# Full wwPDB EM Validation Report ⓘ

Nov 20, 2022 – 11:36 AM EST

| | | |
|---|---|---|
| PDB ID | : | 7MFF |
| EMDB ID | : | EMD-23815 |
| Title | : | Dimeric (BRAF)2:(14-3-3)2 complex bound to SB590885 Inhibitor |
| Authors | : | Martinez Fiesco, J.A.; Ping, Z.; Durrant, D.E.; Morrison, D.K. |
| Deposited on | : | 2021-04-09 |
| Resolution | : | 3.89 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.

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

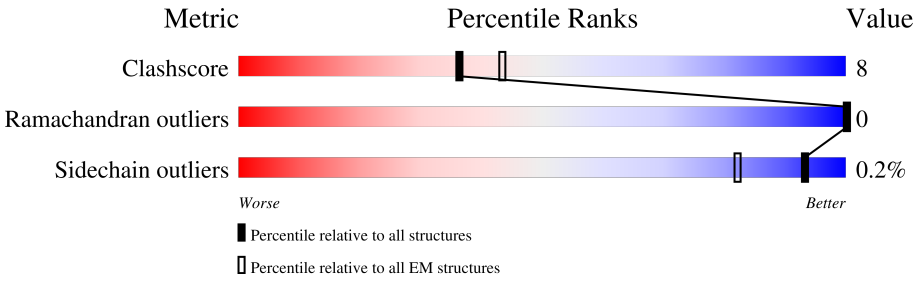
| | | |
|---|---|---|
| EMDB validation analysis | : | 0.0.1.dev43 |
| Mogul | : | 1.8.5 (274361), CSD as541be (2020) |
| MolProbity | : | 4.02b-467 |
| buster-report | : | 1.1.7 (2018) |
| Percentile statistics | : | 20191225.v01 (using entries in the PDB archive December 25th 2019) |
| MapQ | : | 1.9.9 |
| 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 3.89 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 | C | 245 | 18% 74% 20% 7% |
| 1 | D | 245 | 19% 77% 16% 7% |
| 2 | A | 766 | 6% 27% 8% 65% |
| 2 | B | 766 | 9% 27% 9% 64% |

# 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 8003 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.

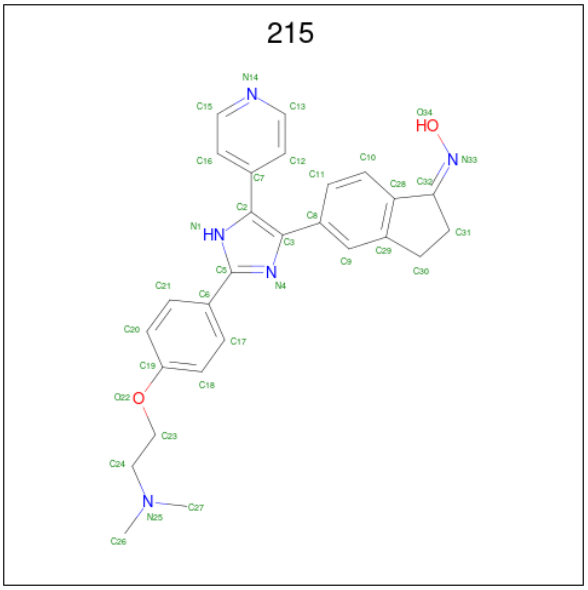
- Molecule 1 is a protein called 14-3-3 protein zeta/delta.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 1 | C | 229 | Total | C | N | O | S | 0 | 0 |
| | | | 1808 | 1135 | 302 | 362 | 9 | | |
| 1 | D | 228 | Total | C | N | O | S | 0 | 0 |
| | | | 1793 | 1125 | 297 | 361 | 10 | | |

- Molecule 2 is a protein called Serine/threonine-protein kinase B-raf.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| 2 | A | 271 | Total | C | N | O | P | S | 0 | 0 |
| | | | 2163 | 1382 | 378 | 389 | 1 | 13 | | |
| 2 | B | 272 | Total | C | N | O | P | S | 0 | 0 |
| | | | 2171 | 1388 | 379 | 390 | 1 | 13 | | |

- Molecule 3 is (1Z)-5-(2-{4-[2-(DIMETHYLAMINO)ETHOXY]PHENYL}-5-PYRIDIN-4-YL-1H-IMIDAZOL-4-YL)INDAN-1-ONE OXIME (three-letter code: 215) (formula: $C_{27}H_{27}N_5O_2$).



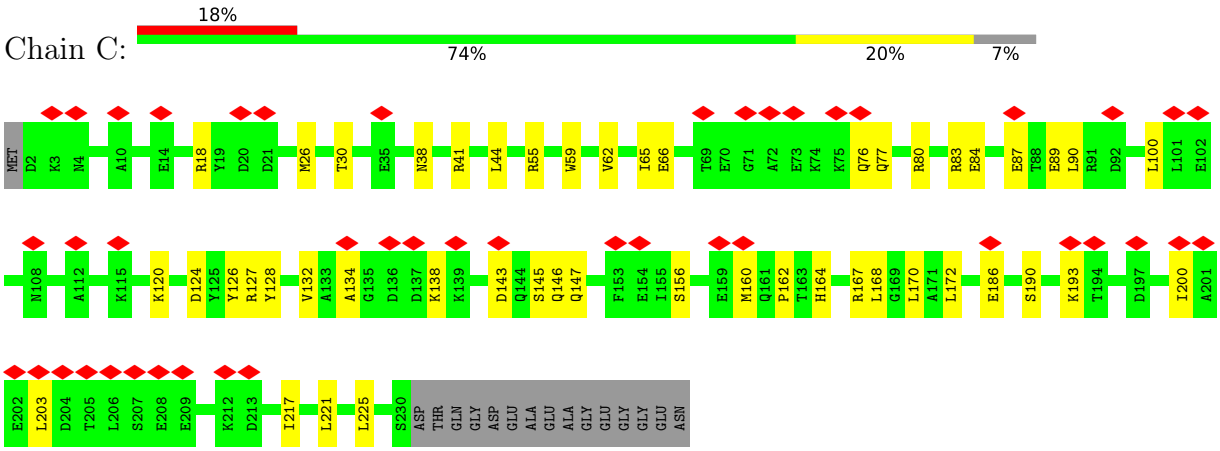
| Mol | Chain | Residues | Atoms | | | | AltConf |
|---|---|---|---|---|---|---|---|
| 3 | A | 1 | Total | C | N | O | 0 |
| | | | 34 | 27 | 5 | 2 | |
| 3 | B | 1 | Total | C | N | O | 0 |
| | | | 34 | 27 | 5 | 2 | |

