# wwPDB X-ray Structure Validation Summary Report (i)

May 26, 2020 – 02:49 am BST

| | | |
|---|---|---|
| PDB ID | : | 6DWU |
| Title | : | Crystal structure of complex of BBKI and Bovine Trypsin |
| Authors | : | Li, M.; Wlodawer, A.; Gustchina, A. |
| Deposited on | : | 2018-06-28 |
| Resolution | : | 3.96 Å(reported) |

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

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

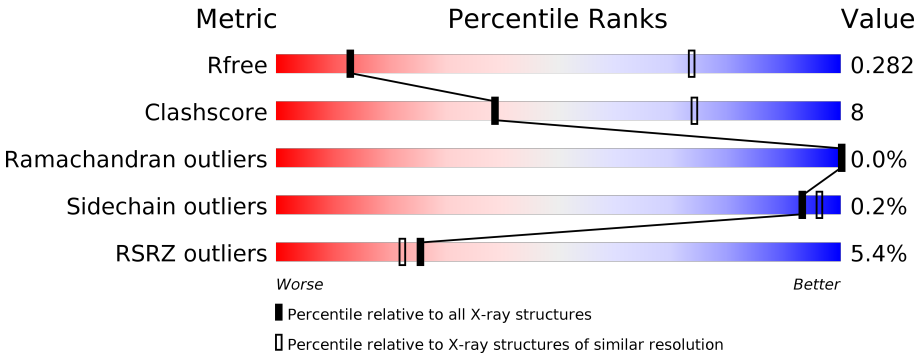
| | | |
|---|---|---|
| MolProbity | : | 4.02b-467 |
| Xtriage (Phenix) | : | 1.13 |
| EDS | : | 2.11 |
| Percentile statistics | : | 20191225.v01 (using entries in the PDB archive December 25th 2019) |
| Refmac | : | 5.8.0158 |
| CCP4 | : | 7.0.044 (Gargrove) |
| Ideal geometry (proteins) | : | Engh & Huber (2001) |
| Ideal geometry (DNA, RNA) | : | Parkinson et al. (1996) |
| Validation Pipeline (wwPDB-VP) | : | 2.11 |

# 1 Overall quality at a glance (i)

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

The reported resolution of this entry is 3.96 Å.

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




| Metric | Whole archive (#Entries) | Similar resolution (#Entries, resolution range(Å)) |
|---|---|---|
| $R_{free}$ | 130704 | 1025 (4.22-3.70) |
| Clashscore | 141614 | 1085 (4.22-3.70) |
| Ramachandran outliers | 138981 | 1047 (4.22-3.70) |
| Sidechain outliers | 138945 | 1039 (4.22-3.70) |
| RSRZ outliers | 127900 | 1013 (4.28-3.64) |

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

| Mol | Chain | Length | Quality of chain |
|---|---|---|---|
| 1 | AA | 223 | 3% 83% 17% |
| 1 | AC | 223 | 12% 80% 20% |
| 1 | AE | 223 | 6% 83% 17% |
| 1 | AG | 223 | 4% 87% 13% |
| 1 | AI | 223 | 8% 85% 15% |
| 1 | AK | 223 | 85% 15% |

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| Mol | Chain | Length | Quality of chain |
|---|---|---|---|
| 1 | AM | 223 | 3% 86% 14% |
| 1 | AO | 223 | 7% 83% 17% |
| 1 | AQ | 223 | 3% 81% 19% |
| 1 | AS | 223 | 4% 84% 16% |
| 1 | AU | 223 | 20% 85% 15% |
| 1 | BA | 223 | 4% 84% 16% |
| 1 | BC | 223 | 21% 92% 8% |
| 1 | BE | 223 | 9% 87% 13% |
| 1 | BG | 223 | 2% 85% 15% |
| 1 | BI | 223 | 6% 86% 14% |
| 1 | BK | 223 | 6% 87% 13% |
| 1 | BM | 223 | 4% 83% 17% |
| 1 | BO | 223 | 86% 14% |
| 1 | BQ | 223 | 5% 79% 21% |
| 1 | BS | 223 | 18% 80% 20% |
| 1 | BU | 223 | 7% 84% 16% |
| 1 | CA | 223 | 13% 84% 16% |
| 1 | CC | 223 | 15% 82% 18% |
| 1 | CE | 223 | 4% 87% 13% |
| 1 | CG | 223 | 2% 82% 18% |
| 1 | CI | 223 | 2% 92% 8% |
| 1 | CK | 223 | 2% 84% 16% |
| 1 | CM | 223 | 6% 87% 13% |
| 1 | CO | 223 | 13% 83% 17% |
| 1 | CQ | 223 | 4% 79% 21% |

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| Mol | Chain | Length | Quality of chain |
|---|---|---|---|
| 1 | CS | 223 | 17% 83% 17% |
| 1 | CU | 223 | 10% 82% 18% |
| 1 | DA | 223 | 13% 85% 15% |
| 1 | DC | 223 | % 88% 12% |
| 1 | DE | 223 | 20% 84% 16% |
| 1 | DG | 223 | 3% 89% 11% |
| 1 | DI | 223 | 2% 81% 19% |
| 1 | DK | 223 | 2% 86% 14% |
| 1 | DM | 223 | % 86% 14% |
| 1 | DO | 223 | % 85% 15% |
| 1 | DQ | 223 | 7% 82% 17% |
| 1 | DS | 223 | 2% 84% 16% |
| 1 | DU | 223 | 11% 86% 14% |
| 2 | AB | 163 | 4% 81% 19% |
| 2 | AD | 163 | 4% 82% 18% |
| 2 | AF | 163 | % 83% 17% |
| 2 | AH | 163 | % 79% 21% |
| 2 | AJ | 163 | 86% 14% |
| 2 | AL | 163 | % 79% 21% |
| 2 | AN | 163 | % 80% 20% |
| 2 | AP | 163 | 3% 80% 20% |
| 2 | AR | 163 | 7% 80% 19% |
| 2 | AT | 163 | % 82% 18% |
| 2 | AV | 163 | 6% 80% 20% |
| 2 | BB | 163 | % 83% 17% |

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| Mol | Chain | Length | Quality of chain |
|---|---|---|---|
| 2 | BD | 163 | 4% 72% 28% |
| 2 | BF | 163 | 12% 83% 17% |
| 2 | BH | 163 | 3% 82% 18% |
| 2 | BJ | 163 | % 82% 18% |
| 2 | BL | 163 | % 77% 22% |
| 2 | BN | 163 | % 85% 14% |
| 2 | BP | 163 | 4% 83% 16% |
| 2 | BR | 163 | % 85% 15% |
| 2 | BT | 163 | 2% 83% 17% |
| 2 | BV | 163 | 10% 83% 17% |
| 2 | CB | 163 | 6% 76% 24% |
| 2 | CD | 163 | 9% 68% 32% |
| 2 | CF | 163 | 4% 85% 15% |
| 2 | CH | 163 | 82% 18% |
| 2 | CJ | 163 | 2% 83% 17% |
| 2 | CL | 163 | 2% 83% 17% |
| 2 | CN | 163 | 85% 15% |
| 2 | CP | 163 | 10% 77% 23% |
| 2 | CR | 163 | % 71% 28% |
| 2 | CT | 163 | 2% 80% 20% |
| 2 | CV | 163 | 7% 84% 16% |
| 2 | DB | 163 | 7% 86% 13% |
| 2 | DD | 163 | % 86% 13% |
| 2 | DF | 163 | 4% 74% 26% |
| 2 | DH | 163 | % 81% 19% |

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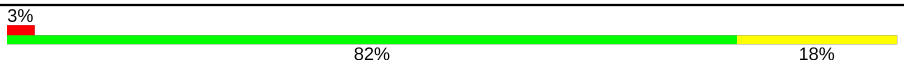
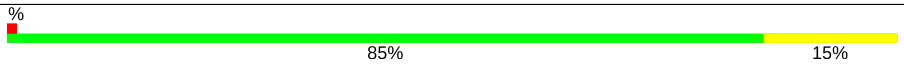
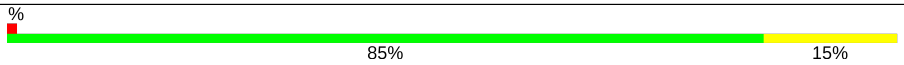
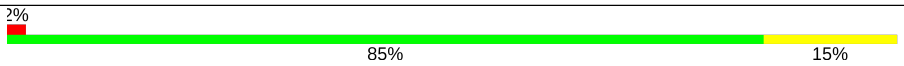
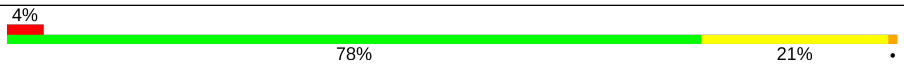
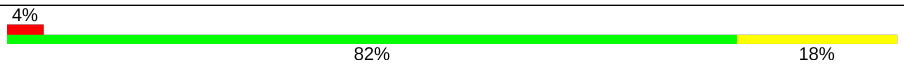
| Mol | Chain | Length | Quality of chain |
|---|---|---|---|
| 2 | DJ | 163 |   |
| 2 | DL | 163 |   |
| 2 | DN | 163 |   |
| 2 | DP | 163 |   |
| 2 | DR | 163 |   |
| 2 | DT | 163 |   |
| 2 | DV | 163 |   |

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 127116 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Cationic trypsin.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| 1 | AA | 223 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1629 | 1012 | 279 | 324 | 14 | | | |
| 1 | AC | 223 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1629 | 1012 | 279 | 324 | 14 | | | |
| 1 | AE | 223 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1629 | 1012 | 279 | 324 | 14 | | | |
| 1 | AG | 223 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1629 | 1012 | 279 | 324 | 14 | | | |
| 1 | AI | 223 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1629 | 1012 | 279 | 324 | 14 | | | |
| 1 | AK | 223 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1629 | 1012 | 279 | 324 | 14 | | | |
| 1 | AM | 223 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1629 | 1012 | 279 | 324 | 14 | | | |
| 1 | AO | 223 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1629 | 1012 | 279 | 324 | 14 | | | |
| 1 | AQ | 223 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1629 | 1012 | 279 | 324 | 14 | | | |
| 1 | AS | 223 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1629 | 1012 | 279 | 324 | 14 | | | |
| 1 | AU | 223 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1629 | 1012 | 279 | 324 | 14 | | | |
| 1 | BA | 223 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1629 | 1012 | 279 | 324 | 14 | | | |
| 1 | BC | 223 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1629 | 1012 | 279 | 324 | 14 | | | |
| 1 | BE | 223 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1629 | 1012 | 279 | 324 | 14 | | | |
| 1 | BG | 223 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1629 | 1012 | 279 | 324 | 14 | | | |
| 1 | BI | 223 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1629 | 1012 | 279 | 324 | 14 | | | |

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| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| 1 | BK | 223 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1629 | 1012 | 279 | 324 | 14 | | | |
| 1 | BM | 223 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1629 | 1012 | 279 | 324 | 14 | | | |
| 1 | BO | 223 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1629 | 1012 | 279 | 324 | 14 | | | |
| 1 | BQ | 223 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1629 | 1012 | 279 | 324 | 14 | | | |
| 1 | BS | 223 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1629 | 1012 | 279 | 324 | 14 | | | |
| 1 | BU | 223 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1629 | 1012 | 279 | 324 | 14 | | | |
| 1 | CA | 223 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1629 | 1012 | 279 | 324 | 14 | | | |
| 1 | CC | 223 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1629 | 1012 | 279 | 324 | 14 | | | |
| 1 | CE | 223 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1629 | 1012 | 279 | 324 | 14 | | | |
| 1 | CG | 223 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1629 | 1012 | 279 | 324 | 14 | | | |
| 1 | CI | 223 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1629 | 1012 | 279 | 324 | 14 | | | |
| 1 | CK | 223 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1629 | 1012 | 279 | 324 | 14 | | | |
| 1 | CM | 223 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1629 | 1012 | 279 | 324 | 14 | | | |
| 1 | CO | 223 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1629 | 1012 | 279 | 324 | 14 | | | |
| 1 | CQ | 223 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1629 | 1012 | 279 | 324 | 14 | | | |
| 1 | CS | 223 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1629 | 1012 | 279 | 324 | 14 | | | |
| 1 | CU | 223 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1629 | 1012 | 279 | 324 | 14 | | | |
| 1 | DA | 223 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1629 | 1012 | 279 | 324 | 14 | | | |
| 1 | DC | 223 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1629 | 1012 | 279 | 324 | 14 | | | |
| 1 | DE | 223 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1629 | 1012 | 279 | 324 | 14 | | | |
| 1 | DG | 223 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1629 | 1012 | 279 | 324 | 14 | | | |

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| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| 1 | DI | 223 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1629 | 1012 | 279 | 324 | 14 | | | |
| 1 | DK | 223 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1629 | 1012 | 279 | 324 | 14 | | | |
| 1 | DM | 223 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1629 | 1012 | 279 | 324 | 14 | | | |
| 1 | DO | 223 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1629 | 1012 | 279 | 324 | 14 | | | |
| 1 | DQ | 223 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1629 | 1012 | 279 | 324 | 14 | | | |
| 1 | DS | 223 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1629 | 1012 | 279 | 324 | 14 | | | |
| 1 | DU | 223 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1629 | 1012 | 279 | 324 | 14 | | | |

- Molecule 2 is a protein called Kunitz-type inihibitor.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| 2 | AB | 163 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1260 | 807 | 217 | 235 | 1 | | | |
| 2 | AD | 163 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1260 | 807 | 217 | 235 | 1 | | | |
| 2 | AF | 163 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1260 | 807 | 217 | 235 | 1 | | | |
| 2 | AH | 163 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1260 | 807 | 217 | 235 | 1 | | | |
| 2 | AJ | 163 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1260 | 807 | 217 | 235 | 1 | | | |
| 2 | AL | 163 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1260 | 807 | 217 | 235 | 1 | | | |
| 2 | AN | 163 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1260 | 807 | 217 | 235 | 1 | | | |
| 2 | AP | 163 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1260 | 807 | 217 | 235 | 1 | | | |
| 2 | AR | 163 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1260 | 807 | 217 | 235 | 1 | | | |
| 2 | AT | 163 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1260 | 807 | 217 | 235 | 1 | | | |
| 2 | AV | 163 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1260 | 807 | 217 | 235 | 1 | | | |
| 2 | BB | 163 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1260 | 807 | 217 | 235 | 1 | | | |

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| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| 2 | BD | 163 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1260 | 807 | 217 | 235 | 1 | | | |
| 2 | BF | 163 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1260 | 807 | 217 | 235 | 1 | | | |
| 2 | BH | 163 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1260 | 807 | 217 | 235 | 1 | | | |
| 2 | BJ | 163 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1260 | 807 | 217 | 235 | 1 | | | |
| 2 | BL | 163 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1260 | 807 | 217 | 235 | 1 | | | |
| 2 | BN | 163 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1260 | 807 | 217 | 235 | 1 | | | |
| 2 | BP | 163 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1260 | 807 | 217 | 235 | 1 | | | |
| 2 | BR | 163 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1260 | 807 | 217 | 235 | 1 | | | |
| 2 | BT | 163 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1260 | 807 | 217 | 235 | 1 | | | |
| 2 | BV | 163 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1260 | 807 | 217 | 235 | 1 | | | |
| 2 | CB | 163 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1260 | 807 | 217 | 235 | 1 | | | |
| 2 | CD | 163 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1260 | 807 | 217 | 235 | 1 | | | |
| 2 | CF | 163 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1260 | 807 | 217 | 235 | 1 | | | |
| 2 | CH | 163 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1260 | 807 | 217 | 235 | 1 | | | |
| 2 | CJ | 163 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1260 | 807 | 217 | 235 | 1 | | | |
| 2 | CL | 163 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1260 | 807 | 217 | 235 | 1 | | | |
| 2 | CN | 163 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1260 | 807 | 217 | 235 | 1 | | | |
| 2 | CP | 163 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1260 | 807 | 217 | 235 | 1 | | | |
| 2 | CR | 163 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1260 | 807 | 217 | 235 | 1 | | | |
| 2 | CT | 163 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1260 | 807 | 217 | 235 | 1 | | | |
| 2 | CV | 163 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1260 | 807 | 217 | 235 | 1 | | | |

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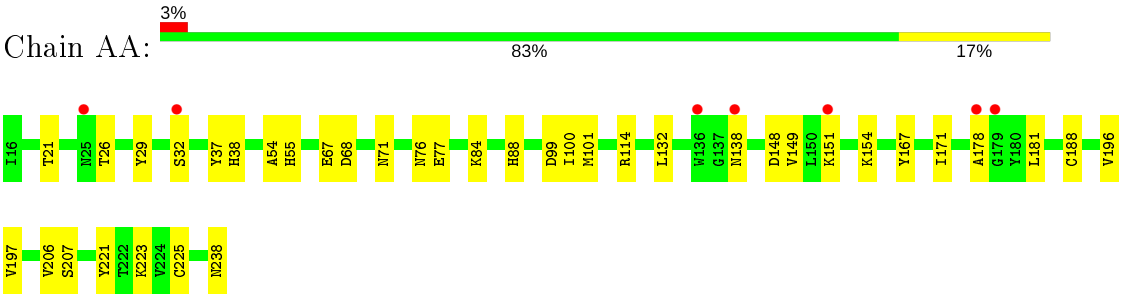
| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| 2 | DB | 163 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1260 | 807 | 217 | 235 | 1 | | | |
| 2 | DD | 163 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1260 | 807 | 217 | 235 | 1 | | | |
| 2 | DF | 163 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1260 | 807 | 217 | 235 | 1 | | | |
| 2 | DH | 163 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1260 | 807 | 217 | 235 | 1 | | | |
| 2 | DJ | 163 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1260 | 807 | 217 | 235 | 1 | | | |
| 2 | DL | 163 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1260 | 807 | 217 | 235 | 1 | | | |
| 2 | DN | 163 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1260 | 807 | 217 | 235 | 1 | | | |
| 2 | DP | 163 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1260 | 807 | 217 | 235 | 1 | | | |
| 2 | DR | 163 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1260 | 807 | 217 | 235 | 1 | | | |
| 2 | DT | 163 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1260 | 807 | 217 | 235 | 1 | | | |
| 2 | DV | 163 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1260 | 807 | 217 | 235 | 1 | | | |

# 3 Residue-property plots (i)

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

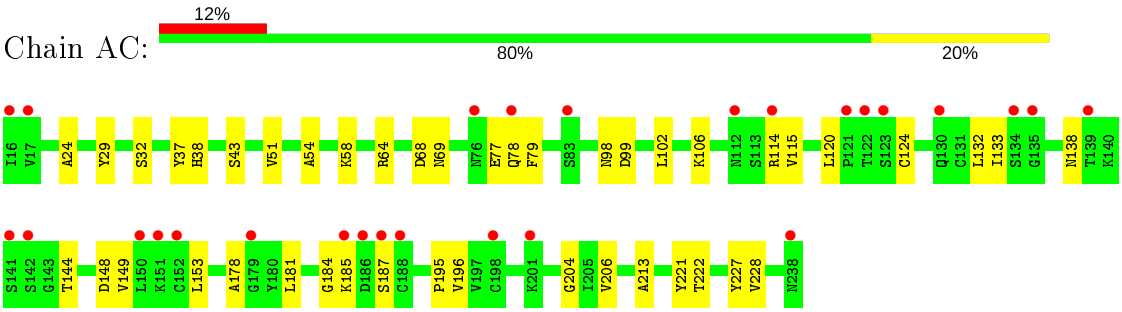
- Molecule 1: Cationic trypsin

Chain AA:



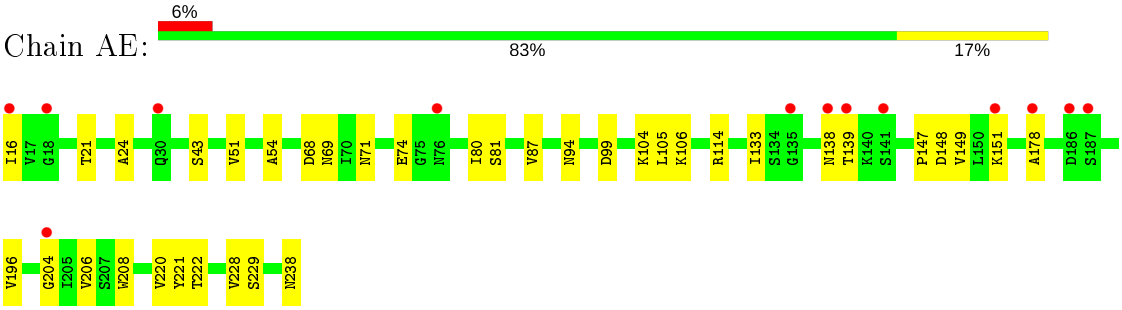

- Molecule 1: Cationic trypsin

Chain AC:



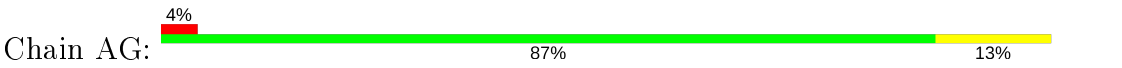

- Molecule 1: Cationic trypsin

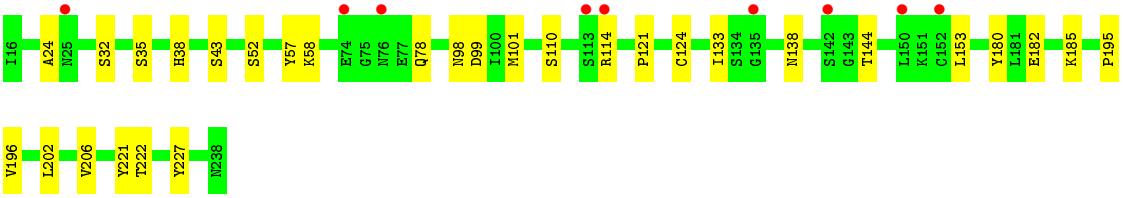
Chain AE:




- Molecule 1: Cationic trypsin

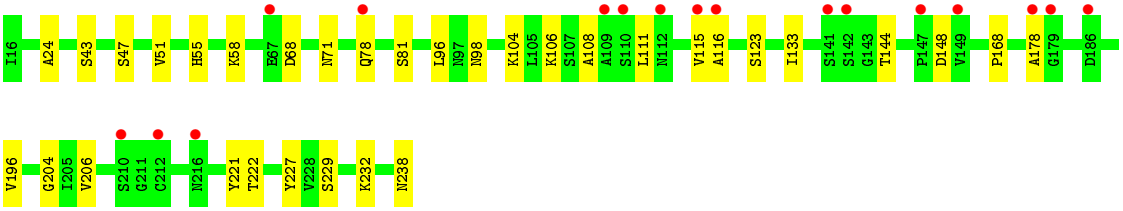
Chain AG:





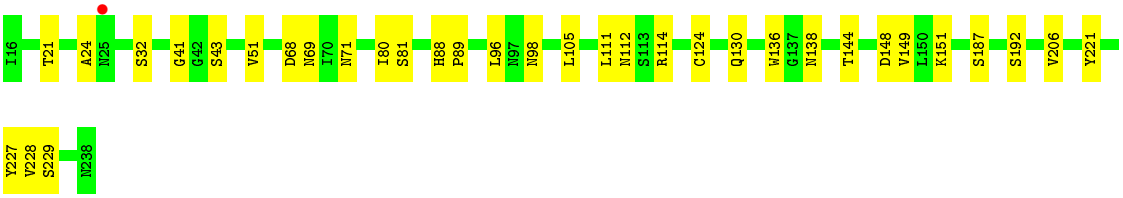

- Molecule 1: Cationic trypsin

Chain AI:

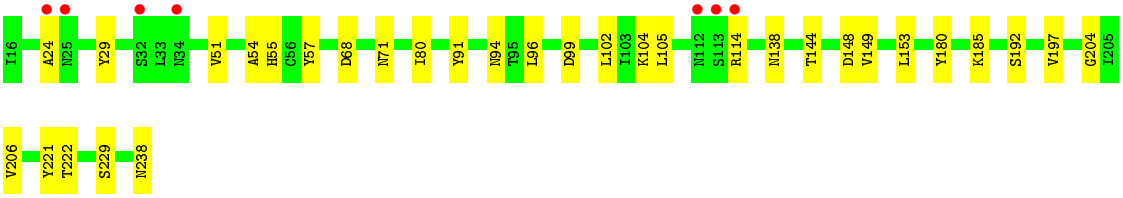

- Molecule 1: Cationic trypsin

Chain AK:

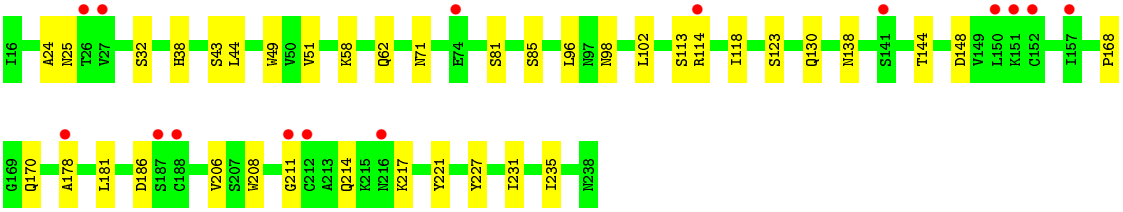

- Molecule 1: Cationic trypsin

Chain AM:

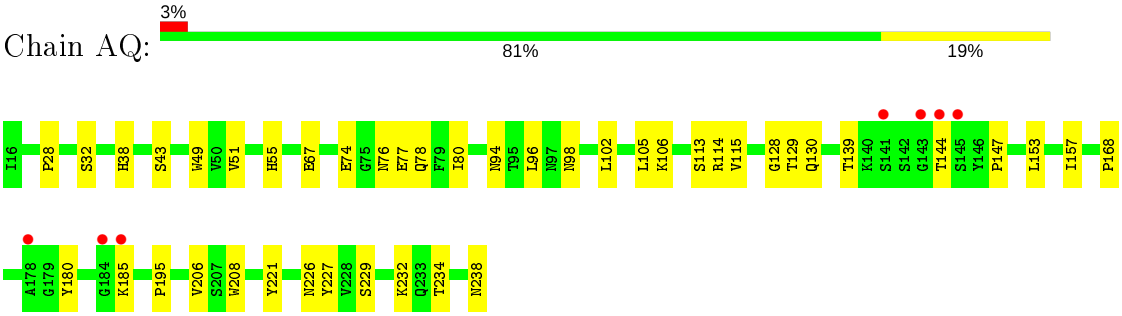

- Molecule 1: Cationic trypsin

Chain AO:

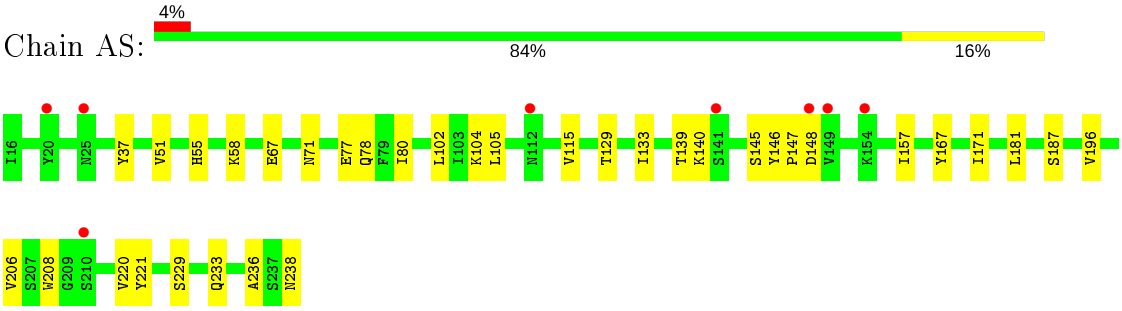
• Molecule 1: Cationic trypsin

Chain AQ:



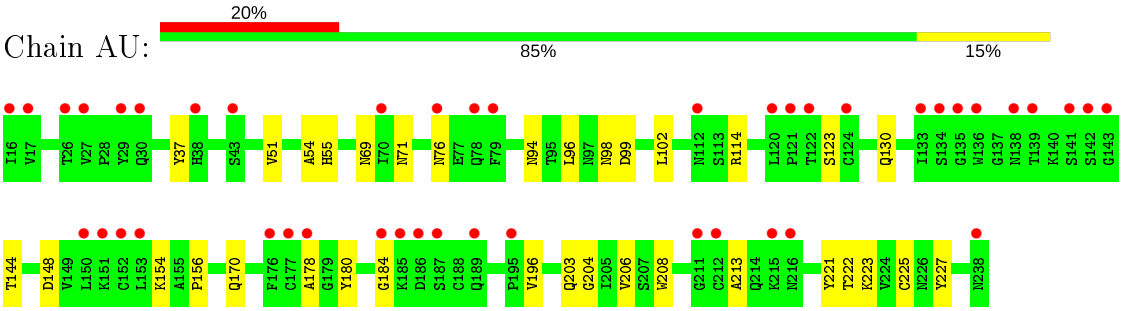

• Molecule 1: Cationic trypsin

Chain AS:



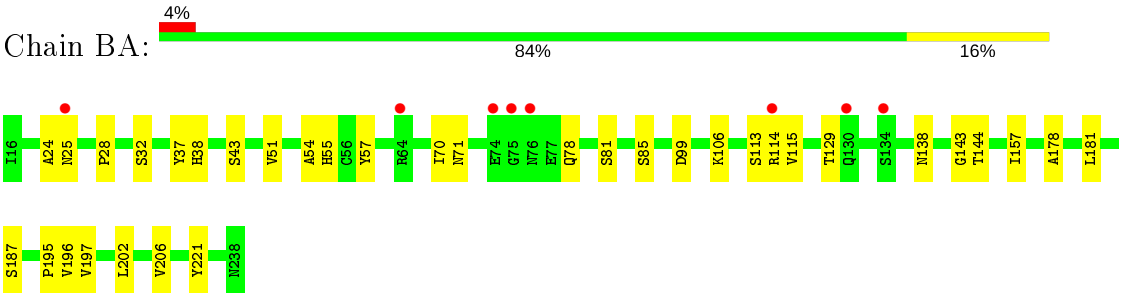

• Molecule 1: Cationic trypsin

Chain AU:



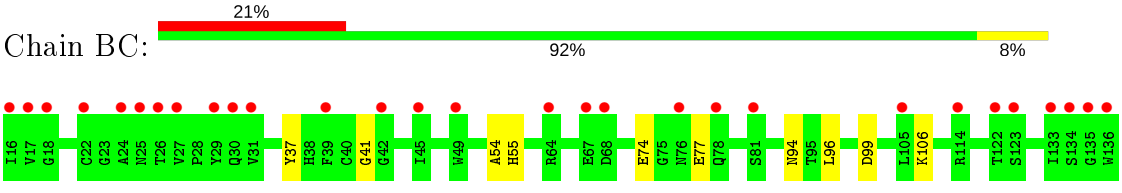

• Molecule 1: Cationic trypsin

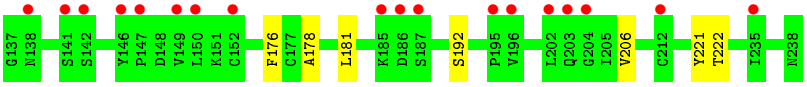
Chain BA:




• Molecule 1: Cationic trypsin

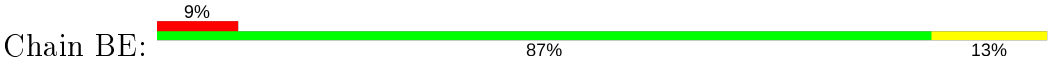
Chain BC:

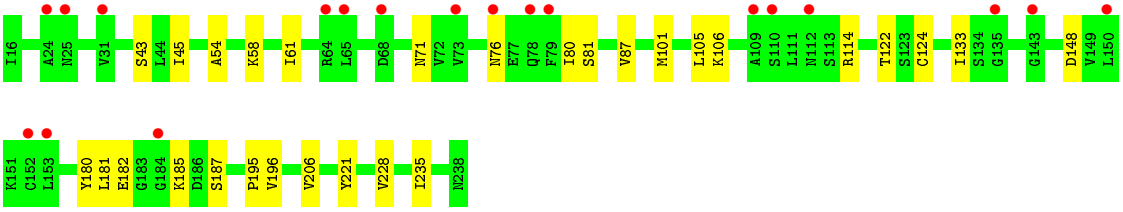





- Molecule 1: Cationic trypsin

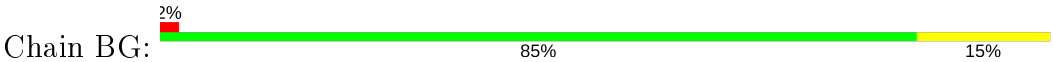
Chain BE:

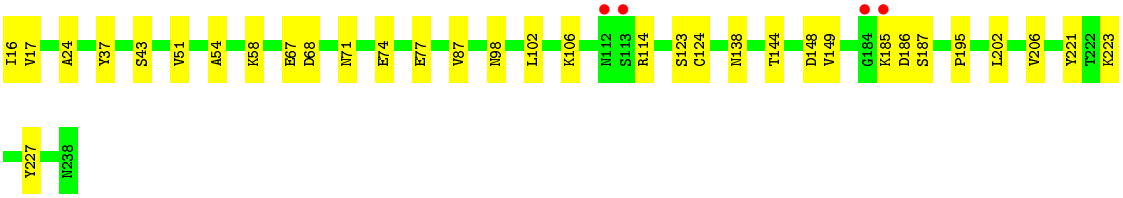



- Molecule 1: Cationic trypsin

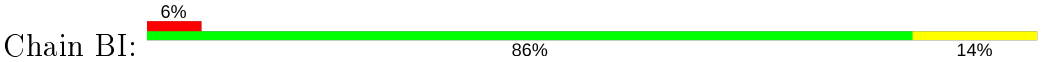
Chain BG:

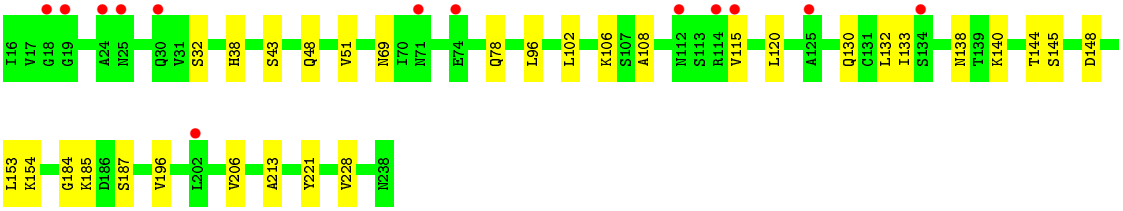



- Molecule 1: Cationic trypsin

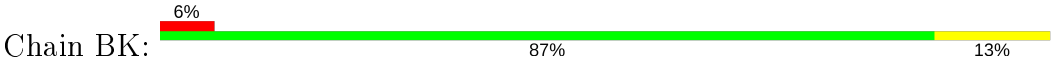
Chain BI:

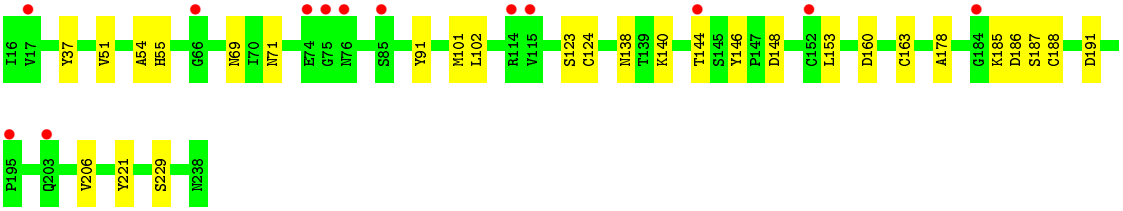



- Molecule 1: Cationic trypsin

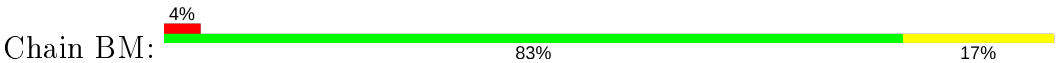
Chain BK:

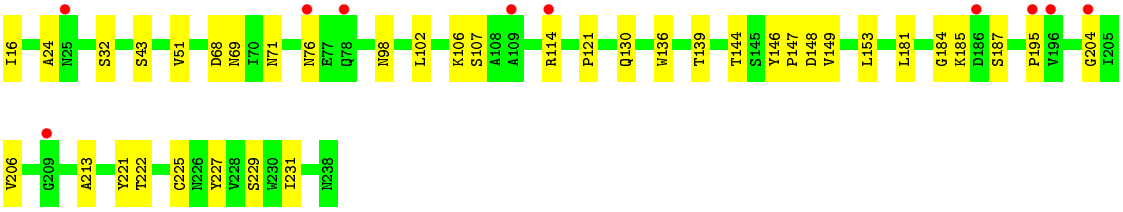



- Molecule 1: Cationic trypsin

Chain BM:





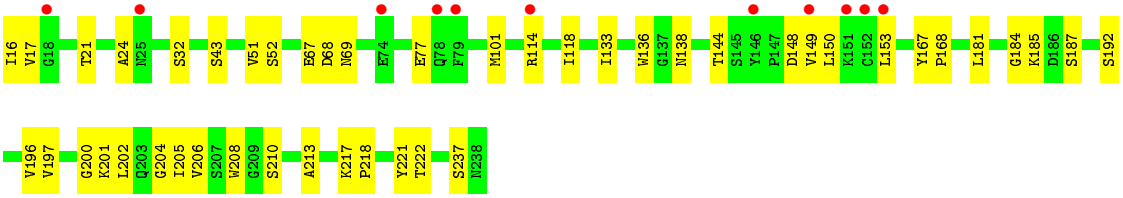

- Molecule 1: Cationic trypsin

Chain BO:



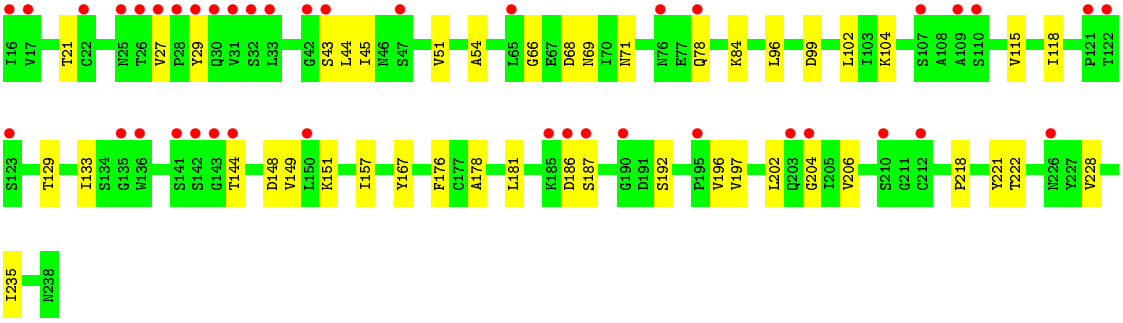
- Molecule 1: Cationic trypsin

Chain BQ:

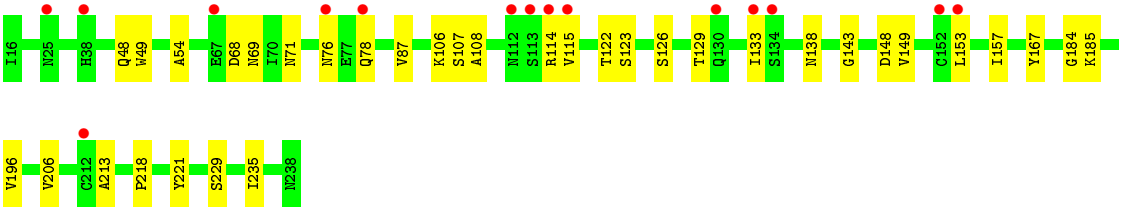

- Molecule 1: Cationic trypsin

Chain BS:

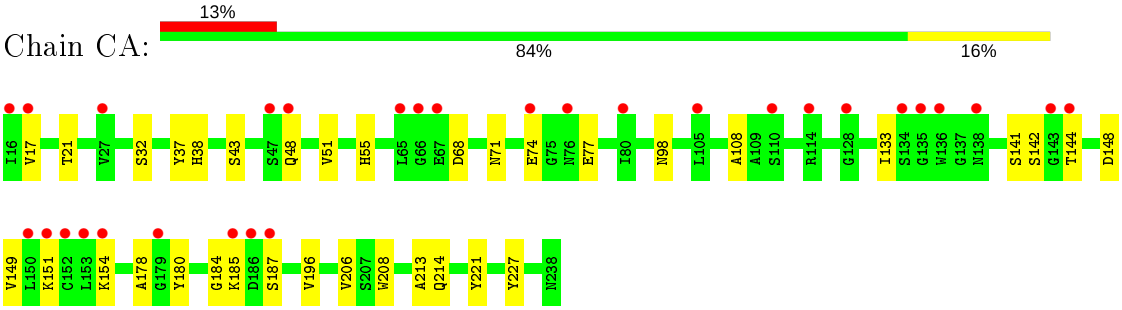

- Molecule 1: Cationic trypsin

Chain BU:

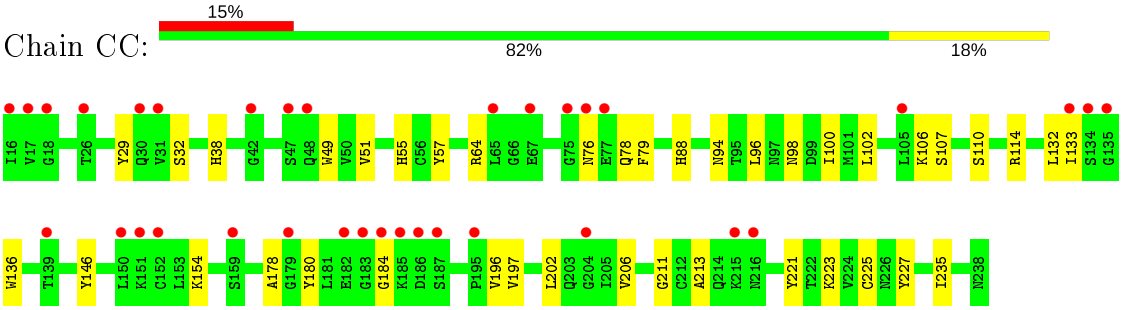
• Molecule 1: Cationic trypsin

Chain CA:



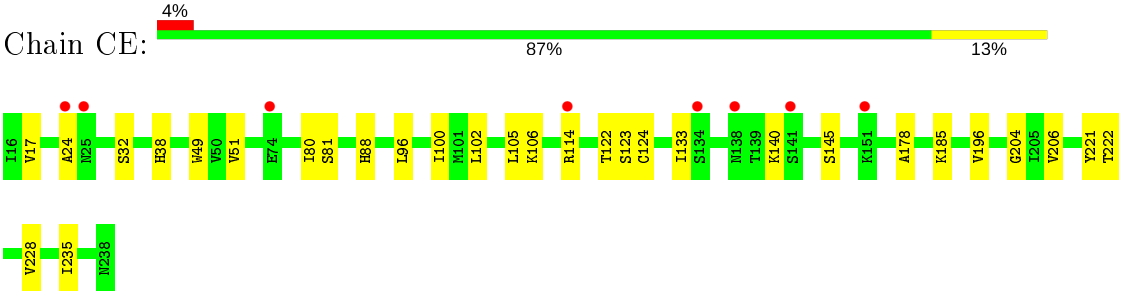

• Molecule 1: Cationic trypsin

Chain CC:



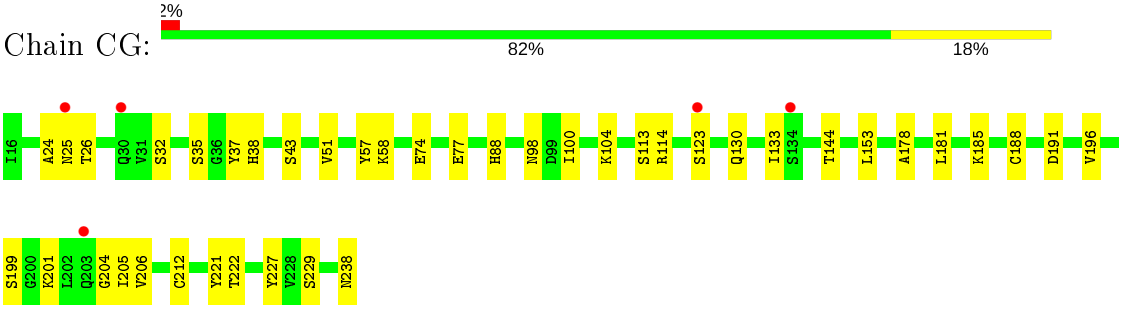

• Molecule 1: Cationic trypsin

Chain CE:



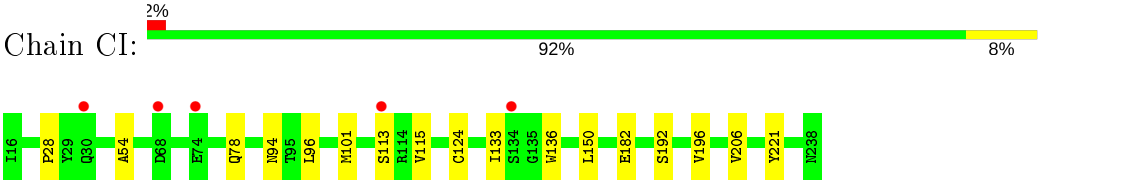

• Molecule 1: Cationic trypsin

Chain CG:



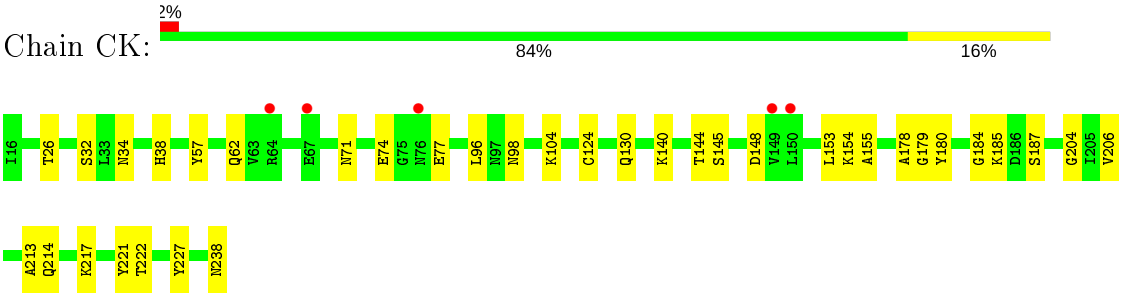

• Molecule 1: Cationic trypsin

Chain CI:



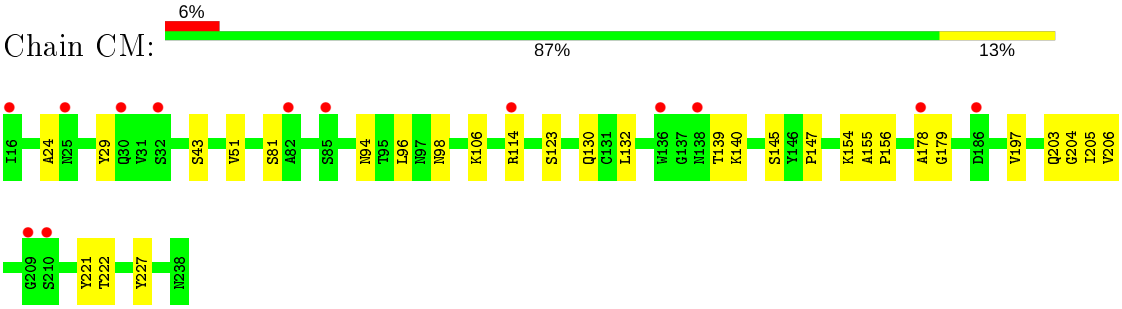
- Molecule 1: Cationic trypsin

Chain CK:



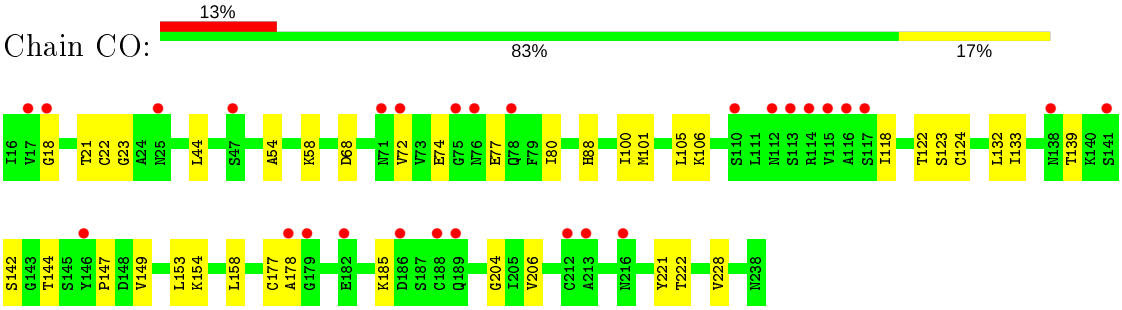

- Molecule 1: Cationic trypsin

Chain CM:



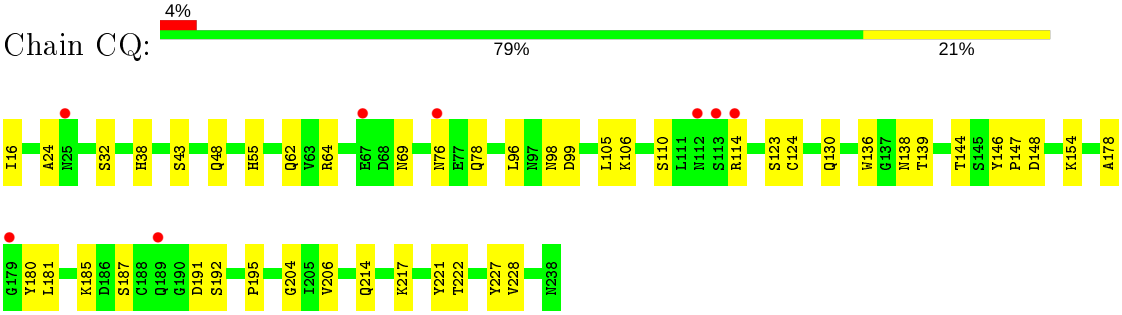

- Molecule 1: Cationic trypsin

Chain CO:



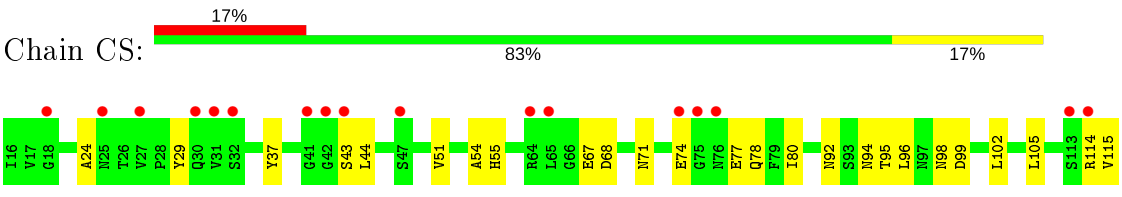

- Molecule 1: Cationic trypsin

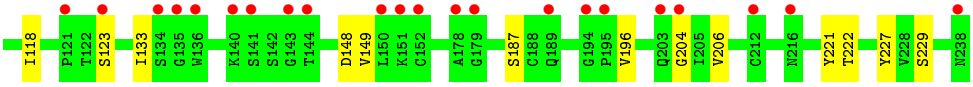
Chain CQ:




- Molecule 1: Cationic trypsin

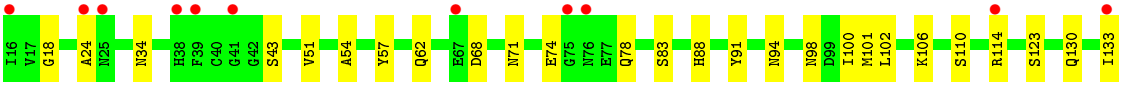
Chain CS:

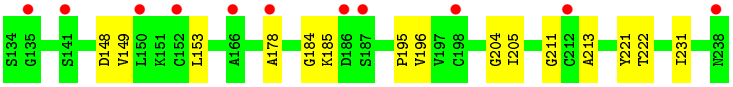





• Molecule 1: Cationic trypsin

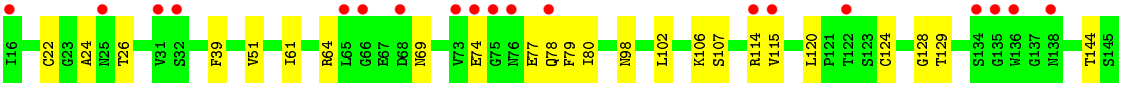
Chain CU:

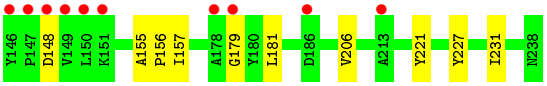




• Molecule 1: Cationic trypsin

Chain DA:

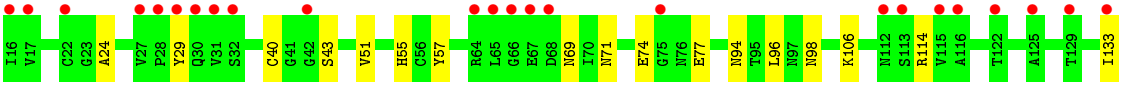

• Molecule 1: Cationic trypsin

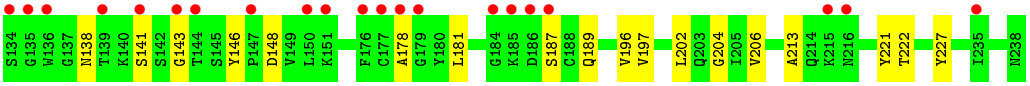
Chain DC:



• Molecule 1: Cationic trypsin

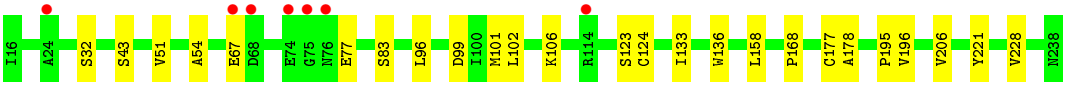
Chain DE:

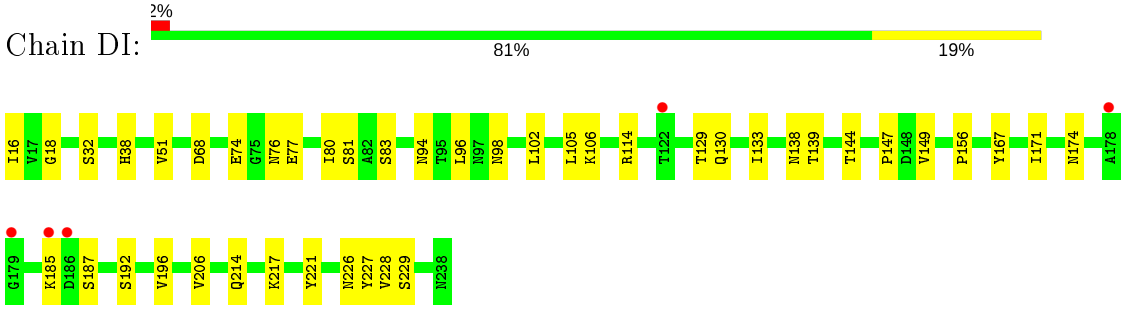

• Molecule 1: Cationic trypsin

Chain DG:

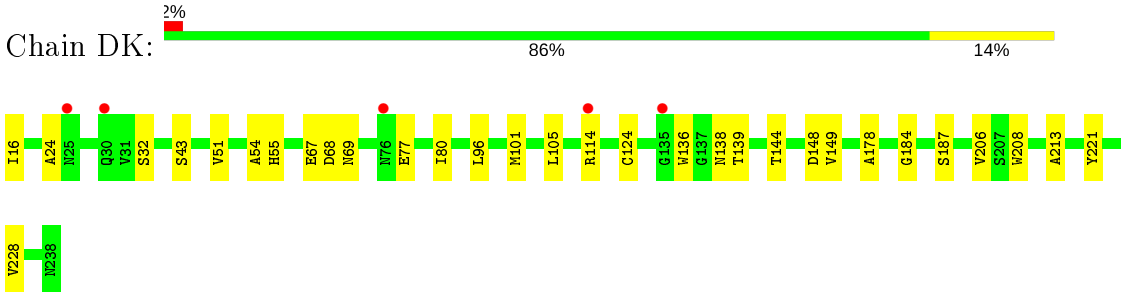
• Molecule 1: Cationic trypsin

Chain DI:



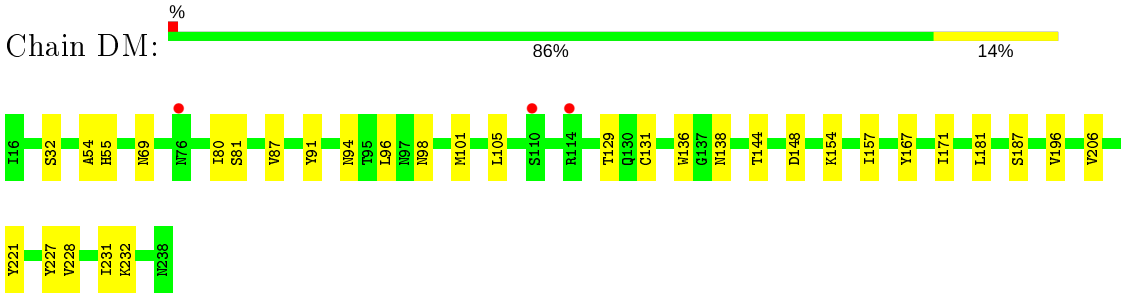

• Molecule 1: Cationic trypsin

Chain DK:



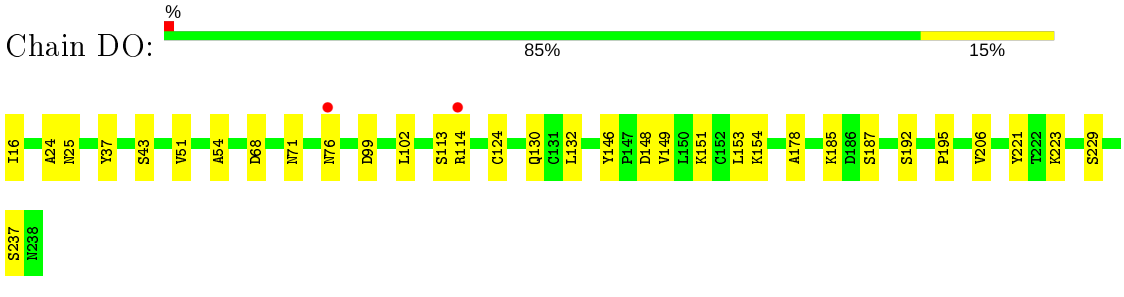

• Molecule 1: Cationic trypsin

Chain DM:



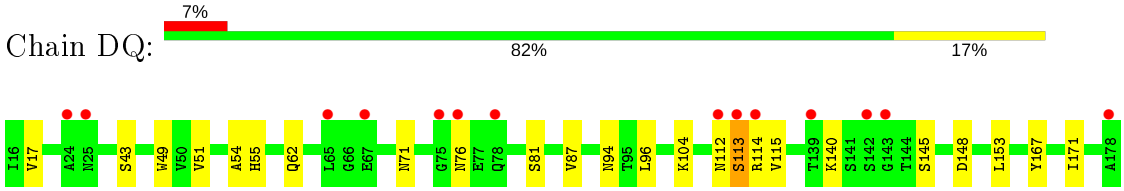

• Molecule 1: Cationic trypsin

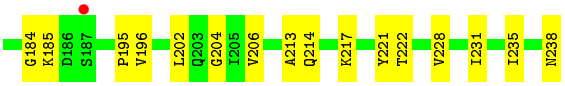
Chain DO:




• Molecule 1: Cationic trypsin

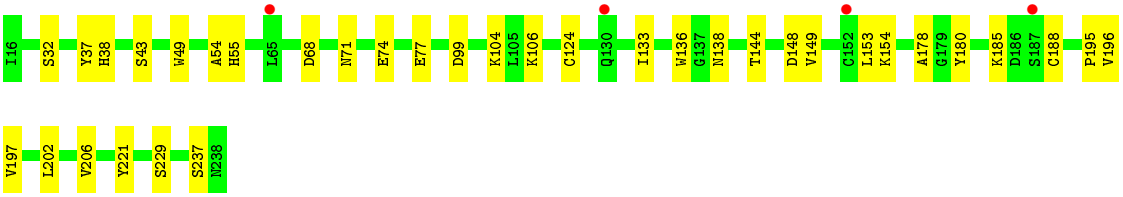
Chain DQ:





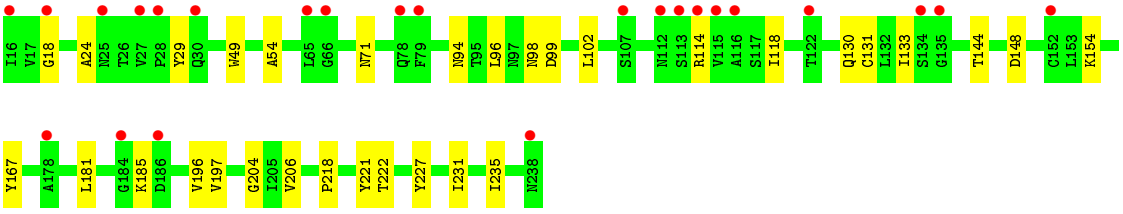

• Molecule 1: Cationic trypsin

Chain DS:

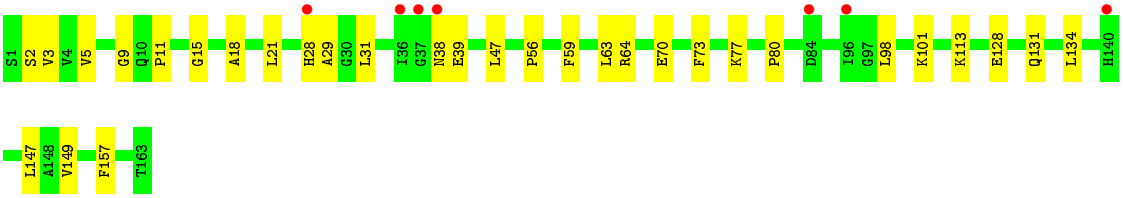

• Molecule 1: Cationic trypsin

Chain DU:

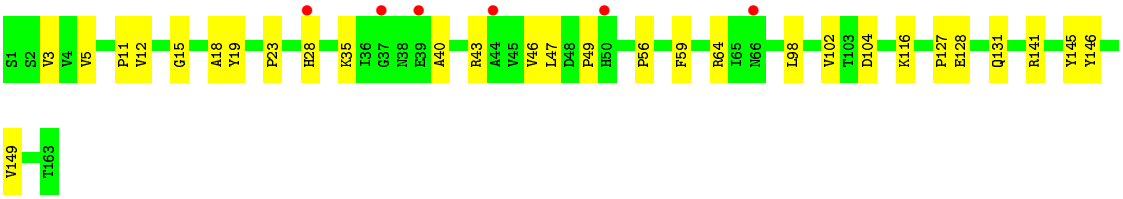

• Molecule 2: Kunitz-type inihibitor

Chain AB:


• Molecule 2: Kunitz-type inihibitor

Chain AD:

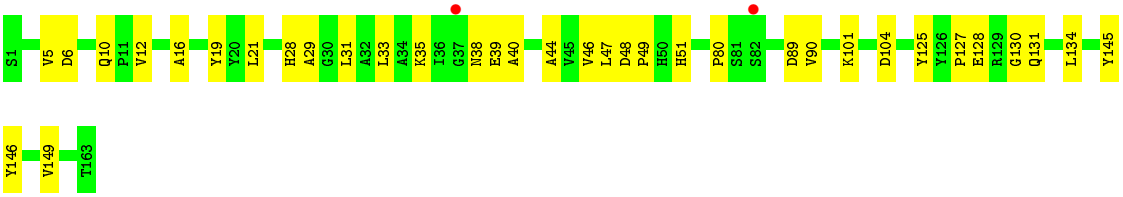




• Molecule 2: Kunitz-type inihibitor

Chain AF:

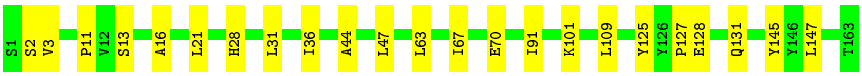

• Molecule 2: Kunitz-type inihibitor

Chain AH:

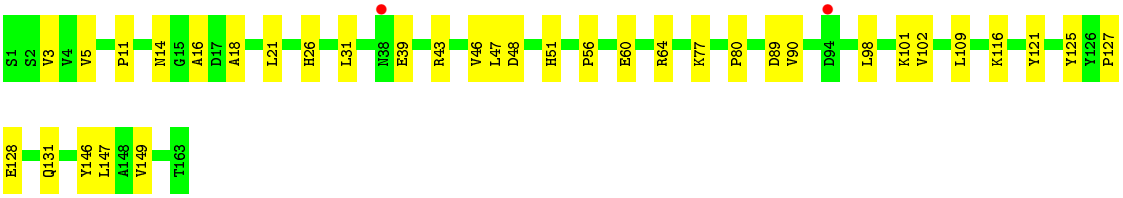

• Molecule 2: Kunitz-type inihibitor

Chain AJ:

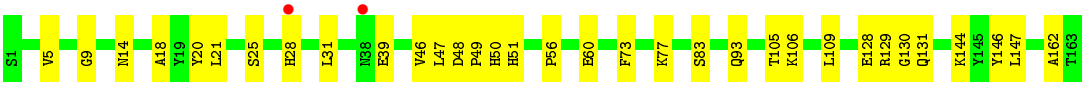

• Molecule 2: Kunitz-type inihibitor

Chain AL:


• Molecule 2: Kunitz-type inihibitor

Chain AN:


• Molecule 2: Kunitz-type inihibitor

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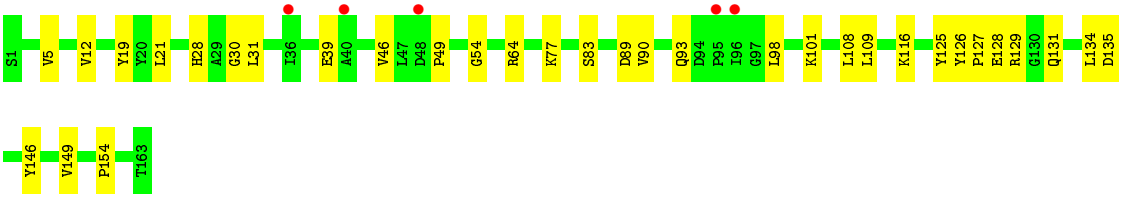

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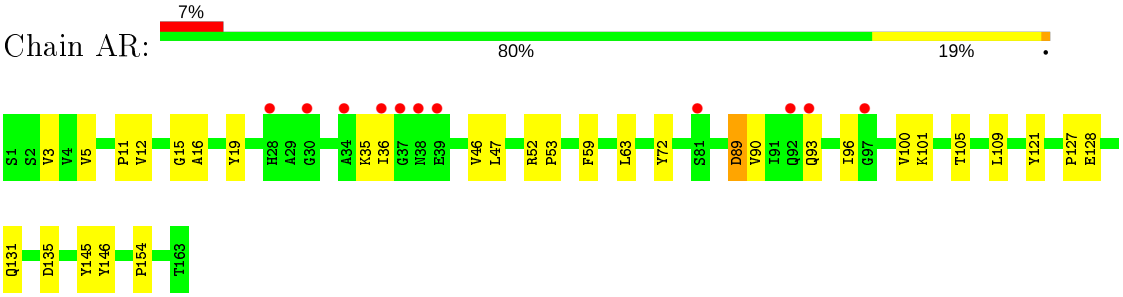
Chain AR:

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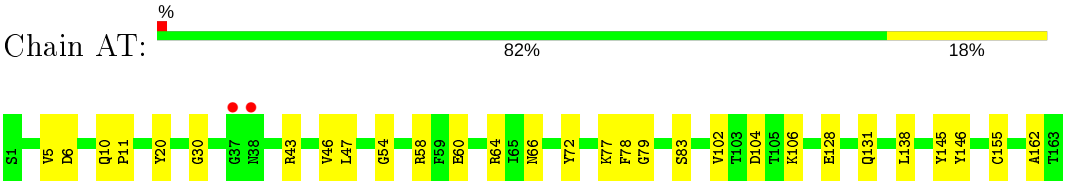


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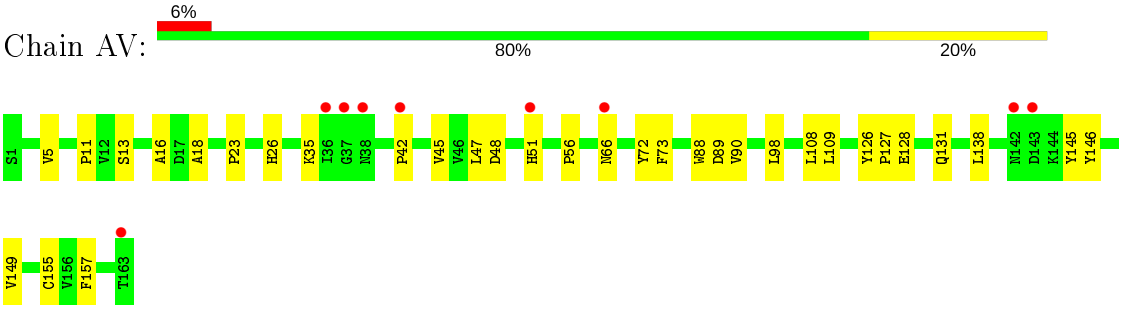
Chain AV:

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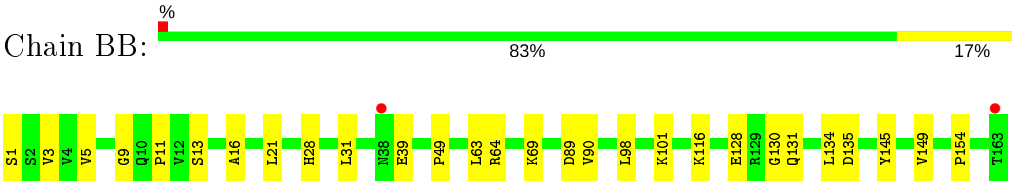
Chain BB:

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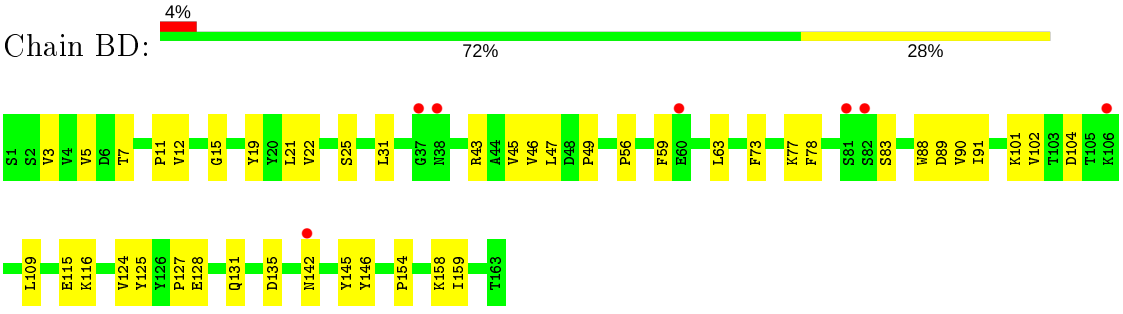
Chain BD:




• Molecule 2: Kunitz-type inihibitor

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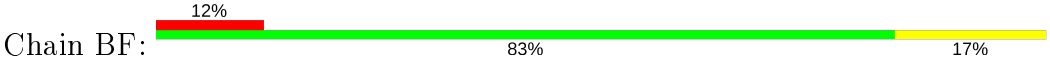

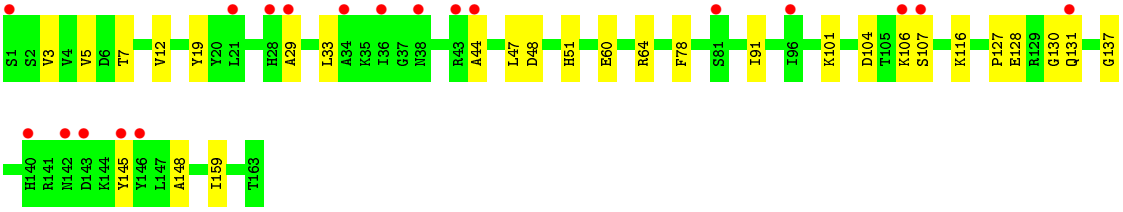


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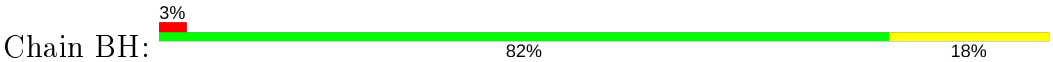


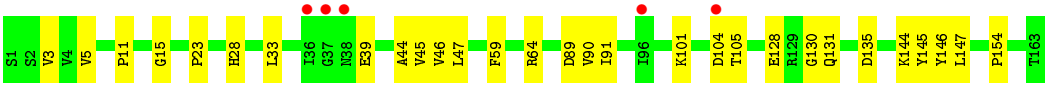


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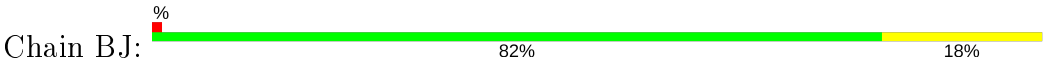
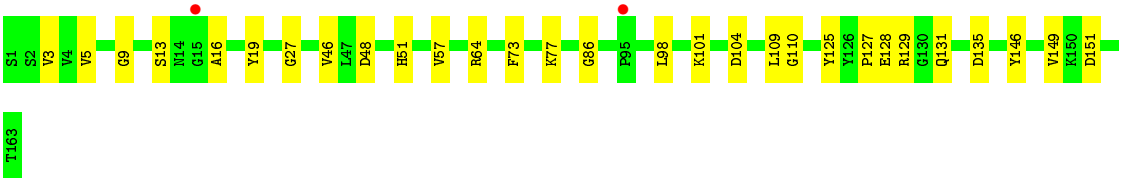
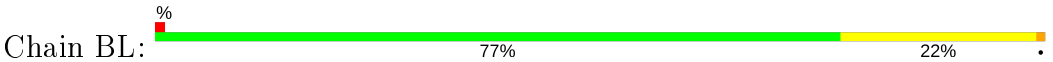
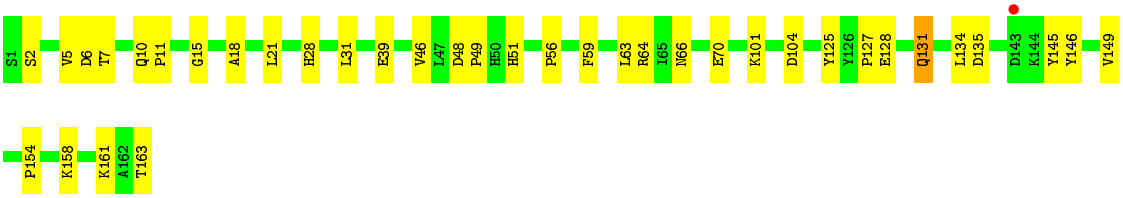



• Molecule 2: Kunitz-type inihibitor

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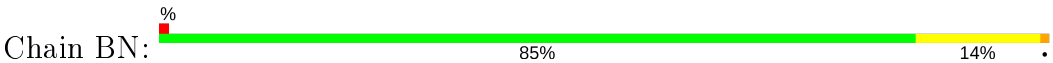


