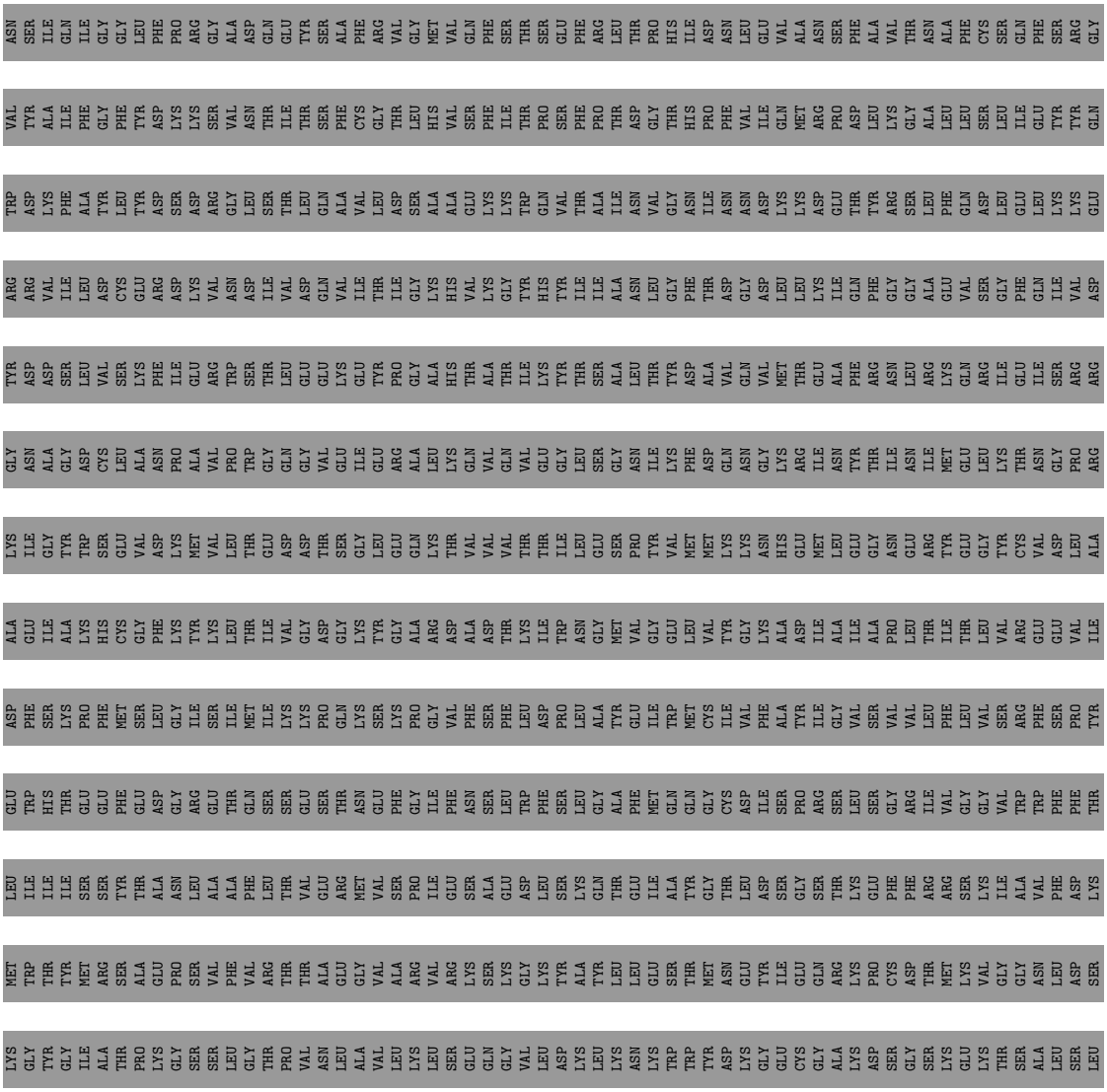
Chain D:

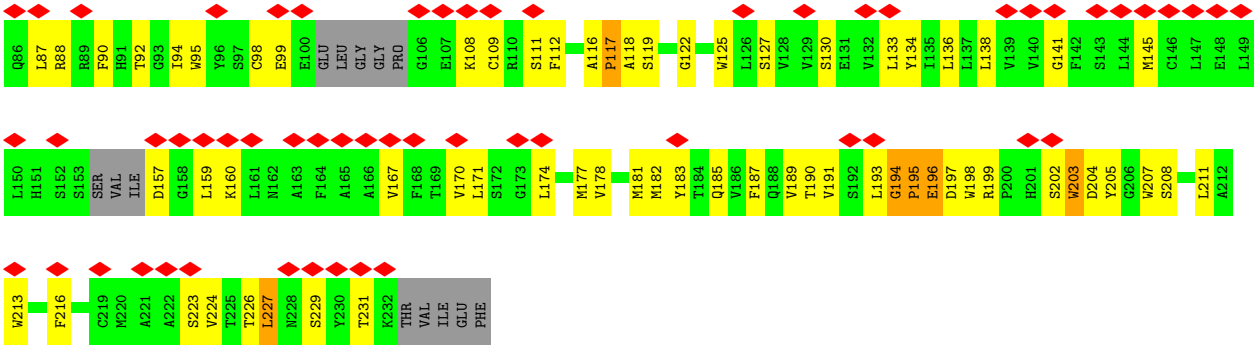






• Molecule 1: Glutamate receptor 2,Germ cell-specific gene 1-like protein

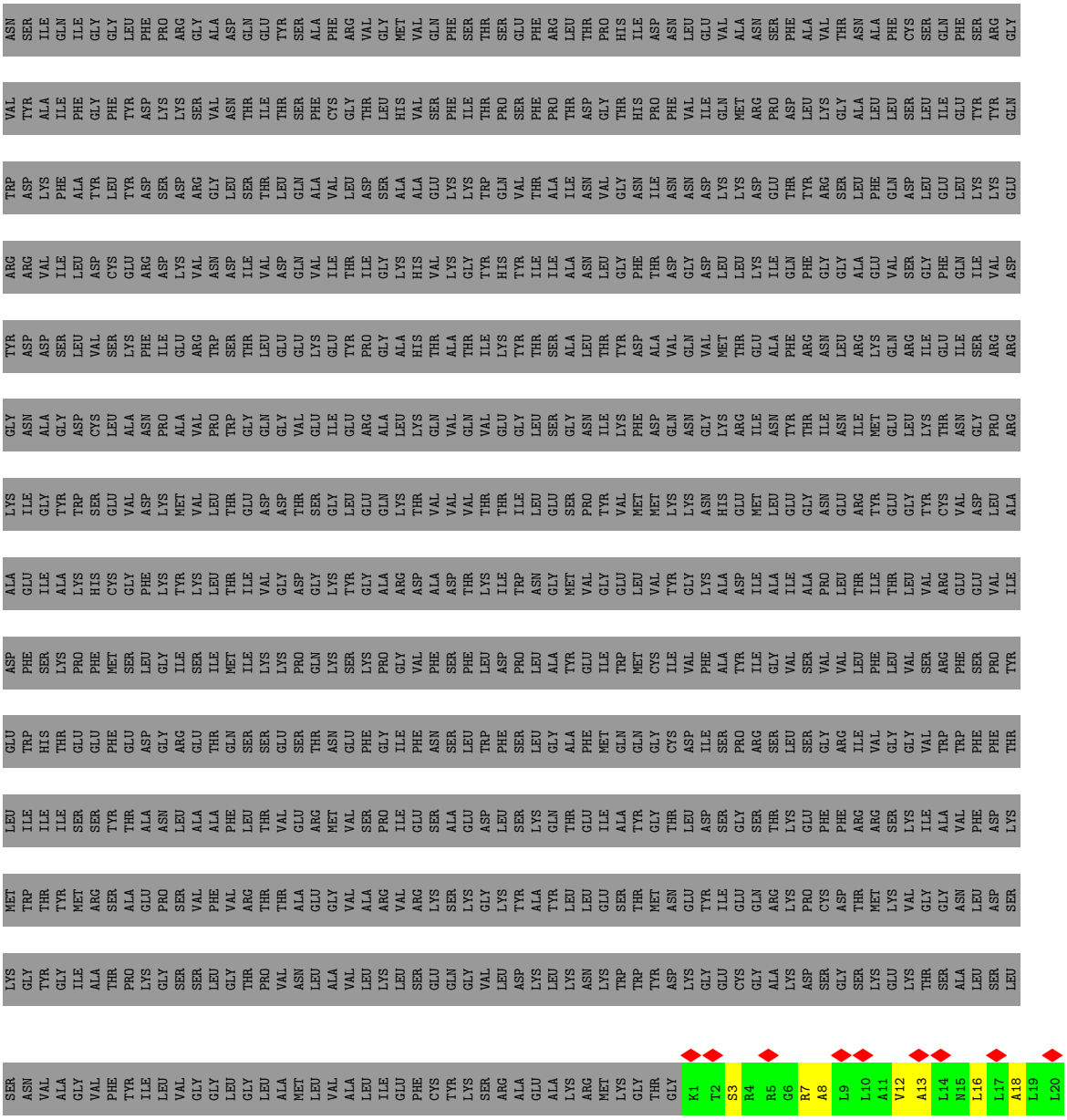
Chain E:

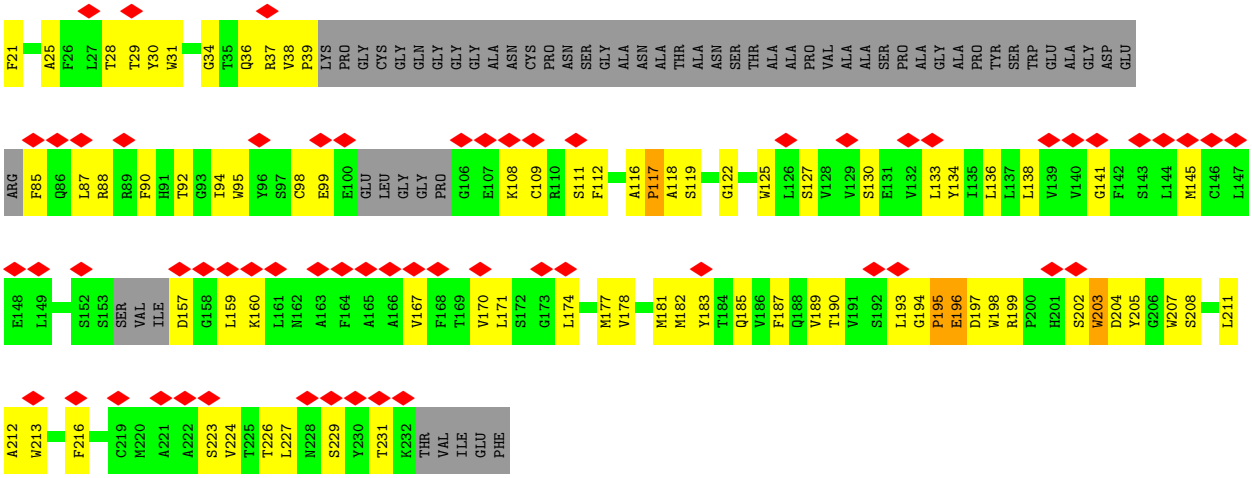






• Molecule 1: Glutamate receptor 2,Germ cell-specific gene 1-like protein

Chain F: 7% 9% 8% 83%




F21 A25 F26 L27 T28 T29 Y30 W31 G34 T35 Q36 R37 V38 P39 LYS PRO GLY CYS GLY GLN GLY GLY GLY GLY ALA ASN CYS PRO ASN SER GLY ALA ASN ALA THR ALA ASN SER THR ALA ALA PRO VAL ALA ALA SER PRO ALA GLY ALA PRO TYR SER TRP GLU ALA GLY ASP GLU
ARG F85 Q86 L87 R88 R89 F90 H91 T92 G93 I94 W95 Y96 S97 C98 E99 E100 GLU LEU GLY GLY PRO G106 E107 K108 C109 R110 S111 F112 A116 P117 A118 S119 G122 W125 L126 S127 V128 V129 S130 E131 V132 L133 Y134 I135 L136 L137 L138 V139 V140 G141 F142 S143 L144 M145 C146 L147
E148 L149 S152 S153 SER VAL ILE D157 G158 L159 K160 L161 N162 A163 F164 A165 A166 V167 F168 T169 V170 L171 S172 G173 L174 M177 V178 M181 M182 Y183 T184 Q185 V186 F187 Q188 V189 T190 V191 S192 L193 G194 P195 E196 D197 W198 R199 P200 H201 S202 W203 D204 Y205 G206 W207 S208 L211
A212 W213 F216 C219 M220 A221 A222 S223 V224 T225 T226 L227 N228 S229 Y230 T231 K232 THR VAL ILE GLU PHE

# 4 Experimental information (i)

| Property | Value | Source |
|---|---|---|
| EM reconstruction method | SINGLE PARTICLE | Depositor |
| Imposed symmetry | POINT, C2 | Depositor |
| Number of particles used | 51130 | Depositor |
| Resolution determination method | FSC 0.143 CUT-OFF | Depositor |
| CTF correction method | PHASE FLIPPING AND AMPLITUDE CORRECTION | Depositor |
| Microscope | FEI POLARA 300 | Depositor |
| Voltage (kV) | 300 | Depositor |
| Electron dose ($e^-/Å^2$) | 67 | Depositor |
| Minimum defocus (nm) | Not provided | |
| Maximum defocus (nm) | Not provided | |
| Magnification | Not provided | |
| Image detector | GATAN K2 SUMMIT (4k x 4k) | Depositor |
| Maximum map value | 0.053 | Depositor |
| Minimum map value | -0.026 | Depositor |
| Average map value | 0.000 | Depositor |
| Map value standard deviation | 0.002 | Depositor |
| Recommended contour level | 0.015 | Depositor |
| Map size (Å) | 352.80002, 352.80002, 352.80002 | wwPDB |
| Map dimensions | 360, 360, 360 | wwPDB |
| Map angles (°) | 90.0, 90.0, 90.0 | wwPDB |
| Pixel spacing (Å) | 0.9800001, 0.9800001, 0.9800001 | Depositor |

# 5 Model quality

## 5.1 Standard geometry

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

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 | 0.32 | 0/6287 | 0.50 | 0/8493 |
| 1 | B | 0.33 | 0/6265 | 0.56 | 4/8464 (0.0%) |
| 1 | C | 0.32 | 0/6287 | 0.50 | 1/8493 (0.0%) |
| 1 | D | 0.35 | 1/6265 (0.0%) | 0.57 | 5/8464 (0.1%) |
| 1 | E | 0.29 | 0/1443 | 0.49 | 0/1959 |
| 1 | F | 0.29 | 0/1443 | 0.48 | 0/1959 |
| All | All | 0.33 | 1/27990 (0.0%) | 0.53 | 10/37832 (0.0%) |

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

| Mol | Chain | #Chirality outliers | #Planarity outliers |
|---|---|---|---|
| 1 | D | 0 | 1 |

All (1) bond length outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(Å) | Ideal(Å) |
|---|---|---|---|---|---|---|---|
| 1 | D | 786 | ALA | C-N | -11.69 | 1.07 | 1.34 |

All (10) bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed($^o$) | Ideal($^o$) |
|---|---|---|---|---|---|---|---|
| 1 | B | 506 | LYS | C-N-CD | -17.67 | 81.72 | 120.60 |
| 1 | D | 506 | LYS | C-N-CD | -17.65 | 81.76 | 120.60 |
| 1 | B | 631 | SER | C-N-CD | -16.78 | 83.69 | 120.60 |
| 1 | D | 631 | SER | C-N-CD | -16.76 | 83.72 | 120.60 |
| 1 | D | 786 | ALA | O-C-N | -8.83 | 108.58 | 122.70 |
| 1 | D | 386 | ASP | CB-CG-OD2 | 5.23 | 123.00 | 118.30 |

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| Mol | Chain | Res | Type | Atoms | Z | Observed($^o$) | Ideal($^o$) |
|---|---|---|---|---|---|---|---|
| 1 | B | 386 | ASP | CB-CG-OD2 | 5.21 | 122.99 | 118.30 |
| 1 | C | 456 | ASP | CB-CG-OD2 | 5.21 | 122.98 | 118.30 |
| 1 | D | 456 | ASP | CB-CG-OD2 | 5.20 | 122.98 | 118.30 |
| 1 | B | 456 | ASP | CB-CG-OD2 | 5.19 | 122.97 | 118.30 |

There are no chirality outliers.

All (1) planarity outliers are listed below:

| Mol | Chain | Res | Type | Group |
|---|---|---|---|---|
| 1 | D | 786 | ALA | Mainchain |

## 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 | A | 6159 | 0 | 6157 | 283 | 0 |
| 1 | B | 6137 | 0 | 6132 | 321 | 0 |
| 1 | C | 6159 | 0 | 6157 | 309 | 0 |
| 1 | D | 6137 | 0 | 6131 | 291 | 0 |
| 1 | E | 1408 | 0 | 1406 | 61 | 0 |
| 1 | F | 1408 | 0 | 1406 | 54 | 0 |
| 2 | A | 13 | 0 | 6 | 0 | 0 |
| 2 | B | 13 | 0 | 6 | 0 | 0 |
| 2 | C | 13 | 0 | 6 | 0 | 0 |
| 2 | D | 13 | 0 | 6 | 0 | 0 |
| All | All | 27460 | 0 | 27413 | 1177 | 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 21.

All (1177) 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:C:506:LYS:CE | 1:C:721:MET:HB2 | 1.20 | 1.65 |
| 1:A:506:LYS:CE | 1:A:721:MET:HB2 | 1.16 | 1.58 |

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| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|---|---|---|---|
| 1:A:506:LYS:HE3 | 1:A:721:MET:CB | 1.33 | 1.57 |
| 1:C:506:LYS:HE3 | 1:C:721:MET:CB | 1.35 | 1.56 |
| 1:A:506:LYS:CE | 1:A:721:MET:CB | 1.86 | 1.53 |
| 1:C:506:LYS:HE2 | 1:C:721:MET:CG | 1.41 | 1.51 |
| 1:C:506:LYS:CE | 1:C:721:MET:CB | 1.87 | 1.48 |
| 1:A:506:LYS:HE2 | 1:A:721:MET:CG | 1.43 | 1.45 |
| 1:B:512:PRO:HB3 | 1:B:516:SER:CB | 1.46 | 1.43 |
| 1:A:483:LEU:CD2 | 1:D:755:GLU:OE2 | 1.71 | 1.37 |
| 1:B:512:PRO:CB | 1:B:516:SER:CB | 2.03 | 1.36 |
| 1:B:453:ARG:HD2 | 1:B:460:TRP:NE1 | 1.40 | 1.33 |
| 1:B:755:GLU:OE2 | 1:C:483:LEU:CD2 | 1.77 | 1.30 |
| 1:B:512:PRO:HB2 | 1:B:516:SER:OG | 1.18 | 1.28 |
| 1:C:627:GLU:O | 1:C:630:VAL:HG13 | 1.34 | 1.28 |
| 1:B:512:PRO:CB | 1:B:516:SER:HB3 | 1.64 | 1.24 |
| 1:B:453:ARG:HD2 | 1:B:460:TRP:CE2 | 1.73 | 1.23 |
| 1:A:512:PRO:HB2 | 1:A:515:PHE:CD2 | 1.75 | 1.22 |
| 1:C:512:PRO:HB2 | 1:C:515:PHE:CD2 | 1.75 | 1.22 |
| 1:B:512:PRO:CB | 1:B:516:SER:OG | 1.89 | 1.21 |
| 1:D:512:PRO:HB2 | 1:D:516:SER:OG | 1.43 | 1.18 |
| 1:C:634:GLU:CG | 1:C:723:VAL:HB | 1.73 | 1.18 |
| 1:A:483:LEU:HD21 | 1:D:755:GLU:OE2 | 1.30 | 1.17 |
| 1:C:663:LYS:HE2 | 1:C:663:LYS:HA | 1.29 | 1.14 |
| 1:D:631:SER:HB3 | 1:D:632:PRO:CD | 1.78 | 1.14 |
| 1:B:631:SER:HB3 | 1:B:632:PRO:CD | 1.78 | 1.13 |
| 1:B:657:GLU:OE2 | 1:B:661:ARG:NH1 | 1.81 | 1.12 |
| 1:D:512:PRO:CB | 1:D:516:SER:CB | 2.27 | 1.12 |
| 1:B:755:GLU:OE2 | 1:C:483:LEU:HD21 | 1.40 | 1.10 |
| 1:A:504:ILE:HD11 | 1:A:723:VAL:HG13 | 1.25 | 1.10 |
| 1:A:506:LYS:HE2 | 1:A:721:MET:SD | 1.93 | 1.09 |
| 1:A:627:GLU:O | 1:A:630:VAL:HG13 | 1.51 | 1.09 |
| 1:D:633:ILE:HD11 | 1:D:645:ILE:CD1 | 1.83 | 1.08 |
| 1:C:506:LYS:CE | 1:C:721:MET:CG | 2.19 | 1.08 |
| 1:D:633:ILE:CD1 | 1:D:645:ILE:CD1 | 2.32 | 1.07 |
| 1:B:393:LYS:HG2 | 1:B:394:THR:N | 1.69 | 1.07 |
| 1:B:633:ILE:CD1 | 1:B:645:ILE:CD1 | 2.33 | 1.06 |
| 1:B:633:ILE:HD11 | 1:B:645:ILE:CD1 | 1.84 | 1.06 |
| 1:B:453:ARG:CD | 1:B:460:TRP:CE2 | 2.39 | 1.05 |
| 1:C:506:LYS:HE3 | 1:C:721:MET:CA | 1.86 | 1.05 |
| 1:D:663:LYS:HE2 | 1:D:663:LYS:HA | 1.32 | 1.05 |
| 1:B:713:GLU:OE2 | 1:B:776:LYS:HE3 | 1.57 | 1.04 |
| 1:C:506:LYS:HE2 | 1:C:721:MET:SD | 1.97 | 1.04 |