# 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.

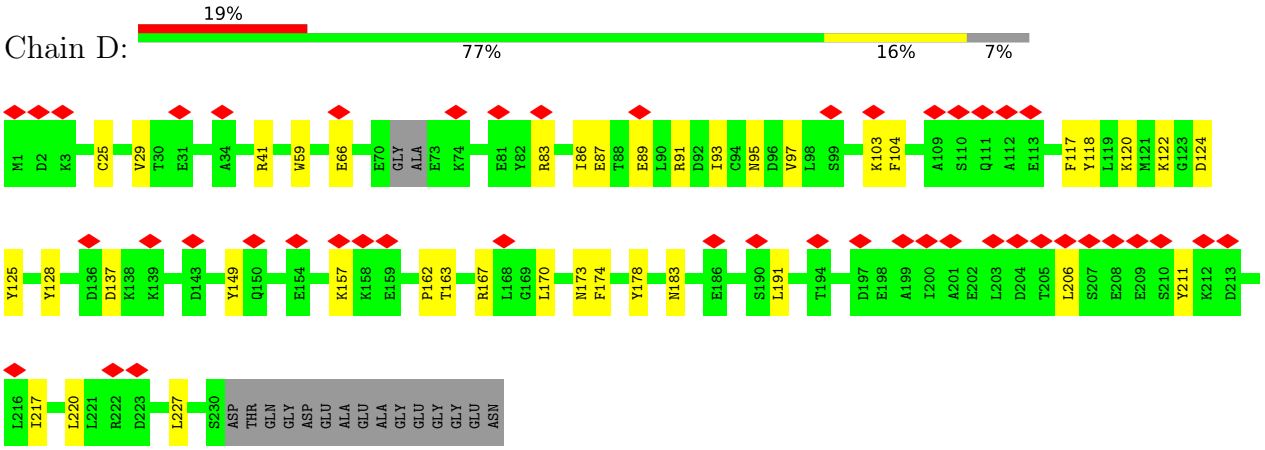
• Molecule 1: 14-3-3 protein zeta/delta

Chain C:



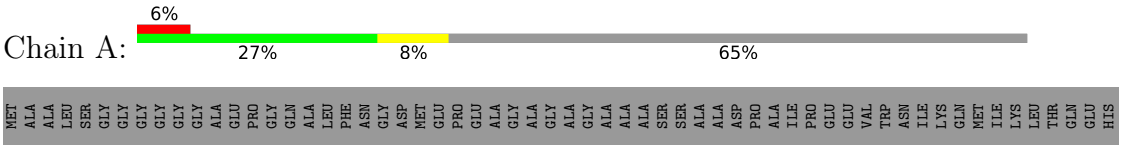

• Molecule 1: 14-3-3 protein zeta/delta

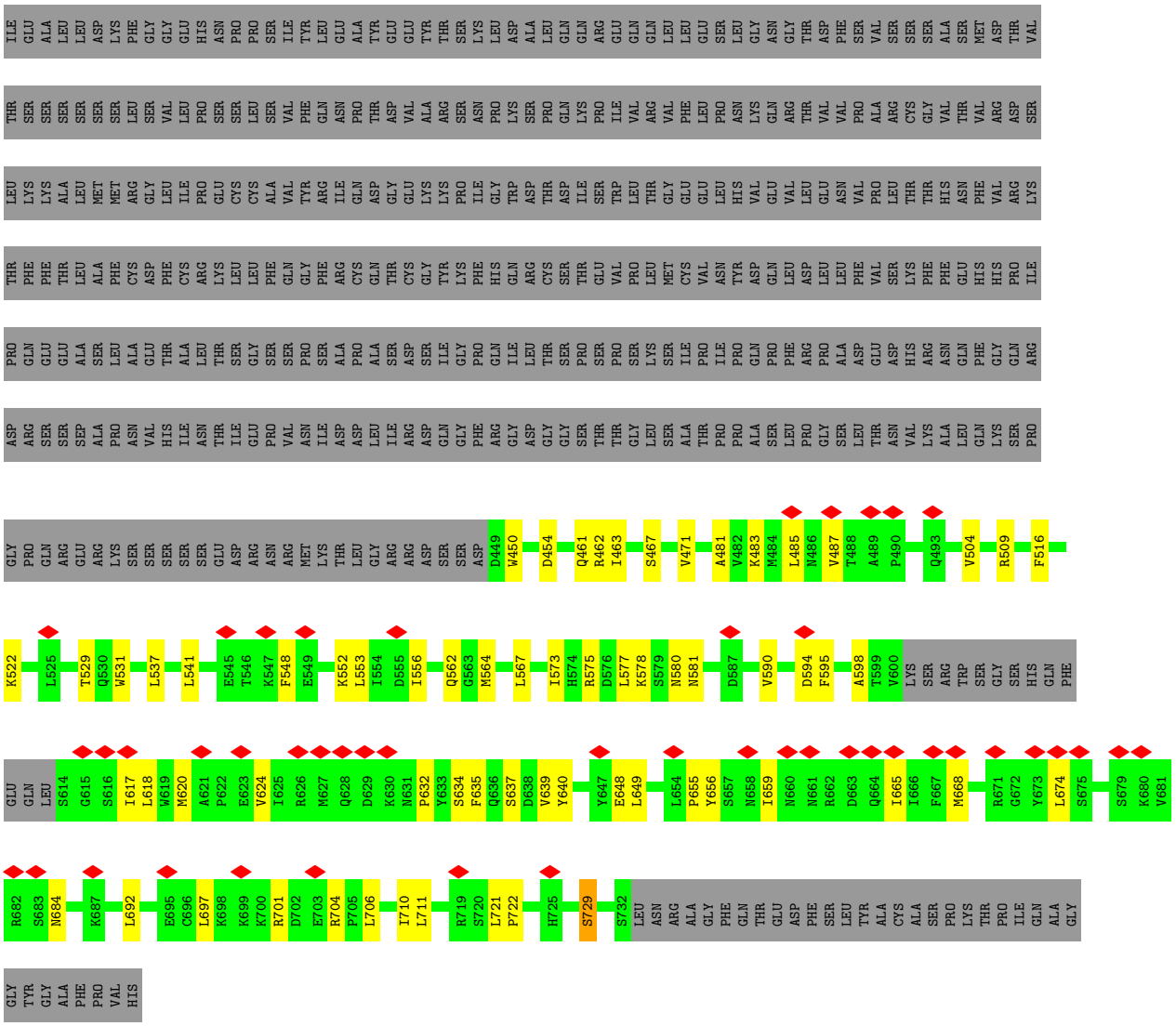
Chain D:




• Molecule 2: Serine/threonine-protein kinase B-raf

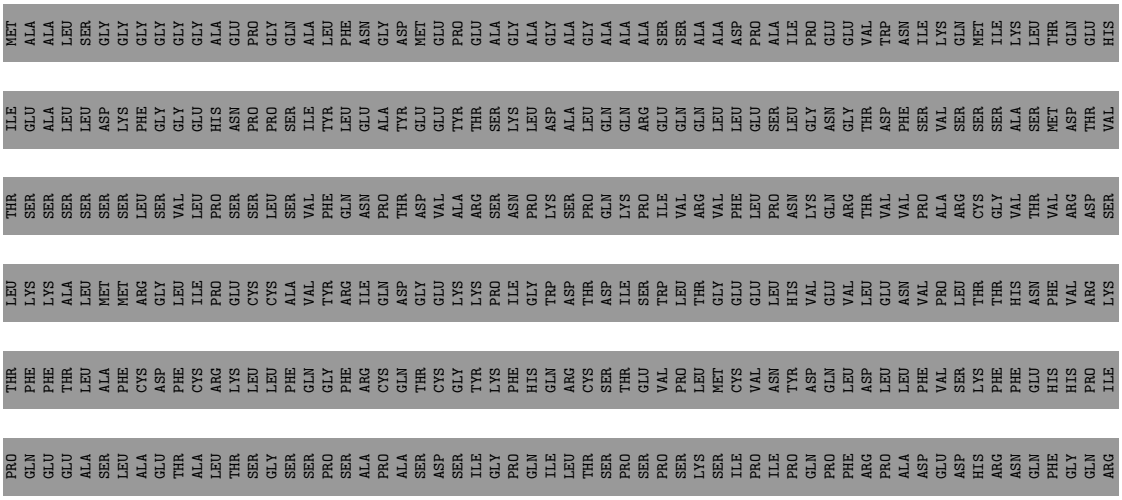
Chain A:

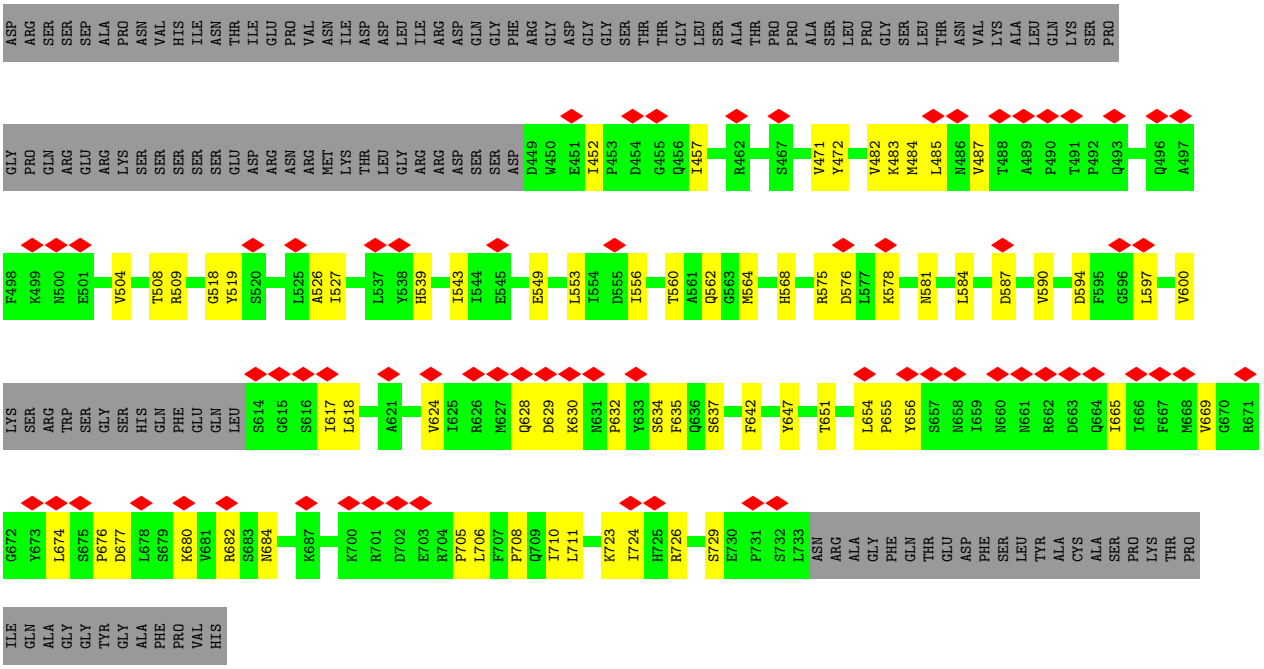




• Molecule 2: Serine/threonine-protein kinase B-raf

Chain B:


ASP ARG SER SER SEP ALA PRO ASN VAL HIS ILE ASN THR ILE GLU PRO VAL ASN ILE ASP ASP LEU ILE ARG ASP GLN GLY PHE ARG GLY ASP GLY GLY SER THR THR GLY LEU SER ALA THR PRO PRO ALA SER LEU PRO GLY SER LEU THR ASN VAL LYS ALA LEU GLN LYS SER PRO
GLY PRO GLN ARG GLU ARG LYS SER SER SER SER GLU ASP ARG ASN ARG MET LYS THR LEU GLY ARG ARG ASP SER SER ASP D449 W450 E451 T452 P453 D454 G455 Q456 I457 R462 S467 V471 Y472 V482 K483 M484 L485 M486 V487 T488 A489 P490 T491 P492 Q493 Q496 A497
F498 K499 N500 E501 V504 T508 R509 G518 Y519 S520 L525 A526 I527 L537 Y538 H539 I543 I544 E545 E549 L553 I564 D555 I556 T560 A561 Q562 G563 M564 H568 R575 D576 L577 K578 N581 L584 D587 V590 D594 F595 G596 L597 V600
LYS SER ARG TRP SER GLY SER HIS GLN PHE GLU GLN LEU S614 G615 S616 I617 L618 A621 V624 I625 R626 M627 Q628 D629 K630 N631 P632 Y633 S634 F635 Q636 S637 F642 Y647 T651 L654 P655 Y656 S657 N658 I659 N660 N661 R662 D663 Q664 I665 I666 F667 M668 V669 G670 R671
G672 Y673 L674 S675 P676 D677 L678 S679 K680 V681 R682 S683 N684 K687 K700 R701 D702 E703 R704 P705 L706 F707 P708 Q709 I710 L711 K723 I724 H725 R726 S729 E730 P731 S732 L733 ASN ARG ALA GLY PHE GLN THR GLU ASP PHE SER LEU TYR ALA CYS ALA SER PRO LYS THR PRO
ILE GLN ALA GLY GLY TYR GLY ALA PHE PRO VAL HIS

# 4 Experimental information (i)

| Property | Value | Source |
|---|---|---|
| EM reconstruction method | SINGLE PARTICLE | Depositor |
| Imposed symmetry | POINT, Not provided | |
| Number of particles used | 203343 | Depositor |
| Resolution determination method | FSC 0.143 CUT-OFF | Depositor |
| CTF correction method | PHASE FLIPPING AND AMPLITUDE CORRECTION | Depositor |
| Microscope | FEI TITAN KRIOS | Depositor |
| Voltage (kV) | 300 | Depositor |
| Electron dose ($e^-/Å^2$) | 57 | 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 | 0.313 | Depositor |
| Minimum map value | -0.200 | Depositor |
| Average map value | 0.001 | Depositor |
| Map value standard deviation | 0.010 | Depositor |
| Recommended contour level | 0.049 | Depositor |
| Map size (Å) | 175.24, 175.24, 175.24 | wwPDB |
| Map dimensions | 130, 130, 130 | wwPDB |
| Map angles (°) | 90.0, 90.0, 90.0 | wwPDB |
| Pixel spacing (Å) | 1.348, 1.348, 1.348 | Depositor |

# 5 Model quality

## 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: SEP, 215

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 | C | 0.24 | 0/1833 | 0.44 | 0/2470 |
| 1 | D | 0.24 | 0/1817 | 0.47 | 0/2451 |
| 2 | A | 0.24 | 0/2199 | 0.48 | 0/2967 |
| 2 | B | 0.24 | 0/2207 | 0.48 | 0/2978 |
| All | All | 0.24 | 0/8056 | 0.47 | 0/10866 |

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

## 5.2 Too-close contacts

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

| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|---|---|---|---|---|---|---|
| 1 | C | 1808 | 0 | 1769 | 27 | 0 |
| 1 | D | 1793 | 0 | 1736 | 27 | 0 |
| 2 | A | 2163 | 0 | 2198 | 42 | 0 |
| 2 | B | 2171 | 0 | 2209 | 43 | 0 |
| 3 | A | 34 | 0 | 27 | 1 | 0 |
| 3 | B | 34 | 0 | 27 | 0 | 0 |
| All | All | 8003 | 0 | 7966 | 134 | 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 8.