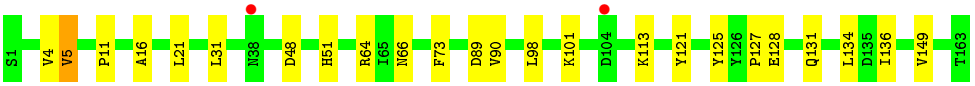


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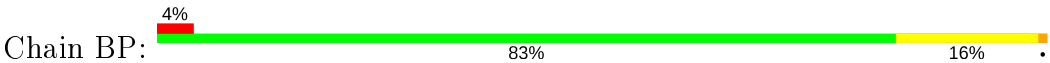
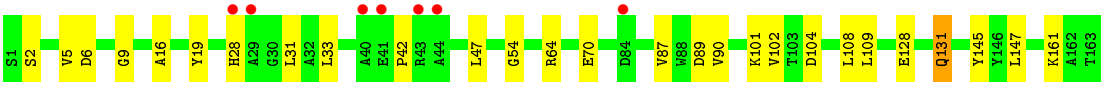
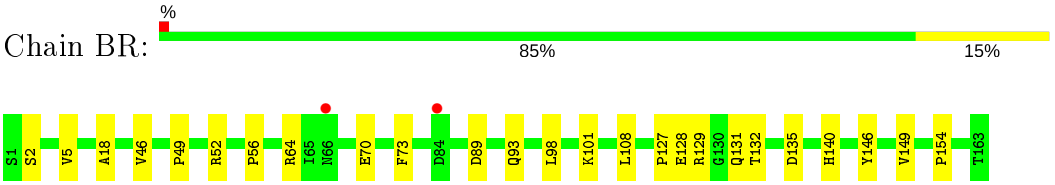


• Molecule 2: Kunitz-type inihibitor

Chain BR:




• Molecule 2: Kunitz-type inihibitor

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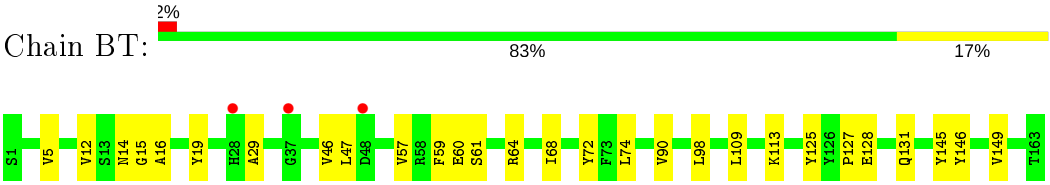
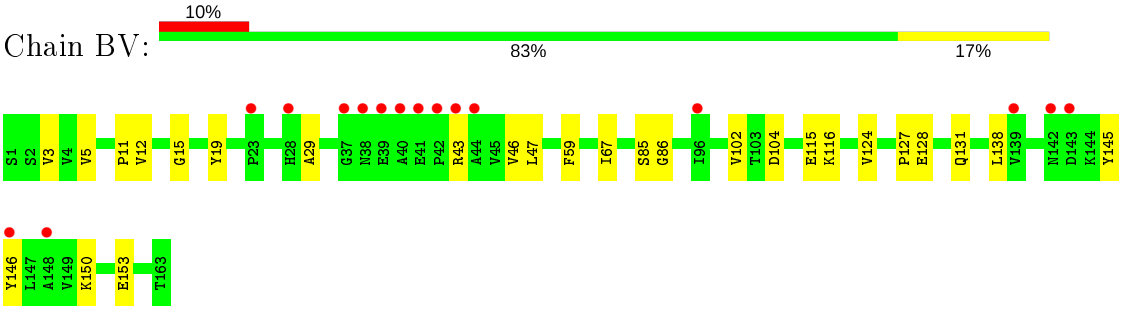


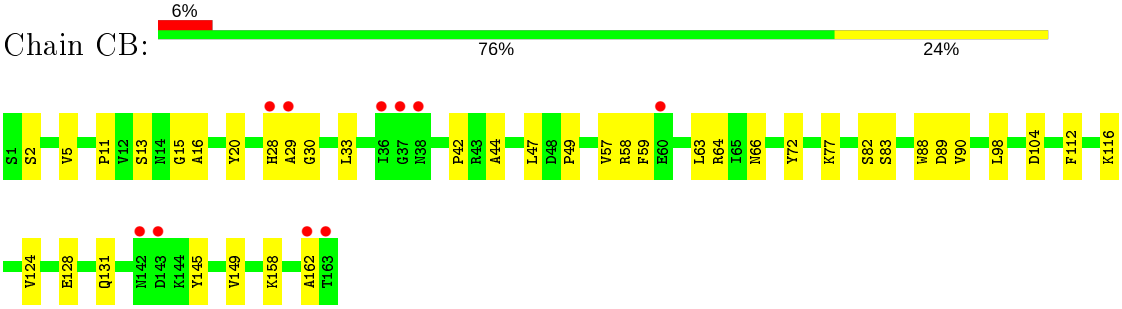

• Molecule 2: Kunitz-type inihibitor

Chain BV:



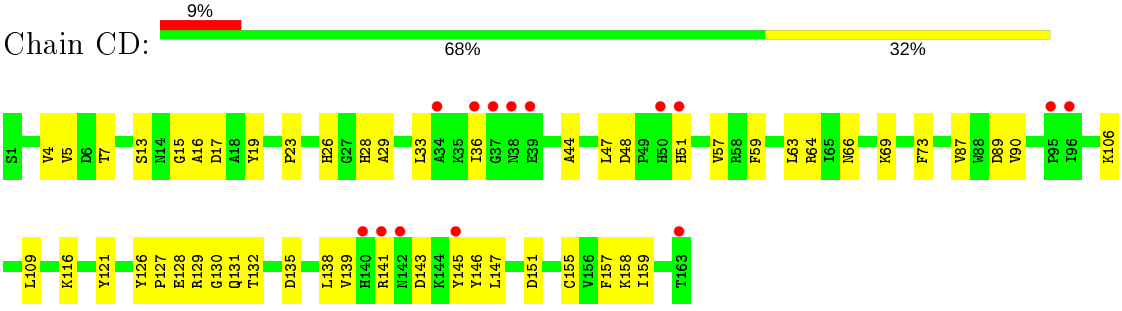

• Molecule 2: Kunitz-type inihibitor

Chain CB:



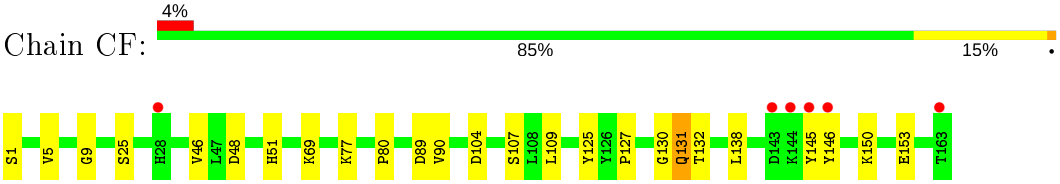

• Molecule 2: Kunitz-type inihibitor

Chain CD:



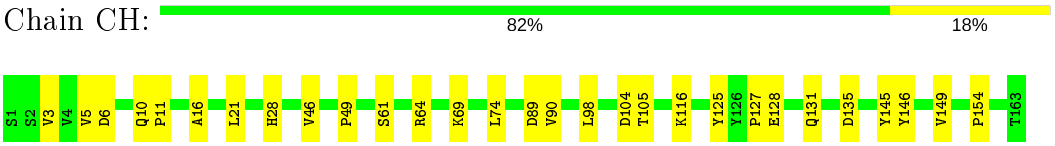

• Molecule 2: Kunitz-type inihibitor

Chain CF:



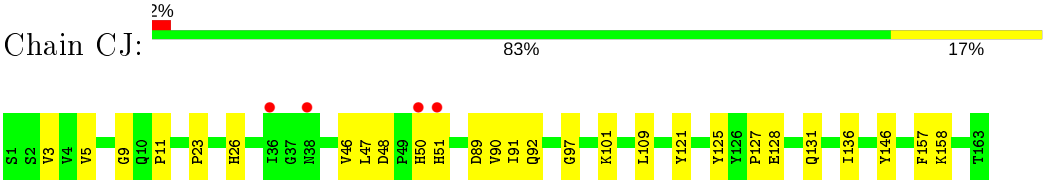

• Molecule 2: Kunitz-type inihibitor

Chain CH:



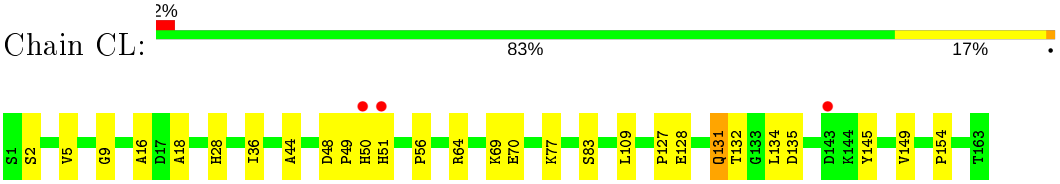

• Molecule 2: Kunitz-type inihibitor

Chain CJ:



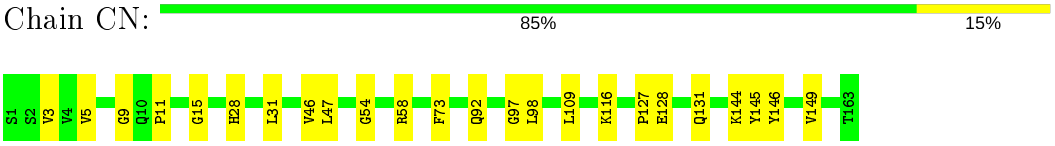

• Molecule 2: Kunitz-type inihibitor

Chain CL:



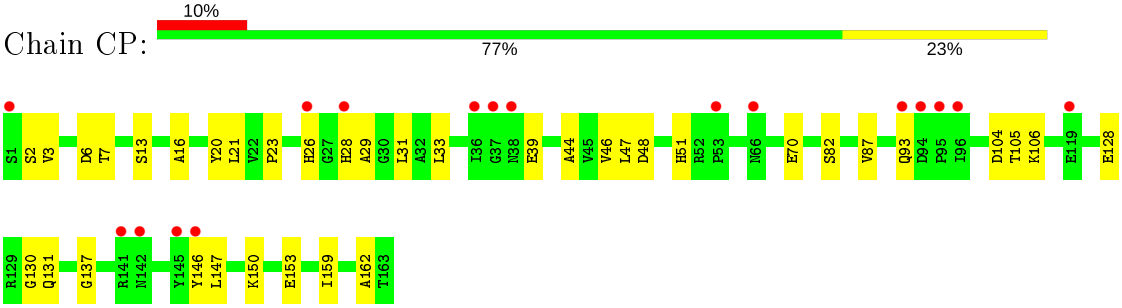

• Molecule 2: Kunitz-type inihibitor

Chain CN:




• Molecule 2: Kunitz-type inihibitor

Chain CP:




• Molecule 2: Kunitz-type inihibitor

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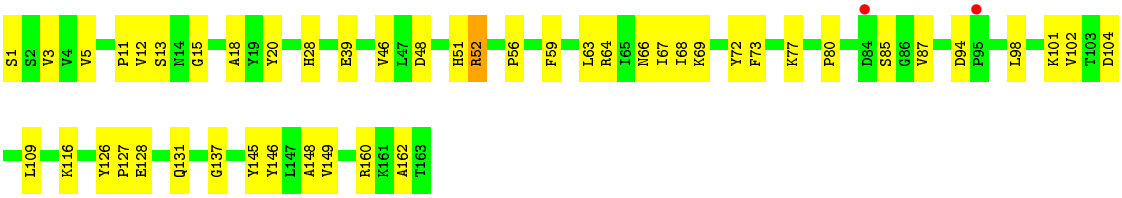
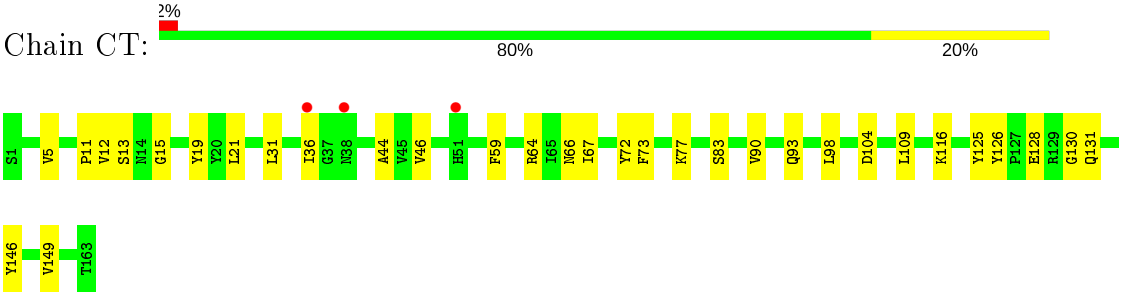


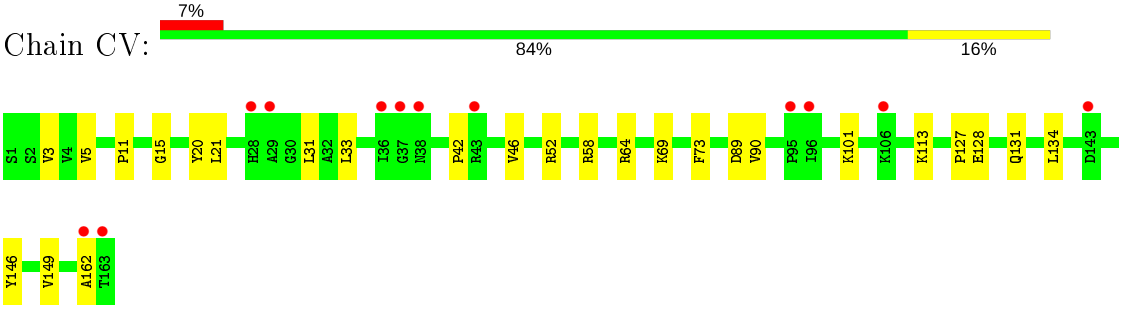

• Molecule 2: Kunitz-type inihibitor

Chain CT:



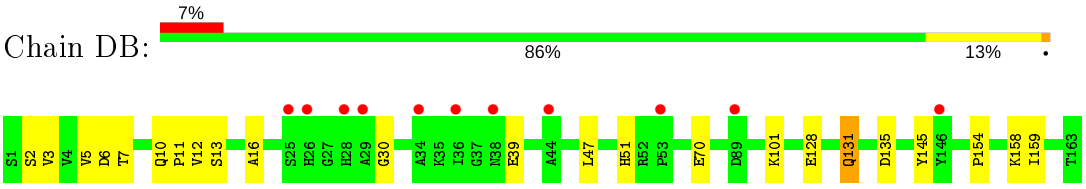

• Molecule 2: Kunitz-type inihibitor

Chain CV:



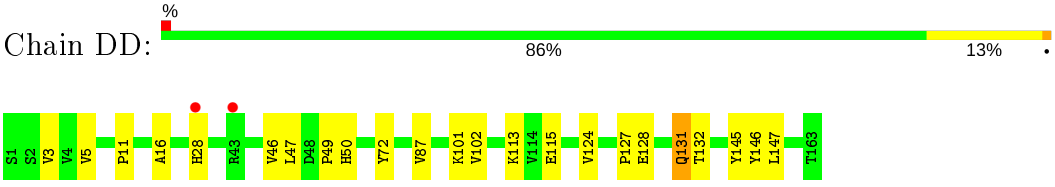

• Molecule 2: Kunitz-type inihibitor

Chain DB:



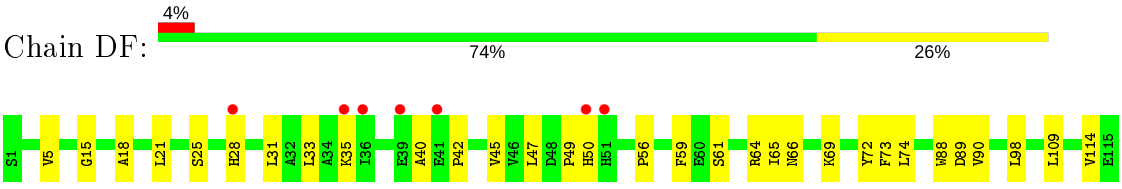

• Molecule 2: Kunitz-type inihibitor

Chain DD:



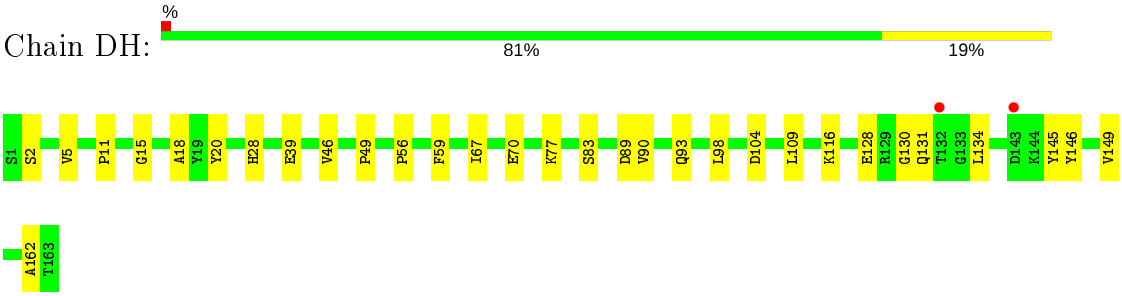

• Molecule 2: Kunitz-type inihibitor

Chain DF:



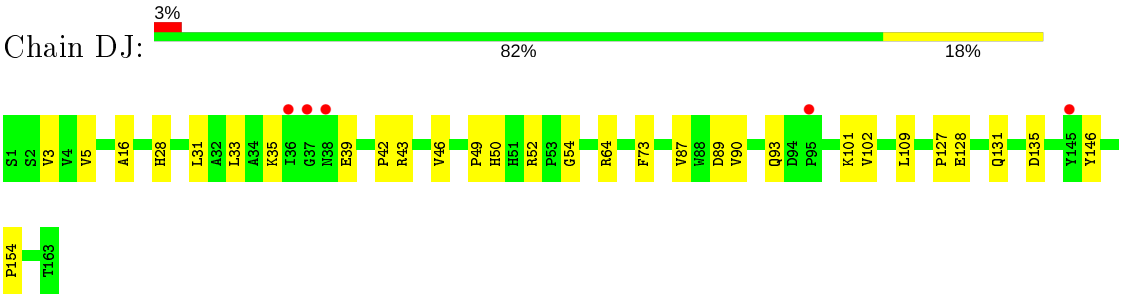

• Molecule 2: Kunitz-type inihibitor

Chain DH:



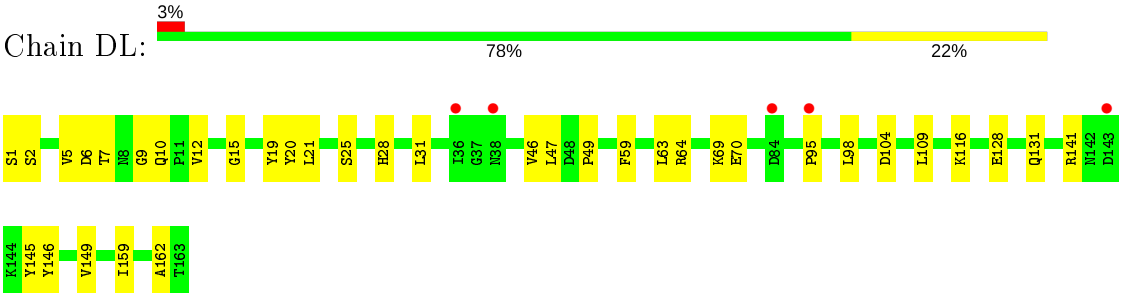

• Molecule 2: Kunitz-type inihibitor

Chain DJ:



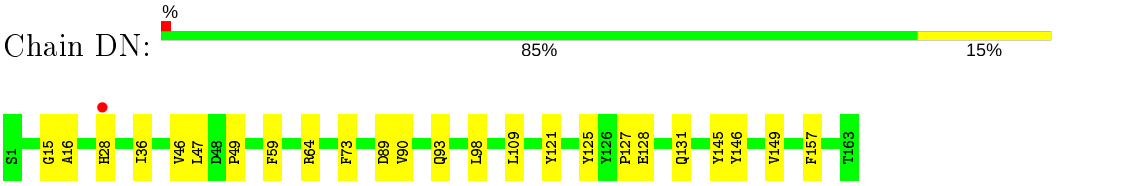

• Molecule 2: Kunitz-type inihibitor

Chain DL:



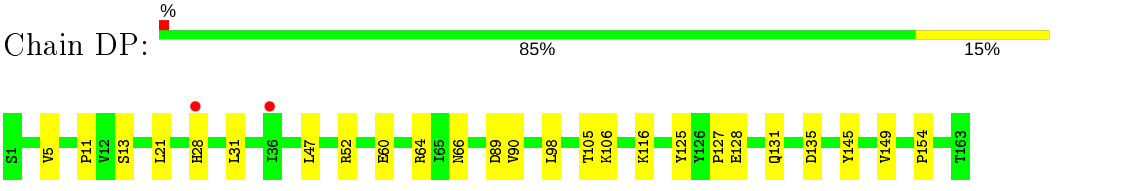

• Molecule 2: Kunitz-type inihibitor

Chain DN:



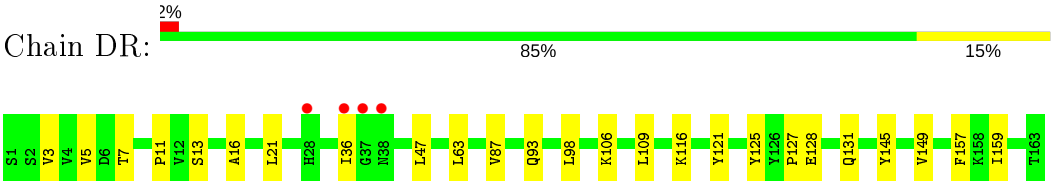

• Molecule 2: Kunitz-type inihibitor

Chain DP:



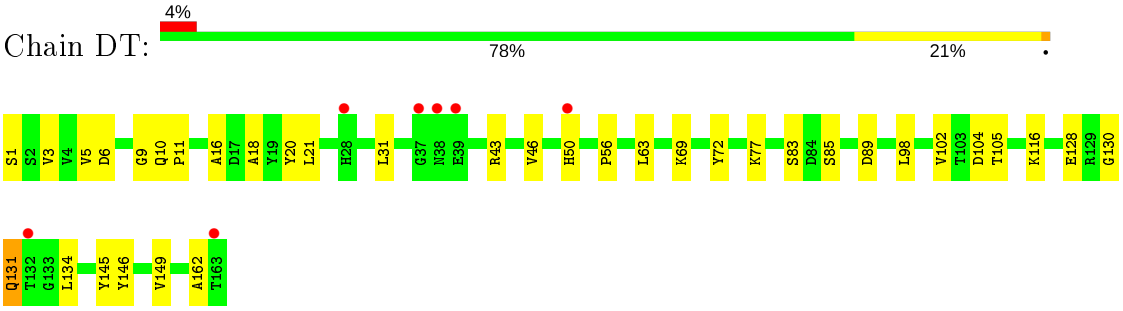
• Molecule 2: Kunitz-type inihibitor

Chain DR:



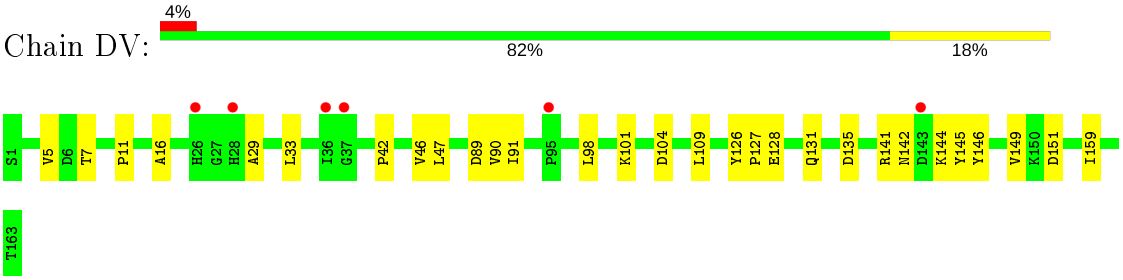

• Molecule 2: Kunitz-type inihibitor

Chain DT:




• Molecule 2: Kunitz-type inihibitor

Chain DV:



# 4 Data and refinement statistics (i)

| Property | Value | Source |
|---|---|---|
| Space group | P 1 21 1 | Depositor |
| Cell constants<br>a, b, c, $\alpha$, $\beta$, $\gamma$ | 137.17Å 483.88Å 137.01Å<br>90.00° 116.76° 90.00° | Depositor |
| Resolution (Å) | 49.23 – 3.96<br>49.23 – 3.94 | Depositor<br>EDS |
| % Data completeness<br>(in resolution range) | 85.1 (49.23-3.96)<br>85.1 (49.23-3.94) | Depositor<br>EDS |
| $R_{merge}$ | (Not available) | Depositor |
| $R_{sym}$ | 0.14 | Depositor |
| $< I/\sigma(I) >$ [1] | 3.59 (at 4.00Å) | Xtriage |
| Refinement program | PHENIX (1.12_2829) | Depositor |
| R, $R_{free}$ | 0.226 , 0.281<br>0.226 , 0.282 | Depositor<br>DCC |
| $R_{free}$ test set | 5830 reflections (4.92%) | wwPDB-VP |
| Wilson B-factor (Å$^2$) | 52.0 | Xtriage |
| Anisotropy | 0.368 | Xtriage |
| Bulk solvent $k_{sol}$(e/Å$^3$), $B_{sol}$(Å$^2$) | 0.24 , 26.7 | EDS |
| L-test for twinning[2] | $< \|L\| > = 0.49$, $< L^2 > = 0.32$ | Xtriage |
| Estimated twinning fraction | 0.028 for l,-k,h | Xtriage |
| $F_o$,$F_c$ correlation | 0.81 | EDS |
| Total number of atoms | 127116 | wwPDB-VP |
| Average B, all atoms (Å$^2$) | 71.0 | wwPDB-VP |

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.66% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

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

# 5 Model quality

## 5.1 Standard geometry

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 | AA | 0.28 | 0/1660 | 0.50 | 0/2250 |
| 1 | AC | 0.28 | 0/1660 | 0.50 | 0/2250 |
| 1 | AE | 0.28 | 0/1660 | 0.50 | 0/2250 |
| 1 | AG | 0.28 | 0/1660 | 0.50 | 0/2250 |
| 1 | AI | 0.28 | 0/1660 | 0.52 | 0/2250 |
| 1 | AK | 0.29 | 0/1660 | 0.50 | 0/2250 |
| 1 | AM | 0.28 | 0/1660 | 0.49 | 0/2250 |
| 1 | AO | 0.27 | 0/1660 | 0.49 | 0/2250 |
| 1 | AQ | 0.29 | 0/1660 | 0.51 | 0/2250 |
| 1 | AS | 0.28 | 0/1660 | 0.49 | 0/2250 |
| 1 | AU | 0.27 | 0/1660 | 0.49 | 0/2250 |
| 1 | BA | 0.27 | 0/1660 | 0.50 | 0/2250 |
| 1 | BC | 0.27 | 0/1660 | 0.49 | 0/2250 |
| 1 | BE | 0.28 | 0/1660 | 0.50 | 0/2250 |
| 1 | BG | 0.28 | 0/1660 | 0.51 | 0/2250 |
| 1 | BI | 0.27 | 0/1660 | 0.50 | 0/2250 |
| 1 | BK | 0.27 | 0/1660 | 0.51 | 0/2250 |
| 1 | BM | 0.28 | 0/1660 | 0.53 | 0/2250 |
| 1 | BO | 0.28 | 0/1660 | 0.50 | 0/2250 |
| 1 | BQ | 0.28 | 0/1660 | 0.51 | 0/2250 |
| 1 | BS | 0.27 | 0/1660 | 0.48 | 0/2250 |
| 1 | BU | 0.27 | 0/1660 | 0.50 | 0/2250 |
| 1 | CA | 0.28 | 0/1660 | 0.50 | 0/2250 |
| 1 | CC | 0.27 | 0/1660 | 0.50 | 0/2250 |
| 1 | CE | 0.29 | 0/1660 | 0.52 | 0/2250 |
| 1 | CG | 0.30 | 0/1660 | 0.50 | 0/2250 |
| 1 | CI | 0.31 | 0/1660 | 0.53 | 0/2250 |
| 1 | CK | 0.29 | 0/1660 | 0.52 | 0/2250 |
| 1 | CM | 0.28 | 0/1660 | 0.50 | 0/2250 |
| 1 | CO | 0.28 | 0/1660 | 0.51 | 0/2250 |
| 1 | CQ | 0.29 | 0/1660 | 0.51 | 0/2250 |
| 1 | CS | 0.27 | 0/1660 | 0.50 | 0/2250 |
| 1 | CU | 0.27 | 0/1660 | 0.49 | 0/2250 |
| 1 | DA | 0.29 | 0/1660 | 0.50 | 0/2250 |

| Mol | Chain | Bond lengths | | Bond angles | |
|---|---|---|---|---|---|
| | | RMSZ | #\|Z\| >5 | RMSZ | #\|Z\| >5 |
| 1 | DC | 0.29 | 0/1660 | 0.49 | 0/2250 |
| 1 | DE | 0.27 | 0/1660 | 0.49 | 0/2250 |
| 1 | DG | 0.28 | 0/1660 | 0.51 | 0/2250 |
| 1 | DI | 0.29 | 0/1660 | 0.52 | 0/2250 |
| 1 | DK | 0.30 | 0/1660 | 0.53 | 0/2250 |
| 1 | DM | 0.28 | 0/1660 | 0.50 | 0/2250 |
| 1 | DO | 0.29 | 0/1660 | 0.53 | 0/2250 |
| 1 | DQ | 0.28 | 0/1660 | 0.50 | 0/2250 |
| 1 | DS | 0.28 | 0/1660 | 0.50 | 0/2250 |
| 1 | DU | 0.27 | 0/1660 | 0.49 | 0/2250 |
| 2 | AB | 0.28 | 0/1291 | 0.55 | 0/1754 |
| 2 | AD | 0.29 | 0/1291 | 0.53 | 0/1754 |
| 2 | AF | 0.33 | 0/1291 | 0.57 | 0/1754 |
| 2 | AH | 0.29 | 0/1291 | 0.56 | 0/1754 |
| 2 | AJ | 0.30 | 0/1291 | 0.55 | 0/1754 |
| 2 | AL | 0.31 | 0/1291 | 0.52 | 0/1754 |
| 2 | AN | 0.30 | 0/1291 | 0.52 | 0/1754 |
| 2 | AP | 0.29 | 0/1291 | 0.53 | 0/1754 |
| 2 | AR | 0.28 | 0/1291 | 0.53 | 0/1754 |
| 2 | AT | 0.30 | 0/1291 | 0.54 | 0/1754 |
| 2 | AV | 0.30 | 0/1291 | 0.53 | 0/1754 |
| 2 | BB | 0.29 | 0/1291 | 0.55 | 0/1754 |
| 2 | BD | 0.29 | 0/1291 | 0.53 | 0/1754 |
| 2 | BF | 0.28 | 0/1291 | 0.50 | 0/1754 |
| 2 | BH | 0.30 | 0/1291 | 0.55 | 0/1754 |
| 2 | BJ | 0.30 | 0/1291 | 0.53 | 0/1754 |
| 2 | BL | 0.29 | 0/1291 | 0.54 | 0/1754 |
| 2 | BN | 0.32 | 0/1291 | 0.54 | 1/1754 (0.1%) |
| 2 | BP | 0.30 | 0/1291 | 0.55 | 0/1754 |
| 2 | BR | 0.31 | 0/1291 | 0.55 | 0/1754 |
| 2 | BT | 0.28 | 0/1291 | 0.51 | 0/1754 |
| 2 | BV | 0.28 | 0/1291 | 0.51 | 0/1754 |
| 2 | CB | 0.30 | 0/1291 | 0.53 | 0/1754 |
| 2 | CD | 0.30 | 0/1291 | 0.57 | 0/1754 |
| 2 | CF | 0.29 | 0/1291 | 0.53 | 0/1754 |
| 2 | CH | 0.31 | 0/1291 | 0.55 | 0/1754 |
| 2 | CJ | 0.31 | 0/1291 | 0.56 | 0/1754 |
| 2 | CL | 0.31 | 0/1291 | 0.53 | 0/1754 |
| 2 | CN | 0.30 | 0/1291 | 0.53 | 0/1754 |
| 2 | CP | 0.28 | 0/1291 | 0.51 | 0/1754 |
| 2 | CR | 0.30 | 0/1291 | 0.52 | 0/1754 |
| 2 | CT | 0.30 | 0/1291 | 0.52 | 0/1754 |
| 2 | CV | 0.27 | 0/1291 | 0.51 | 0/1754 |

| Mol | Chain | Bond lengths | | Bond angles | |
|---|---|---|---|---|---|
| | | RMSZ | #\|Z\| >5 | RMSZ | #\|Z\| >5 |
| 2 | DB | 0.30 | 0/1291 | 0.53 | 0/1754 |
| 2 | DD | 0.32 | 0/1291 | 0.56 | 1/1754 (0.1%) |
| 2 | DF | 0.34 | 0/1291 | 0.57 | 0/1754 |
| 2 | DH | 0.30 | 0/1291 | 0.53 | 0/1754 |
| 2 | DJ | 0.31 | 0/1291 | 0.52 | 0/1754 |
| 2 | DL | 0.31 | 0/1291 | 0.56 | 0/1754 |
| 2 | DN | 0.30 | 0/1291 | 0.55 | 0/1754 |
| 2 | DP | 0.31 | 0/1291 | 0.53 | 0/1754 |
| 2 | DR | 0.29 | 0/1291 | 0.54 | 0/1754 |
| 2 | DT | 0.29 | 0/1291 | 0.53 | 0/1754 |
| 2 | DV | 0.29 | 0/1291 | 0.53 | 0/1754 |
| All | All | 0.29 | 0/129844 | 0.52 | 2/176176 (0.0%) |

There are no bond length outliers.

All (2) bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed($^o$) | Ideal($^o$) |
|---|---|---|---|---|---|---|---|
| 2 | DD | 131 | GLN | CA-CB-CG | -6.06 | 100.07 | 113.40 |
| 2 | BN | 5 | VAL | CG1-CB-CG2 | 5.25 | 119.31 | 110.90 |

There are no chirality outliers.

There are no planarity outliers.

## 5.2 Too-close contacts (i)

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

| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|---|---|---|---|---|---|---|
| 1 | AA | 1629 | 0 | 1588 | 23 | 0 |
| 1 | AC | 1629 | 0 | 1588 | 28 | 1 |
| 1 | AE | 1629 | 0 | 1588 | 25 | 0 |
| 1 | AG | 1629 | 0 | 1588 | 20 | 0 |
| 1 | AI | 1629 | 0 | 1588 | 24 | 0 |
| 1 | AK | 1629 | 0 | 1588 | 26 | 0 |
| 1 | AM | 1629 | 0 | 1588 | 20 | 0 |
| 1 | AO | 1629 | 0 | 1588 | 28 | 0 |
| 1 | AQ | 1629 | 0 | 1588 | 40 | 0 |

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| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|---|---|---|---|---|---|---|
| 1 | AS | 1629 | 0 | 1588 | 24 | 0 |
| 1 | AU | 1629 | 0 | 1588 | 24 | 0 |
| 1 | BA | 1629 | 0 | 1588 | 27 | 0 |
| 1 | BC | 1629 | 0 | 1588 | 15 | 0 |
| 1 | BE | 1629 | 0 | 1588 | 22 | 0 |
| 1 | BG | 1629 | 0 | 1588 | 22 | 0 |
| 1 | BI | 1629 | 0 | 1588 | 21 | 0 |
| 1 | BK | 1629 | 0 | 1588 | 22 | 0 |
| 1 | BM | 1629 | 0 | 1588 | 25 | 1 |
| 1 | BO | 1629 | 0 | 1588 | 22 | 0 |
| 1 | BQ | 1629 | 0 | 1588 | 31 | 0 |
| 1 | BS | 1629 | 0 | 1588 | 32 | 0 |
| 1 | BU | 1629 | 0 | 1588 | 24 | 0 |
| 1 | CA | 1629 | 0 | 1588 | 24 | 0 |
| 1 | CC | 1629 | 0 | 1588 | 30 | 0 |
| 1 | CE | 1629 | 0 | 1588 | 20 | 0 |
| 1 | CG | 1629 | 0 | 1588 | 30 | 0 |
| 1 | CI | 1629 | 0 | 1588 | 12 | 0 |
| 1 | CK | 1629 | 0 | 1588 | 23 | 0 |
| 1 | CM | 1629 | 0 | 1588 | 23 | 0 |
| 1 | CO | 1629 | 0 | 1588 | 33 | 0 |
| 1 | CQ | 1629 | 0 | 1588 | 34 | 0 |
| 1 | CS | 1629 | 0 | 1588 | 26 | 0 |
| 1 | CU | 1629 | 0 | 1588 | 28 | 1 |
| 1 | DA | 1629 | 0 | 1588 | 19 | 1 |
| 1 | DC | 1629 | 0 | 1588 | 20 | 1 |
| 1 | DE | 1629 | 0 | 1588 | 30 | 0 |
| 1 | DG | 1629 | 0 | 1588 | 16 | 0 |
| 1 | DI | 1629 | 0 | 1588 | 41 | 0 |
| 1 | DK | 1629 | 0 | 1588 | 24 | 0 |
| 1 | DM | 1629 | 0 | 1588 | 25 | 0 |
| 1 | DO | 1629 | 0 | 1588 | 28 | 0 |
| 1 | DQ | 1629 | 0 | 1588 | 29 | 1 |
| 1 | DS | 1629 | 0 | 1588 | 24 | 0 |
| 1 | DU | 1629 | 0 | 1588 | 20 | 0 |
| 2 | AB | 1260 | 0 | 1265 | 27 | 0 |
| 2 | AD | 1260 | 0 | 1265 | 25 | 0 |
| 2 | AF | 1260 | 0 | 1265 | 28 | 0 |
| 2 | AH | 1260 | 0 | 1265 | 34 | 0 |
| 2 | AJ | 1260 | 0 | 1265 | 23 | 0 |
| 2 | AL | 1260 | 0 | 1265 | 32 | 0 |
| 2 | AN | 1260 | 0 | 1265 | 36 | 0 |