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| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|---|---|---|---|
| 1:C:506:LYS:HE2 | 1:C:721:MET:HG3 | 1.38 | 1.04 |
| 1:A:512:PRO:HB2 | 1:A:515:PHE:HD2 | 0.89 | 1.03 |
| 1:C:506:LYS:HE2 | 1:C:721:MET:CB | 1.67 | 1.03 |
| 1:A:663:LYS:HE2 | 1:A:663:LYS:HA | 1.39 | 1.02 |
| 1:D:393:LYS:HG2 | 1:D:394:THR:N | 1.69 | 1.02 |
| 1:D:631:SER:HB3 | 1:D:632:PRO:HD2 | 1.02 | 1.02 |
| 1:A:506:LYS:CE | 1:A:721:MET:CG | 2.20 | 1.02 |
| 1:C:512:PRO:HB2 | 1:C:515:PHE:HD2 | 0.89 | 1.02 |
| 1:A:506:LYS:HE3 | 1:A:721:MET:CA | 1.90 | 1.02 |
| 1:B:512:PRO:HB3 | 1:B:516:SER:HB3 | 1.18 | 1.01 |
| 1:A:634:GLU:HG3 | 1:A:723:VAL:HB | 1.43 | 1.01 |
| 1:B:631:SER:HB3 | 1:B:632:PRO:HD2 | 1.02 | 1.01 |
| 1:C:742:LEU:O | 1:C:745:PRO:HG2 | 1.61 | 1.01 |
| 1:B:742:LEU:O | 1:B:745:PRO:HG2 | 1.61 | 1.01 |
| 1:C:634:GLU:HG2 | 1:C:723:VAL:HB | 1.39 | 1.01 |
| 1:D:742:LEU:O | 1:D:745:PRO:HG2 | 1.61 | 1.00 |
| 1:B:631:SER:CB | 1:B:632:PRO:HD2 | 1.89 | 1.00 |
| 1:B:755:GLU:OE2 | 1:C:483:LEU:HD23 | 1.58 | 1.00 |
| 1:D:631:SER:CB | 1:D:632:PRO:HD2 | 1.89 | 1.00 |
| 1:C:634:GLU:HG3 | 1:C:723:VAL:HB | 1.44 | 1.00 |
| 1:A:506:LYS:HE2 | 1:A:721:MET:CB | 1.68 | 0.99 |
| 1:C:512:PRO:CB | 1:C:515:PHE:HD2 | 1.76 | 0.99 |
| 1:C:513:GLY:O | 1:C:514:VAL:HG23 | 1.63 | 0.99 |
| 1:A:744:THR:OG1 | 1:A:745:PRO:HD3 | 1.63 | 0.98 |
| 1:D:713:GLU:OE2 | 1:D:776:LYS:HE3 | 1.61 | 0.98 |
| 1:A:512:PRO:CB | 1:A:515:PHE:HD2 | 1.76 | 0.98 |
| 1:A:775:ALA:C | 1:A:777:ASP:H | 1.63 | 0.98 |
| 1:A:513:GLY:O | 1:A:514:VAL:HG23 | 1.63 | 0.97 |
| 1:D:634:GLU:N | 1:D:638:ASP:OD2 | 1.97 | 0.97 |
| 1:B:633:ILE:HD11 | 1:B:645:ILE:HD11 | 1.44 | 0.97 |
| 1:D:512:PRO:HB3 | 1:D:516:SER:CB | 1.90 | 0.97 |
| 1:D:633:ILE:HD11 | 1:D:645:ILE:HD11 | 1.45 | 0.97 |
| 1:D:684:ARG:NH1 | 1:D:688:GLU:OE1 | 1.97 | 0.97 |
| 1:C:504:ILE:HD11 | 1:C:723:VAL:CG1 | 1.94 | 0.96 |
| 1:A:525:ILE:HG12 | 1:B:789:LEU:HB2 | 1.45 | 0.96 |
| 1:C:503:MET:HB2 | 1:C:709:ASN:OD1 | 1.64 | 0.96 |
| 1:D:512:PRO:CB | 1:D:516:SER:HB3 | 1.92 | 0.96 |
| 1:C:504:ILE:HD13 | 1:C:504:ILE:H | 1.30 | 0.95 |
| 1:A:506:LYS:HE2 | 1:A:721:MET:HG3 | 1.45 | 0.95 |
| 1:B:663:LYS:HA | 1:B:663:LYS:HE2 | 1.46 | 0.95 |
| 1:A:483:LEU:HD23 | 1:D:755:GLU:OE2 | 1.61 | 0.95 |

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| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|---|---|---|---|
| 1:B:512:PRO:HB2 | 1:B:516:SER:HG | 1.30 | 0.95 |
| 1:A:504:ILE:HD11 | 1:A:723:VAL:CG1 | 1.96 | 0.95 |
| 1:F:31:TRP:HE1 | 1:F:208:SER:HG | 1.15 | 0.94 |
| 1:B:455:ALA:O | 1:B:456:ASP:HB2 | 1.66 | 0.94 |
| 1:C:506:LYS:CD | 1:C:721:MET:HB2 | 1.97 | 0.94 |
| 1:C:775:ALA:C | 1:C:777:ASP:H | 1.63 | 0.93 |
| 1:D:455:ALA:O | 1:D:456:ASP:HB2 | 1.66 | 0.93 |
| 1:C:455:ALA:O | 1:C:456:ASP:HB2 | 1.66 | 0.93 |
| 1:A:436:CYS:SG | 1:A:745:PRO:HB2 | 2.09 | 0.93 |
| 1:C:627:GLU:O | 1:C:630:VAL:CG1 | 2.16 | 0.92 |
| 1:A:56:PHE:CE2 | 1:B:91:THR:HG21 | 2.03 | 0.92 |
| 1:A:742:LEU:O | 1:A:746:VAL:HG23 | 1.69 | 0.92 |
| 1:C:512:PRO:CB | 1:C:515:PHE:CD2 | 2.52 | 0.90 |
| 1:D:633:ILE:HG23 | 1:D:638:ASP:HB3 | 1.53 | 0.90 |
| 1:A:634:GLU:CG | 1:A:723:VAL:HB | 2.01 | 0.90 |
| 1:D:595:SER:HA | 1:D:599:ARG:HB3 | 1.53 | 0.90 |
| 1:A:506:LYS:CD | 1:A:721:MET:HB2 | 2.00 | 0.90 |
| 1:B:663:LYS:HA | 1:B:663:LYS:CE | 2.00 | 0.90 |
| 1:E:31:TRP:HE1 | 1:E:208:SER:HG | 1.14 | 0.89 |
| 1:B:512:PRO:HB3 | 1:B:516:SER:HB2 | 1.52 | 0.89 |
| 1:D:512:PRO:HB2 | 1:D:516:SER:CB | 1.95 | 0.88 |
| 1:B:178:ARG:NH2 | 1:D:237:PHE:CE2 | 2.43 | 0.86 |
| 1:A:512:PRO:CB | 1:A:515:PHE:CD2 | 2.52 | 0.86 |
| 1:D:634:GLU:O | 1:D:635:SER:HB3 | 1.75 | 0.86 |
| 1:B:633:ILE:HD13 | 1:B:645:ILE:CD1 | 2.07 | 0.85 |
| 1:B:453:ARG:CD | 1:B:460:TRP:NE1 | 2.33 | 0.85 |
| 1:D:633:ILE:HD13 | 1:D:645:ILE:CD1 | 2.04 | 0.85 |
| 1:C:56:PHE:CE2 | 1:D:91:THR:HG21 | 2.12 | 0.85 |
| 1:B:453:ARG:HD2 | 1:B:460:TRP:HE1 | 1.38 | 0.84 |
| 1:A:513:GLY:O | 1:A:514:VAL:CG2 | 2.26 | 0.84 |
| 1:C:87:SER:OG | 1:D:54:ASN:OD1 | 1.95 | 0.83 |
| 1:C:506:LYS:CE | 1:C:721:MET:HG3 | 2.01 | 0.83 |
| 1:C:513:GLY:O | 1:C:514:VAL:CG2 | 2.26 | 0.83 |
| 1:B:634:GLU:N | 1:B:638:ASP:OD2 | 2.10 | 0.83 |
| 1:A:744:THR:OG1 | 1:A:745:PRO:CD | 2.27 | 0.82 |
| 1:C:455:ALA:O | 1:C:456:ASP:CB | 2.27 | 0.81 |
| 1:B:455:ALA:O | 1:B:456:ASP:CB | 2.27 | 0.81 |
| 1:C:504:ILE:HD11 | 1:C:723:VAL:HG13 | 1.62 | 0.81 |
| 1:B:453:ARG:CD | 1:B:460:TRP:CZ2 | 2.63 | 0.81 |
| 1:B:512:PRO:CA | 1:B:516:SER:HB3 | 2.10 | 0.81 |
| 1:A:188:LYS:HD2 | 1:A:190:ARG:HH22 | 1.46 | 0.80 |

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| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|---|---|---|---|
| 1:D:633:ILE:CD1 | 1:D:645:ILE:HD12 | 2.10 | 0.80 |
| 1:B:393:LYS:CG | 1:B:394:THR:N | 2.45 | 0.80 |
| 1:B:631:SER:CB | 1:B:632:PRO:CD | 2.40 | 0.80 |
| 1:C:775:ALA:O | 1:C:777:ASP:N | 2.15 | 0.80 |
| 1:D:455:ALA:O | 1:D:456:ASP:CB | 2.27 | 0.80 |
| 1:A:16:GLY:H | 1:A:65:GLN:HE22 | 1.30 | 0.80 |
| 1:B:729:SER:HB3 | 1:C:729:SER:CB | 2.12 | 0.80 |
| 1:A:56:PHE:CD2 | 1:B:91:THR:HG21 | 2.17 | 0.79 |
| 1:A:627:GLU:O | 1:A:630:VAL:CG1 | 2.30 | 0.79 |
| 1:C:337:GLN:HE21 | 1:C:346:LYS:HE2 | 1.47 | 0.79 |
| 1:C:684:ARG:HH21 | 1:C:684:ARG:HG3 | 1.45 | 0.79 |
| 1:C:786:ALA:O | 1:C:787:LEU:HB2 | 1.81 | 0.79 |
| 1:B:453:ARG:HD3 | 1:B:460:TRP:CZ2 | 2.16 | 0.79 |
| 1:B:633:ILE:HD13 | 1:B:645:ILE:HD13 | 1.65 | 0.79 |
| 1:C:663:LYS:HA | 1:C:663:LYS:CE | 2.04 | 0.79 |
| 1:A:786:ALA:O | 1:A:787:LEU:HB2 | 1.81 | 0.79 |
| 1:C:595:SER:H | 1:C:599:ARG:HE | 1.28 | 0.79 |
| 1:B:729:SER:HB3 | 1:C:729:SER:OG | 1.83 | 0.78 |
| 1:C:742:LEU:O | 1:C:745:PRO:CG | 2.31 | 0.78 |
| 1:D:742:LEU:O | 1:D:745:PRO:CG | 2.31 | 0.78 |
| 1:A:775:ALA:O | 1:A:777:ASP:N | 2.15 | 0.78 |
| 1:B:742:LEU:O | 1:B:745:PRO:CG | 2.31 | 0.78 |
| 1:A:455:ALA:O | 1:A:456:ASP:CB | 2.32 | 0.78 |
| 1:A:506:LYS:CE | 1:A:721:MET:HG3 | 2.05 | 0.78 |
| 1:D:134:ALA:HB3 | 1:D:192:VAL:HG22 | 1.66 | 0.78 |
| 1:D:393:LYS:CG | 1:D:394:THR:N | 2.45 | 0.78 |
| 1:B:134:ALA:HB3 | 1:B:192:VAL:HG22 | 1.66 | 0.78 |
| 1:D:372:GLY:HA2 | 1:D:383:THR:HG23 | 1.66 | 0.78 |
| 1:A:83:ASN:ND2 | 1:B:80:LYS:HA | 1.97 | 0.77 |
| 1:B:237:PHE:CE2 | 1:D:178:ARG:NH2 | 2.53 | 0.77 |
| 1:B:633:ILE:HG23 | 1:B:638:ASP:HB3 | 1.65 | 0.77 |
| 1:B:214:HIS:HE1 | 1:D:212:GLY:CA | 1.98 | 0.77 |
| 1:B:595:SER:HA | 1:B:599:ARG:HB2 | 1.65 | 0.77 |
| 1:C:506:LYS:HE3 | 1:C:721:MET:HB2 | 0.78 | 0.77 |
| 1:D:512:PRO:HB3 | 1:D:516:SER:HB2 | 1.64 | 0.77 |
| 1:B:512:PRO:HB2 | 1:B:516:SER:CB | 1.90 | 0.77 |
| 1:B:215:VAL:HG11 | 1:D:215:VAL:HG11 | 1.68 | 0.76 |
| 1:D:355:ASN:N | 1:D:376:GLU:OE2 | 2.19 | 0.76 |
| 1:B:619:ASN:ND2 | 1:C:787:LEU:HG | 2.00 | 0.76 |
| 1:C:775:ALA:C | 1:C:777:ASP:N | 2.35 | 0.76 |
| 1:A:77:TYR:HE2 | 1:A:98:THR:HG21 | 1.49 | 0.75 |

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| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|---|---|---|---|
| 1:B:633:ILE:CD1 | 1:B:645:ILE:HD12 | 2.16 | 0.75 |
| 1:C:504:ILE:HD11 | 1:C:723:VAL:HG11 | 1.66 | 0.75 |
| 1:B:247:ILE:HG23 | 1:B:248:VAL:HG23 | 1.67 | 0.75 |
| 1:D:392:GLN:NE2 | 1:D:437:GLY:O | 2.20 | 0.75 |
| 1:A:504:ILE:HD12 | 1:A:723:VAL:HG22 | 1.68 | 0.75 |
| 1:A:742:LEU:O | 1:A:745:PRO:HD2 | 1.87 | 0.75 |
| 1:D:633:ILE:HD13 | 1:D:645:ILE:HD13 | 1.69 | 0.75 |
| 1:B:392:GLN:NE2 | 1:B:437:GLY:O | 2.20 | 0.74 |
| 1:A:729:SER:OG | 1:D:729:SER:HB3 | 1.87 | 0.74 |
| 1:D:634:GLU:O | 1:D:635:SER:CB | 2.35 | 0.74 |
| 1:A:80:LYS:HA | 1:B:83:ASN:ND2 | 2.02 | 0.74 |
| 1:A:513:GLY:O | 1:A:514:VAL:CB | 2.36 | 0.74 |
| 1:B:77:TYR:OH | 1:B:101:PHE:O | 2.06 | 0.74 |
| 1:C:80:LYS:HA | 1:D:83:ASN:ND2 | 2.01 | 0.74 |
| 1:C:506:LYS:CG | 1:C:721:MET:HB2 | 2.18 | 0.74 |
| 1:D:721:MET:HG3 | 1:D:776:LYS:HE2 | 1.69 | 0.74 |
| 1:B:503:MET:HB2 | 1:B:709:ASN:OD1 | 1.88 | 0.74 |
| 1:C:16:GLY:H | 1:C:65:GLN:HE22 | 1.33 | 0.74 |
| 1:D:523:TYR:HA | 1:D:526:TRP:HD1 | 1.52 | 0.73 |
| 1:C:513:GLY:O | 1:C:514:VAL:CB | 2.36 | 0.73 |
| 1:C:83:ASN:ND2 | 1:D:80:LYS:HA | 2.02 | 0.73 |
| 1:D:744:THR:N | 1:D:745:PRO:HD2 | 2.03 | 0.73 |
| 1:C:88:PHE:CE1 | 1:D:56:PHE:HD1 | 2.06 | 0.73 |
| 1:A:729:SER:CB | 1:D:729:SER:HB3 | 2.18 | 0.73 |
| 1:A:14:ILE:HD13 | 1:A:43:LEU:HD23 | 1.70 | 0.73 |
| 1:C:372:GLY:HA2 | 1:C:383:THR:OG1 | 1.89 | 0.73 |
| 1:D:308:ARG:NH2 | 1:D:325:GLN:OE1 | 2.22 | 0.73 |
| 1:B:744:THR:N | 1:B:745:PRO:HD2 | 2.03 | 0.73 |
| 1:C:77:TYR:HE2 | 1:C:98:THR:HG21 | 1.51 | 0.72 |
| 1:A:594:ARG:HD3 | 1:B:575:ASN:HB2 | 1.71 | 0.72 |
| 1:B:729:SER:HB3 | 1:C:729:SER:HB3 | 1.69 | 0.72 |
| 1:D:77:TYR:OH | 1:D:101:PHE:O | 2.08 | 0.72 |
| 1:D:101:PHE:HA | 1:D:114:ARG:HD2 | 1.72 | 0.72 |
| 1:A:599:ARG:HH22 | 1:B:581:LEU:HB3 | 1.53 | 0.72 |
| 1:C:14:ILE:HD13 | 1:C:43:LEU:HD23 | 1.69 | 0.72 |
| 1:D:633:ILE:CG2 | 1:D:638:ASP:HB3 | 2.18 | 0.72 |
| 1:D:505:LYS:O | 1:D:506:LYS:O | 2.08 | 0.72 |
| 1:A:706:SER:O | 1:A:710:GLU:HG2 | 1.90 | 0.71 |
| 1:B:706:SER:O | 1:B:710:GLU:HG2 | 1.90 | 0.71 |
| 1:C:744:THR:N | 1:C:745:PRO:HD2 | 2.03 | 0.71 |
| 1:D:512:PRO:CA | 1:D:516:SER:HB3 | 2.20 | 0.71 |

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| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|---|---|---|---|
| 1:B:193:ILE:HG12 | 1:B:221:ILE:HB | 1.73 | 0.71 |
| 1:B:209:ILE:HA | 1:B:214:HIS:HD2 | 1.55 | 0.71 |
| 1:D:247:ILE:HG23 | 1:D:248:VAL:HG23 | 1.71 | 0.71 |
| 1:B:246:GLN:HE21 | 1:B:248:VAL:H | 1.37 | 0.71 |
| 1:C:633:ILE:O | 1:C:633:ILE:HG13 | 1.90 | 0.70 |
| 1:B:523:TYR:HA | 1:B:526:TRP:HD1 | 1.56 | 0.70 |
| 1:C:789:LEU:HG | 1:C:793:ALA:HB2 | 1.73 | 0.70 |
| 1:B:505:LYS:O | 1:B:506:LYS:O | 2.08 | 0.70 |
| 1:B:633:ILE:CD1 | 1:B:645:ILE:HD13 | 2.20 | 0.70 |
| 1:A:595:SER:H | 1:A:599:ARG:HE | 1.39 | 0.70 |
| 1:C:706:SER:O | 1:C:710:GLU:HG2 | 1.90 | 0.70 |
| 1:F:98:CYS:HA | 1:F:109:CYS:HA | 1.74 | 0.70 |
| 1:A:633:ILE:HG13 | 1:A:633:ILE:O | 1.90 | 0.70 |
| 1:D:193:ILE:HG12 | 1:D:221:ILE:HB | 1.72 | 0.70 |
| 1:D:512:PRO:CB | 1:D:516:SER:OG | 2.26 | 0.70 |
| 1:D:706:SER:O | 1:D:710:GLU:HG2 | 1.90 | 0.70 |
| 1:A:88:PHE:CE1 | 1:B:56:PHE:HD1 | 2.09 | 0.70 |
| 1:C:91:THR:HG21 | 1:D:56:PHE:CE2 | 2.27 | 0.70 |
| 1:C:718:CYS:CB | 1:C:773:CYS:HG | 2.03 | 0.70 |
| 1:D:663:LYS:HA | 1:D:663:LYS:CE | 2.00 | 0.70 |
| 1:A:684:ARG:NH2 | 1:A:684:ARG:HB2 | 2.07 | 0.69 |
| 1:B:101:PHE:HA | 1:B:114:ARG:HD2 | 1.73 | 0.69 |
| 1:B:263:SER:O | 1:B:274:HIS:ND1 | 2.25 | 0.69 |
| 1:B:376:GLU:HG2 | 1:B:377:VAL:HG13 | 1.73 | 0.69 |
| 1:B:375:SER:HB3 | 1:B:378:ASP:HB2 | 1.74 | 0.69 |
| 1:C:504:ILE:HD13 | 1:C:504:ILE:N | 2.05 | 0.69 |
| 1:A:506:LYS:HE3 | 1:A:721:MET:HB2 | 0.70 | 0.69 |
| 1:E:98:CYS:HA | 1:E:109:CYS:HA | 1.75 | 0.69 |
| 1:A:637:GLU:HG2 | 1:A:641:LYS:HE3 | 1.74 | 0.69 |
| 1:C:344:ASN:HD21 | 1:C:346:LYS:HE3 | 1.58 | 0.69 |
| 1:C:393:LYS:O | 1:C:393:LYS:HG2 | 1.92 | 0.69 |
| 1:B:13:GLN:HA | 1:B:44:THR:HB | 1.74 | 0.69 |
| 1:B:209:ILE:HA | 1:B:214:HIS:CD2 | 2.27 | 0.69 |
| 1:D:393:LYS:HG2 | 1:D:394:THR:H | 1.57 | 0.69 |
| 1:D:631:SER:CB | 1:D:632:PRO:CD | 2.40 | 0.69 |
| 1:B:214:HIS:CE1 | 1:D:212:GLY:CA | 2.76 | 0.68 |
| 1:D:637:GLU:HG2 | 1:D:641:LYS:HE3 | 1.74 | 0.68 |
| 1:A:393:LYS:O | 1:A:393:LYS:HG2 | 1.92 | 0.68 |
| 1:A:586:GLN:HA | 1:D:587:GLN:HE21 | 1.57 | 0.68 |
| 1:B:637:GLU:HG2 | 1:B:641:LYS:HE3 | 1.74 | 0.68 |
| 1:D:590:ASP:O | 1:D:592:SER:N | 2.24 | 0.68 |