All (134) 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:A:578:LYS:HZ2 | 2:A:580:ASN:HB2 | 1.50 | 0.76 |
| 2:B:628:GLN:HG2 | 2:B:629:ASP:H | 1.52 | 0.75 |
| 1:C:162:PRO:HA | 1:C:167:ARG:HE | 1.55 | 0.72 |
| 2:A:668:MET:HG2 | 2:A:674:LEU:HB2 | 1.71 | 0.72 |
| 1:D:157:LYS:HA | 1:D:167:ARG:HH21 | 1.55 | 0.71 |
| 2:B:654:LEU:HD12 | 2:B:655:PRO:HD2 | 1.73 | 0.71 |
| 2:B:576:ASP:OD1 | 2:B:578:LYS:NZ | 2.23 | 0.70 |
| 2:A:564:MET:HE3 | 2:A:577:LEU:HD21 | 1.74 | 0.70 |
| 2:B:723:LYS:O | 2:B:726:ARG:NH2 | 2.26 | 0.69 |
| 1:D:120:LYS:HB2 | 1:D:170:LEU:HD13 | 1.75 | 0.68 |
| 2:A:516:PHE:HA | 2:A:529:THR:HG22 | 1.76 | 0.67 |
| 2:A:721:LEU:HD12 | 2:A:722:PRO:HD2 | 1.78 | 0.66 |
| 2:B:484:MET:HB3 | 2:B:526:ALA:HB2 | 1.75 | 0.66 |
| 1:D:227:LEU:HD11 | 2:B:726:ARG:HE | 1.61 | 0.66 |
| 1:C:66:GLU:O | 1:C:76:GLN:NE2 | 2.29 | 0.66 |
| 1:C:84:GLU:HA | 1:C:87:GLU:HB2 | 1.78 | 0.66 |
| 1:D:149:TYR:HB3 | 1:D:174:PHE:HD1 | 1.61 | 0.64 |
| 1:C:38:ASN:HA | 1:C:41:ARG:HH11 | 1.63 | 0.63 |
| 2:A:640:TYR:HE1 | 2:A:697:LEU:HD23 | 1.65 | 0.61 |
| 2:B:519:TYR:HA | 2:B:527:ILE:HA | 1.82 | 0.61 |
| 2:B:618:LEU:HD23 | 2:B:655:PRO:HG2 | 1.84 | 0.60 |
| 2:A:454:ASP:HB3 | 2:A:522:LYS:HG3 | 1.83 | 0.59 |
| 1:D:103:LYS:HG3 | 1:D:104:PHE:HD2 | 1.67 | 0.59 |
| 2:A:509:ARG:NH2 | 2:B:508:THR:O | 2.36 | 0.58 |
| 1:C:156:SER:HB2 | 1:C:167:ARG:HG3 | 1.84 | 0.58 |
| 1:D:149:TYR:HB3 | 1:D:174:PHE:CD1 | 2.38 | 0.58 |
| 2:A:467:SER:H | 2:A:483:LYS:HZ1 | 1.52 | 0.58 |
| 2:B:624:VAL:HG12 | 2:B:632:PRO:HB2 | 1.86 | 0.58 |
| 1:C:134:ALA:HA | 1:C:138:LYS:HD2 | 1.84 | 0.58 |
| 2:A:656:TYR:HB3 | 2:A:659:ILE:HD13 | 1.86 | 0.58 |
| 2:A:463:ILE:HB | 2:A:471:VAL:HG23 | 1.85 | 0.57 |
| 1:D:178:TYR:O | 1:D:183:ASN:N | 2.38 | 0.57 |
| 1:C:77:GLN:HA | 1:C:80:ARG:HH12 | 1.69 | 0.56 |
| 2:A:624:VAL:HG12 | 2:A:632:PRO:HB2 | 1.87 | 0.56 |
| 2:B:584:LEU:HG | 2:B:587:ASP:HA | 1.86 | 0.56 |
| 1:D:206:LEU:HD13 | 1:D:211:TYR:HB3 | 1.86 | 0.56 |
| 1:C:120:LYS:HB2 | 1:C:170:LEU:HD13 | 1.87 | 0.56 |
| 2:A:618:LEU:HD11 | 2:A:655:PRO:HG2 | 1.88 | 0.56 |
| 1:D:170:LEU:O | 1:D:174:PHE:N | 2.38 | 0.56 |
| 2:B:669:VAL:HG22 | 2:B:674:LEU:HB3 | 1.89 | 0.55 |