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| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|---|---|---|---|---|---|---|
| 2 | AP | 1260 | 0 | 1265 | 32 | 0 |
| 2 | AR | 1260 | 0 | 1265 | 29 | 0 |
| 2 | AT | 1260 | 0 | 1265 | 25 | 0 |
| 2 | AV | 1260 | 0 | 1265 | 30 | 1 |
| 2 | BB | 1260 | 0 | 1265 | 27 | 1 |
| 2 | BD | 1260 | 0 | 1265 | 40 | 1 |
| 2 | BF | 1260 | 0 | 1265 | 22 | 0 |
| 2 | BH | 1260 | 0 | 1265 | 25 | 0 |
| 2 | BJ | 1260 | 0 | 1265 | 32 | 0 |
| 2 | BL | 1260 | 0 | 1265 | 29 | 0 |
| 2 | BN | 1260 | 0 | 1265 | 23 | 0 |
| 2 | BP | 1260 | 0 | 1265 | 27 | 0 |
| 2 | BR | 1260 | 0 | 1265 | 27 | 0 |
| 2 | BT | 1260 | 0 | 1265 | 25 | 0 |
| 2 | BV | 1260 | 0 | 1265 | 17 | 1 |
| 2 | CB | 1260 | 0 | 1265 | 32 | 0 |
| 2 | CD | 1260 | 0 | 1265 | 48 | 0 |
| 2 | CF | 1260 | 0 | 1265 | 21 | 0 |
| 2 | CH | 1260 | 0 | 1265 | 29 | 0 |
| 2 | CJ | 1260 | 0 | 1265 | 24 | 0 |
| 2 | CL | 1260 | 0 | 1265 | 29 | 1 |
| 2 | CN | 1260 | 0 | 1265 | 28 | 0 |
| 2 | CP | 1260 | 0 | 1265 | 29 | 0 |
| 2 | CR | 1260 | 0 | 1265 | 41 | 0 |
| 2 | CT | 1260 | 0 | 1265 | 28 | 0 |
| 2 | CV | 1260 | 0 | 1265 | 18 | 0 |
| 2 | DB | 1260 | 0 | 1265 | 19 | 0 |
| 2 | DD | 1260 | 0 | 1265 | 22 | 0 |
| 2 | DF | 1260 | 0 | 1265 | 53 | 0 |
| 2 | DH | 1260 | 0 | 1265 | 28 | 0 |
| 2 | DJ | 1260 | 0 | 1265 | 28 | 0 |
| 2 | DL | 1260 | 0 | 1265 | 38 | 0 |
| 2 | DN | 1260 | 0 | 1265 | 24 | 0 |
| 2 | DP | 1260 | 0 | 1265 | 22 | 0 |
| 2 | DR | 1260 | 0 | 1265 | 22 | 0 |
| 2 | DT | 1260 | 0 | 1265 | 33 | 1 |
| 2 | DV | 1260 | 0 | 1265 | 25 | 2 |
| All | All | 127116 | 0 | 125532 | 1896 | 7 |

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 8.

The worst 5 of 1896 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) |
|---|---|---|---|
| 2:AL:5:VAL:HG22 | 2:AN:131:GLN:HG2 | 1.03 | 1.03 |
| 2:AL:5:VAL:HG22 | 2:AN:131:GLN:CG | 1.91 | 0.99 |
| 2:AL:5:VAL:CG2 | 2:AN:131:GLN:HG2 | 1.91 | 0.99 |
| 1:CE:32:SER:HG | 1:CE:38:HIS:HD1 | 0.99 | 0.98 |
| 2:CJ:5:VAL:HG22 | 2:CL:131:GLN:HG2 | 1.45 | 0.97 |

The worst 5 of 7 symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|---|---|---|---|
| 1:AC:124:CYS:O | 2:AV:145:TYR:OH[2_545] | 1.99 | 0.21 |
| 1:DA:124:CYS:O | 2:DT:145:TYR:OH[2_646] | 2.04 | 0.16 |
| 2:BD:142:ASN:OD1 | 1:DQ:76:ASN:ND2[1_554] | 2.06 | 0.14 |
| 1:CU:74:GLU:O | 2:DV:141:ARG:NH2[2_646] | 2.09 | 0.11 |
| 1:BM:76:ASN:OD1 | 2:CL:50:HIS:NE2[1_554] | 2.10 | 0.10 |

## 5.3 Torsion angles (i)

### 5.3.1 Protein backbone (i)

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

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

| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles | |
|---|---|---|---|---|---|---|---|
| 1 | AA | 221/223 (99%) | 215 (97%) | 6 (3%) | 0 | 100 | 100 |
| 1 | AC | 221/223 (99%) | 216 (98%) | 5 (2%) | 0 | 100 | 100 |
| 1 | AE | 221/223 (99%) | 215 (97%) | 6 (3%) | 0 | 100 | 100 |
| 1 | AG | 221/223 (99%) | 216 (98%) | 5 (2%) | 0 | 100 | 100 |
| 1 | AI | 221/223 (99%) | 218 (99%) | 3 (1%) | 0 | 100 | 100 |
| 1 | AK | 221/223 (99%) | 217 (98%) | 4 (2%) | 0 | 100 | 100 |
| 1 | AM | 221/223 (99%) | 216 (98%) | 5 (2%) | 0 | 100 | 100 |
| 1 | AO | 221/223 (99%) | 216 (98%) | 5 (2%) | 0 | 100 | 100 |
| 1 | AQ | 221/223 (99%) | 215 (97%) | 6 (3%) | 0 | 100 | 100 |
| 1 | AS | 221/223 (99%) | 215 (97%) | 6 (3%) | 0 | 100 | 100 |

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| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles | |
|---|---|---|---|---|---|---|---|
| 1 | AU | 221/223 (99%) | 216 (98%) | 5 (2%) | 0 | 100 | 100 |
| 1 | BA | 221/223 (99%) | 214 (97%) | 7 (3%) | 0 | 100 | 100 |
| 1 | BC | 221/223 (99%) | 216 (98%) | 5 (2%) | 0 | 100 | 100 |
| 1 | BE | 221/223 (99%) | 216 (98%) | 5 (2%) | 0 | 100 | 100 |
| 1 | BG | 221/223 (99%) | 216 (98%) | 5 (2%) | 0 | 100 | 100 |
| 1 | BI | 221/223 (99%) | 217 (98%) | 4 (2%) | 0 | 100 | 100 |
| 1 | BK | 221/223 (99%) | 217 (98%) | 4 (2%) | 0 | 100 | 100 |
| 1 | BM | 221/223 (99%) | 215 (97%) | 6 (3%) | 0 | 100 | 100 |
| 1 | BO | 221/223 (99%) | 217 (98%) | 4 (2%) | 0 | 100 | 100 |
| 1 | BQ | 221/223 (99%) | 217 (98%) | 4 (2%) | 0 | 100 | 100 |
| 1 | BS | 221/223 (99%) | 216 (98%) | 5 (2%) | 0 | 100 | 100 |
| 1 | BU | 221/223 (99%) | 217 (98%) | 4 (2%) | 0 | 100 | 100 |
| 1 | CA | 221/223 (99%) | 215 (97%) | 6 (3%) | 0 | 100 | 100 |
| 1 | CC | 221/223 (99%) | 216 (98%) | 5 (2%) | 0 | 100 | 100 |
| 1 | CE | 221/223 (99%) | 217 (98%) | 4 (2%) | 0 | 100 | 100 |
| 1 | CG | 221/223 (99%) | 216 (98%) | 5 (2%) | 0 | 100 | 100 |
| 1 | CI | 221/223 (99%) | 216 (98%) | 5 (2%) | 0 | 100 | 100 |
| 1 | CK | 221/223 (99%) | 218 (99%) | 3 (1%) | 0 | 100 | 100 |
| 1 | CM | 221/223 (99%) | 217 (98%) | 4 (2%) | 0 | 100 | 100 |
| 1 | CO | 221/223 (99%) | 215 (97%) | 5 (2%) | 1 (0%) | 29 | 66 |
| 1 | CQ | 221/223 (99%) | 214 (97%) | 7 (3%) | 0 | 100 | 100 |
| 1 | CS | 221/223 (99%) | 215 (97%) | 6 (3%) | 0 | 100 | 100 |
| 1 | CU | 221/223 (99%) | 216 (98%) | 5 (2%) | 0 | 100 | 100 |
| 1 | DA | 221/223 (99%) | 214 (97%) | 7 (3%) | 0 | 100 | 100 |
| 1 | DC | 221/223 (99%) | 217 (98%) | 4 (2%) | 0 | 100 | 100 |
| 1 | DE | 221/223 (99%) | 217 (98%) | 4 (2%) | 0 | 100 | 100 |
| 1 | DG | 221/223 (99%) | 216 (98%) | 5 (2%) | 0 | 100 | 100 |
| 1 | DI | 221/223 (99%) | 215 (97%) | 6 (3%) | 0 | 100 | 100 |
| 1 | DK | 221/223 (99%) | 216 (98%) | 5 (2%) | 0 | 100 | 100 |
| 1 | DM | 221/223 (99%) | 216 (98%) | 5 (2%) | 0 | 100 | 100 |
| 1 | DO | 221/223 (99%) | 215 (97%) | 6 (3%) | 0 | 100 | 100 |

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| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles |
|---|---|---|---|---|---|---|
| 1 | DQ | 221/223 (99%) | 214 (97%) | 5 (2%) | 2 (1%) | 17 54 |
| 1 | DS | 221/223 (99%) | 217 (98%) | 4 (2%) | 0 | 100 100 |
| 1 | DU | 221/223 (99%) | 215 (97%) | 6 (3%) | 0 | 100 100 |
| 2 | AB | 161/163 (99%) | 154 (96%) | 7 (4%) | 0 | 100 100 |
| 2 | AD | 161/163 (99%) | 152 (94%) | 9 (6%) | 0 | 100 100 |
| 2 | AF | 161/163 (99%) | 154 (96%) | 7 (4%) | 0 | 100 100 |
| 2 | AH | 161/163 (99%) | 153 (95%) | 8 (5%) | 0 | 100 100 |
| 2 | AJ | 161/163 (99%) | 152 (94%) | 9 (6%) | 0 | 100 100 |
| 2 | AL | 161/163 (99%) | 153 (95%) | 8 (5%) | 0 | 100 100 |
| 2 | AN | 161/163 (99%) | 153 (95%) | 8 (5%) | 0 | 100 100 |
| 2 | AP | 161/163 (99%) | 154 (96%) | 7 (4%) | 0 | 100 100 |
| 2 | AR | 161/163 (99%) | 153 (95%) | 8 (5%) | 0 | 100 100 |
| 2 | AT | 161/163 (99%) | 153 (95%) | 8 (5%) | 0 | 100 100 |
| 2 | AV | 161/163 (99%) | 153 (95%) | 8 (5%) | 0 | 100 100 |
| 2 | BB | 161/163 (99%) | 154 (96%) | 7 (4%) | 0 | 100 100 |
| 2 | BD | 161/163 (99%) | 154 (96%) | 7 (4%) | 0 | 100 100 |
| 2 | BF | 161/163 (99%) | 150 (93%) | 10 (6%) | 1 (1%) | 25 63 |
| 2 | BH | 161/163 (99%) | 154 (96%) | 7 (4%) | 0 | 100 100 |
| 2 | BJ | 161/163 (99%) | 153 (95%) | 8 (5%) | 0 | 100 100 |
| 2 | BL | 161/163 (99%) | 153 (95%) | 8 (5%) | 0 | 100 100 |
| 2 | BN | 161/163 (99%) | 154 (96%) | 7 (4%) | 0 | 100 100 |
| 2 | BP | 161/163 (99%) | 154 (96%) | 7 (4%) | 0 | 100 100 |
| 2 | BR | 161/163 (99%) | 153 (95%) | 8 (5%) | 0 | 100 100 |
| 2 | BT | 161/163 (99%) | 154 (96%) | 7 (4%) | 0 | 100 100 |
| 2 | BV | 161/163 (99%) | 154 (96%) | 7 (4%) | 0 | 100 100 |
| 2 | CB | 161/163 (99%) | 154 (96%) | 7 (4%) | 0 | 100 100 |
| 2 | CD | 161/163 (99%) | 154 (96%) | 7 (4%) | 0 | 100 100 |
| 2 | CF | 161/163 (99%) | 150 (93%) | 10 (6%) | 1 (1%) | 25 63 |
| 2 | CH | 161/163 (99%) | 153 (95%) | 8 (5%) | 0 | 100 100 |
| 2 | CJ | 161/163 (99%) | 153 (95%) | 8 (5%) | 0 | 100 100 |
| 2 | CL | 161/163 (99%) | 152 (94%) | 9 (6%) | 0 | 100 100 |

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| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles | |
|---|---|---|---|---|---|---|---|
| 2 | CN | 161/163 (99%) | 153 (95%) | 8 (5%) | 0 | 100 | 100 |
| 2 | CP | 161/163 (99%) | 154 (96%) | 7 (4%) | 0 | 100 | 100 |
| 2 | CR | 161/163 (99%) | 153 (95%) | 8 (5%) | 0 | 100 | 100 |
| 2 | CT | 161/163 (99%) | 152 (94%) | 9 (6%) | 0 | 100 | 100 |
| 2 | CV | 161/163 (99%) | 152 (94%) | 9 (6%) | 0 | 100 | 100 |
| 2 | DB | 161/163 (99%) | 154 (96%) | 7 (4%) | 0 | 100 | 100 |
| 2 | DD | 161/163 (99%) | 152 (94%) | 9 (6%) | 0 | 100 | 100 |
| 2 | DF | 161/163 (99%) | 152 (94%) | 9 (6%) | 0 | 100 | 100 |
| 2 | DH | 161/163 (99%) | 154 (96%) | 7 (4%) | 0 | 100 | 100 |
| 2 | DJ | 161/163 (99%) | 152 (94%) | 9 (6%) | 0 | 100 | 100 |
| 2 | DL | 161/163 (99%) | 153 (95%) | 8 (5%) | 0 | 100 | 100 |
| 2 | DN | 161/163 (99%) | 154 (96%) | 7 (4%) | 0 | 100 | 100 |
| 2 | DP | 161/163 (99%) | 153 (95%) | 8 (5%) | 0 | 100 | 100 |
| 2 | DR | 161/163 (99%) | 153 (95%) | 8 (5%) | 0 | 100 | 100 |
| 2 | DT | 161/163 (99%) | 153 (95%) | 8 (5%) | 0 | 100 | 100 |
| 2 | DV | 161/163 (99%) | 154 (96%) | 7 (4%) | 0 | 100 | 100 |
| All | All | 16808/16984 (99%) | 16235 (97%) | 568 (3%) | 5 (0%) | 100 | 100 |

All (5) Ramachandran outliers are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 2 | BF | 107 | SER |
| 2 | CF | 107 | SER |
| 1 | CO | 22 | CYS |
| 1 | DQ | 113 | SER |
| 1 | DQ | 112 | ASN |

### 5.3.2 Protein sidechains (i)

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

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

| Mol | Chain | Analysed | Rotameric | Outliers | Percentiles | |
|---|---|---|---|---|---|---|
| 1 | AA | 184/184 (100%) | 184 (100%) | 0 | 100 | 100 |
| 1 | AC | 184/184 (100%) | 184 (100%) | 0 | 100 | 100 |
| 1 | AE | 184/184 (100%) | 184 (100%) | 0 | 100 | 100 |
| 1 | AG | 184/184 (100%) | 184 (100%) | 0 | 100 | 100 |
| 1 | AI | 184/184 (100%) | 184 (100%) | 0 | 100 | 100 |
| 1 | AK | 184/184 (100%) | 183 (100%) | 1 (0%) | 88 | 93 |
| 1 | AM | 184/184 (100%) | 184 (100%) | 0 | 100 | 100 |
| 1 | AO | 184/184 (100%) | 183 (100%) | 1 (0%) | 88 | 93 |
| 1 | AQ | 184/184 (100%) | 184 (100%) | 0 | 100 | 100 |
| 1 | AS | 184/184 (100%) | 184 (100%) | 0 | 100 | 100 |
| 1 | AU | 184/184 (100%) | 184 (100%) | 0 | 100 | 100 |
| 1 | BA | 184/184 (100%) | 184 (100%) | 0 | 100 | 100 |
| 1 | BC | 184/184 (100%) | 184 (100%) | 0 | 100 | 100 |
| 1 | BE | 184/184 (100%) | 184 (100%) | 0 | 100 | 100 |
| 1 | BG | 184/184 (100%) | 184 (100%) | 0 | 100 | 100 |
| 1 | BI | 184/184 (100%) | 183 (100%) | 1 (0%) | 88 | 93 |
| 1 | BK | 184/184 (100%) | 184 (100%) | 0 | 100 | 100 |
| 1 | BM | 184/184 (100%) | 183 (100%) | 1 (0%) | 88 | 93 |
| 1 | BO | 184/184 (100%) | 184 (100%) | 0 | 100 | 100 |
| 1 | BQ | 184/184 (100%) | 184 (100%) | 0 | 100 | 100 |
| 1 | BS | 184/184 (100%) | 184 (100%) | 0 | 100 | 100 |
| 1 | BU | 184/184 (100%) | 184 (100%) | 0 | 100 | 100 |
| 1 | CA | 184/184 (100%) | 184 (100%) | 0 | 100 | 100 |
| 1 | CC | 184/184 (100%) | 184 (100%) | 0 | 100 | 100 |
| 1 | CE | 184/184 (100%) | 184 (100%) | 0 | 100 | 100 |
| 1 | CG | 184/184 (100%) | 183 (100%) | 1 (0%) | 88 | 93 |
| 1 | CI | 184/184 (100%) | 184 (100%) | 0 | 100 | 100 |
| 1 | CK | 184/184 (100%) | 183 (100%) | 1 (0%) | 88 | 93 |
| 1 | CM | 184/184 (100%) | 184 (100%) | 0 | 100 | 100 |
| 1 | CO | 184/184 (100%) | 184 (100%) | 0 | 100 | 100 |
| 1 | CQ | 184/184 (100%) | 183 (100%) | 1 (0%) | 88 | 93 |
| 1 | CS | 184/184 (100%) | 184 (100%) | 0 | 100 | 100 |