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| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|---|---|---|---|
| 1:A:453:ARG:O | 1:A:453:ARG:HG2 | 1.93 | 0.68 |
| 1:B:24:GLN:HE21 | 1:B:278:ILE:HG13 | 1.58 | 0.68 |
| 1:D:13:GLN:HA | 1:D:44:THR:HB | 1.76 | 0.68 |
| 1:D:24:GLN:HE21 | 1:D:278:ILE:HG13 | 1.58 | 0.68 |
| 1:C:637:GLU:HG2 | 1:C:641:LYS:HE3 | 1.74 | 0.68 |
| 1:D:309:ARG:HG2 | 1:D:311:ASN:H | 1.58 | 0.68 |
| 1:A:375:SER:HB3 | 1:A:378:ASP:HB2 | 1.75 | 0.67 |
| 1:B:790:SER:OG | 1:E:185:GLN:NE2 | 2.25 | 0.67 |
| 1:B:16:GLY:H | 1:B:65:GLN:HE22 | 1.40 | 0.67 |
| 1:D:785:SER:O | 1:D:786:ALA:HB3 | 1.95 | 0.67 |
| 1:C:520:PRO:O | 1:C:619:ASN:ND2 | 2.28 | 0.67 |
| 1:A:56:PHE:HD1 | 1:B:88:PHE:CD2 | 2.12 | 0.67 |
| 1:A:634:GLU:O | 1:A:634:GLU:HG2 | 1.93 | 0.67 |
| 1:B:619:ASN:HD21 | 1:C:786:ALA:HB1 | 1.58 | 0.67 |
| 1:C:718:CYS:HG | 1:C:773:CYS:HG | 1.36 | 0.67 |
| 1:A:729:SER:HB3 | 1:D:729:SER:HB3 | 1.77 | 0.67 |
| 1:B:309:ARG:HG2 | 1:B:311:ASN:H | 1.60 | 0.67 |
| 1:B:453:ARG:HD2 | 1:B:460:TRP:CZ2 | 2.26 | 0.67 |
| 1:B:346:LYS:HD3 | 1:B:355:ASN:HD22 | 1.60 | 0.67 |
| 1:D:246:GLN:HE21 | 1:D:248:VAL:H | 1.40 | 0.67 |
| 1:B:785:SER:O | 1:B:786:ALA:HB3 | 1.95 | 0.66 |
| 1:C:375:SER:HB3 | 1:C:378:ASP:HB2 | 1.75 | 0.66 |
| 1:A:91:THR:HG21 | 1:B:56:PHE:CD2 | 2.30 | 0.66 |
| 1:C:56:PHE:CD2 | 1:D:91:THR:HG21 | 2.31 | 0.66 |
| 1:A:91:THR:HG21 | 1:B:56:PHE:CE2 | 2.30 | 0.66 |
| 1:A:506:LYS:HE2 | 1:A:721:MET:HB2 | 1.38 | 0.66 |
| 1:A:523:TYR:HA | 1:A:526:TRP:HD1 | 1.61 | 0.66 |
| 1:B:209:ILE:CG2 | 1:D:209:ILE:CG2 | 2.73 | 0.66 |
| 1:B:757:GLY:HA3 | 1:C:663:LYS:HG3 | 1.78 | 0.66 |
| 1:C:91:THR:HG21 | 1:D:56:PHE:CD2 | 2.31 | 0.66 |
| 1:C:246:GLN:HE21 | 1:C:248:VAL:H | 1.41 | 0.66 |
| 1:D:592:SER:O | 1:D:599:ARG:NH2 | 2.29 | 0.66 |
| 1:A:236:GLN:NE2 | 1:A:365:THR:O | 2.29 | 0.66 |
| 1:B:178:ARG:NE | 1:D:237:PHE:CE1 | 2.63 | 0.66 |
| 1:B:520:PRO:O | 1:B:619:ASN:ND2 | 2.29 | 0.66 |
| 1:C:80:LYS:HA | 1:D:83:ASN:HD22 | 1.61 | 0.66 |
| 1:C:634:GLU:HG3 | 1:C:723:VAL:CB | 2.24 | 0.66 |
| 1:A:206:ASP:HA | 1:A:209:ILE:HD12 | 1.77 | 0.65 |
| 1:B:619:ASN:HD22 | 1:C:787:LEU:HG | 1.59 | 0.65 |
| 1:B:628:ARG:HG3 | 1:B:628:ARG:O | 1.95 | 0.65 |
| 1:D:375:SER:HB3 | 1:D:378:ASP:HB2 | 1.78 | 0.65 |

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| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|---|---|---|---|
| 1:D:592:SER:HB3 | 1:D:599:ARG:HB2 | 1.78 | 0.65 |
| 1:A:504:ILE:HD13 | 1:A:504:ILE:N | 2.11 | 0.65 |
| 1:D:51:GLU:HG3 | 1:D:53:ALA:H | 1.61 | 0.65 |
| 1:B:721:MET:HG3 | 1:B:776:LYS:HE2 | 1.78 | 0.65 |
| 1:C:523:TYR:HA | 1:C:526:TRP:HD1 | 1.61 | 0.65 |
| 1:D:348:ASP:OD1 | 1:D:352:LYS:N | 2.30 | 0.65 |
| 1:A:56:PHE:N | 1:B:87:SER:OG | 2.29 | 0.65 |
| 1:C:742:LEU:O | 1:C:745:PRO:HD2 | 1.97 | 0.65 |
| 1:A:246:GLN:HE21 | 1:A:248:VAL:H | 1.44 | 0.65 |
| 1:A:504:ILE:HD13 | 1:A:504:ILE:H | 1.62 | 0.65 |
| 1:C:13:GLN:HA | 1:C:44:THR:HB | 1.79 | 0.65 |
| 1:C:502:ILE:HG12 | 1:C:703:LEU:CD2 | 2.26 | 0.65 |
| 1:A:506:LYS:CG | 1:A:721:MET:HB2 | 2.26 | 0.65 |
| 1:B:156:LYS:O | 1:B:157:LYS:HG3 | 1.96 | 0.65 |
| 1:C:307:SER:O | 1:C:308:ARG:NH1 | 2.25 | 0.65 |
| 1:D:209:ILE:HA | 1:D:214:HIS:CD2 | 2.32 | 0.65 |
| 1:B:393:LYS:CG | 1:B:394:THR:H | 2.10 | 0.65 |
| 1:A:247:ILE:HG23 | 1:A:248:VAL:HG23 | 1.79 | 0.64 |
| 1:B:305:GLU:O | 1:B:325:GLN:NE2 | 2.29 | 0.64 |
| 1:C:88:PHE:CE1 | 1:D:56:PHE:CD1 | 2.83 | 0.64 |
| 1:B:579:PHE:HZ | 1:B:590:ASP:H | 1.45 | 0.64 |
| 1:A:504:ILE:HD13 | 1:A:721:MET:O | 1.97 | 0.64 |
| 1:D:16:GLY:H | 1:D:65:GLN:HE22 | 1.45 | 0.64 |
| 1:C:663:LYS:HE2 | 1:C:663:LYS:CA | 2.19 | 0.64 |
| 1:D:78:ASP:OD1 | 1:D:79:LYS:N | 2.30 | 0.64 |
| 1:D:263:SER:O | 1:D:274:HIS:ND1 | 2.31 | 0.64 |
| 1:D:161:THR:OG1 | 1:D:187:LYS:NZ | 2.28 | 0.64 |
| 1:A:513:GLY:C | 1:A:514:VAL:HG23 | 2.18 | 0.64 |
| 1:B:348:ASP:OD1 | 1:B:352:LYS:N | 2.31 | 0.64 |
| 1:B:742:LEU:O | 1:B:745:PRO:HD2 | 1.97 | 0.64 |
| 1:D:742:LEU:O | 1:D:745:PRO:HD2 | 1.97 | 0.64 |
| 1:C:742:LEU:O | 1:C:745:PRO:CD | 2.46 | 0.64 |
| 1:A:775:ALA:C | 1:A:777:ASP:N | 2.35 | 0.63 |
| 1:C:11:SER:OG | 1:C:44:THR:OG1 | 2.15 | 0.63 |
| 1:C:337:GLN:HG3 | 1:C:346:LYS:HG2 | 1.81 | 0.63 |
| 1:A:88:PHE:CE1 | 1:B:56:PHE:CD1 | 2.87 | 0.63 |
| 1:B:178:ARG:NE | 1:D:237:PHE:CD1 | 2.67 | 0.63 |
| 1:D:513:GLY:O | 1:D:514:VAL:HB | 1.99 | 0.63 |
| 1:D:633:ILE:CD1 | 1:D:645:ILE:HD13 | 2.24 | 0.63 |
| 1:A:130:TRP:CD2 | 1:A:191:ARG:HD3 | 2.34 | 0.63 |
| 1:A:633:ILE:HA | 1:A:638:ASP:OD2 | 1.97 | 0.63 |

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| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|---|---|---|---|
| 1:C:513:GLY:C | 1:C:514:VAL:HG23 | 2.18 | 0.63 |
| 1:A:628:ARG:NH1 | 1:D:622:ALA:O | 2.32 | 0.63 |
| 1:B:78:ASP:OD1 | 1:B:79:LYS:N | 2.31 | 0.63 |
| 1:D:742:LEU:O | 1:D:745:PRO:CD | 2.47 | 0.63 |
| 1:A:11:SER:OG | 1:A:44:THR:OG1 | 2.16 | 0.62 |
| 1:A:520:PRO:O | 1:A:619:ASN:ND2 | 2.32 | 0.62 |
| 1:C:56:PHE:HD1 | 1:D:88:PHE:CE2 | 2.17 | 0.62 |
| 1:C:633:ILE:HA | 1:C:638:ASP:OD2 | 1.98 | 0.62 |
| 1:A:455:ALA:O | 1:A:456:ASP:HB3 | 1.99 | 0.62 |
| 1:A:391:GLU:OE2 | 1:A:391:GLU:HA | 1.99 | 0.62 |
| 1:B:161:THR:OG1 | 1:B:187:LYS:NZ | 2.33 | 0.62 |
| 1:C:504:ILE:HD12 | 1:C:723:VAL:HG22 | 1.81 | 0.62 |
| 1:C:513:GLY:O | 1:C:514:VAL:HB | 1.99 | 0.62 |
| 1:C:78:ASP:OD1 | 1:C:79:LYS:N | 2.32 | 0.62 |
| 1:B:742:LEU:O | 1:B:745:PRO:CD | 2.47 | 0.62 |
| 1:C:718:CYS:HB3 | 1:C:773:CYS:SG | 2.40 | 0.62 |
| 1:B:393:LYS:HG2 | 1:B:394:THR:H | 1.57 | 0.62 |
| 1:E:37:ARG:HD2 | 1:E:87:LEU:HD22 | 1.82 | 0.62 |
| 1:A:78:ASP:OD1 | 1:A:79:LYS:N | 2.33 | 0.61 |
| 1:C:334:LYS:HD3 | 1:C:349:GLN:HA | 1.82 | 0.61 |
| 1:A:786:ALA:HB1 | 1:D:619:ASN:HD21 | 1.66 | 0.61 |
| 1:A:13:GLN:HA | 1:A:44:THR:HB | 1.81 | 0.61 |
| 1:B:623:PHE:CZ | 1:C:786:ALA:HB2 | 2.35 | 0.61 |
| 1:F:31:TRP:N | 1:F:92:THR:O | 2.32 | 0.61 |
| 1:A:513:GLY:O | 1:A:514:VAL:HB | 1.99 | 0.61 |
| 1:C:259:ILE:HA | 1:C:262:TRP:HB3 | 1.82 | 0.61 |
| 1:C:595:SER:N | 1:C:599:ARG:HE | 1.96 | 0.61 |
| 1:D:752:LYS:O | 1:D:756:GLN:HG3 | 2.01 | 0.61 |
| 1:B:164:ASN:OD1 | 1:B:165:VAL:N | 2.34 | 0.61 |
| 1:B:178:ARG:CZ | 1:D:237:PHE:CE2 | 2.83 | 0.61 |
| 1:C:752:LYS:O | 1:C:756:GLN:HG3 | 2.01 | 0.61 |
| 1:B:334:LYS:NZ | 1:B:349:GLN:O | 2.26 | 0.61 |
| 1:B:752:LYS:O | 1:B:756:GLN:HG3 | 2.01 | 0.61 |
| 1:A:525:ILE:CG1 | 1:B:789:LEU:HB2 | 2.25 | 0.60 |
| 1:A:594:ARG:HB3 | 1:B:578:TRP:HE3 | 1.66 | 0.60 |
| 1:B:661:ARG:HG3 | 1:B:661:ARG:O | 2.00 | 0.60 |
| 1:E:31:TRP:N | 1:E:92:THR:O | 2.32 | 0.60 |
| 1:C:744:THR:OG1 | 1:C:745:PRO:HD3 | 2.01 | 0.60 |
| 1:D:630:VAL:HG22 | 1:D:630:VAL:O | 2.00 | 0.60 |
| 1:A:30:ARG:NH1 | 1:A:269:GLU:O | 2.35 | 0.60 |
| 1:B:744:THR:OG1 | 1:B:745:PRO:HD3 | 2.01 | 0.60 |

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| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|---|---|---|---|
| 1:D:744:THR:OG1 | 1:D:745:PRO:HD3 | 2.01 | 0.60 |
| 1:D:583:ALA:HA | 1:D:589:CYS:H | 1.67 | 0.60 |
| 1:F:37:ARG:HD2 | 1:F:87:LEU:HD22 | 1.81 | 0.60 |
| 1:B:633:ILE:CG2 | 1:B:638:ASP:HB3 | 2.32 | 0.60 |
| 1:D:393:LYS:CG | 1:D:394:THR:H | 2.10 | 0.60 |
| 1:A:80:LYS:HA | 1:B:83:ASN:HD22 | 1.67 | 0.60 |
| 1:A:752:LYS:O | 1:A:756:GLN:HG3 | 2.01 | 0.59 |
| 1:B:214:HIS:CE1 | 1:D:212:GLY:HA2 | 2.37 | 0.59 |
| 1:B:513:GLY:O | 1:B:514:VAL:HB | 2.02 | 0.59 |
| 1:C:130:TRP:CD2 | 1:C:191:ARG:HD3 | 2.36 | 0.59 |
| 1:C:262:TRP:CZ2 | 1:C:273:ALA:HA | 2.37 | 0.59 |
| 1:A:514:VAL:HA | 1:A:794:GLY:HA3 | 1.83 | 0.59 |
| 1:B:178:ARG:NE | 1:D:237:PHE:CZ | 2.70 | 0.59 |
| 1:F:18:ALA:HA | 1:F:21:PHE:HD2 | 1.67 | 0.59 |
| 1:A:78:ASP:N | 1:A:81:SER:OG | 2.34 | 0.59 |
| 1:B:372:GLY:HA2 | 1:B:383:THR:HG23 | 1.84 | 0.59 |
| 1:D:579:PHE:HZ | 1:D:590:ASP:H | 1.50 | 0.59 |
| 1:A:663:LYS:HA | 1:A:663:LYS:CE | 2.10 | 0.59 |
| 1:B:77:TYR:HE2 | 1:B:98:THR:HG21 | 1.67 | 0.59 |
| 1:B:502:ILE:HG12 | 1:B:703:LEU:CD2 | 2.33 | 0.59 |
| 1:A:718:CYS:CB | 1:A:773:CYS:SG | 2.91 | 0.59 |
| 1:D:477:ALA:HB1 | 1:D:478:PRO:HD2 | 1.85 | 0.59 |
| 1:D:586:GLN:O | 1:D:588:GLY:N | 2.36 | 0.59 |
| 1:A:56:PHE:HD1 | 1:B:88:PHE:CE2 | 2.20 | 0.59 |
| 1:A:308:ARG:HB3 | 1:A:311:ASN:HD22 | 1.67 | 0.59 |
| 1:B:477:ALA:HB1 | 1:B:478:PRO:HD2 | 1.85 | 0.59 |
| 1:C:477:ALA:HB1 | 1:C:478:PRO:HD2 | 1.85 | 0.59 |
| 1:D:663:LYS:HE2 | 1:D:663:LYS:CA | 2.21 | 0.59 |
| 1:A:787:LEU:HD12 | 1:D:521:LEU:HA | 1.85 | 0.59 |
| 1:C:38:THR:HG21 | 1:C:297:ARG:HH21 | 1.67 | 0.59 |
| 1:A:595:SER:N | 1:A:599:ARG:HE | 2.01 | 0.58 |
| 1:B:35:GLN:OE1 | 1:B:261:ARG:NH2 | 2.36 | 0.58 |
| 1:C:23:ASP:HB3 | 1:C:271:PRO:HG2 | 1.84 | 0.58 |
| 1:C:236:GLN:NE2 | 1:C:365:THR:O | 2.35 | 0.58 |
| 1:C:590:ASP:O | 1:C:592:SER:N | 2.30 | 0.58 |
| 1:D:594:ARG:O | 1:D:596:LEU:N | 2.36 | 0.58 |
| 1:C:387:THR:C | 1:C:389:GLY:H | 2.07 | 0.58 |
| 1:C:416:GLU:OE1 | 1:C:417:GLY:N | 2.30 | 0.58 |
| 1:D:597:SER:O | 1:D:600:ILE:HG12 | 2.02 | 0.58 |
| 1:B:328:GLU:OE2 | 1:B:331:ARG:NH1 | 2.34 | 0.58 |
| 1:D:785:SER:O | 1:D:786:ALA:CB | 2.52 | 0.58 |

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| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|---|---|---|---|
| 1:A:477:ALA:HB1 | 1:A:478:PRO:HD2 | 1.85 | 0.58 |
| 1:B:630:VAL:O | 1:B:630:VAL:HG13 | 2.03 | 0.58 |
| 1:A:30:ARG:NH2 | 1:A:269:GLU:OE2 | 2.35 | 0.58 |
| 1:C:502:ILE:HG12 | 1:C:703:LEU:HD23 | 1.84 | 0.58 |
| 1:A:684:ARG:HB2 | 1:A:684:ARG:CZ | 2.33 | 0.58 |
| 1:A:783:LYS:HG2 | 1:A:783:LYS:O | 2.04 | 0.58 |
| 1:C:783:LYS:O | 1:C:783:LYS:HG2 | 2.04 | 0.58 |
| 1:D:657:GLU:OE2 | 1:D:661:ARG:CZ | 2.51 | 0.58 |
| 1:B:625:THR:HG21 | 1:C:625:THR:HG23 | 1.84 | 0.58 |
| 1:E:18:ALA:HA | 1:E:21:PHE:HD2 | 1.69 | 0.58 |
| 1:B:178:ARG:HD3 | 1:D:237:PHE:CD1 | 2.39 | 0.57 |
| 1:B:250:TYR:HA | 1:B:255:VAL:HG11 | 1.87 | 0.57 |
| 1:C:504:ILE:HD12 | 1:C:723:VAL:CG2 | 2.34 | 0.57 |
| 1:C:13:GLN:HB3 | 1:C:70:VAL:HG12 | 1.86 | 0.57 |
| 1:C:520:PRO:HB2 | 1:C:616:TYR:CE1 | 2.40 | 0.57 |
| 1:A:50:LEU:HD23 | 1:A:57:ALA:HB1 | 1.87 | 0.57 |
| 1:B:214:HIS:CE1 | 1:D:212:GLY:HA3 | 2.39 | 0.57 |
| 1:B:684:ARG:NH1 | 1:B:688:GLU:OE1 | 2.37 | 0.57 |
| 1:D:25:GLU:HG2 | 1:D:76:PHE:HZ | 1.69 | 0.57 |
| 1:F:195:PRO:HD2 | 1:F:199:ARG:HB3 | 1.87 | 0.57 |
| 1:B:25:GLU:HG2 | 1:B:76:PHE:HZ | 1.68 | 0.57 |
| 1:B:785:SER:O | 1:B:786:ALA:CB | 2.52 | 0.57 |
| 1:A:387:THR:C | 1:A:389:GLY:H | 2.07 | 0.57 |
| 1:C:308:ARG:HB3 | 1:C:311:ASN:HD22 | 1.68 | 0.57 |
| 1:B:209:ILE:CG2 | 1:D:209:ILE:HG22 | 2.34 | 0.57 |
| 1:E:37:ARG:HA | 1:E:87:LEU:HA | 1.85 | 0.57 |
| 1:C:503:MET:CB | 1:C:709:ASN:OD1 | 2.44 | 0.56 |
| 1:C:347:PHE:HE1 | 1:C:353:ARG:HG2 | 1.70 | 0.56 |
| 1:A:266:GLU:HG2 | 1:A:268:LYS:H | 1.70 | 0.56 |
| 1:B:586:GLN:O | 1:B:588:GLY:N | 2.38 | 0.56 |
| 1:B:587:GLN:HE21 | 1:C:586:GLN:HA | 1.69 | 0.56 |
| 1:B:630:VAL:O | 1:B:631:SER:C | 2.44 | 0.56 |
| 1:C:345:ILE:HG12 | 1:C:353:ARG:NH2 | 2.21 | 0.56 |
| 1:C:503:MET:HA | 1:C:721:MET:O | 2.04 | 0.56 |
| 1:C:594:ARG:HB3 | 1:D:578:TRP:HE3 | 1.69 | 0.56 |
| 1:A:262:TRP:CZ2 | 1:A:273:ALA:HA | 2.41 | 0.56 |
| 1:B:215:VAL:HG11 | 1:D:215:VAL:CG1 | 2.33 | 0.56 |
| 1:C:684:ARG:HG3 | 1:C:684:ARG:NH2 | 2.19 | 0.56 |
| 1:B:520:PRO:O | 1:C:787:LEU:HD12 | 2.06 | 0.56 |
| 1:C:594:ARG:HD3 | 1:D:575:ASN:HB2 | 1.87 | 0.56 |
| 1:D:236:GLN:NE2 | 1:D:364:LYS:O | 2.38 | 0.56 |