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| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|---|---|---|---|
| 2:B:564:MET:O | 2:B:568:HIS:ND1 | 2.32 | 0.55 |
| 2:A:450:TRP:CH2 | 2:B:509:ARG:HG3 | 2.43 | 0.54 |
| 1:C:26:MET:HG3 | 1:C:44:LEU:HD13 | 1.90 | 0.54 |
| 2:A:548:PHE:HB2 | 2:A:553:LEU:HD22 | 1.91 | 0.53 |
| 2:B:504:VAL:HG22 | 2:B:600:VAL:HG23 | 1.89 | 0.53 |
| 2:A:541:LEU:HD13 | 2:A:648:GLU:HG2 | 1.91 | 0.52 |
| 2:B:562:GLN:HA | 2:B:711:LEU:HD11 | 1.90 | 0.52 |
| 1:C:126:TYR:HB3 | 1:C:145:SER:HB3 | 1.92 | 0.52 |
| 2:A:467:SER:OG | 2:A:594:ASP:OD1 | 2.26 | 0.52 |
| 1:C:55:ARG:NE | 1:C:89:GLU:OE2 | 2.41 | 0.51 |
| 2:B:682:ARG:NH1 | 2:B:684:ASN:OD1 | 2.44 | 0.51 |
| 2:A:581:ASN:ND2 | 2:A:594:ASP:HB3 | 2.25 | 0.50 |
| 2:A:692:LEU:HD11 | 2:A:710:ILE:HG23 | 1.93 | 0.50 |
| 2:A:556:ILE:HG23 | 2:A:590:VAL:HG21 | 1.93 | 0.50 |
| 2:B:560:THR:HG22 | 2:B:590:VAL:HG11 | 1.92 | 0.50 |
| 2:A:573:ILE:HG22 | 2:A:575:ARG:HG3 | 1.93 | 0.49 |
| 1:C:66:GLU:OE1 | 1:C:83:ARG:NH1 | 2.45 | 0.49 |
| 2:B:556:ILE:HG13 | 2:B:590:VAL:HG21 | 1.94 | 0.49 |
| 1:C:193:LYS:HD2 | 1:C:225:LEU:HD13 | 1.94 | 0.49 |
| 1:D:66:GLU:OE2 | 1:D:83:ARG:NH2 | 2.46 | 0.49 |
| 1:D:217:ILE:HA | 1:D:220:LEU:HD12 | 1.95 | 0.49 |
| 1:D:125:TYR:HA | 1:D:128:TYR:HD2 | 1.79 | 0.48 |
| 2:A:634:SER:O | 2:A:637:SER:OG | 2.27 | 0.48 |
| 1:D:162:PRO:HD2 | 1:D:163:THR:H | 1.78 | 0.47 |
| 2:A:552:LYS:O | 2:A:556:ILE:HG13 | 2.14 | 0.47 |
| 1:D:124:ASP:CG | 1:D:173:ASN:HD21 | 2.17 | 0.47 |
| 2:B:647:TYR:O | 2:B:651:THR:OG1 | 2.19 | 0.47 |
| 1:C:18:ARG:NH1 | 1:D:89:GLU:OE1 | 2.40 | 0.47 |
| 2:B:452:ILE:HD11 | 2:B:518:GLY:HA3 | 1.97 | 0.47 |
| 1:D:162:PRO:HA | 1:D:167:ARG:HD3 | 1.97 | 0.47 |
| 2:A:578:LYS:NZ | 2:A:580:ASN:HB2 | 2.24 | 0.47 |
| 2:B:647:TYR:OH | 2:B:677:ASP:O | 2.20 | 0.47 |
| 2:A:454:ASP:N | 2:A:454:ASP:OD1 | 2.45 | 0.46 |
| 2:B:581:ASN:HD21 | 2:B:594:ASP:HB2 | 1.80 | 0.46 |
| 1:C:143:ASP:O | 1:C:147:GLN:HG3 | 2.16 | 0.46 |
| 2:A:461:GLN:NE2 | 2:A:462:ARG:O | 2.49 | 0.46 |
| 2:B:617:ILE:HG13 | 2:B:618:LEU:HD12 | 1.97 | 0.46 |
| 2:A:634:SER:OG | 2:A:701:ARG:NH1 | 2.49 | 0.46 |
| 2:A:640:TYR:HB2 | 2:A:704:ARG:NH1 | 2.31 | 0.46 |
| 2:B:485:LEU:H | 2:B:485:LEU:HD23 | 1.80 | 0.46 |
| 2:B:575:ARG:NH2 | 2:B:597:LEU:O | 2.49 | 0.46 |

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| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|---|---|---|---|
| 2:B:581:ASN:ND2 | 2:B:594:ASP:HB2 | 2.30 | 0.46 |
| 2:A:481:ALA:HB2 | 2:A:531:TRP:HE3 | 1.81 | 0.45 |
| 2:A:485:LEU:HD23 | 2:A:485:LEU:H | 1.81 | 0.45 |
| 2:A:504:VAL:HG11 | 2:A:598:ALA:HB3 | 1.97 | 0.45 |
| 2:B:472:TYR:N | 2:B:482:VAL:O | 2.47 | 0.45 |
| 1:C:124:ASP:OD1 | 1:C:127:ARG:NH2 | 2.47 | 0.45 |
| 1:D:91:ARG:O | 1:D:95:ASN:ND2 | 2.36 | 0.45 |
| 2:B:642:PHE:HE2 | 2:B:710:ILE:HG21 | 1.82 | 0.45 |
| 1:C:186:GLU:O | 1:C:190:SER:OG | 2.23 | 0.45 |
| 1:D:174:PHE:HE2 | 1:D:191:LEU:HD22 | 1.82 | 0.45 |
| 1:D:59:TRP:HB2 | 1:D:86:ILE:HG21 | 1.99 | 0.44 |
| 2:B:539:HIS:HA | 2:B:543:ILE:HG12 | 1.99 | 0.44 |
| 2:B:568:HIS:HD2 | 2:B:635:PHE:CD1 | 2.36 | 0.44 |
| 2:B:628:GLN:CG | 2:B:629:ASP:H | 2.27 | 0.44 |
| 2:A:485:LEU:HG | 2:A:487:VAL:H | 1.83 | 0.44 |
| 1:D:41:ARG:HD2 | 1:D:117:PHE:CG | 2.53 | 0.43 |
| 1:C:62:VAL:HA | 1:C:65:ILE:HD12 | 2.00 | 0.43 |
| 1:C:168:LEU:HB3 | 1:C:217:ILE:HG21 | 1.99 | 0.43 |
| 2:A:659:ILE:HG21 | 2:A:665:ILE:HD11 | 2.00 | 0.43 |
| 2:B:471:VAL:HA | 2:B:483:LYS:HA | 2.00 | 0.43 |
| 2:B:656:TYR:CD2 | 2:B:665:ILE:HD11 | 2.53 | 0.43 |
| 1:C:172:LEU:HD12 | 1:C:221:LEU:HG | 2.00 | 0.43 |
| 2:B:549:GLU:O | 2:B:553:LEU:N | 2.49 | 0.43 |
| 2:B:705:PRO:HG2 | 2:B:710:ILE:HD11 | 1.99 | 0.43 |
| 1:C:59:TRP:CE2 | 1:C:132:VAL:HG23 | 2.53 | 0.42 |
| 2:A:617:ILE:HG22 | 2:A:620:MET:HE3 | 2.01 | 0.42 |
| 1:D:93:ILE:O | 1:D:97:VAL:HG23 | 2.18 | 0.42 |
| 1:D:118:TYR:O | 1:D:122:LYS:N | 2.46 | 0.42 |
| 2:A:537:LEU:HD21 | 2:A:649:LEU:HD21 | 2.00 | 0.42 |
| 1:D:137:ASP:N | 1:D:137:ASP:OD1 | 2.50 | 0.42 |
| 2:B:706:LEU:HB3 | 2:B:708:PRO:HD2 | 2.02 | 0.42 |
| 1:C:128:TYR:OH | 2:A:729:SEP:O3P | 2.21 | 0.42 |
| 2:A:701:ARG:HA | 2:A:704:ARG:HH21 | 1.84 | 0.42 |
| 1:D:87:GLU:O | 1:D:91:ARG:N | 2.46 | 0.42 |
| 2:B:680:LYS:HD3 | 2:B:680:LYS:HA | 1.88 | 0.42 |
| 1:C:30:THR:HG21 | 1:C:100:LEU:HD21 | 2.01 | 0.42 |
| 1:D:25:CYS:O | 1:D:29:VAL:HG23 | 2.20 | 0.42 |
| 2:A:706:LEU:O | 2:A:710:ILE:HG13 | 2.20 | 0.42 |
| 1:C:160:MET:SD | 1:C:164:HIS:ND1 | 2.89 | 0.41 |
| 2:B:656:TYR:OH | 2:B:676:PRO:HD3 | 2.20 | 0.41 |
| 2:B:724:ILE:HA | 2:B:726:ARG:NH2 | 2.36 | 0.41 |