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| Mol | Chain | Analysed | Rotameric | Outliers | Percentiles |
|---|---|---|---|---|---|
| 1 | CU | 184/184 (100%) | 184 (100%) | 0 | 100 100 |
| 1 | DA | 184/184 (100%) | 184 (100%) | 0 | 100 100 |
| 1 | DC | 184/184 (100%) | 184 (100%) | 0 | 100 100 |
| 1 | DE | 184/184 (100%) | 184 (100%) | 0 | 100 100 |
| 1 | DG | 184/184 (100%) | 184 (100%) | 0 | 100 100 |
| 1 | DI | 184/184 (100%) | 184 (100%) | 0 | 100 100 |
| 1 | DK | 184/184 (100%) | 184 (100%) | 0 | 100 100 |
| 1 | DM | 184/184 (100%) | 184 (100%) | 0 | 100 100 |
| 1 | DO | 184/184 (100%) | 183 (100%) | 1 (0%) | 88 93 |
| 1 | DQ | 184/184 (100%) | 184 (100%) | 0 | 100 100 |
| 1 | DS | 184/184 (100%) | 184 (100%) | 0 | 100 100 |
| 1 | DU | 184/184 (100%) | 183 (100%) | 1 (0%) | 88 93 |
| 2 | AB | 137/137 (100%) | 137 (100%) | 0 | 100 100 |
| 2 | AD | 137/137 (100%) | 137 (100%) | 0 | 100 100 |
| 2 | AF | 137/137 (100%) | 137 (100%) | 0 | 100 100 |
| 2 | AH | 137/137 (100%) | 137 (100%) | 0 | 100 100 |
| 2 | AJ | 137/137 (100%) | 137 (100%) | 0 | 100 100 |
| 2 | AL | 137/137 (100%) | 137 (100%) | 0 | 100 100 |
| 2 | AN | 137/137 (100%) | 137 (100%) | 0 | 100 100 |
| 2 | AP | 137/137 (100%) | 137 (100%) | 0 | 100 100 |
| 2 | AR | 137/137 (100%) | 136 (99%) | 1 (1%) | 84 90 |
| 2 | AT | 137/137 (100%) | 137 (100%) | 0 | 100 100 |
| 2 | AV | 137/137 (100%) | 137 (100%) | 0 | 100 100 |
| 2 | BB | 137/137 (100%) | 137 (100%) | 0 | 100 100 |
| 2 | BD | 137/137 (100%) | 137 (100%) | 0 | 100 100 |
| 2 | BF | 137/137 (100%) | 137 (100%) | 0 | 100 100 |
| 2 | BH | 137/137 (100%) | 137 (100%) | 0 | 100 100 |
| 2 | BJ | 137/137 (100%) | 137 (100%) | 0 | 100 100 |
| 2 | BL | 137/137 (100%) | 136 (99%) | 1 (1%) | 84 90 |
| 2 | BN | 137/137 (100%) | 137 (100%) | 0 | 100 100 |
| 2 | BP | 137/137 (100%) | 136 (99%) | 1 (1%) | 84 90 |

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| Mol | Chain | Analysed | Rotameric | Outliers | Percentiles |
|---|---|---|---|---|---|
| 2 | BR | 137/137 (100%) | 136 (99%) | 1 (1%) | 84 90 |
| 2 | BT | 137/137 (100%) | 137 (100%) | 0 | 100 100 |
| 2 | BV | 137/137 (100%) | 137 (100%) | 0 | 100 100 |
| 2 | CB | 137/137 (100%) | 137 (100%) | 0 | 100 100 |
| 2 | CD | 137/137 (100%) | 137 (100%) | 0 | 100 100 |
| 2 | CF | 137/137 (100%) | 136 (99%) | 1 (1%) | 84 90 |
| 2 | CH | 137/137 (100%) | 137 (100%) | 0 | 100 100 |
| 2 | CJ | 137/137 (100%) | 137 (100%) | 0 | 100 100 |
| 2 | CL | 137/137 (100%) | 136 (99%) | 1 (1%) | 84 90 |
| 2 | CN | 137/137 (100%) | 137 (100%) | 0 | 100 100 |
| 2 | CP | 137/137 (100%) | 137 (100%) | 0 | 100 100 |
| 2 | CR | 137/137 (100%) | 136 (99%) | 1 (1%) | 84 90 |
| 2 | CT | 137/137 (100%) | 137 (100%) | 0 | 100 100 |
| 2 | CV | 137/137 (100%) | 136 (99%) | 1 (1%) | 84 90 |
| 2 | DB | 137/137 (100%) | 136 (99%) | 1 (1%) | 84 90 |
| 2 | DD | 137/137 (100%) | 137 (100%) | 0 | 100 100 |
| 2 | DF | 137/137 (100%) | 137 (100%) | 0 | 100 100 |
| 2 | DH | 137/137 (100%) | 137 (100%) | 0 | 100 100 |
| 2 | DJ | 137/137 (100%) | 136 (99%) | 1 (1%) | 84 90 |
| 2 | DL | 137/137 (100%) | 137 (100%) | 0 | 100 100 |
| 2 | DN | 137/137 (100%) | 137 (100%) | 0 | 100 100 |
| 2 | DP | 137/137 (100%) | 137 (100%) | 0 | 100 100 |
| 2 | DR | 137/137 (100%) | 137 (100%) | 0 | 100 100 |
| 2 | DT | 137/137 (100%) | 134 (98%) | 3 (2%) | 52 71 |
| 2 | DV | 137/137 (100%) | 137 (100%) | 0 | 100 100 |
| All | All | 14124/14124 (100%) | 14102 (100%) | 22 (0%) | 93 96 |

5 of 22 residues with a non-rotameric sidechain are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 1 | CG | 130 | GLN |
| 1 | CQ | 130 | GLN |
| 2 | DT | 131 | GLN |

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| Mol | Chain | Res | Type |
|---|---|---|---|
| 1 | CK | 130 | GLN |
| 2 | CL | 131 | GLN |

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 30 such sidechains are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 2 | BR | 131 | GLN |
| 2 | CF | 131 | GLN |
| 1 | DQ | 78 | GLN |
| 1 | CE | 34 | ASN |
| 1 | CI | 94 | ASN |

#### 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 carbohydrates in this entry.

### 5.6 Ligand geometry

There are no ligands in this entry.

### 5.7 Other polymers

There are no such residues in this entry.

### 5.8 Polymer linkage issues

There are no chain breaks in this entry.

# 6 Fit of model and data

## 6.1 Protein, DNA and RNA chains

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

| Mol | Chain | Analysed | <RSRZ> | #RSRZ>2 | OWAB(Å$^2$) | Q<0.9 |
|---|---|---|---|---|---|---|
| 1 | AA | 223/223 (100%) | 0.27 | 7 (3%) 49 38 | 49, 69, 94, 105 | 0 |
| 1 | AC | 223/223 (100%) | 0.68 | 27 (12%) 4 5 | 63, 107, 139, 151 | 0 |
| 1 | AE | 223/223 (100%) | 0.40 | 13 (5%) 23 19 | 39, 63, 90, 105 | 0 |
| 1 | AG | 223/223 (100%) | 0.19 | 9 (4%) 38 31 | 31, 59, 92, 116 | 0 |
| 1 | AI | 223/223 (100%) | 0.44 | 17 (7%) 13 11 | 53, 92, 130, 145 | 0 |
| 1 | AK | 223/223 (100%) | -0.19 | 1 (0%) 92 87 | 21, 34, 52, 67 | 0 |
| 1 | AM | 223/223 (100%) | 0.20 | 7 (3%) 49 38 | 40, 58, 77, 89 | 0 |
| 1 | AO | 223/223 (100%) | 0.36 | 15 (6%) 17 14 | 61, 78, 98, 111 | 0 |
| 1 | AQ | 223/223 (100%) | 0.27 | 7 (3%) 49 38 | 43, 72, 94, 105 | 0 |
| 1 | AS | 223/223 (100%) | 0.23 | 8 (3%) 42 34 | 51, 67, 87, 98 | 0 |
| 1 | AU | 223/223 (100%) | 0.96 | 44 (19%) 1 1 | 82, 115, 141, 149 | 0 |
| 1 | BA | 223/223 (100%) | 0.41 | 8 (3%) 42 34 | 68, 85, 101, 114 | 0 |
| 1 | BC | 223/223 (100%) | 1.08 | 47 (21%) 1 1 | 87, 114, 141, 160 | 0 |
| 1 | BE | 223/223 (100%) | 0.53 | 19 (8%) 10 9 | 55, 82, 109, 121 | 0 |
| 1 | BG | 223/223 (100%) | -0.13 | 4 (1%) 68 59 | 26, 39, 57, 67 | 0 |
| 1 | BI | 223/223 (100%) | 0.55 | 13 (5%) 23 19 | 47, 73, 100, 112 | 0 |
| 1 | BK | 223/223 (100%) | 0.36 | 13 (5%) 23 19 | 46, 83, 119, 141 | 0 |
| 1 | BM | 223/223 (100%) | 0.22 | 10 (4%) 33 27 | 44, 60, 74, 81 | 0 |
| 1 | BO | 223/223 (100%) | -0.11 | 0 100 100 | 33, 47, 60, 67 | 0 |
| 1 | BQ | 223/223 (100%) | 0.40 | 11 (4%) 29 25 | 49, 68, 90, 101 | 0 |
| 1 | BS | 223/223 (100%) | 0.90 | 41 (18%) 1 1 | 70, 112, 151, 166 | 0 |
| 1 | BU | 223/223 (100%) | 0.40 | 15 (6%) 17 14 | 68, 91, 121, 125 | 0 |
| 1 | CA | 223/223 (100%) | 0.66 | 30 (13%) 3 3 | 47, 104, 149, 165 | 0 |
| 1 | CC | 223/223 (100%) | 0.76 | 34 (15%) 2 2 | 55, 89, 113, 129 | 0 |

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| Mol | Chain | Analysed | <RSRZ> | #RSRZ>2 | OWAB(Å$^2$) | Q<0.9 |
|---|---|---|---|---|---|---|
| 1 | CE | 223/223 (100%) | 0.22 | 8 (3%) 42 34 | 21, 61, 87, 92 | 0 |
| 1 | CG | 223/223 (100%) | 0.07 | 5 (2%) 62 52 | 29, 61, 97, 110 | 0 |
| 1 | CI | 223/223 (100%) | 0.04 | 5 (2%) 62 52 | 23, 39, 61, 75 | 0 |
| 1 | CK | 223/223 (100%) | 0.03 | 5 (2%) 62 52 | 20, 50, 85, 108 | 0 |
| 1 | CM | 223/223 (100%) | 0.44 | 13 (5%) 23 19 | 57, 75, 101, 117 | 0 |
| 1 | CO | 223/223 (100%) | 0.64 | 28 (12%) 3 5 | 60, 96, 135, 155 | 0 |
| 1 | CQ | 223/223 (100%) | 0.17 | 8 (3%) 42 34 | 42, 65, 88, 94 | 0 |
| 1 | CS | 223/223 (100%) | 0.83 | 39 (17%) 1 2 | 63, 94, 126, 137 | 0 |
| 1 | CU | 223/223 (100%) | 0.72 | 22 (9%) 7 7 | 80, 119, 151, 166 | 0 |
| 1 | DA | 223/223 (100%) | 0.55 | 29 (13%) 3 4 | 49, 81, 120, 136 | 0 |
| 1 | DC | 223/223 (100%) | 0.13 | 3 (1%) 77 68 | 44, 66, 96, 111 | 0 |
| 1 | DE | 223/223 (100%) | 1.06 | 45 (20%) 1 1 | 77, 99, 119, 130 | 0 |
| 1 | DG | 223/223 (100%) | 0.18 | 7 (3%) 49 38 | 39, 56, 78, 92 | 0 |
| 1 | DI | 223/223 (100%) | 0.31 | 5 (2%) 62 52 | 42, 82, 109, 122 | 0 |
| 1 | DK | 223/223 (100%) | 0.00 | 5 (2%) 62 52 | 28, 41, 55, 66 | 0 |
| 1 | DM | 223/223 (100%) | 0.14 | 3 (1%) 77 68 | 29, 61, 83, 92 | 0 |
| 1 | DO | 223/223 (100%) | 0.02 | 2 (0%) 84 77 | 25, 46, 66, 82 | 0 |
| 1 | DQ | 223/223 (100%) | 0.17 | 15 (6%) 17 14 | 43, 73, 101, 118 | 0 |
| 1 | DS | 223/223 (100%) | 0.10 | 4 (1%) 68 59 | 25, 51, 81, 96 | 0 |
| 1 | DU | 223/223 (100%) | 0.73 | 24 (10%) 5 5 | 66, 95, 125, 141 | 0 |
| 2 | AB | 163/163 (100%) | 0.27 | 7 (4%) 35 29 | 42, 72, 110, 134 | 0 |
| 2 | AD | 163/163 (100%) | 0.15 | 6 (3%) 41 32 | 39, 64, 87, 114 | 0 |
| 2 | AF | 163/163 (100%) | -0.08 | 1 (0%) 89 84 | 22, 42, 67, 91 | 0 |
| 2 | AH | 163/163 (100%) | -0.13 | 2 (1%) 79 70 | 24, 39, 66, 82 | 0 |
| 2 | AJ | 163/163 (100%) | -0.16 | 0 100 100 | 31, 46, 81, 111 | 0 |
| 2 | AL | 163/163 (100%) | -0.03 | 2 (1%) 79 70 | 20, 45, 94, 112 | 0 |
| 2 | AN | 163/163 (100%) | -0.17 | 2 (1%) 79 70 | 32, 44, 70, 95 | 0 |
| 2 | AP | 163/163 (100%) | 0.19 | 5 (3%) 49 38 | 52, 65, 98, 122 | 0 |
| 2 | AR | 163/163 (100%) | 0.41 | 11 (6%) 17 14 | 47, 75, 118, 142 | 0 |
| 2 | AT | 163/163 (100%) | -0.08 | 2 (1%) 79 70 | 39, 56, 80, 99 | 0 |
| 2 | AV | 163/163 (100%) | 0.40 | 9 (5%) 25 22 | 64, 87, 128, 146 | 0 |

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| Mol | Chain | Analysed | <RSRZ> | #RSRZ>2 | OWAB(Å$^2$) | Q<0.9 |
|---|---|---|---|---|---|---|
| 2 | BB | 163/163 (100%) | 0.01 | 2 (1%) 79 70 | 45, 67, 90, 116 | 0 |
| 2 | BD | 163/163 (100%) | 0.29 | 7 (4%) 35 29 | 56, 80, 110, 136 | 0 |
| 2 | BF | 163/163 (100%) | 0.69 | 19 (11%) 4 5 | 56, 93, 145, 157 | 0 |
| 2 | BH | 163/163 (100%) | 0.04 | 5 (3%) 49 38 | 28, 55, 94, 135 | 0 |
| 2 | BJ | 163/163 (100%) | -0.17 | 2 (1%) 79 70 | 28, 40, 63, 87 | 0 |
| 2 | BL | 163/163 (100%) | -0.05 | 1 (0%) 89 84 | 42, 59, 89, 110 | 0 |
| 2 | BN | 163/163 (100%) | -0.01 | 2 (1%) 79 70 | 37, 53, 81, 104 | 0 |
| 2 | BP | 163/163 (100%) | 0.12 | 7 (4%) 35 29 | 34, 51, 82, 90 | 0 |
| 2 | BR | 163/163 (100%) | -0.19 | 2 (1%) 79 70 | 37, 52, 86, 101 | 0 |
| 2 | BT | 163/163 (100%) | 0.31 | 3 (1%) 68 59 | 57, 85, 115, 129 | 0 |
| 2 | BV | 163/163 (100%) | 0.62 | 16 (9%) 7 7 | 58, 97, 145, 164 | 0 |
| 2 | CB | 163/163 (100%) | 0.37 | 10 (6%) 21 17 | 62, 97, 142, 165 | 0 |
| 2 | CD | 163/163 (100%) | 0.58 | 14 (8%) 10 9 | 43, 91, 161, 187 | 0 |
| 2 | CF | 163/163 (100%) | 0.08 | 6 (3%) 41 32 | 31, 59, 105, 118 | 0 |
| 2 | CH | 163/163 (100%) | -0.25 | 0 100 100 | 17, 32, 66, 94 | 0 |
| 2 | CJ | 163/163 (100%) | -0.20 | 4 (2%) 57 47 | 16, 36, 80, 107 | 0 |
| 2 | CL | 163/163 (100%) | -0.19 | 3 (1%) 68 59 | 16, 33, 66, 81 | 0 |
| 2 | CN | 163/163 (100%) | 0.04 | 0 100 100 | 46, 60, 77, 93 | 0 |
| 2 | CP | 163/163 (100%) | 0.68 | 17 (10%) 6 6 | 71, 109, 152, 162 | 0 |
| 2 | CR | 163/163 (100%) | 0.11 | 2 (1%) 79 70 | 39, 78, 120, 138 | 0 |
| 2 | CT | 163/163 (100%) | 0.05 | 3 (1%) 68 59 | 32, 57, 94, 121 | 0 |
| 2 | CV | 163/163 (100%) | 0.44 | 12 (7%) 14 12 | 51, 87, 130, 144 | 0 |
| 2 | DB | 163/163 (100%) | 0.51 | 11 (6%) 17 14 | 53, 87, 138, 157 | 0 |
| 2 | DD | 163/163 (100%) | 0.07 | 2 (1%) 79 70 | 40, 62, 99, 118 | 0 |
| 2 | DF | 163/163 (100%) | 0.32 | 7 (4%) 35 29 | 66, 88, 130, 147 | 0 |
| 2 | DH | 163/163 (100%) | 0.02 | 2 (1%) 79 70 | 37, 52, 85, 112 | 0 |
| 2 | DJ | 163/163 (100%) | 0.04 | 5 (3%) 49 38 | 33, 52, 92, 109 | 0 |
| 2 | DL | 163/163 (100%) | -0.12 | 5 (3%) 49 38 | 17, 37, 72, 93 | 0 |
| 2 | DN | 163/163 (100%) | -0.24 | 1 (0%) 89 84 | 20, 41, 83, 107 | 0 |
| 2 | DP | 163/163 (100%) | -0.13 | 2 (1%) 79 70 | 25, 39, 65, 88 | 0 |
| 2 | DR | 163/163 (100%) | 0.13 | 4 (2%) 57 47 | 27, 55, 94, 109 | 0 |

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| Mol | Chain | Analysed | <RSRZ> | #RSRZ>2 | OWAB(Å$^2$) | Q<0.9 |
|---|---|---|---|---|---|---|
| 2 | DT | 163/163 (100%) | -0.01 | 7 (4%) 35 29 | 33, 53, 88, 107 | 0 |
| 2 | DV | 163/163 (100%) | 0.15 | 6 (3%) 41 32 | 41, 64, 106, 131 | 0 |
| All | All | 16984/16984 (100%) | 0.26 | 911 (5%) 25 22 | 16, 68, 123, 187 | 0 |

The worst 5 of 911 RSRZ outliers are listed below:

| Mol | Chain | Res | Type | RSRZ |
|---|---|---|---|---|
| 1 | AM | 25 | ASN | 6.8 |
| 1 | CO | 76 | ASN | 6.4 |
| 1 | CS | 135 | GLY | 6.3 |
| 1 | BC | 25 | ASN | 6.2 |
| 1 | DE | 134 | SER | 6.1 |

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

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

## 6.3 Carbohydrates (i)

There are no carbohydrates in this entry.

## 6.4 Ligands (i)

There are no ligands in this entry.

## 6.5 Other polymers (i)

There are no such residues in this entry.