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| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|---|---|---|---|
| 1:A:134:ALA:HB3 | 1:A:192:VAL:HG22 | 1.85 | 0.56 |
| 1:A:334:LYS:HD3 | 1:A:349:GLN:HA | 1.86 | 0.56 |
| 1:C:371:ILE:O | 1:C:383:THR:N | 2.31 | 0.56 |
| 1:B:308:ARG:HH21 | 1:B:325:GLN:H | 1.53 | 0.56 |
| 1:C:25:GLU:OE1 | 1:C:25:GLU:N | 2.34 | 0.56 |
| 1:A:13:GLN:HB3 | 1:A:70:VAL:HG12 | 1.87 | 0.56 |
| 1:A:307:SER:O | 1:A:308:ARG:NH1 | 2.39 | 0.56 |
| 1:F:37:ARG:HA | 1:F:87:LEU:HA | 1.86 | 0.56 |
| 1:A:77:TYR:OH | 1:A:101:PHE:O | 2.13 | 0.56 |
| 1:A:628:ARG:HH21 | 1:D:628:ARG:HG2 | 1.70 | 0.56 |
| 1:B:600:ILE:HG22 | 1:C:581:LEU:HD11 | 1.87 | 0.56 |
| 1:E:36:GLN:NE2 | 1:E:197:ASP:O | 2.35 | 0.56 |
| 1:A:578:TRP:CG | 1:D:595:SER:HB3 | 2.41 | 0.55 |
| 1:C:50:LEU:HD23 | 1:C:57:ALA:HB1 | 1.88 | 0.55 |
| 1:C:504:ILE:CD1 | 1:C:723:VAL:HG22 | 2.36 | 0.55 |
| 1:C:634:GLU:HG2 | 1:C:634:GLU:O | 2.06 | 0.55 |
| 1:D:633:ILE:HD13 | 1:D:645:ILE:HD12 | 1.83 | 0.55 |
| 1:E:122:GLY:HA2 | 1:E:125:TRP:HD1 | 1.71 | 0.55 |
| 1:F:13:ALA:HA | 1:F:16:LEU:HD12 | 1.89 | 0.55 |
| 1:A:587:GLN:NE2 | 1:B:587:GLN:OE1 | 2.40 | 0.55 |
| 1:C:525:ILE:HG12 | 1:D:789:LEU:HD13 | 1.89 | 0.55 |
| 1:C:390:LEU:HD12 | 1:C:391:GLU:HG3 | 1.89 | 0.55 |
| 1:C:742:LEU:C | 1:C:745:PRO:HD2 | 2.27 | 0.55 |
| 1:B:742:LEU:C | 1:B:745:PRO:HD2 | 2.27 | 0.55 |
| 1:C:504:ILE:CD1 | 1:C:723:VAL:CG2 | 2.85 | 0.55 |
| 1:A:25:GLU:N | 1:A:25:GLU:OE1 | 2.36 | 0.55 |
| 1:A:66:PHE:CZ | 1:A:312:ALA:HB1 | 2.42 | 0.55 |
| 1:C:586:GLN:O | 1:C:588:GLY:N | 2.39 | 0.55 |
| 1:F:122:GLY:HA2 | 1:F:125:TRP:HD1 | 1.72 | 0.55 |
| 1:A:177:TYR:CD2 | 1:A:207:GLN:HG3 | 2.42 | 0.55 |
| 1:A:584:PHE:CZ | 1:D:606:TRP:HZ3 | 2.25 | 0.55 |
| 1:C:78:ASP:N | 1:C:81:SER:OG | 2.39 | 0.55 |
| 1:C:587:GLN:NE2 | 1:D:587:GLN:OE1 | 2.40 | 0.55 |
| 1:E:195:PRO:HD2 | 1:E:199:ARG:HB3 | 1.88 | 0.55 |
| 1:A:393:LYS:O | 1:A:394:THR:HB | 2.07 | 0.55 |
| 1:E:191:VAL:HA | 1:E:195:PRO:HG3 | 1.89 | 0.55 |
| 1:C:744:THR:N | 1:C:745:PRO:CD | 2.70 | 0.55 |
| 1:D:742:LEU:C | 1:D:745:PRO:HD2 | 2.27 | 0.55 |
| 1:C:504:ILE:H | 1:C:504:ILE:CD1 | 2.13 | 0.54 |
| 1:B:744:THR:N | 1:B:745:PRO:CD | 2.70 | 0.54 |
| 1:C:170:ASN:HA | 1:C:173:LYS:HB2 | 1.89 | 0.54 |

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| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|---|---|---|---|
| 1:D:225:LEU:HD22 | 1:D:247:ILE:HB | 1.89 | 0.54 |
| 1:B:178:ARG:CZ | 1:D:237:PHE:CZ | 2.90 | 0.54 |
| 1:B:608:PHE:CZ | 1:B:612:ILE:HD11 | 2.43 | 0.54 |
| 1:C:393:LYS:O | 1:C:394:THR:HB | 2.07 | 0.54 |
| 1:B:209:ILE:HG22 | 1:D:209:ILE:CG2 | 2.36 | 0.54 |
| 1:C:316:LEU:HD22 | 1:D:60:ASN:HA | 1.89 | 0.54 |
| 1:A:625:THR:HG23 | 1:D:625:THR:HG21 | 1.89 | 0.54 |
| 1:B:219:HIS:HD2 | 1:B:241:GLU:HB2 | 1.73 | 0.54 |
| 1:C:789:LEU:O | 1:C:793:ALA:HB2 | 2.08 | 0.54 |
| 1:A:586:GLN:O | 1:A:588:GLY:N | 2.41 | 0.54 |
| 1:A:590:ASP:OD1 | 1:A:591:ILE:N | 2.37 | 0.54 |
| 1:B:177:TYR:CD2 | 1:B:207:GLN:HG3 | 2.42 | 0.54 |
| 1:C:718:CYS:HB3 | 1:C:773:CYS:HG | 1.72 | 0.54 |
| 1:D:76:PHE:HE1 | 1:D:99:PRO:HG2 | 1.73 | 0.54 |
| 1:D:744:THR:N | 1:D:745:PRO:CD | 2.70 | 0.54 |
| 1:B:610:LEU:HD21 | 1:C:613:ILE:HG21 | 1.89 | 0.54 |
| 1:B:619:ASN:ND2 | 1:C:786:ALA:HB1 | 2.22 | 0.54 |
| 1:C:66:PHE:CZ | 1:C:312:ALA:HB1 | 2.43 | 0.54 |
| 1:C:211:ILE:HG13 | 1:C:213:LYS:H | 1.73 | 0.54 |
| 1:B:512:PRO:HA | 1:B:516:SER:HB3 | 1.87 | 0.53 |
| 1:B:627:GLU:HG2 | 1:B:629:MET:CE | 2.38 | 0.53 |
| 1:D:800:VAL:HA | 1:D:803:LEU:HD12 | 1.89 | 0.53 |
| 1:B:592:SER:O | 1:B:599:ARG:NH2 | 2.41 | 0.53 |
| 1:B:661:ARG:HB2 | 1:B:661:ARG:CZ | 2.38 | 0.53 |
| 1:E:133:LEU:HD23 | 1:E:136:LEU:HD12 | 1.91 | 0.53 |
| 1:C:112:GLN:HE21 | 1:C:352:LYS:HA | 1.74 | 0.53 |
| 1:C:247:ILE:HG23 | 1:C:248:VAL:HG23 | 1.91 | 0.53 |
| 1:D:227:PHE:CD1 | 1:D:244:GLY:HA3 | 2.42 | 0.53 |
| 1:E:13:ALA:HA | 1:E:16:LEU:HD12 | 1.91 | 0.53 |
| 1:A:79:LYS:NZ | 1:A:140:ASP:HA | 2.24 | 0.53 |
| 1:A:263:SER:O | 1:A:274:HIS:ND1 | 2.42 | 0.53 |
| 1:A:455:ALA:O | 1:A:456:ASP:HB2 | 2.07 | 0.53 |
| 1:E:29:THR:HG23 | 1:E:30:TYR:CD1 | 2.44 | 0.53 |
| 1:B:76:PHE:HE1 | 1:B:99:PRO:HG2 | 1.73 | 0.53 |
| 1:C:134:ALA:HB3 | 1:C:192:VAL:HG22 | 1.89 | 0.53 |
| 1:F:29:THR:HG23 | 1:F:30:TYR:CD1 | 2.44 | 0.53 |
| 1:B:453:ARG:CG | 1:B:460:TRP:CE2 | 2.91 | 0.53 |
| 1:D:644:GLU:HG2 | 1:D:645:ILE:HG13 | 1.90 | 0.53 |
| 1:C:138:ASP:OD1 | 1:C:139:SER:N | 2.41 | 0.53 |
| 1:D:161:THR:HG1 | 1:D:187:LYS:HZ2 | 1.56 | 0.53 |
| 1:B:225:LEU:HD22 | 1:B:247:ILE:HB | 1.89 | 0.53 |

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| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|---|---|---|---|
| 1:F:34:GLY:O | 1:F:90:PHE:N | 2.42 | 0.53 |
| 1:A:718:CYS:HB2 | 1:A:773:CYS:SG | 2.49 | 0.52 |
| 1:B:237:PHE:CD1 | 1:D:178:ARG:NE | 2.77 | 0.52 |
| 1:D:512:PRO:HA | 1:D:516:SER:HB3 | 1.89 | 0.52 |
| 1:E:34:GLY:O | 1:E:90:PHE:N | 2.42 | 0.52 |
| 1:B:237:PHE:CE2 | 1:D:178:ARG:CZ | 2.93 | 0.52 |
| 1:A:786:ALA:CB | 1:D:619:ASN:HD21 | 2.23 | 0.52 |
| 1:C:77:TYR:CE2 | 1:C:100:SER:HB2 | 2.45 | 0.52 |
| 1:C:316:LEU:HD11 | 1:D:63:CYS:SG | 2.50 | 0.52 |
| 1:F:36:GLN:NE2 | 1:F:197:ASP:O | 2.38 | 0.52 |
| 1:F:39:PRO:O | 1:F:85:PHE:N | 2.42 | 0.52 |
| 1:A:80:LYS:HG2 | 1:B:83:ASN:ND2 | 2.24 | 0.52 |
| 1:A:685:THR:OG1 | 1:A:688:GLU:HG3 | 2.09 | 0.52 |
| 1:B:237:PHE:CE1 | 1:D:178:ARG:NE | 2.78 | 0.52 |
| 1:B:590:ASP:O | 1:B:599:ARG:NE | 2.43 | 0.52 |
| 1:C:590:ASP:CG | 1:C:591:ILE:H | 2.13 | 0.52 |
| 1:D:77:TYR:HE2 | 1:D:98:THR:HG21 | 1.74 | 0.52 |
| 1:D:721:MET:HG3 | 1:D:776:LYS:CE | 2.37 | 0.52 |
| 1:B:236:GLN:HA | 1:B:363:LEU:HD21 | 1.91 | 0.52 |
| 1:B:532:ALA:O | 1:B:536:VAL:HG23 | 2.10 | 0.52 |
| 1:C:600:ILE:HA | 1:D:581:LEU:HD21 | 1.91 | 0.52 |
| 1:D:330:GLU:HA | 1:D:333:LEU:HD12 | 1.91 | 0.52 |
| 1:B:502:ILE:HG12 | 1:B:703:LEU:HD23 | 1.91 | 0.52 |
| 1:B:579:PHE:CZ | 1:B:591:ILE:HG22 | 2.44 | 0.52 |
| 1:D:791:ASN:OD1 | 1:D:792:VAL:HG23 | 2.09 | 0.52 |
| 1:E:39:PRO:O | 1:E:85:PHE:N | 2.43 | 0.52 |
| 1:F:127:SER:O | 1:F:130:SER:OG | 2.23 | 0.52 |
| 1:A:56:PHE:CD1 | 1:B:88:PHE:CD2 | 2.97 | 0.52 |
| 1:A:786:ALA:O | 1:A:787:LEU:CB | 2.55 | 0.52 |
| 1:B:261:ARG:O | 1:B:264:THR:OG1 | 2.21 | 0.52 |
| 1:C:363:LEU:HA | 1:C:368:PRO:HA | 1.91 | 0.52 |
| 1:D:219:HIS:CD2 | 1:D:241:GLU:HB2 | 2.45 | 0.52 |
| 1:C:56:PHE:HD1 | 1:D:88:PHE:CD2 | 2.27 | 0.52 |
| 1:C:453:ARG:HD2 | 1:C:460:TRP:CH2 | 2.45 | 0.52 |
| 1:A:581:LEU:HD21 | 1:D:600:ILE:HA | 1.92 | 0.51 |
| 1:B:594:ARG:O | 1:B:596:LEU:N | 2.42 | 0.51 |
| 1:A:259:ILE:HA | 1:A:262:TRP:HB3 | 1.93 | 0.51 |
| 1:A:746:VAL:HG12 | 1:A:746:VAL:O | 2.10 | 0.51 |
| 1:B:219:HIS:CD2 | 1:B:241:GLU:HB2 | 2.45 | 0.51 |
| 1:B:606:TRP:HZ3 | 1:C:584:PHE:CZ | 2.28 | 0.51 |
| 1:C:387:THR:O | 1:C:389:GLY:N | 2.38 | 0.51 |

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| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|---|---|---|---|
| 1:D:346:LYS:HD3 | 1:D:355:ASN:HD22 | 1.76 | 0.51 |
| 1:A:539:VAL:HA | 1:A:542:LEU:HD12 | 1.93 | 0.51 |
| 1:D:261:ARG:O | 1:D:264:THR:OG1 | 2.18 | 0.51 |
| 1:A:317:ALA:O | 1:A:320:ALA:N | 2.44 | 0.51 |
| 1:A:355:ASN:N | 1:A:376:GLU:OE2 | 2.22 | 0.51 |
| 1:E:127:SER:O | 1:E:130:SER:OG | 2.22 | 0.51 |
| 1:A:504:ILE:CD1 | 1:A:723:VAL:HG22 | 2.38 | 0.51 |
| 1:A:721:MET:HE2 | 1:A:723:VAL:HG12 | 1.93 | 0.51 |
| 1:B:178:ARG:CD | 1:D:237:PHE:CE1 | 2.93 | 0.51 |
| 1:C:121:LEU:HA | 1:C:245:PHE:CZ | 2.45 | 0.51 |
| 1:D:130:TRP:CD2 | 1:D:191:ARG:HD3 | 2.46 | 0.51 |
| 1:D:219:HIS:HD2 | 1:D:241:GLU:HB2 | 1.76 | 0.51 |
| 1:D:348:ASP:OD1 | 1:D:351:GLY:N | 2.43 | 0.51 |
| 1:D:388:SER:OG | 1:D:389:GLY:N | 2.43 | 0.51 |
| 1:A:581:LEU:HD11 | 1:D:600:ILE:HG22 | 1.93 | 0.51 |
| 1:C:263:SER:O | 1:C:274:HIS:ND1 | 2.44 | 0.51 |
| 1:D:608:PHE:CZ | 1:D:612:ILE:HD11 | 2.45 | 0.51 |
| 1:E:177:MET:O | 1:E:181:MET:HG2 | 2.11 | 0.51 |
| 1:D:794:GLY:HA2 | 1:D:797:TYR:CD2 | 2.45 | 0.51 |
| 1:B:130:TRP:CE2 | 1:B:191:ARG:HD3 | 2.46 | 0.51 |
| 1:C:504:ILE:N | 1:C:504:ILE:CD1 | 2.73 | 0.51 |
| 1:D:309:ARG:HD3 | 1:D:311:ASN:HB2 | 1.94 | 0.51 |
| 1:A:387:THR:O | 1:A:389:GLY:N | 2.38 | 0.50 |
| 1:B:174:ASP:CG | 1:B:178:ARG:HH12 | 2.14 | 0.50 |
| 1:B:348:ASP:OD1 | 1:B:351:GLY:N | 2.45 | 0.50 |
| 1:C:718:CYS:CB | 1:C:773:CYS:SG | 2.98 | 0.50 |
| 1:E:157:ASP:HB3 | 1:E:160:LYS:HB2 | 1.93 | 0.50 |
| 1:A:763:LYS:O | 1:A:767:TRP:HB2 | 2.11 | 0.50 |
| 1:B:130:TRP:CD2 | 1:B:191:ARG:HD3 | 2.45 | 0.50 |
| 1:B:190:ARG:HD3 | 1:B:218:TYR:CE1 | 2.46 | 0.50 |
| 1:C:178:ARG:NH1 | 1:C:211:ILE:HG22 | 2.27 | 0.50 |
| 1:C:619:ASN:ND2 | 1:D:787:LEU:HB2 | 2.26 | 0.50 |
| 1:D:99:PRO:HA | 1:D:113:MET:HB2 | 1.93 | 0.50 |
| 1:A:347:PHE:HE1 | 1:A:353:ARG:HG2 | 1.77 | 0.50 |
| 1:C:211:ILE:HD12 | 1:C:213:LYS:HD2 | 1.94 | 0.50 |
| 1:C:763:LYS:O | 1:C:767:TRP:HB2 | 2.12 | 0.50 |
| 1:A:77:TYR:CE2 | 1:A:100:SER:HB2 | 2.47 | 0.50 |
| 1:B:453:ARG:HG3 | 1:B:460:TRP:CG | 2.47 | 0.50 |
| 1:D:130:TRP:CE2 | 1:D:191:ARG:HD3 | 2.46 | 0.50 |
| 1:A:17:LEU:HB2 | 1:A:75:GLY:HA3 | 1.93 | 0.50 |
| 1:B:789:LEU:O | 1:B:789:LEU:HG | 2.12 | 0.50 |

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| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|---|---|---|---|
| 1:C:392:GLN:C | 1:C:394:THR:H | 2.15 | 0.50 |
| 1:D:763:LYS:O | 1:D:767:TRP:HB2 | 2.11 | 0.50 |
| 1:F:157:ASP:HB3 | 1:F:160:LYS:HB2 | 1.94 | 0.50 |
| 1:A:584:PHE:HD1 | 1:A:605:TRP:HZ2 | 1.59 | 0.50 |
| 1:B:326:GLY:HA2 | 1:B:329:ILE:HD12 | 1.93 | 0.50 |
| 1:D:595:SER:HA | 1:D:599:ARG:CB | 2.35 | 0.50 |
| 1:B:132:LYS:NZ | 1:B:189:GLU:OE2 | 2.44 | 0.50 |
| 1:C:521:LEU:O | 1:C:526:TRP:NE1 | 2.44 | 0.50 |
| 1:D:190:ARG:HD3 | 1:D:218:TYR:CE1 | 2.47 | 0.50 |
| 1:B:178:ARG:NE | 1:D:237:PHE:CE2 | 2.80 | 0.49 |
| 1:B:453:ARG:HG3 | 1:B:460:TRP:CD1 | 2.47 | 0.49 |
| 1:B:763:LYS:O | 1:B:767:TRP:HB2 | 2.11 | 0.49 |
| 1:C:644:GLU:HG2 | 1:C:645:ILE:HG13 | 1.93 | 0.49 |
| 1:D:77:TYR:CE2 | 1:D:100:SER:HB2 | 2.47 | 0.49 |
| 1:D:392:GLN:CD | 1:D:437:GLY:O | 2.50 | 0.49 |
| 1:D:593:PRO:HD2 | 1:D:596:LEU:HD23 | 1.93 | 0.49 |
| 1:D:595:SER:O | 1:D:597:SER:N | 2.44 | 0.49 |
| 1:F:133:LEU:HD23 | 1:F:136:LEU:HD12 | 1.92 | 0.49 |
| 1:A:101:PHE:HA | 1:A:114:ARG:HH11 | 1.78 | 0.49 |
| 1:C:597:SER:O | 1:C:600:ILE:HG12 | 2.13 | 0.49 |
| 1:D:803:LEU:O | 1:D:807:MET:HG2 | 2.12 | 0.49 |
| 1:A:135:TYR:HH | 1:A:145:THR:HG1 | 1.59 | 0.49 |
| 1:A:744:THR:CB | 1:A:745:PRO:HD3 | 2.42 | 0.49 |
| 1:C:115:PRO:HB3 | 1:C:356:TYR:CG | 2.48 | 0.49 |
| 1:C:267:GLU:HG3 | 1:C:271:PRO:HA | 1.94 | 0.49 |
| 1:D:627:GLU:HG2 | 1:D:629:MET:HE2 | 1.93 | 0.49 |
| 1:A:130:TRP:CZ3 | 1:A:191:ARG:HB3 | 2.47 | 0.49 |
| 1:A:392:GLN:C | 1:A:394:THR:H | 2.15 | 0.49 |
| 1:B:77:TYR:CE2 | 1:B:100:SER:HB2 | 2.48 | 0.49 |
| 1:A:77:TYR:CE2 | 1:A:98:THR:HG21 | 2.40 | 0.49 |
| 1:B:627:GLU:HG2 | 1:B:629:MET:HE3 | 1.94 | 0.49 |
| 1:D:177:TYR:CD2 | 1:D:207:GLN:HG3 | 2.47 | 0.49 |
| 1:D:337:GLN:OE1 | 1:D:346:LYS:NZ | 2.33 | 0.49 |
| 1:D:532:ALA:O | 1:D:536:VAL:HG23 | 2.12 | 0.49 |
| 1:A:124:LEU:HD11 | 1:A:128:TYR:HE1 | 1.77 | 0.49 |
| 1:C:504:ILE:CD1 | 1:C:723:VAL:HG13 | 2.36 | 0.49 |
| 1:C:786:ALA:O | 1:C:787:LEU:CB | 2.55 | 0.49 |
| 1:D:246:GLN:HE21 | 1:D:248:VAL:N | 2.09 | 0.49 |
| 1:D:627:GLU:HG2 | 1:D:629:MET:CE | 2.43 | 0.49 |
| 1:A:316:LEU:HD11 | 1:B:63:CYS:SG | 2.53 | 0.49 |
| 1:B:24:GLN:NE2 | 1:B:278:ILE:HG13 | 2.27 | 0.49 |