*Continued on next page...*

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| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|---|---|---|---|
| 2:B:457:ILE:H | 2:B:457:ILE:HD12 | 1.85 | 0.41 |
| 2:B:485:LEU:O | 2:B:487:VAL:HG23 | 2.21 | 0.41 |
| 2:B:634:SER:O | 2:B:637:SER:OG | 2.30 | 0.41 |
| 1:D:174:PHE:CE2 | 1:D:191:LEU:HD22 | 2.55 | 0.41 |
| 1:C:200:ILE:HD13 | 1:C:203:LEU:HD11 | 2.03 | 0.40 |
| 2:A:562:GLN:OE1 | 2:A:711:LEU:HD11 | 2.21 | 0.40 |
| 2:A:635:PHE:O | 2:A:639:VAL:HG23 | 2.22 | 0.40 |
| 2:A:567:LEU:HD11 | 2:A:595:PHE:CZ | 2.56 | 0.40 |
| 1:C:90:LEU:HD22 | 1:C:132:VAL:HG11 | 2.03 | 0.40 |
| 1:C:143:ASP:O | 1:C:146:GLN:HG2 | 2.22 | 0.40 |
| 1:D:124:ASP:HB3 | 1:D:128:TYR:CE2 | 2.57 | 0.40 |
| 2:A:594:ASP:HA | 3:A:801:215:O34 | 2.21 | 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 | C | 227/245 (93%) | 226 (100%) | 1 (0%) | 0 | 100 | 100 |
| 1 | D | 224/245 (91%) | 221 (99%) | 3 (1%) | 0 | 100 | 100 |
| 2 | A | 266/766 (35%) | 251 (94%) | 15 (6%) | 0 | 100 | 100 |
| 2 | B | 267/766 (35%) | 251 (94%) | 16 (6%) | 0 | 100 | 100 |
| All | All | 984/2022 (49%) | 949 (96%) | 35 (4%) | 0 | 100 | 100 |

There are no Ramachandran outliers to report.

### 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 | C | 191/209 (91%) | 191 (100%) | 0 | 100 100 |
| 1 | D | 189/209 (90%) | 189 (100%) | 0 | 100 100 |
| 2 | A | 237/656 (36%) | 236 (100%) | 1 (0%) | 91 94 |
| 2 | B | 238/656 (36%) | 237 (100%) | 1 (0%) | 91 94 |
| All | All | 855/1730 (49%) | 853 (100%) | 2 (0%) | 93 96 |

All (2) residues with a non-rotameric sidechain are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 2 | A | 684 | ASN |
| 2 | B | 630 | LYS |

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 2 | A | 580 | ASN |
| 2 | A | 581 | ASN |

### 5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

2 non-standard protein/DNA/RNA residues 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 | SEP | B | 729 | 2 | 8,9,10 | 1.53 | 1 (12%) | 8,12,14 | 1.51 | 2 (25%) |
| 2 | SEP | A | 729 | 2 | 8,9,10 | 1.54 | 1 (12%) | 8,12,14 | 1.84 | 2 (25%) |

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 | SEP | B | 729 | 2 | - | 0/5/8/10 | - |
| 2 | SEP | A | 729 | 2 | - | 4/5/8/10 | - |

All (2) bond length outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(Å) | Ideal(Å) |
|---|---|---|---|---|---|---|---|
| 2 | B | 729 | SEP | P-O1P | 3.34 | 1.61 | 1.50 |
| 2 | A | 729 | SEP | P-O1P | 3.33 | 1.61 | 1.50 |

All (4) bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed($^o$) | Ideal($^o$) |
|---|---|---|---|---|---|---|---|
| 2 | A | 729 | SEP | P-OG-CB | -3.47 | 108.74 | 118.30 |
| 2 | A | 729 | SEP | OG-CB-CA | 3.35 | 111.41 | 108.14 |
| 2 | B | 729 | SEP | OG-CB-CA | 2.88 | 110.95 | 108.14 |
| 2 | B | 729 | SEP | P-OG-CB | -2.44 | 111.57 | 118.30 |

There are no chirality outliers.

All (4) torsion outliers are listed below:

| Mol | Chain | Res | Type | Atoms |
|---|---|---|---|---|
| 2 | A | 729 | SEP | N-CA-CB-OG |
| 2 | A | 729 | SEP | CB-OG-P-O1P |
| 2 | A | 729 | SEP | CB-OG-P-O2P |
| 2 | A | 729 | SEP | CB-OG-P-O3P |

There are no ring outliers.

1 monomer is involved in 1 short contact:

| Mol | Chain | Res | Type | Clashes | Symm-Clashes |
|---|---|---|---|---|---|
| 2 | A | 729 | SEP | 1 | 0 |

## 5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry (i)

2 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 | $\#\|Z\|>2$ |
| 3 | 215 | A | 801 | - | 33,38,38 | 0.81 | 0 | 31,53,53 | 0.38 | 0 |
| 3 | 215 | B | 801 | - | 33,38,38 | 0.81 | 0 | 31,53,53 | 0.39 | 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 |
|---|---|---|---|---|---|---|---|
| 3 | 215 | A | 801 | - | - | 5/8/29/29 | 0/5/5/5 |
| 3 | 215 | B | 801 | - | - | 3/8/29/29 | 0/5/5/5 |

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 |
|---|---|---|---|---|
| 3 | A | 801 | 215 | C31-C32-N33-O34 |
| 3 | A | 801 | 215 | C23-C24-N25-C26 |
| 3 | B | 801 | 215 | C31-C32-N33-O34 |
| 3 | B | 801 | 215 | C23-C24-N25-C26 |
| 3 | A | 801 | 215 | C20-C19-O22-C23 |
| 3 | A | 801 | 215 | C18-C19-O22-C23 |