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| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|---|---|---|---|
| 1:B:227:PHE:CD1 | 1:B:244:GLY:HA3 | 2.48 | 0.49 |
| 1:C:607:PHE:O | 1:C:611:ILE:HG12 | 2.12 | 0.49 |
| 1:F:170:VAL:O | 1:F:174:LEU:HG | 2.13 | 0.49 |
| 1:A:97:ILE:HG13 | 1:A:111:ILE:HB | 1.93 | 0.49 |
| 1:A:247:ILE:HG13 | 1:A:342:SER:HB2 | 1.93 | 0.49 |
| 1:A:785:SER:O | 1:A:786:ALA:HB2 | 2.13 | 0.49 |
| 1:C:619:ASN:HD21 | 1:D:787:LEU:HB2 | 1.78 | 0.49 |
| 1:D:243:SER:OG | 1:D:362:GLU:HG2 | 2.13 | 0.49 |
| 1:A:640:SER:O | 1:A:669:LYS:HE3 | 2.13 | 0.49 |
| 1:B:794:GLY:HA2 | 1:B:797:TYR:CD2 | 2.48 | 0.49 |
| 1:D:174:ASP:CG | 1:D:178:ARG:HH12 | 2.16 | 0.49 |
| 1:D:209:ILE:HA | 1:D:214:HIS:HD2 | 1.77 | 0.49 |
| 1:D:782:GLU:O | 1:D:783:LYS:HG3 | 2.13 | 0.49 |
| 1:A:138:ASP:OD1 | 1:A:139:SER:N | 2.46 | 0.48 |
| 1:B:329:ILE:O | 1:B:333:LEU:HG | 2.13 | 0.48 |
| 1:C:525:ILE:HG12 | 1:D:789:LEU:HB2 | 1.94 | 0.48 |
| 1:C:785:SER:O | 1:C:786:ALA:HB2 | 2.13 | 0.48 |
| 1:D:640:SER:O | 1:D:669:LYS:HE3 | 2.13 | 0.48 |
| 1:A:316:LEU:HD22 | 1:B:60:ASN:HA | 1.95 | 0.48 |
| 1:B:178:ARG:CD | 1:D:237:PHE:CD1 | 2.96 | 0.48 |
| 1:C:337:GLN:NE2 | 1:C:346:LYS:HE2 | 2.23 | 0.48 |
| 1:D:25:GLU:OE1 | 1:D:25:GLU:N | 2.44 | 0.48 |
| 1:B:35:GLN:HG2 | 1:B:286:TYR:OH | 2.13 | 0.48 |
| 1:C:291:VAL:HG13 | 1:C:336:VAL:HG11 | 1.95 | 0.48 |
| 1:C:97:ILE:HG13 | 1:C:111:ILE:HB | 1.96 | 0.48 |
| 1:C:514:VAL:HA | 1:C:794:GLY:HA3 | 1.96 | 0.48 |
| 1:C:789:LEU:O | 1:C:793:ALA:CB | 2.62 | 0.48 |
| 1:D:326:GLY:HA2 | 1:D:329:ILE:HD12 | 1.95 | 0.48 |
| 1:F:159:LEU:HD12 | 1:F:229:SER:HB3 | 1.95 | 0.48 |
| 1:A:23:ASP:HB3 | 1:A:271:PRO:HG2 | 1.95 | 0.48 |
| 1:D:250:TYR:HA | 1:D:255:VAL:HG11 | 1.94 | 0.48 |
| 1:F:36:GLN:NE2 | 1:F:199:ARG:H | 2.12 | 0.48 |
| 1:A:14:ILE:HG13 | 1:A:45:PRO:HA | 1.95 | 0.48 |
| 1:B:161:THR:HG1 | 1:B:187:LYS:HZ2 | 1.62 | 0.48 |
| 1:B:237:PHE:CD1 | 1:D:178:ARG:HD3 | 2.49 | 0.48 |
| 1:B:417:GLY:HA2 | 1:B:441:LYS:NZ | 2.29 | 0.48 |
| 1:B:789:LEU:HD21 | 1:E:181:MET:CE | 2.44 | 0.48 |
| 1:F:7:ARG:HH21 | 1:F:224:VAL:HG13 | 1.79 | 0.48 |
| 1:A:417:GLY:HA2 | 1:A:441:LYS:NZ | 2.29 | 0.48 |
| 1:A:633:ILE:HD13 | 1:A:645:ILE:CD1 | 2.43 | 0.48 |
| 1:D:592:SER:OG | 1:D:596:LEU:HB3 | 2.12 | 0.48 |

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| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|---|---|---|---|
| 1:B:640:SER:O | 1:B:669:LYS:HE3 | 2.13 | 0.48 |
| 1:C:640:SER:O | 1:C:669:LYS:HE3 | 2.13 | 0.48 |
| 1:F:28:THR:HG23 | 1:F:207:TRP:CD1 | 2.48 | 0.48 |
| 1:A:348:ASP:OD1 | 1:A:352:LYS:N | 2.46 | 0.48 |
| 1:C:77:TYR:OH | 1:C:101:PHE:O | 2.16 | 0.48 |
| 1:A:255:VAL:O | 1:A:259:ILE:HG12 | 2.13 | 0.48 |
| 1:A:784:THR:O | 1:A:786:ALA:N | 2.47 | 0.48 |
| 1:B:309:ARG:HD3 | 1:B:311:ASN:HB2 | 1.96 | 0.48 |
| 1:B:800:VAL:HA | 1:B:803:LEU:HD12 | 1.94 | 0.48 |
| 1:A:256:SER:O | 1:A:260:GLU:HG3 | 2.14 | 0.47 |
| 1:A:744:THR:CB | 1:A:745:PRO:CD | 2.91 | 0.47 |
| 1:B:25:GLU:OE1 | 1:B:25:GLU:N | 2.45 | 0.47 |
| 1:C:364:LYS:HG3 | 1:C:369:ARG:NH2 | 2.29 | 0.47 |
| 1:B:306:ILE:HA | 1:B:325:GLN:HE21 | 1.78 | 0.47 |
| 1:C:634:GLU:HG2 | 1:C:723:VAL:CB | 2.28 | 0.47 |
| 1:E:28:THR:HG23 | 1:E:207:TRP:CD1 | 2.49 | 0.47 |
| 1:A:236:GLN:HA | 1:A:363:LEU:HD21 | 1.97 | 0.47 |
| 1:B:78:ASP:N | 1:B:81:SER:OG | 2.48 | 0.47 |
| 1:B:243:SER:OG | 1:B:362:GLU:HG2 | 2.14 | 0.47 |
| 1:B:579:PHE:CE1 | 1:B:591:ILE:HG22 | 2.49 | 0.47 |
| 1:C:299:LEU:O | 1:C:303:ARG:N | 2.45 | 0.47 |
| 1:C:633:ILE:HD13 | 1:C:645:ILE:CD1 | 2.45 | 0.47 |
| 1:C:657:GLU:OE2 | 1:C:661:ARG:CZ | 2.62 | 0.47 |
| 1:C:784:THR:O | 1:C:786:ALA:N | 2.47 | 0.47 |
| 1:D:24:GLN:HE22 | 1:D:279:LYS:H | 1.62 | 0.47 |
| 1:D:35:GLN:HG2 | 1:D:286:TYR:OH | 2.14 | 0.47 |
| 1:D:417:GLY:HA2 | 1:D:441:LYS:NZ | 2.29 | 0.47 |
| 1:A:522:ALA:H | 1:A:525:ILE:HD12 | 1.79 | 0.47 |
| 1:C:14:ILE:HG13 | 1:C:45:PRO:HA | 1.96 | 0.47 |
| 1:C:56:PHE:CD1 | 1:D:88:PHE:CE2 | 3.02 | 0.47 |
| 1:C:308:ARG:HB3 | 1:C:311:ASN:ND2 | 2.29 | 0.47 |
| 1:D:592:SER:OG | 1:D:595:SER:O | 2.26 | 0.47 |
| 1:D:633:ILE:CG2 | 1:D:638:ASP:CB | 2.92 | 0.47 |
| 1:E:227:LEU:O | 1:E:231:THR:HG23 | 2.14 | 0.47 |
| 1:A:607:PHE:O | 1:A:611:ILE:HG12 | 2.14 | 0.47 |
| 1:D:512:PRO:HB3 | 1:D:516:SER:HB3 | 1.67 | 0.47 |
| 1:A:585:MET:HG3 | 1:D:603:GLY:HA2 | 1.97 | 0.47 |
| 1:A:629:MET:O | 1:A:630:VAL:O | 2.33 | 0.47 |
| 1:A:634:GLU:HG2 | 1:A:723:VAL:HB | 1.93 | 0.47 |
| 1:B:506:LYS:CG | 1:B:507:PRO:HD2 | 2.45 | 0.47 |
| 1:B:782:GLU:O | 1:B:783:LYS:HG3 | 2.13 | 0.47 |

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| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|---|---|---|---|
| 1:C:417:GLY:HA2 | 1:C:441:LYS:NZ | 2.29 | 0.47 |
| 1:E:36:GLN:NE2 | 1:E:199:ARG:H | 2.13 | 0.47 |
| 1:E:159:LEU:HD12 | 1:E:229:SER:HB3 | 1.95 | 0.47 |
| 1:A:506:LYS:NZ | 1:A:721:MET:HG3 | 2.30 | 0.47 |
| 1:A:613:ILE:HG21 | 1:D:610:LEU:HD21 | 1.95 | 0.47 |
| 1:B:95:SER:HA | 1:B:109:PHE:HB3 | 1.97 | 0.47 |
| 1:B:663:LYS:HE2 | 1:B:663:LYS:CA | 2.33 | 0.47 |
| 1:D:534:ILE:O | 1:D:537:SER:OG | 2.27 | 0.47 |
| 1:E:7:ARG:HH21 | 1:E:224:VAL:HG13 | 1.80 | 0.47 |
| 1:B:24:GLN:HE22 | 1:B:279:LYS:H | 1.61 | 0.47 |
| 1:A:87:SER:OG | 1:B:54:ASN:OD1 | 2.32 | 0.47 |
| 1:D:790:SER:OG | 1:F:185:GLN:NE2 | 2.39 | 0.47 |
| 1:E:38:VAL:HG11 | 1:E:85:PHE:HD2 | 1.79 | 0.47 |
| 1:F:187:PHE:HE2 | 1:F:203:TRP:CD1 | 2.32 | 0.47 |
| 1:C:122:LEU:HA | 1:C:125:ILE:HD12 | 1.97 | 0.47 |
| 1:C:776:LYS:HD2 | 1:C:776:LYS:HA | 1.52 | 0.47 |
| 1:F:141:GLY:O | 1:F:145:MET:HG3 | 2.15 | 0.47 |
| 1:A:526:TRP:HA | 1:A:529:ILE:HG22 | 1.98 | 0.46 |
| 1:B:24:GLN:NE2 | 1:B:279:LYS:H | 2.13 | 0.46 |
| 1:B:330:GLU:HA | 1:B:333:LEU:HD12 | 1.98 | 0.46 |
| 1:D:197:GLU:O | 1:D:201:VAL:HG23 | 2.15 | 0.46 |
| 1:F:38:VAL:HG11 | 1:F:85:PHE:HD2 | 1.79 | 0.46 |
| 1:A:541:PHE:HE2 | 1:E:226:THR:HG23 | 1.80 | 0.46 |
| 1:A:594:ARG:O | 1:A:596:LEU:N | 2.49 | 0.46 |
| 1:B:595:SER:HB3 | 1:C:578:TRP:CG | 2.51 | 0.46 |
| 1:F:189:VAL:O | 1:F:193:LEU:HD13 | 2.15 | 0.46 |
| 1:D:215:VAL:HA | 1:D:238:GLY:O | 2.16 | 0.46 |
| 1:E:187:PHE:HE2 | 1:E:203:TRP:CD1 | 2.33 | 0.46 |
| 1:B:526:TRP:HA | 1:B:529:ILE:HG22 | 1.97 | 0.46 |
| 1:D:506:LYS:HA | 1:D:507:PRO:HD3 | 1.44 | 0.46 |
| 1:E:94:ILE:HG12 | 1:E:95:TRP:CD1 | 2.51 | 0.46 |
| 1:C:83:ASN:ND2 | 1:D:80:LYS:CA | 2.75 | 0.46 |
| 1:C:323:TRP:CE3 | 1:C:325:GLN:HB2 | 2.50 | 0.46 |
| 1:A:597:SER:O | 1:A:600:ILE:HG12 | 2.16 | 0.46 |
| 1:A:721:MET:CE | 1:A:723:VAL:HG12 | 2.46 | 0.46 |
| 1:B:308:ARG:NH2 | 1:B:325:GLN:HG2 | 2.29 | 0.46 |
| 1:C:721:MET:CE | 1:C:723:VAL:HG12 | 2.46 | 0.46 |
| 1:D:124:LEU:HD11 | 1:D:128:TYR:HE1 | 1.81 | 0.46 |
| 1:B:178:ARG:NE | 1:D:237:PHE:CD2 | 2.83 | 0.46 |
| 1:B:309:ARG:HG2 | 1:B:311:ASN:N | 2.30 | 0.46 |
| 1:C:132:LYS:HD3 | 1:C:159:GLN:OE1 | 2.16 | 0.46 |

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| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|---|---|---|---|
| 1:D:506:LYS:CG | 1:D:507:PRO:HD2 | 2.45 | 0.46 |
| 1:D:529:ILE:HD12 | 1:D:612:ILE:HD13 | 1.97 | 0.46 |
| 1:D:721:MET:CE | 1:D:723:VAL:HG12 | 2.46 | 0.46 |
| 1:F:94:ILE:HG12 | 1:F:95:TRP:CD1 | 2.51 | 0.46 |
| 1:D:592:SER:N | 1:D:599:ARG:HH21 | 2.14 | 0.46 |
| 1:A:246:GLN:HE21 | 1:A:248:VAL:N | 2.12 | 0.46 |
| 1:C:80:LYS:HG2 | 1:D:83:ASN:ND2 | 2.31 | 0.46 |
| 1:D:95:SER:HA | 1:D:109:PHE:HB3 | 1.97 | 0.46 |
| 1:E:204:ASP:OD1 | 1:E:205:TYR:N | 2.49 | 0.46 |
| 1:F:195:PRO:O | 1:F:197:ASP:N | 2.49 | 0.46 |
| 1:A:330:GLU:HG2 | 1:A:334:LYS:HE3 | 1.98 | 0.46 |
| 1:A:786:ALA:HB1 | 1:D:619:ASN:ND2 | 2.29 | 0.46 |
| 1:C:112:GLN:NE2 | 1:C:352:LYS:HG2 | 2.31 | 0.46 |
| 1:D:329:ILE:O | 1:D:333:LEU:HG | 2.16 | 0.46 |
| 1:D:513:GLY:O | 1:D:514:VAL:CB | 2.64 | 0.46 |
| 1:E:196:GLU:OE1 | 1:E:198:TRP:NE1 | 2.48 | 0.46 |
| 1:A:113:MET:HB3 | 1:A:284:LEU:HD22 | 1.98 | 0.45 |
| 1:A:188:LYS:HD2 | 1:A:190:ARG:NH2 | 2.22 | 0.45 |
| 1:A:261:ARG:O | 1:A:265:LEU:HG | 2.16 | 0.45 |
| 1:A:628:ARG:NH1 | 1:D:623:PHE:HA | 2.31 | 0.45 |
| 1:B:146:LEU:HA | 1:B:149:VAL:HG22 | 1.98 | 0.45 |
| 1:B:250:TYR:OH | 1:B:277:THR:HB | 2.16 | 0.45 |
| 1:B:345:ILE:HG12 | 1:B:353:ARG:NH2 | 2.31 | 0.45 |
| 1:C:813:GLU:O | 1:C:817:LYS:HG3 | 2.16 | 0.45 |
| 1:D:371:ILE:HB | 1:D:386:ASP:OD2 | 2.15 | 0.45 |
| 1:E:170:VAL:O | 1:E:174:LEU:HG | 2.15 | 0.45 |
| 1:F:213:TRP:O | 1:F:216:PHE:HB3 | 2.16 | 0.45 |
| 1:A:130:TRP:CE2 | 1:A:191:ARG:HD3 | 2.51 | 0.45 |
| 1:B:453:ARG:HG3 | 1:B:460:TRP:CD2 | 2.51 | 0.45 |
| 1:B:721:MET:CE | 1:B:723:VAL:HG12 | 2.46 | 0.45 |
| 1:C:346:LYS:HD2 | 1:C:355:ASN:HD22 | 1.81 | 0.45 |
| 1:F:178:VAL:O | 1:F:181:MET:HB2 | 2.16 | 0.45 |
| 1:A:227:PHE:CD1 | 1:A:244:GLY:HA3 | 2.51 | 0.45 |
| 1:A:326:GLY:HA2 | 1:A:329:ILE:HD12 | 1.97 | 0.45 |
| 1:A:521:LEU:O | 1:A:526:TRP:NE1 | 2.49 | 0.45 |
| 1:B:417:GLY:HA2 | 1:B:441:LYS:HZ2 | 1.81 | 0.45 |
| 1:C:255:VAL:O | 1:C:259:ILE:HG12 | 2.16 | 0.45 |
| 1:D:345:ILE:HG12 | 1:D:353:ARG:NH2 | 2.31 | 0.45 |
| 1:E:34:GLY:HA3 | 1:E:90:PHE:HB2 | 1.99 | 0.45 |
| 1:F:195:PRO:HB2 | 1:F:198:TRP:O | 2.16 | 0.45 |
| 1:A:80:LYS:CA | 1:B:83:ASN:ND2 | 2.77 | 0.45 |

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| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|---|---|---|---|
| 1:A:598:GLY:O | 1:A:601:VAL:HB | 2.16 | 0.45 |
| 1:B:236:GLN:NE2 | 1:B:364:LYS:O | 2.47 | 0.45 |
| 1:B:347:PHE:HE1 | 1:B:353:ARG:HG2 | 1.82 | 0.45 |
| 1:C:177:TYR:HE1 | 1:C:204:ILE:HG12 | 1.82 | 0.45 |
| 1:D:607:PHE:O | 1:D:611:ILE:HG12 | 2.16 | 0.45 |
| 1:F:117:PRO:O | 1:F:119:SER:N | 2.49 | 0.45 |
| 1:B:607:PHE:O | 1:B:611:ILE:HG12 | 2.16 | 0.45 |
| 1:D:122:LEU:O | 1:D:126:GLU:HG3 | 2.16 | 0.45 |
| 1:D:526:TRP:HA | 1:D:529:ILE:HG22 | 1.98 | 0.45 |
| 1:E:141:GLY:O | 1:E:145:MET:HG3 | 2.16 | 0.45 |
| 1:E:195:PRO:HB2 | 1:E:198:TRP:O | 2.16 | 0.45 |
| 1:C:18:PHE:O | 1:C:49:ASN:HA | 2.16 | 0.45 |
| 1:C:197:GLU:O | 1:C:201:VAL:HG23 | 2.16 | 0.45 |
| 1:C:684:ARG:NH2 | 1:C:684:ARG:CG | 2.75 | 0.45 |
| 1:D:204:ILE:O | 1:D:208:VAL:HG23 | 2.16 | 0.45 |
| 1:D:598:GLY:O | 1:D:601:VAL:HB | 2.17 | 0.45 |
| 1:A:504:ILE:N | 1:A:504:ILE:CD1 | 2.77 | 0.45 |
| 1:C:121:LEU:HA | 1:C:245:PHE:HZ | 1.81 | 0.45 |
| 1:C:169:ASN:HD21 | 1:C:172:LYS:HE3 | 1.82 | 0.45 |
| 1:C:185:GLU:HA | 1:C:188:LYS:HA | 1.97 | 0.45 |
| 1:C:506:LYS:NZ | 1:C:721:MET:HG3 | 2.31 | 0.45 |
| 1:A:684:ARG:NH2 | 1:A:684:ARG:CB | 2.79 | 0.45 |
| 1:A:742:LEU:O | 1:A:745:PRO:CD | 2.61 | 0.45 |
| 1:B:122:LEU:O | 1:B:126:GLU:HG3 | 2.17 | 0.45 |
| 1:B:131:ASP:OD1 | 1:B:132:LYS:N | 2.50 | 0.45 |
| 1:B:506:LYS:HA | 1:B:507:PRO:HD3 | 1.44 | 0.45 |
| 1:C:76:PHE:CD1 | 1:C:99:PRO:HD2 | 2.52 | 0.45 |
| 1:C:124:LEU:HD11 | 1:C:128:TYR:HE1 | 1.82 | 0.45 |
| 1:C:348:ASP:OD1 | 1:C:352:LYS:N | 2.50 | 0.45 |
| 1:E:213:TRP:O | 1:E:216:PHE:HB3 | 2.17 | 0.45 |
| 1:A:392:GLN:C | 1:A:394:THR:N | 2.70 | 0.45 |
| 1:A:534:ILE:O | 1:A:537:SER:OG | 2.24 | 0.45 |
| 1:B:540:LEU:HD12 | 1:B:580:SER:HB3 | 1.99 | 0.45 |
| 1:A:541:PHE:CZ | 1:E:227:LEU:HD13 | 2.52 | 0.45 |
| 1:B:595:SER:H | 1:B:599:ARG:HG3 | 1.81 | 0.45 |
| 1:C:517:PHE:O | 1:C:520:PRO:HD2 | 2.17 | 0.45 |
| 1:C:594:ARG:O | 1:C:596:LEU:N | 2.48 | 0.45 |
| 1:E:178:VAL:O | 1:E:182:MET:HG2 | 2.17 | 0.45 |
| 1:A:18:PHE:O | 1:A:49:ASN:HA | 2.17 | 0.44 |
| 1:A:629:MET:O | 1:A:630:VAL:C | 2.55 | 0.44 |
| 1:B:124:LEU:HD11 | 1:B:128:TYR:HE1 | 1.82 | 0.44 |

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| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|---|---|---|---|
| 1:C:598:GLY:O | 1:C:601:VAL:HB | 2.16 | 0.44 |
| 1:C:789:LEU:O | 1:C:793:ALA:N | 2.47 | 0.44 |
| 1:D:116:ASP:OD1 | 1:D:118:LYS:HG2 | 2.17 | 0.44 |
| 1:F:31:TRP:CE2 | 1:F:183:TYR:HE2 | 2.36 | 0.44 |
| 1:A:384:GLU:O | 1:A:386:ASP:N | 2.50 | 0.44 |
| 1:B:237:PHE:CZ | 1:D:178:ARG:NE | 2.85 | 0.44 |
| 1:C:267:GLU:CG | 1:C:271:PRO:HA | 2.48 | 0.44 |
| 1:C:809:VAL:HA | 1:C:812:ILE:HG12 | 1.99 | 0.44 |
| 1:D:325:GLN:O | 1:D:329:ILE:HG13 | 2.16 | 0.44 |
| 1:D:391:GLU:O | 1:D:392:GLN:HG3 | 2.17 | 0.44 |
| 1:E:8:ALA:O | 1:E:12:VAL:HG23 | 2.16 | 0.44 |
| 1:A:107:HIS:HA | 1:A:108:PRO:HD3 | 1.84 | 0.44 |
| 1:A:172:LYS:O | 1:A:174:ASP:N | 2.48 | 0.44 |
| 1:A:663:LYS:O | 1:A:663:LYS:HD3 | 2.18 | 0.44 |
| 1:B:198:ARG:CZ | 1:B:230:GLY:HA2 | 2.47 | 0.44 |
| 1:B:503:MET:HA | 1:B:721:MET:O | 2.17 | 0.44 |
| 1:C:130:TRP:CZ3 | 1:C:191:ARG:HB3 | 2.53 | 0.44 |
| 1:A:190:ARG:HD3 | 1:A:218:TYR:CE1 | 2.53 | 0.44 |
| 1:B:68:ARG:HB3 | 1:B:70:VAL:HG13 | 1.99 | 0.44 |
| 1:B:112:GLN:HE21 | 1:B:352:LYS:HA | 1.82 | 0.44 |
| 1:B:204:ILE:O | 1:B:208:VAL:HG23 | 2.18 | 0.44 |
| 1:B:391:GLU:O | 1:B:392:GLN:HG3 | 2.17 | 0.44 |
| 1:C:250:TYR:HA | 1:C:255:VAL:HG11 | 1.99 | 0.44 |
| 1:C:599:ARG:HH22 | 1:D:581:LEU:HB3 | 1.83 | 0.44 |
| 1:A:595:SER:HB2 | 1:B:578:TRP:CG | 2.53 | 0.44 |
| 1:A:781:LYS:O | 1:A:784:THR:HG23 | 2.17 | 0.44 |
| 1:B:99:PRO:HA | 1:B:113:MET:HB2 | 1.99 | 0.44 |
| 1:B:237:PHE:CZ | 1:D:178:ARG:CZ | 3.01 | 0.44 |
| 1:C:306:ILE:HA | 1:C:325:GLN:HE21 | 1.82 | 0.44 |
| 1:C:314:ASP:OD1 | 1:C:315:CYS:N | 2.51 | 0.44 |
| 1:C:392:GLN:C | 1:C:394:THR:N | 2.70 | 0.44 |
| 1:D:24:GLN:NE2 | 1:D:279:LYS:H | 2.16 | 0.44 |
| 1:F:196:GLU:OE1 | 1:F:198:TRP:NE1 | 2.50 | 0.44 |
| 1:B:27:SER:O | 1:B:31:VAL:HG23 | 2.18 | 0.44 |
| 1:B:323:TRP:CE3 | 1:B:325:GLN:HB2 | 2.53 | 0.44 |
| 1:B:388:SER:OG | 1:B:389:GLY:N | 2.43 | 0.44 |
| 1:C:17:LEU:HB2 | 1:C:75:GLY:HA3 | 1.99 | 0.44 |
| 1:C:521:LEU:HA | 1:D:787:LEU:HD23 | 2.00 | 0.44 |
| 1:D:99:PRO:O | 1:D:114:ARG:HB2 | 2.18 | 0.44 |
| 1:E:189:VAL:O | 1:E:193:LEU:HD13 | 2.17 | 0.44 |
| 1:F:177:MET:HE3 | 1:F:212:ALA:HA | 1.99 | 0.44 |

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| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|---|---|---|---|
| 1:A:201:VAL:O | 1:A:205:VAL:HG23 | 2.18 | 0.44 |
| 1:A:504:ILE:HD12 | 1:A:723:VAL:CG2 | 2.43 | 0.44 |
| 1:C:522:ALA:H | 1:C:525:ILE:HD12 | 1.83 | 0.44 |
| 1:C:814:PHE:HA | 1:C:817:LYS:HD2 | 2.00 | 0.44 |
| 1:F:204:ASP:OD1 | 1:F:205:TYR:N | 2.50 | 0.44 |
| 1:A:79:LYS:O | 1:A:82:VAL:HG12 | 2.18 | 0.44 |
| 1:A:174:ASP:OD2 | 1:A:178:ARG:NH2 | 2.45 | 0.44 |
| 1:B:57:ALA:HA | 1:B:60:ASN:ND2 | 2.33 | 0.44 |
| 1:B:619:ASN:HD22 | 1:C:787:LEU:CD1 | 2.31 | 0.44 |
| 1:C:54:ASN:O | 1:C:58:VAL:HG23 | 2.18 | 0.44 |
| 1:C:100:SER:C | 1:C:114:ARG:HD3 | 2.37 | 0.44 |
| 1:C:227:PHE:CD1 | 1:C:244:GLY:HA3 | 2.53 | 0.44 |
| 1:D:309:ARG:HG2 | 1:D:311:ASN:N | 2.31 | 0.44 |
| 1:A:628:ARG:NH2 | 1:D:628:ARG:H | 2.16 | 0.44 |
| 1:C:384:GLU:O | 1:C:386:ASP:N | 2.50 | 0.44 |
| 1:C:453:ARG:NH2 | 1:C:484:VAL:HB | 2.32 | 0.44 |
| 1:C:526:TRP:HA | 1:C:529:ILE:HG22 | 1.99 | 0.44 |
| 1:C:592:SER:HA | 1:C:593:PRO:HD3 | 1.85 | 0.44 |
| 1:C:629:MET:O | 1:C:630:VAL:C | 2.56 | 0.44 |
| 1:D:50:LEU:HD22 | 1:D:61:ALA:HB2 | 1.98 | 0.44 |
| 1:E:37:ARG:HG2 | 1:E:88:ARG:H | 1.83 | 0.44 |
| 1:B:506:LYS:CG | 1:B:507:PRO:CD | 2.96 | 0.43 |
| 1:C:519:ASP:N | 1:C:520:PRO:CD | 2.81 | 0.43 |
| 1:C:781:LYS:O | 1:C:784:THR:HG23 | 2.17 | 0.43 |
| 1:A:314:ASP:OD1 | 1:A:315:CYS:N | 2.50 | 0.43 |
| 1:A:505:LYS:O | 1:A:506:LYS:HG3 | 2.18 | 0.43 |
| 1:A:800:VAL:HA | 1:A:803:LEU:HD12 | 2.01 | 0.43 |
| 1:C:56:PHE:CZ | 1:D:91:THR:HG21 | 2.53 | 0.43 |
| 1:C:506:LYS:HG2 | 1:C:721:MET:SD | 2.57 | 0.43 |
| 1:D:27:SER:O | 1:D:31:VAL:HG23 | 2.18 | 0.43 |
| 1:F:34:GLY:HA3 | 1:F:90:PHE:HB2 | 2.00 | 0.43 |
| 1:F:195:PRO:O | 1:F:198:TRP:N | 2.51 | 0.43 |
| 1:A:56:PHE:CD1 | 1:B:88:PHE:CE2 | 3.03 | 0.43 |
| 1:B:100:SER:HA | 1:B:114:ARG:NH2 | 2.33 | 0.43 |
| 1:B:266:GLU:HG2 | 1:B:268:LYS:H | 1.83 | 0.43 |
| 1:B:308:ARG:NE | 1:B:323:TRP:HB2 | 2.33 | 0.43 |
| 1:B:541:PHE:CD1 | 1:B:573:ILE:HA | 2.53 | 0.43 |
| 1:C:629:MET:O | 1:C:630:VAL:O | 2.36 | 0.43 |
| 1:D:332:ALA:O | 1:D:336:VAL:HG23 | 2.19 | 0.43 |
| 1:D:540:LEU:HD12 | 1:D:580:SER:HB3 | 2.00 | 0.43 |
| 1:D:541:PHE:CD1 | 1:D:573:ILE:HA | 2.53 | 0.43 |

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| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|---|---|---|---|
| 1:E:117:PRO:O | 1:E:119:SER:N | 2.51 | 0.43 |
| 1:F:227:LEU:O | 1:F:231:THR:HG23 | 2.18 | 0.43 |
| 1:B:619:ASN:HD22 | 1:C:787:LEU:CG | 2.27 | 0.43 |
| 1:C:113:MET:O | 1:C:115:PRO:HD3 | 2.19 | 0.43 |
| 1:C:505:LYS:O | 1:C:506:LYS:HG3 | 2.18 | 0.43 |
| 1:D:135:TYR:O | 1:D:162:ALA:HA | 2.18 | 0.43 |
| 1:D:372:GLY:CA | 1:D:383:THR:HG23 | 2.42 | 0.43 |
| 1:D:374:TRP:CH2 | 1:D:376:GLU:HA | 2.54 | 0.43 |
| 1:E:38:VAL:HB | 1:E:85:PHE:HB2 | 2.00 | 0.43 |
| 1:F:8:ALA:O | 1:F:12:VAL:HG23 | 2.17 | 0.43 |
| 1:A:813:GLU:O | 1:A:817:LYS:HG3 | 2.19 | 0.43 |
| 1:B:197:GLU:O | 1:B:201:VAL:HG23 | 2.17 | 0.43 |
| 1:E:167:VAL:O | 1:E:171:LEU:HG | 2.18 | 0.43 |
| 1:F:37:ARG:HG2 | 1:F:88:ARG:H | 1.82 | 0.43 |
| 1:A:24:GLN:HE22 | 1:A:278:ILE:HA | 1.84 | 0.43 |
| 1:A:101:PHE:HA | 1:A:102:PRO:HD3 | 1.80 | 0.43 |
| 1:A:117:LEU:HD11 | 1:A:245:PHE:CG | 2.53 | 0.43 |
| 1:A:595:SER:HA | 1:A:599:ARG:HE | 1.84 | 0.43 |
| 1:C:24:GLN:HE22 | 1:C:278:ILE:HA | 1.83 | 0.43 |
| 1:D:506:LYS:CG | 1:D:507:PRO:CD | 2.96 | 0.43 |
| 1:A:153:ALA:HA | 1:A:158:TRP:HB2 | 2.00 | 0.43 |
| 1:B:619:ASN:OD1 | 1:C:786:ALA:HB1 | 2.18 | 0.43 |
| 1:B:630:VAL:O | 1:B:630:VAL:HG22 | 2.19 | 0.43 |
| 1:D:137:TYR:CE1 | 1:D:164:ASN:HB2 | 2.54 | 0.43 |
| 1:A:776:LYS:HA | 1:A:776:LYS:HD2 | 1.52 | 0.43 |
| 1:C:316:LEU:HD13 | 1:D:63:CYS:CB | 2.48 | 0.43 |
| 1:C:387:THR:C | 1:C:389:GLY:N | 2.72 | 0.43 |
| 1:C:526:TRP:O | 1:C:529:ILE:HG22 | 2.19 | 0.43 |
| 1:D:201:VAL:O | 1:D:205:VAL:HG23 | 2.19 | 0.43 |
| 1:E:227:LEU:O | 1:E:227:LEU:HD12 | 2.19 | 0.43 |
| 1:A:101:PHE:HA | 1:A:114:ARG:HD3 | 2.00 | 0.43 |
| 1:D:146:LEU:HA | 1:D:149:VAL:HG22 | 1.99 | 0.43 |
| 1:A:54:ASN:O | 1:A:58:VAL:HG23 | 2.18 | 0.42 |
| 1:A:387:THR:C | 1:A:389:GLY:N | 2.72 | 0.42 |
| 1:B:533:TYR:OH | 1:B:581:LEU:HA | 2.19 | 0.42 |
| 1:A:83:ASN:ND2 | 1:B:80:LYS:CA | 2.77 | 0.42 |
| 1:B:105:GLY:O | 1:B:107:HIS:ND1 | 2.52 | 0.42 |
| 1:B:135:TYR:O | 1:B:162:ALA:HA | 2.19 | 0.42 |
| 1:B:156:LYS:O | 1:B:157:LYS:CG | 2.67 | 0.42 |
| 1:B:592:SER:HB3 | 1:B:599:ARG:HG2 | 2.01 | 0.42 |
| 1:D:305:GLU:OE2 | 1:D:307:SER:N | 2.52 | 0.42 |

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| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|---|---|---|---|
| 1:E:223:SER:HA | 1:E:226:THR:HG22 | 2.01 | 0.42 |
| 1:B:98:THR:HA | 1:B:99:PRO:HD3 | 1.79 | 0.42 |
| 1:C:220:TYR:HB2 | 1:C:242:VAL:HG22 | 2.01 | 0.42 |
| 1:C:348:ASP:OD2 | 1:C:350:ASN:HB2 | 2.19 | 0.42 |
| 1:C:410:LYS:H | 1:C:410:LYS:HD2 | 1.84 | 0.42 |
| 1:C:599:ARG:NH1 | 1:D:578:TRP:O | 2.52 | 0.42 |
| 1:D:505:LYS:C | 1:D:506:LYS:O | 2.58 | 0.42 |
| 1:D:744:THR:OG1 | 1:D:745:PRO:CD | 2.68 | 0.42 |
| 1:E:182:MET:O | 1:E:185:GLN:HB3 | 2.20 | 0.42 |
| 1:A:267:GLU:HB2 | 1:A:274:HIS:HB3 | 2.02 | 0.42 |
| 1:A:595:SER:CA | 1:A:599:ARG:HE | 2.32 | 0.42 |
| 1:B:198:ARG:NH2 | 1:B:229:ASP:O | 2.52 | 0.42 |
| 1:B:600:ILE:HA | 1:C:581:LEU:HD21 | 2.01 | 0.42 |
| 1:C:115:PRO:HB3 | 1:C:356:TYR:CD1 | 2.54 | 0.42 |
| 1:E:3:SER:O | 1:E:7:ARG:HG2 | 2.20 | 0.42 |
| 1:A:93:HIS:ND1 | 1:A:322:PRO:HG2 | 2.34 | 0.42 |
| 1:A:308:ARG:HB3 | 1:A:311:ASN:ND2 | 2.33 | 0.42 |
| 1:A:318:ASN:HA | 1:A:319:PRO:HA | 1.96 | 0.42 |
| 1:A:434:LYS:HE2 | 1:A:434:LYS:HB3 | 1.53 | 0.42 |
| 1:B:262:TRP:CZ2 | 1:B:273:ALA:HA | 2.54 | 0.42 |
| 1:B:348:ASP:OD2 | 1:B:350:ASN:HB2 | 2.20 | 0.42 |
| 1:C:83:ASN:HD21 | 1:D:80:LYS:HA | 1.81 | 0.42 |
| 1:C:323:TRP:CZ3 | 1:C:325:GLN:HB2 | 2.55 | 0.42 |
| 1:C:364:LYS:HG3 | 1:C:369:ARG:HH21 | 1.84 | 0.42 |
| 1:C:506:LYS:HE3 | 1:C:721:MET:N | 2.33 | 0.42 |
| 1:D:24:GLN:NE2 | 1:D:278:ILE:HG13 | 2.28 | 0.42 |
| 1:D:131:ASP:OD1 | 1:D:132:LYS:N | 2.53 | 0.42 |
| 1:A:113:MET:O | 1:A:115:PRO:HD3 | 2.20 | 0.42 |
| 1:B:141:ARG:HH22 | 1:B:196:CYS:N | 2.18 | 0.42 |
| 1:B:308:ARG:HE | 1:B:323:TRP:HE3 | 1.67 | 0.42 |
| 1:D:299:LEU:HD23 | 1:D:306:ILE:HG21 | 2.01 | 0.42 |
| 1:E:134:TYR:O | 1:E:138:LEU:HG | 2.20 | 0.42 |
| 1:C:502:ILE:HG12 | 1:C:703:LEU:HD21 | 2.00 | 0.42 |
| 1:D:498:LEU:C | 1:D:498:LEU:HD22 | 2.40 | 0.42 |
| 1:A:41:PHE:CE2 | 1:A:297:ARG:HD2 | 2.55 | 0.42 |
| 1:A:198:ARG:HA | 1:A:201:VAL:HB | 2.01 | 0.42 |
| 1:A:464:VAL:O | 1:A:468:VAL:HG23 | 2.20 | 0.42 |
| 1:B:505:LYS:C | 1:B:506:LYS:O | 2.58 | 0.42 |
| 1:C:498:LEU:C | 1:C:498:LEU:HD22 | 2.40 | 0.42 |
| 1:C:503:MET:O | 1:C:503:MET:HG2 | 2.17 | 0.42 |
| 1:D:334:LYS:HA | 1:D:347:PHE:HD2 | 1.84 | 0.42 |

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| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|---|---|---|---|
| 1:A:742:LEU:C | 1:A:745:PRO:HD2 | 2.38 | 0.42 |
| 1:B:212:GLY:CA | 1:D:214:HIS:HE1 | 2.33 | 0.42 |
| 1:B:754:SER:HB3 | 1:B:759:LEU:HD12 | 2.02 | 0.42 |
| 1:C:26:TYR:CE2 | 1:C:30:ARG:HD2 | 2.54 | 0.42 |
| 1:E:10:LEU:O | 1:E:14:LEU:HG | 2.20 | 0.42 |
| 1:E:34:GLY:HA2 | 1:E:202:SER:HB2 | 2.02 | 0.42 |
| 1:A:197:GLU:O | 1:A:201:VAL:HG23 | 2.20 | 0.42 |
| 1:A:634:GLU:HG3 | 1:A:723:VAL:CB | 2.31 | 0.42 |
| 1:B:392:GLN:CD | 1:B:437:GLY:O | 2.58 | 0.42 |
| 1:B:464:VAL:O | 1:B:468:VAL:HG23 | 2.20 | 0.42 |
| 1:B:518:LEU:HD22 | 1:B:526:TRP:CE2 | 2.55 | 0.42 |
| 1:C:30:ARG:NH2 | 1:C:269:GLU:OE2 | 2.53 | 0.42 |
| 1:E:195:PRO:O | 1:E:198:TRP:N | 2.52 | 0.42 |
| 1:F:117:PRO:HG3 | 1:F:193:LEU:HD21 | 2.01 | 0.42 |
| 1:B:619:ASN:HD21 | 1:C:786:ALA:CB | 2.28 | 0.41 |
| 1:B:721:MET:HG3 | 1:B:776:LYS:CE | 2.46 | 0.41 |
| 1:C:383:THR:HG22 | 1:C:385:ASP:H | 1.85 | 0.41 |
| 1:C:666:VAL:HG13 | 1:C:667:PHE:N | 2.36 | 0.41 |
| 1:D:347:PHE:HE1 | 1:D:353:ARG:HG2 | 1.85 | 0.41 |
| 1:E:31:TRP:CE2 | 1:E:183:TYR:HE2 | 2.37 | 0.41 |
| 1:E:194:GLY:O | 1:E:196:GLU:N | 2.53 | 0.41 |
| 1:F:178:VAL:O | 1:F:182:MET:HG2 | 2.19 | 0.41 |
| 1:A:345:ILE:HG12 | 1:A:353:ARG:NH2 | 2.35 | 0.41 |
| 1:B:198:ARG:HG2 | 1:B:279:LYS:NZ | 2.33 | 0.41 |
| 1:C:340:GLY:N | 1:C:343:GLY:O | 2.43 | 0.41 |
| 1:C:595:SER:H | 1:C:599:ARG:NE | 2.05 | 0.41 |
| 1:C:644:GLU:CG | 1:C:645:ILE:HG13 | 2.49 | 0.41 |
| 1:E:21:PHE:HB3 | 1:E:211:LEU:HA | 2.02 | 0.41 |
| 1:E:190:THR:O | 1:E:195:PRO:HG3 | 2.20 | 0.41 |
| 1:F:34:GLY:HA2 | 1:F:202:SER:HB2 | 2.02 | 0.41 |
| 1:F:182:MET:O | 1:F:185:GLN:HB3 | 2.20 | 0.41 |
| 1:F:223:SER:HA | 1:F:226:THR:HG22 | 2.01 | 0.41 |
| 1:A:348:ASP:OD1 | 1:A:351:GLY:N | 2.53 | 0.41 |
| 1:A:666:VAL:HG13 | 1:A:667:PHE:N | 2.35 | 0.41 |
| 1:B:76:PHE:CE1 | 1:B:99:PRO:HG2 | 2.54 | 0.41 |
| 1:B:498:LEU:C | 1:B:498:LEU:HD22 | 2.40 | 0.41 |
| 1:C:575:ASN:O | 1:C:578:TRP:HB2 | 2.20 | 0.41 |
| 1:D:323:TRP:CZ3 | 1:D:325:GLN:HB2 | 2.55 | 0.41 |
| 1:D:464:VAL:O | 1:D:468:VAL:HG23 | 2.20 | 0.41 |
| 1:D:666:VAL:HG13 | 1:D:667:PHE:N | 2.35 | 0.41 |
| 1:D:721:MET:HE2 | 1:D:723:VAL:HG12 | 2.01 | 0.41 |

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| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|---|---|---|---|
| 1:A:498:LEU:C | 1:A:498:LEU:HD22 | 2.40 | 0.41 |
| 1:A:502:ILE:HG22 | 1:A:504:ILE:HG23 | 2.03 | 0.41 |
| 1:B:127:TYR:HB2 | 1:B:380:MET:SD | 2.60 | 0.41 |
| 1:B:212:GLY:CA | 1:D:214:HIS:CE1 | 3.04 | 0.41 |
| 1:B:215:VAL:CG1 | 1:D:215:VAL:HG11 | 2.46 | 0.41 |
| 1:B:591:ILE:HG23 | 1:B:591:ILE:O | 2.21 | 0.41 |
| 1:D:250:TYR:OH | 1:D:277:THR:HB | 2.21 | 0.41 |
| 1:E:195:PRO:O | 1:E:197:ASP:N | 2.53 | 0.41 |
| 1:A:76:PHE:CD1 | 1:A:99:PRO:HD2 | 2.56 | 0.41 |
| 1:A:209:ILE:HA | 1:A:214:HIS:HD2 | 1.86 | 0.41 |
| 1:A:383:THR:HG22 | 1:A:385:ASP:H | 1.85 | 0.41 |
| 1:A:592:SER:HA | 1:A:593:PRO:HD3 | 1.88 | 0.41 |
| 1:A:678:GLU:HA | 1:A:679:PRO:C | 2.41 | 0.41 |
| 1:A:754:SER:HB3 | 1:A:759:LEU:HD12 | 2.02 | 0.41 |
| 1:B:287:ASP:CG | 1:B:341:LEU:H | 2.24 | 0.41 |
| 1:B:453:ARG:HG3 | 1:B:460:TRP:CE2 | 2.55 | 0.41 |
| 1:C:344:ASN:HD21 | 1:C:346:LYS:CE | 2.30 | 0.41 |
| 1:D:100:SER:HA | 1:D:114:ARG:NH2 | 2.35 | 0.41 |
| 1:A:220:TYR:HB2 | 1:A:242:VAL:HG22 | 2.01 | 0.41 |
| 1:B:115:PRO:HG3 | 1:B:353:ARG:CZ | 2.51 | 0.41 |
| 1:B:185:GLU:OE2 | 1:B:213:LYS:NZ | 2.38 | 0.41 |
| 1:B:666:VAL:HG13 | 1:B:667:PHE:N | 2.36 | 0.41 |
| 1:C:306:ILE:HD12 | 1:C:329:ILE:HD11 | 2.03 | 0.41 |
| 1:C:330:GLU:HG2 | 1:C:334:LYS:HE3 | 2.02 | 0.41 |
| 1:C:577:LEU:O | 1:C:580:SER:OG | 2.30 | 0.41 |
| 1:D:10:ASN:N | 1:D:41:PHE:HA | 2.35 | 0.41 |
| 1:F:99:GLU:OE2 | 1:F:108:LYS:HD2 | 2.21 | 0.41 |
| 1:A:87:SER:OG | 1:B:56:PHE:N | 2.38 | 0.41 |
| 1:A:362:GLU:O | 1:A:369:ARG:N | 2.50 | 0.41 |
| 1:A:575:ASN:O | 1:A:578:TRP:HB2 | 2.20 | 0.41 |
| 1:B:228:THR:OG1 | 1:B:246:GLN:OE1 | 2.20 | 0.41 |
| 1:B:678:GLU:HA | 1:B:679:PRO:C | 2.41 | 0.41 |
| 1:C:464:VAL:O | 1:C:468:VAL:HG23 | 2.20 | 0.41 |
| 1:C:754:SER:HB3 | 1:C:759:LEU:HD12 | 2.02 | 0.41 |
| 1:E:159:LEU:CD1 | 1:E:229:SER:HB3 | 2.51 | 0.41 |
| 1:F:116:ALA:HA | 1:F:117:PRO:HA | 1.80 | 0.41 |
| 1:A:39:SER:HA | 1:A:42:ARG:NH2 | 2.36 | 0.41 |
| 1:A:718:CYS:SG | 1:A:718:CYS:O | 2.79 | 0.41 |
| 1:B:99:PRO:O | 1:B:114:ARG:HB2 | 2.20 | 0.41 |
| 1:B:744:THR:OG1 | 1:B:745:PRO:CD | 2.67 | 0.41 |
| 1:C:744:THR:OG1 | 1:C:745:PRO:CD | 2.68 | 0.41 |