*Continued on next page...*

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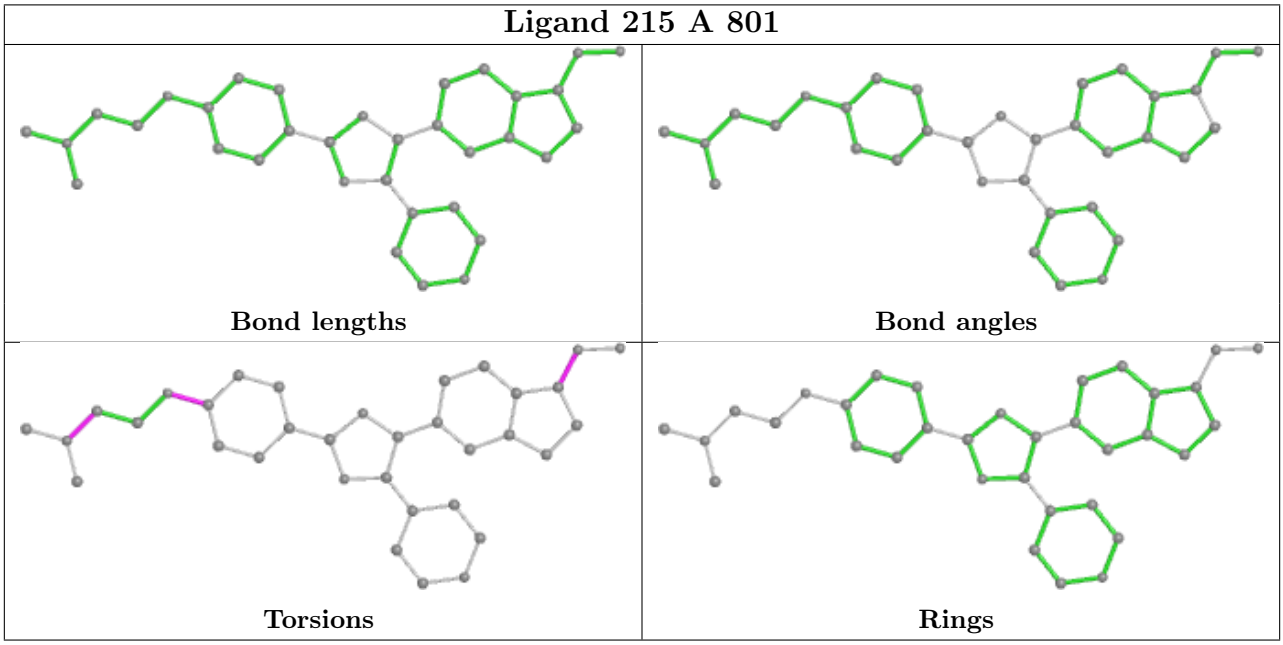
| Mol | Chain | Res | Type | Atoms |
|---|---|---|---|---|
| 3 | A | 801 | 215 | C28-C32-N33-O34 |
| 3 | B | 801 | 215 | C28-C32-N33-O34 |

There are no ring outliers.

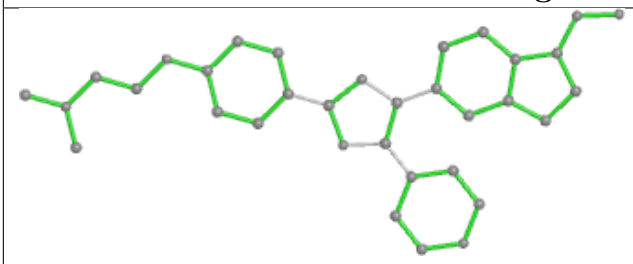
1 monomer is involved in 1 short contact:

| Mol | Chain | Res | Type | Clashes | Symm-Clashes |
|---|---|---|---|---|---|
| 3 | A | 801 | 215 | 1 | 0 |

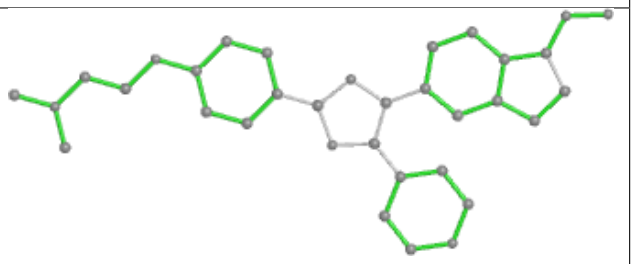
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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



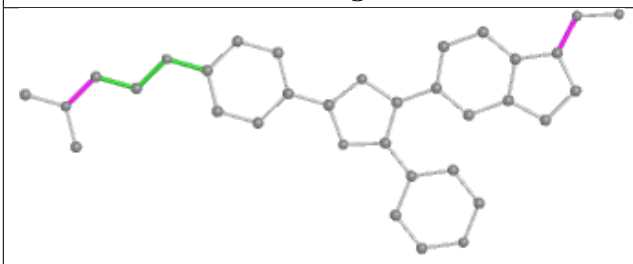
**Ligand 215 B 801**



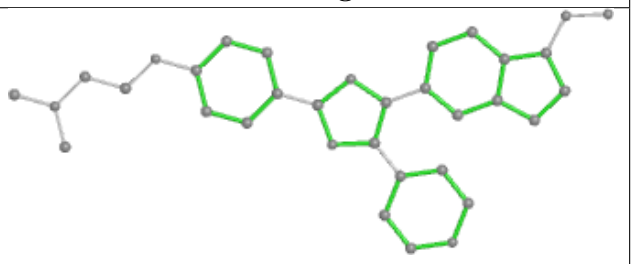
**Bond lengths**



**Bond angles**



**Torsions**



**Rings**

## 5.7 Other polymers (i)

There are no such residues in this entry.

## 5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

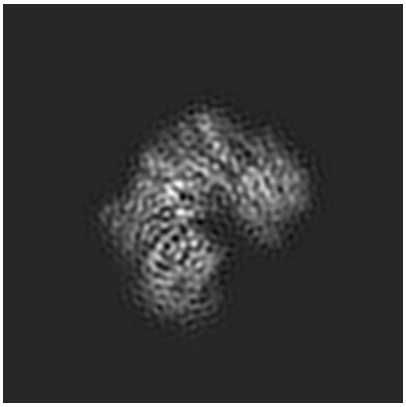
# 6 Map visualisation

This section contains visualisations of the EMDB entry EMD-23815. These allow visual inspection of the internal detail of the map and identification of artifacts.

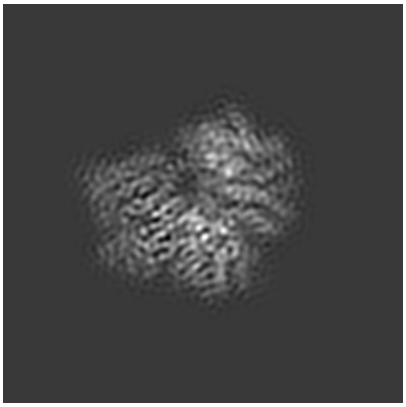
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

## 6.1 Orthogonal projections

### 6.1.1 Primary map



X



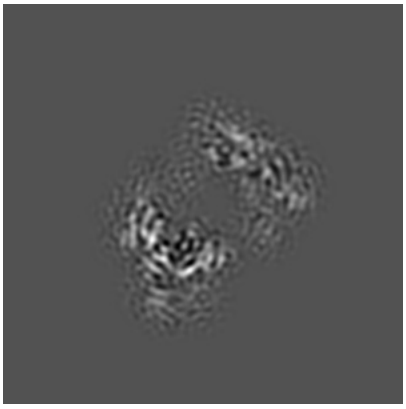
Y

Z

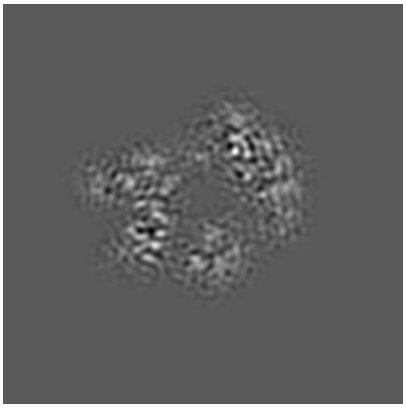
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices