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| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|---|---|---|---|
| 1:A:79:LYS:HB3 | 1:A:101:PHE:HZ | 1.85 | 0.41 |
| 1:A:359:ASN:HA | 1:A:373:TYR:HA | 2.03 | 0.41 |
| 1:A:372:GLY:HA2 | 1:A:383:THR:OG1 | 2.20 | 0.41 |
| 1:A:708:MET:O | 1:A:712:ILE:HG12 | 2.21 | 0.41 |
| 1:B:207:GLN:O | 1:B:211:ILE:HG12 | 2.21 | 0.41 |
| 1:B:325:GLN:O | 1:B:329:ILE:HG13 | 2.21 | 0.41 |
| 1:B:708:MET:O | 1:B:712:ILE:HG12 | 2.21 | 0.41 |
| 1:C:56:PHE:N | 1:D:87:SER:OG | 2.46 | 0.41 |
| 1:C:332:ALA:O | 1:C:336:VAL:HG23 | 2.20 | 0.41 |
| 1:C:453:ARG:HH21 | 1:C:484:VAL:HB | 1.86 | 0.41 |
| 1:C:503:MET:HB2 | 1:C:709:ASN:CG | 2.36 | 0.41 |
| 1:C:506:LYS:CG | 1:C:721:MET:CB | 2.95 | 0.41 |
| 1:C:634:GLU:HA | 1:C:723:VAL:HG21 | 2.02 | 0.41 |
| 1:D:57:ALA:HA | 1:D:60:ASN:ND2 | 2.35 | 0.41 |
| 1:D:512:PRO:HB2 | 1:D:516:SER:HG | 1.70 | 0.41 |
| 1:E:99:GLU:OE2 | 1:E:108:LYS:HD2 | 2.21 | 0.41 |
| 1:F:134:TYR:O | 1:F:138:LEU:HG | 2.21 | 0.41 |
| 1:B:27:SER:HB3 | 1:B:270:TYR:HB3 | 2.03 | 0.41 |
| 1:B:172:LYS:O | 1:B:174:ASP:N | 2.54 | 0.41 |
| 1:B:523:TYR:HA | 1:B:526:TRP:CD1 | 2.46 | 0.41 |
| 1:E:174:LEU:O | 1:E:178:VAL:HG23 | 2.21 | 0.41 |
| 1:A:175:GLU:HA | 1:A:178:ARG:HH11 | 1.86 | 0.40 |
| 1:A:246:GLN:HB2 | 1:A:361:MET:HG3 | 2.03 | 0.40 |
| 1:A:392:GLN:O | 1:A:394:THR:N | 2.54 | 0.40 |
| 1:A:425:CYS:SG | 1:A:477:ALA:HA | 2.61 | 0.40 |
| 1:B:128:TYR:HB3 | 1:B:130:TRP:NE1 | 2.36 | 0.40 |
| 1:B:190:ARG:HA | 1:B:218:TYR:CD1 | 2.56 | 0.40 |
| 1:C:93:HIS:HB3 | 1:C:327:VAL:HG22 | 2.03 | 0.40 |
| 1:C:209:ILE:HA | 1:C:214:HIS:HD2 | 1.86 | 0.40 |
| 1:C:348:ASP:OD1 | 1:C:351:GLY:N | 2.55 | 0.40 |
| 1:C:540:LEU:HD12 | 1:C:580:SER:HB3 | 2.02 | 0.40 |
| 1:D:231:ASP:HB3 | 1:D:234:LYS:HE3 | 2.02 | 0.40 |
| 1:D:371:ILE:O | 1:D:383:THR:OG1 | 2.25 | 0.40 |
| 1:D:743:GLY:C | 1:D:745:PRO:HD2 | 2.41 | 0.40 |
| 1:D:754:SER:HB3 | 1:D:759:LEU:HD12 | 2.02 | 0.40 |
| 1:F:167:VAL:O | 1:F:171:LEU:HG | 2.21 | 0.40 |
| 1:A:112:GLN:NE2 | 1:A:352:LYS:HG2 | 2.36 | 0.40 |
| 1:A:247:ILE:HD13 | 1:A:358:ILE:HG12 | 2.02 | 0.40 |
| 1:A:577:LEU:O | 1:A:580:SER:OG | 2.32 | 0.40 |
| 1:B:50:LEU:HD23 | 1:B:57:ALA:HB1 | 2.03 | 0.40 |
| 1:B:118:LYS:NZ | 1:B:144:SER:OG | 2.54 | 0.40 |

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| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|---|---|---|---|
| 1:B:196:CYS:HB3 | 1:B:200:LYS:HB2 | 2.04 | 0.40 |
| 1:C:79:LYS:O | 1:C:82:VAL:HG12 | 2.21 | 0.40 |
| 1:D:425:CYS:SG | 1:D:477:ALA:HA | 2.62 | 0.40 |
| 1:D:678:GLU:HA | 1:D:679:PRO:C | 2.41 | 0.40 |
| 1:E:116:ALA:HA | 1:E:117:PRO:HA | 1.81 | 0.40 |
| 1:F:38:VAL:HB | 1:F:85:PHE:HB2 | 2.03 | 0.40 |
| 1:F:187:PHE:O | 1:F:190:THR:OG1 | 2.26 | 0.40 |
| 1:A:26:TYR:CE2 | 1:A:30:ARG:HD2 | 2.56 | 0.40 |
| 1:B:215:VAL:HA | 1:B:238:GLY:O | 2.22 | 0.40 |
| 1:B:489:ILE:HD12 | 1:B:735:ALA:HB1 | 2.03 | 0.40 |
| 1:B:521:LEU:HA | 1:C:787:LEU:HD12 | 2.03 | 0.40 |
| 1:C:116:ASP:OD1 | 1:C:118:LYS:HG2 | 2.21 | 0.40 |
| 1:C:425:CYS:SG | 1:C:477:ALA:HA | 2.62 | 0.40 |
| 1:C:489:ILE:HD12 | 1:C:735:ALA:HB1 | 2.03 | 0.40 |
| 1:C:678:GLU:HA | 1:C:679:PRO:C | 2.41 | 0.40 |
| 1:D:489:ILE:HD12 | 1:D:735:ALA:HB1 | 2.03 | 0.40 |
| 1:D:799:LEU:O | 1:D:803:LEU:HG | 2.21 | 0.40 |
| 1:F:3:SER:O | 1:F:7:ARG:HG2 | 2.21 | 0.40 |
| 1:A:532:ALA:O | 1:A:536:VAL:HG23 | 2.21 | 0.40 |
| 1:A:803:LEU:O | 1:A:807:MET:HG2 | 2.21 | 0.40 |
| 1:D:16:GLY:H | 1:D:65:GLN:NE2 | 2.14 | 0.40 |
| 1:D:416:GLU:OE1 | 1:D:417:GLY:N | 2.39 | 0.40 |
| 1:D:708:MET:O | 1:D:712:ILE:HG12 | 2.21 | 0.40 |
| 1:A:671:TRP:O | 1:A:675:ARG:HG2 | 2.22 | 0.40 |
| 1:B:743:GLY:C | 1:B:745:PRO:HD2 | 2.42 | 0.40 |
| 1:C:708:MET:O | 1:C:712:ILE:HG12 | 2.21 | 0.40 |
| 1:F:25:ALA:HB3 | 1:F:211:LEU:HD22 | 2.03 | 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 | A | 779/1057 (74%) | 716 (92%) | 47 (6%) | 16 (2%) | 7 | 36 |
| 1 | B | 776/1057 (73%) | 723 (93%) | 39 (5%) | 14 (2%) | 8 | 40 |
| 1 | C | 779/1057 (74%) | 716 (92%) | 45 (6%) | 18 (2%) | 6 | 34 |
| 1 | D | 776/1057 (73%) | 723 (93%) | 35 (4%) | 18 (2%) | 6 | 34 |
| 1 | E | 171/1057 (16%) | 156 (91%) | 7 (4%) | 8 (5%) | 2 | 21 |
| 1 | F | 171/1057 (16%) | 156 (91%) | 7 (4%) | 8 (5%) | 2 | 21 |
| All | All | 3452/6342 (54%) | 3190 (92%) | 180 (5%) | 82 (2%) | 9 | 33 |

All (82) Ramachandran outliers are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 1 | A | 385 | ASP |
| 1 | A | 456 | ASP |
| 1 | A | 514 | VAL |
| 1 | A | 630 | VAL |
| 1 | A | 776 | LYS |
| 1 | B | 456 | ASP |
| 1 | B | 506 | LYS |
| 1 | B | 507 | PRO |
| 1 | B | 512 | PRO |
| 1 | B | 631 | SER |
| 1 | B | 632 | PRO |
| 1 | B | 786 | ALA |
| 1 | C | 385 | ASP |
| 1 | C | 456 | ASP |
| 1 | C | 514 | VAL |
| 1 | C | 591 | ILE |
| 1 | C | 630 | VAL |
| 1 | C | 776 | LYS |
| 1 | D | 456 | ASP |
| 1 | D | 506 | LYS |
| 1 | D | 507 | PRO |
| 1 | D | 512 | PRO |
| 1 | D | 590 | ASP |
| 1 | D | 591 | ILE |
| 1 | D | 631 | SER |
| 1 | D | 632 | PRO |
| 1 | D | 635 | SER |
| 1 | A | 591 | ILE |
| 1 | A | 633 | ILE |
| 1 | A | 785 | SER |

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| Mol | Chain | Res | Type |
|---|---|---|---|
| 1 | B | 587 | GLN |
| 1 | B | 595 | SER |
| 1 | B | 630 | VAL |
| 1 | C | 174 | ASP |
| 1 | C | 587 | GLN |
| 1 | C | 633 | ILE |
| 1 | C | 785 | SER |
| 1 | D | 520 | PRO |
| 1 | D | 587 | GLN |
| 1 | D | 595 | SER |
| 1 | D | 596 | LEU |
| 1 | E | 111 | SER |
| 1 | E | 117 | PRO |
| 1 | E | 118 | ALA |
| 1 | E | 196 | GLU |
| 1 | E | 203 | TRP |
| 1 | F | 111 | SER |
| 1 | F | 118 | ALA |
| 1 | F | 196 | GLU |
| 1 | F | 203 | TRP |
| 1 | A | 587 | GLN |
| 1 | A | 594 | ARG |
| 1 | A | 595 | SER |
| 1 | A | 786 | ALA |
| 1 | A | 787 | LEU |
| 1 | B | 173 | LYS |
| 1 | B | 174 | ASP |
| 1 | B | 590 | ASP |
| 1 | C | 173 | LYS |
| 1 | C | 594 | ARG |
| 1 | C | 595 | SER |
| 1 | C | 786 | ALA |
| 1 | C | 787 | LEU |
| 1 | D | 786 | ALA |
| 1 | F | 117 | PRO |
| 1 | A | 174 | ASP |
| 1 | A | 775 | ALA |
| 1 | C | 590 | ASP |
| 1 | C | 775 | ALA |
| 1 | D | 594 | ARG |
| 1 | A | 394 | THR |
| 1 | C | 394 | THR |

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| Mol | Chain | Res | Type |
|---|---|---|---|
| 1 | F | 112 | PHE |
| 1 | B | 594 | ARG |
| 1 | E | 112 | PHE |
| 1 | E | 194 | GLY |
| 1 | D | 630 | VAL |
| 1 | F | 194 | GLY |
| 1 | E | 195 | PRO |
| 1 | F | 195 | PRO |
| 1 | D | 514 | VAL |
| 1 | D | 593 | PRO |

### 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 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 | A | 666/888 (75%) | 648 (97%) | 18 (3%) | 44 | 65 |
| 1 | B | 664/888 (75%) | 645 (97%) | 19 (3%) | 42 | 64 |
| 1 | C | 666/888 (75%) | 648 (97%) | 18 (3%) | 44 | 65 |
| 1 | D | 664/888 (75%) | 652 (98%) | 12 (2%) | 59 | 77 |
| 1 | E | 152/888 (17%) | 151 (99%) | 1 (1%) | 84 | 90 |
| 1 | F | 152/888 (17%) | 152 (100%) | 0 | 100 | 100 |
| All | All | 2964/5328 (56%) | 2896 (98%) | 68 (2%) | 53 | 70 |

All (68) residues with a non-rotameric sidechain are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 1 | A | 369 | ARG |
| 1 | A | 388 | SER |
| 1 | A | 390 | LEU |
| 1 | A | 391 | GLU |
| 1 | A | 404 | PRO |
| 1 | A | 416 | GLU |
| 1 | A | 434 | LYS |
| 1 | A | 453 | ARG |

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| Mol | Chain | Res | Type |
|---|---|---|---|
| 1 | A | 498 | LEU |
| 1 | A | 504 | ILE |
| 1 | A | 505 | LYS |
| 1 | A | 509 | LYS |
| 1 | A | 511 | LYS |
| 1 | A | 630 | VAL |
| 1 | A | 661 | ARG |
| 1 | A | 663 | LYS |
| 1 | A | 708 | MET |
| 1 | A | 773 | CYS |
| 1 | B | 384 | GLU |
| 1 | B | 385 | ASP |
| 1 | B | 393 | LYS |
| 1 | B | 404 | PRO |
| 1 | B | 416 | GLU |
| 1 | B | 434 | LYS |
| 1 | B | 453 | ARG |
| 1 | B | 498 | LEU |
| 1 | B | 503 | MET |
| 1 | B | 508 | GLN |
| 1 | B | 628 | ARG |
| 1 | B | 629 | MET |
| 1 | B | 633 | ILE |
| 1 | B | 634 | GLU |
| 1 | B | 661 | ARG |
| 1 | B | 663 | LYS |
| 1 | B | 684 | ARG |
| 1 | B | 708 | MET |
| 1 | B | 789 | LEU |
| 1 | C | 388 | SER |
| 1 | C | 390 | LEU |
| 1 | C | 404 | PRO |
| 1 | C | 410 | LYS |
| 1 | C | 416 | GLU |
| 1 | C | 434 | LYS |
| 1 | C | 498 | LEU |
| 1 | C | 503 | MET |
| 1 | C | 504 | ILE |
| 1 | C | 505 | LYS |
| 1 | C | 509 | LYS |
| 1 | C | 511 | LYS |
| 1 | C | 630 | VAL |

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| Mol | Chain | Res | Type |
|---|---|---|---|
| 1 | C | 644 | GLU |
| 1 | C | 663 | LYS |
| 1 | C | 684 | ARG |
| 1 | C | 708 | MET |
| 1 | C | 773 | CYS |
| 1 | D | 384 | GLU |
| 1 | D | 385 | ASP |
| 1 | D | 393 | LYS |
| 1 | D | 404 | PRO |
| 1 | D | 416 | GLU |
| 1 | D | 434 | LYS |
| 1 | D | 498 | LEU |
| 1 | D | 508 | GLN |
| 1 | D | 633 | ILE |
| 1 | D | 644 | GLU |
| 1 | D | 663 | LYS |
| 1 | D | 708 | MET |
| 1 | E | 227 | LEU |

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (49) such sidechains are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 1 | A | 24 | GLN |
| 1 | A | 46 | HIS |
| 1 | A | 65 | GLN |
| 1 | A | 83 | ASN |
| 1 | A | 246 | GLN |
| 1 | A | 311 | ASN |
| 1 | A | 412 | HIS |
| 1 | A | 435 | HIS |
| 1 | A | 587 | GLN |
| 1 | A | 619 | ASN |
| 1 | B | 24 | GLN |
| 1 | B | 65 | GLN |
| 1 | B | 83 | ASN |
| 1 | B | 214 | HIS |
| 1 | B | 325 | GLN |
| 1 | B | 355 | ASN |
| 1 | B | 392 | GLN |
| 1 | B | 412 | HIS |
| 1 | B | 435 | HIS |
| 1 | B | 587 | GLN |

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| Mol | Chain | Res | Type |
|---|---|---|---|
| 1 | B | 619 | ASN |
| 1 | C | 24 | GLN |
| 1 | C | 46 | HIS |
| 1 | C | 65 | GLN |
| 1 | C | 83 | ASN |
| 1 | C | 112 | GLN |
| 1 | C | 246 | GLN |
| 1 | C | 311 | ASN |
| 1 | C | 325 | GLN |
| 1 | C | 337 | GLN |
| 1 | C | 344 | ASN |
| 1 | C | 355 | ASN |
| 1 | C | 412 | HIS |
| 1 | C | 435 | HIS |
| 1 | C | 587 | GLN |
| 1 | C | 619 | ASN |
| 1 | D | 24 | GLN |
| 1 | D | 65 | GLN |
| 1 | D | 83 | ASN |
| 1 | D | 214 | HIS |
| 1 | D | 355 | ASN |
| 1 | D | 392 | GLN |
| 1 | D | 412 | HIS |
| 1 | D | 435 | HIS |
| 1 | D | 587 | GLN |
| 1 | E | 15 | ASN |
| 1 | E | 180 | HIS |
| 1 | F | 15 | ASN |
| 1 | F | 180 | HIS |

### 5.3.3 RNA

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains

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

## 5.5 Carbohydrates

There are no monosaccharides in this entry.

## 5.6 Ligand geometry (i)

4 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 | QUS | B | 1101 | - | 6,13,13 | 1.25 | 0 | 4,18,18 | 1.40 | 0 |
| 2 | QUS | A | 1101 | - | 6,13,13 | 1.26 | 0 | 4,18,18 | 1.39 | 0 |
| 2 | QUS | D | 1101 | - | 6,13,13 | 1.26 | 0 | 4,18,18 | 1.40 | 0 |
| 2 | QUS | C | 1101 | - | 6,13,13 | 1.25 | 0 | 4,18,18 | 1.40 | 0 |

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 | QUS | B | 1101 | - | - | 2/6/8/8 | 0/1/1/1 |
| 2 | QUS | A | 1101 | - | - | 2/6/8/8 | 0/1/1/1 |
| 2 | QUS | D | 1101 | - | - | 2/6/8/8 | 0/1/1/1 |
| 2 | QUS | C | 1101 | - | - | 2/6/8/8 | 0/1/1/1 |

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (8) torsion outliers are listed below:

| Mol | Chain | Res | Type | Atoms |
|---|---|---|---|---|
| 2 | A | 1101 | QUS | C01-C02-C03-N14 |
| 2 | B | 1101 | QUS | C01-C02-C03-N14 |
| 2 | C | 1101 | QUS | C01-C02-C03-N14 |
| 2 | D | 1101 | QUS | C01-C02-C03-N14 |
| 2 | A | 1101 | QUS | NP3-C02-C03-N14 |
| 2 | B | 1101 | QUS | NP3-C02-C03-N14 |
| 2 | C | 1101 | QUS | NP3-C02-C03-N14 |

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| Mol | Chain | Res | Type | Atoms |
|---|---|---|---|---|
| 2 | D | 1101 | QUS | NP3-C02-C03-N14 |

There are no ring outliers.

No monomer is involved in short contacts.

## 5.7 Other polymers (i)

There are no such residues in this entry.

## 5.8 Polymer linkage issues (i)

The following chains have linkage breaks:

| Mol | Chain | Number of breaks |
|---|---|---|
| 1 | D | 1 |

All chain breaks are listed below:

| Model | Chain | Residue-1 | Atom-1 | Residue-2 | Atom-2 | Distance (Å) |
|---|---|---|---|---|---|---|
| 1 | D | 786:ALA | C | 787:LEU | N | 1.07 |

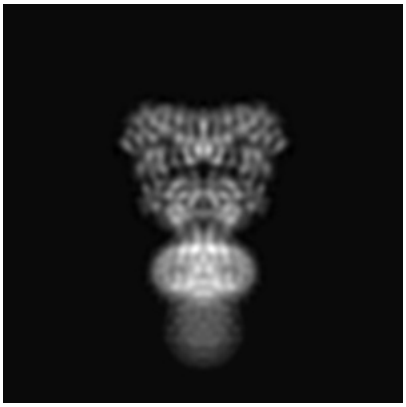
# 6 Map visualisation

This section contains visualisations of the EMDB entry EMD-8688. These allow visual inspection of the internal detail of the map and identification of artifacts.

No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

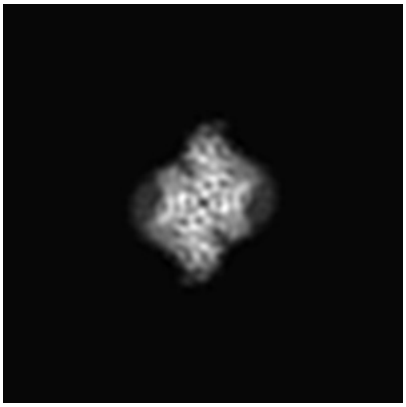
## 6.1 Orthogonal projections

### 6.1.1 Primary map



X

Y



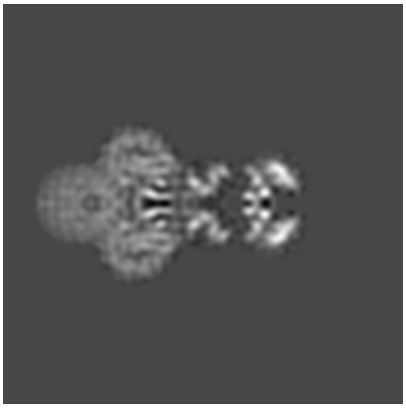
Z

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

## 6.2 Central slices

### 6.2.1 Primary map

X Index: 180



Y Index: 180

Z Index: 180

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: 180

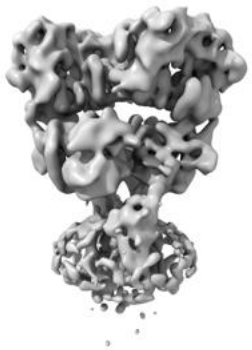
Y Index: 189

Z Index: 227

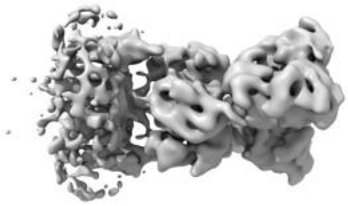
The images above show the largest variance slices of the map in three orthogonal directions.

## 6.4 Orthogonal surface views (i)

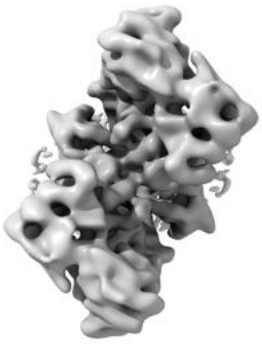
### 6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.015. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

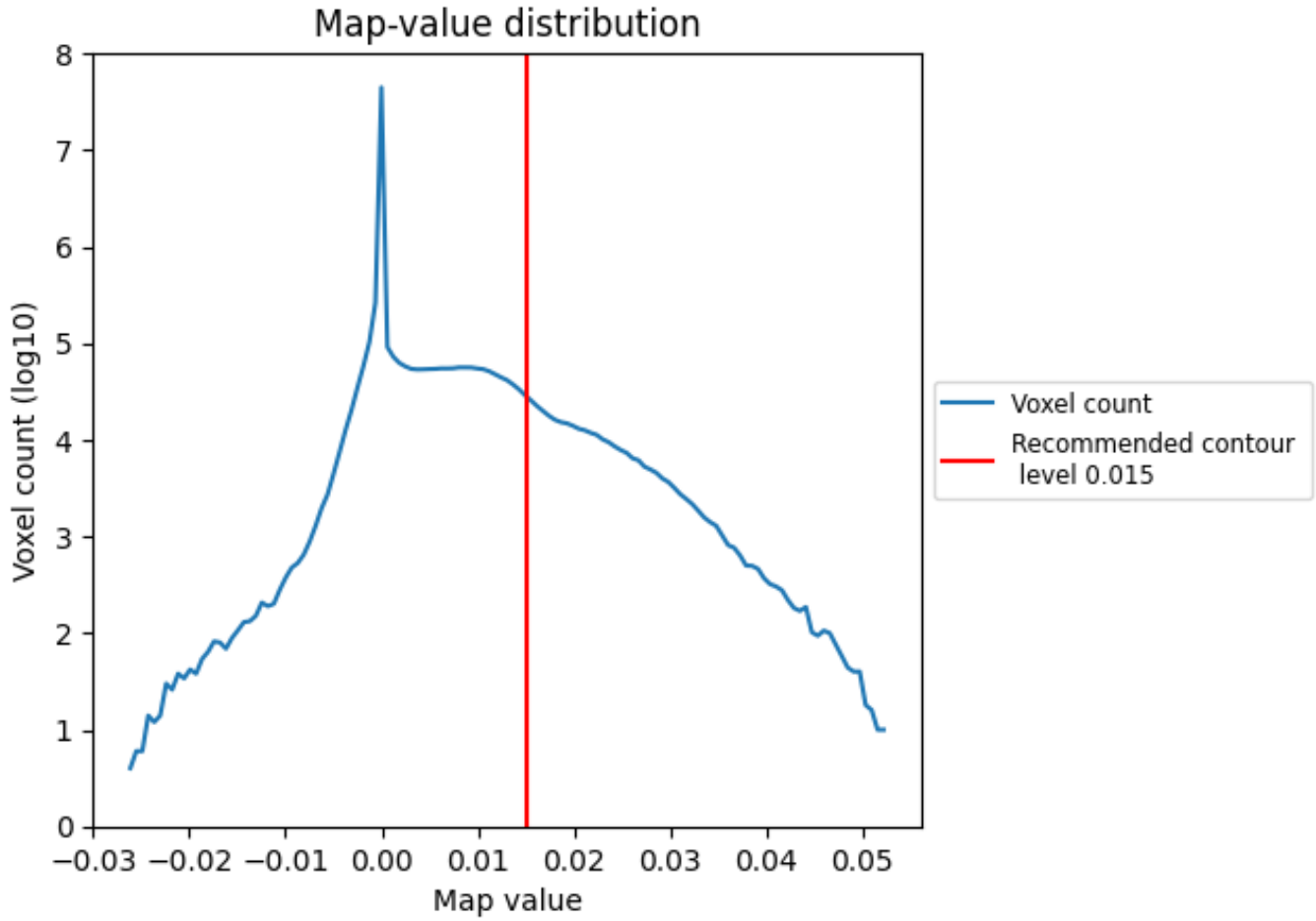
## 6.5 Mask visualisation (i)

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

# 7 Map analysis

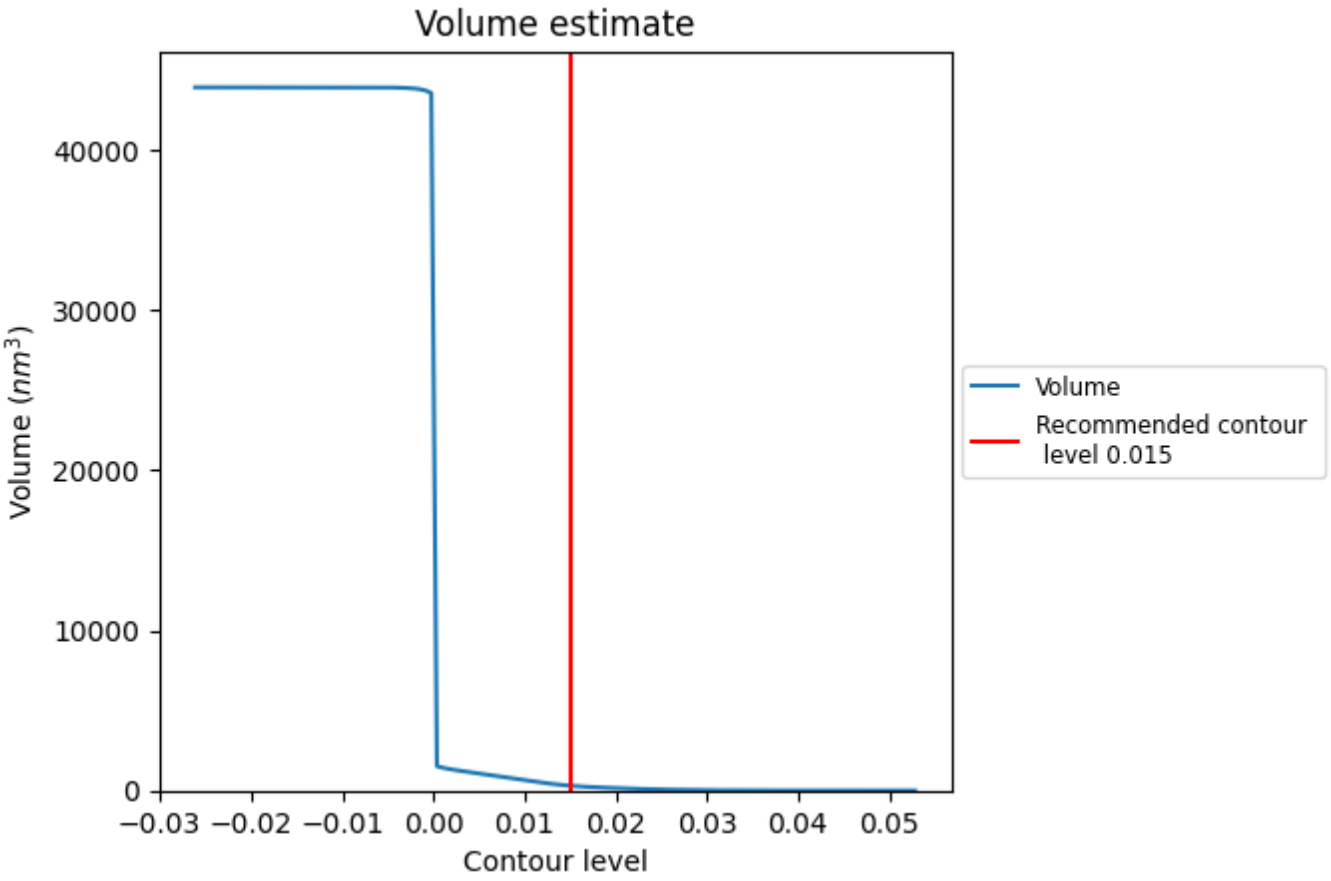
This section contains the results of statistical analysis of the map.

## 7.1 Map-value distribution




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.

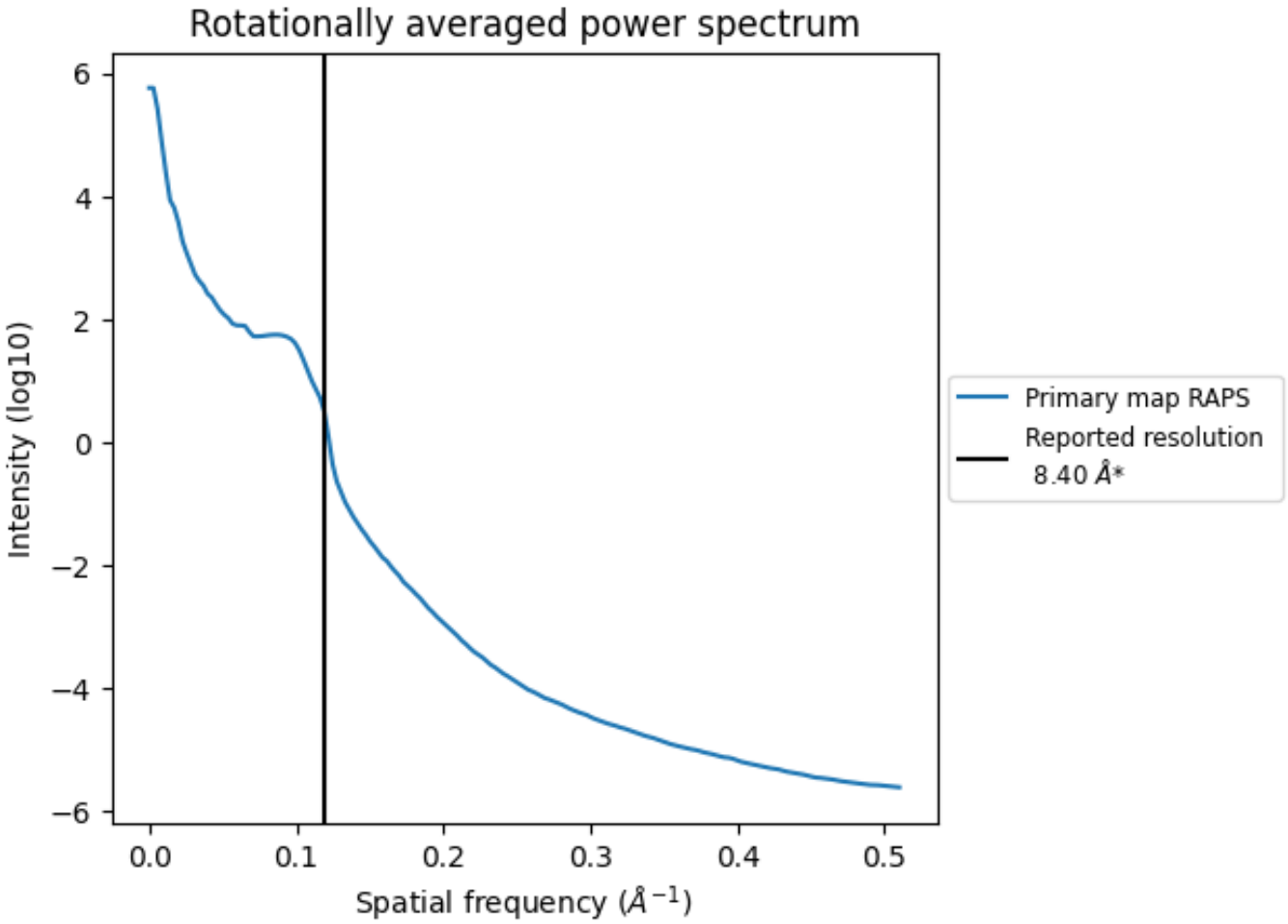
## 7.2 Volume estimate




The volume at the recommended contour level is 303 $nm^3$; this corresponds to an approximate mass of 274 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 (i)




*Reported resolution corresponds to spatial frequency of 0.119 Å$^{-1}$

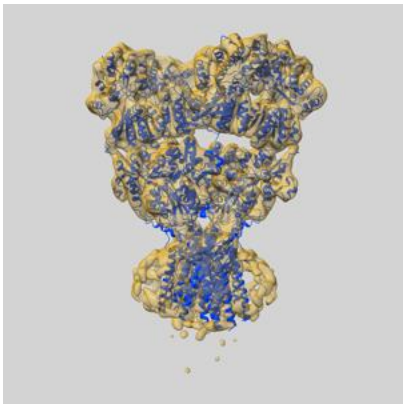
# 8 Fourier-Shell correlation (i)

This section was not generated. No FSC curve or half-maps provided.

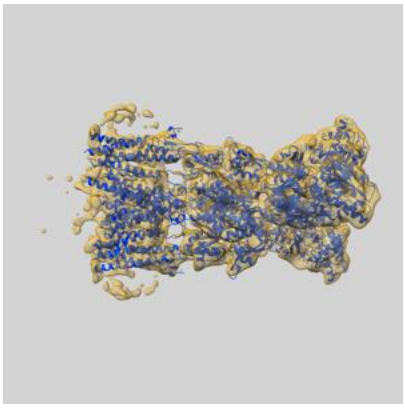
# 9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-8688 and PDB model 5VHZ. Per-residue inclusion information can be found in section 3 on page 7.

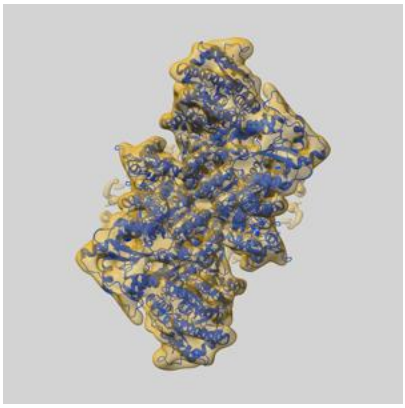
## 9.1 Map-model overlay



X



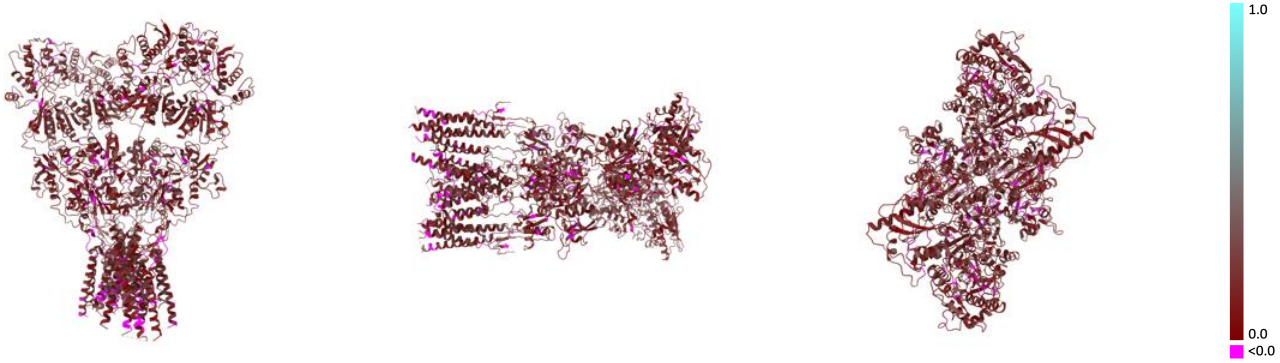
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.015 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

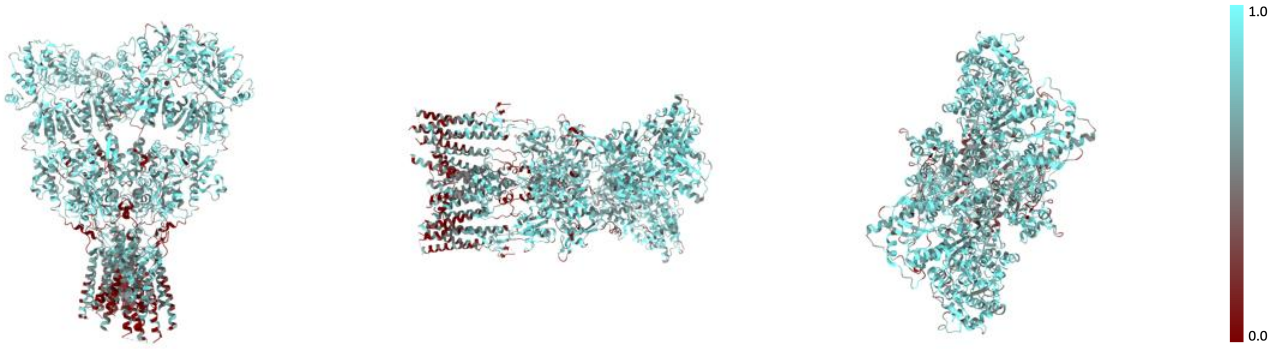
## 9.2 Q-score mapped to coordinate model (i)




X Y Z

The images above show the model with each residue coloured according 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.

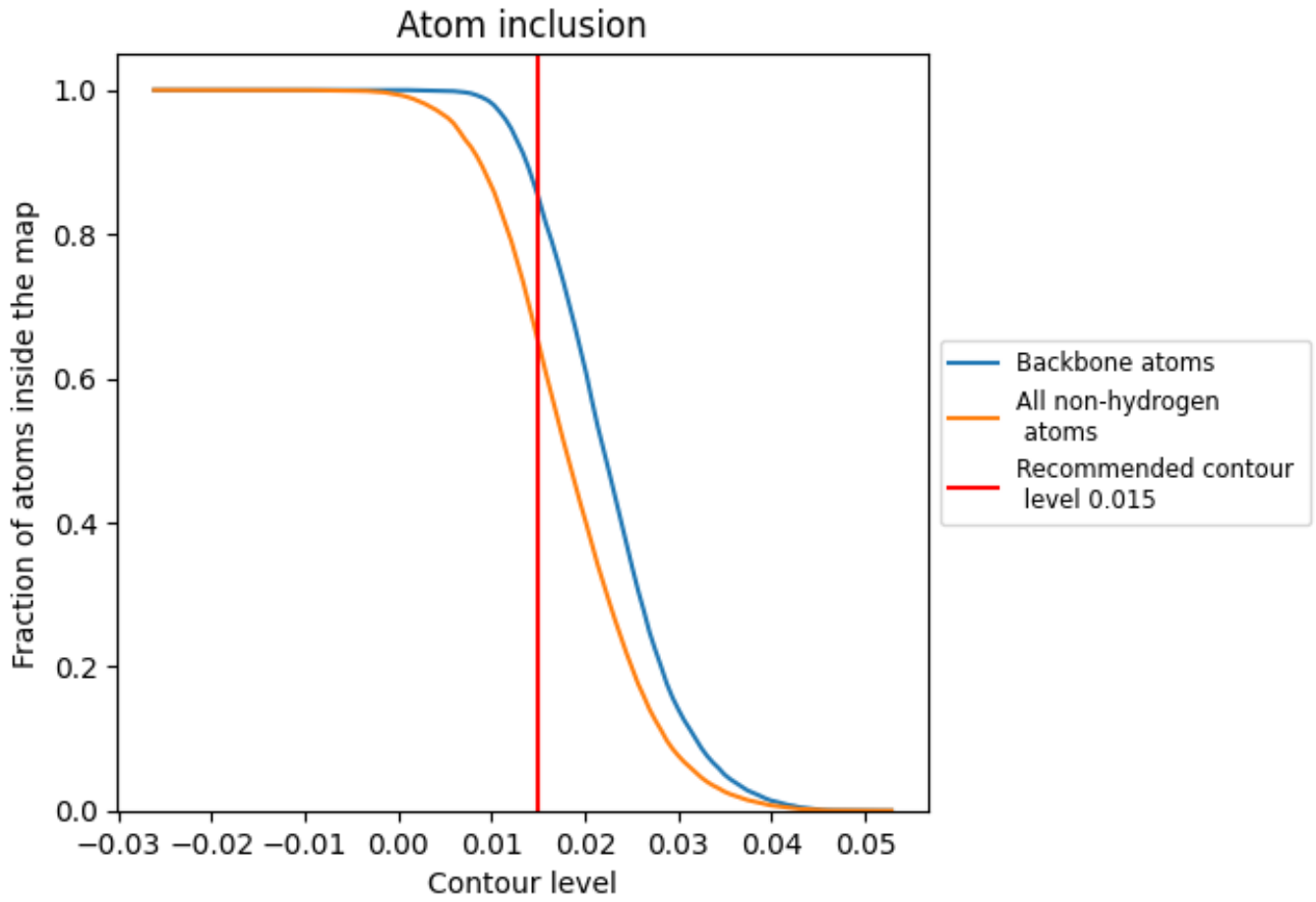
## 9.3 Atom inclusion mapped to coordinate model (i)




X Y Z

The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.015).

## 9.4 Atom inclusion (i)




At the recommended contour level, 85% of all backbone atoms, 65% of all non-hydrogen atoms, are inside the map.

## 9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (0.015) and Q-score for the entire model and for each chain.

| Chain | Atom inclusion | Q-score |
|---|---|---|
| All | 0.6504 | 0.1510 |
| A | 0.6834 | 0.1530 |
| B | 0.6577 | 0.1530 |
| C | 0.6806 | 0.1530 |
| D | 0.6534 | 0.1500 |
| E | 0.4866 | 0.1390 |
| F | 0.4917 | 0.1400 |