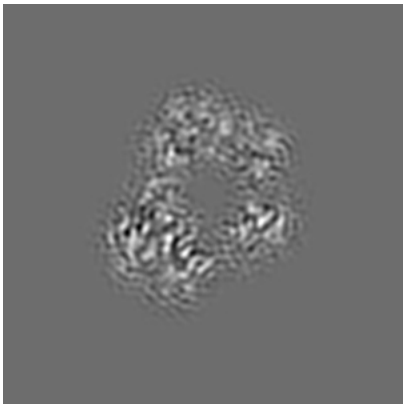
### 6.2.1 Primary map



X Index: 65



Y Index: 65

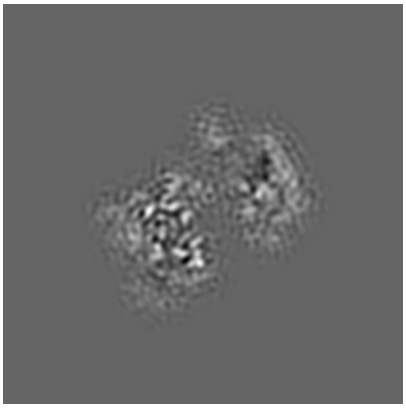


Z Index: 65

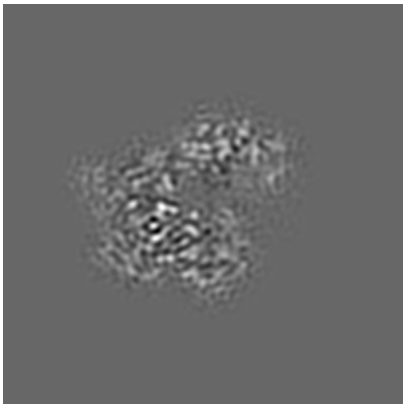
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices (i)

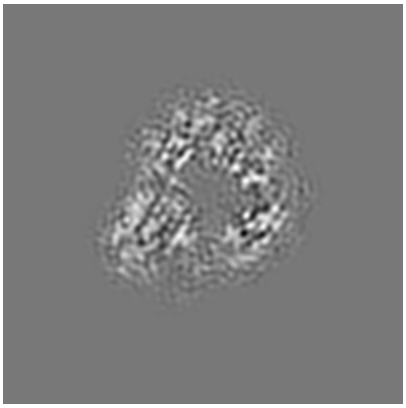
### 6.3.1 Primary map



X Index: 57



Y Index: 58

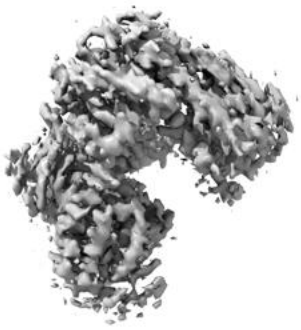


Z Index: 70

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

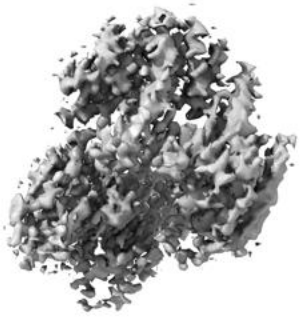
## 6.4 Orthogonal surface views (i)

### 6.4.1 Primary map



X

Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.049. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

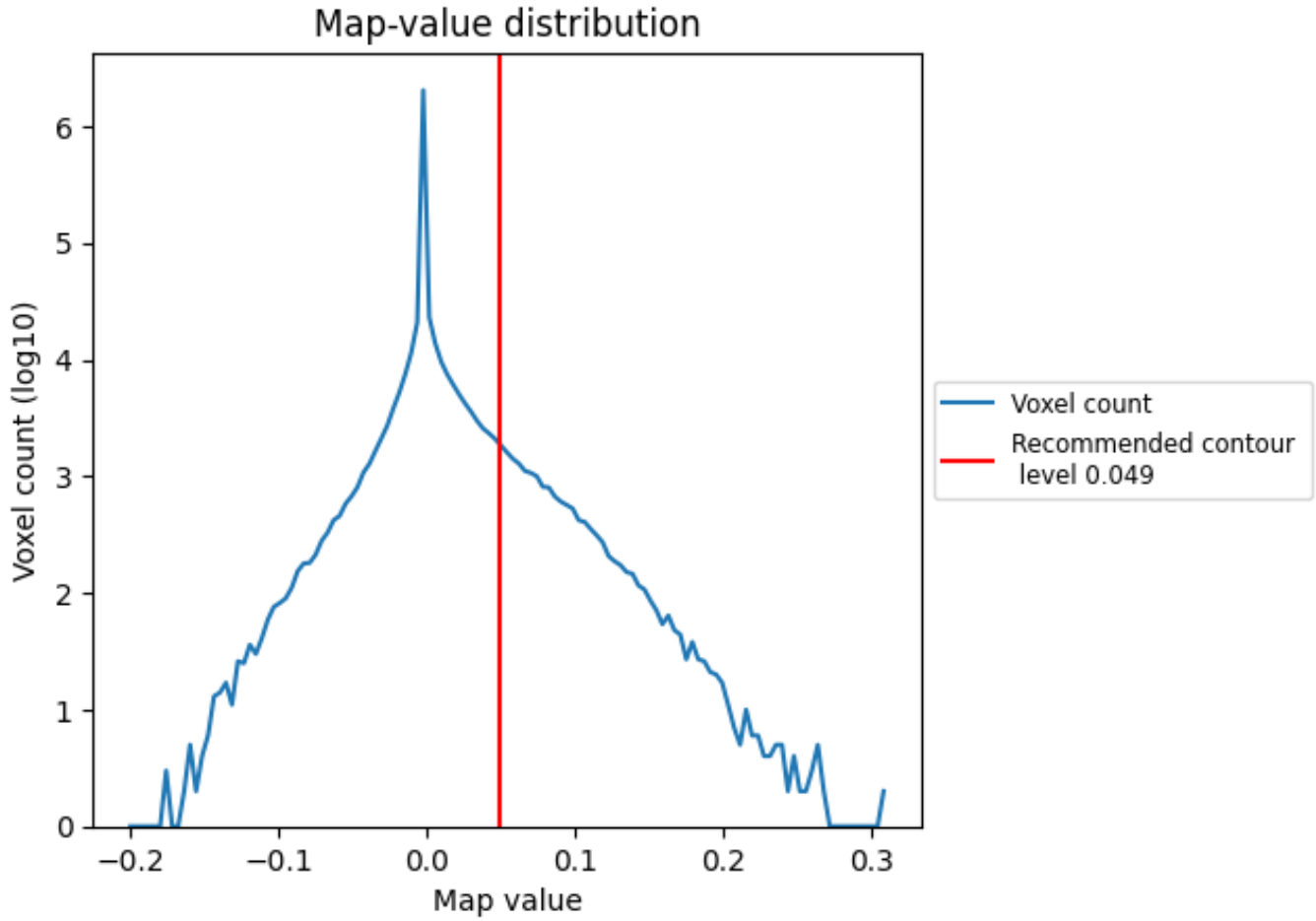
## 6.5 Mask visualisation (i)

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

# 7 Map analysis

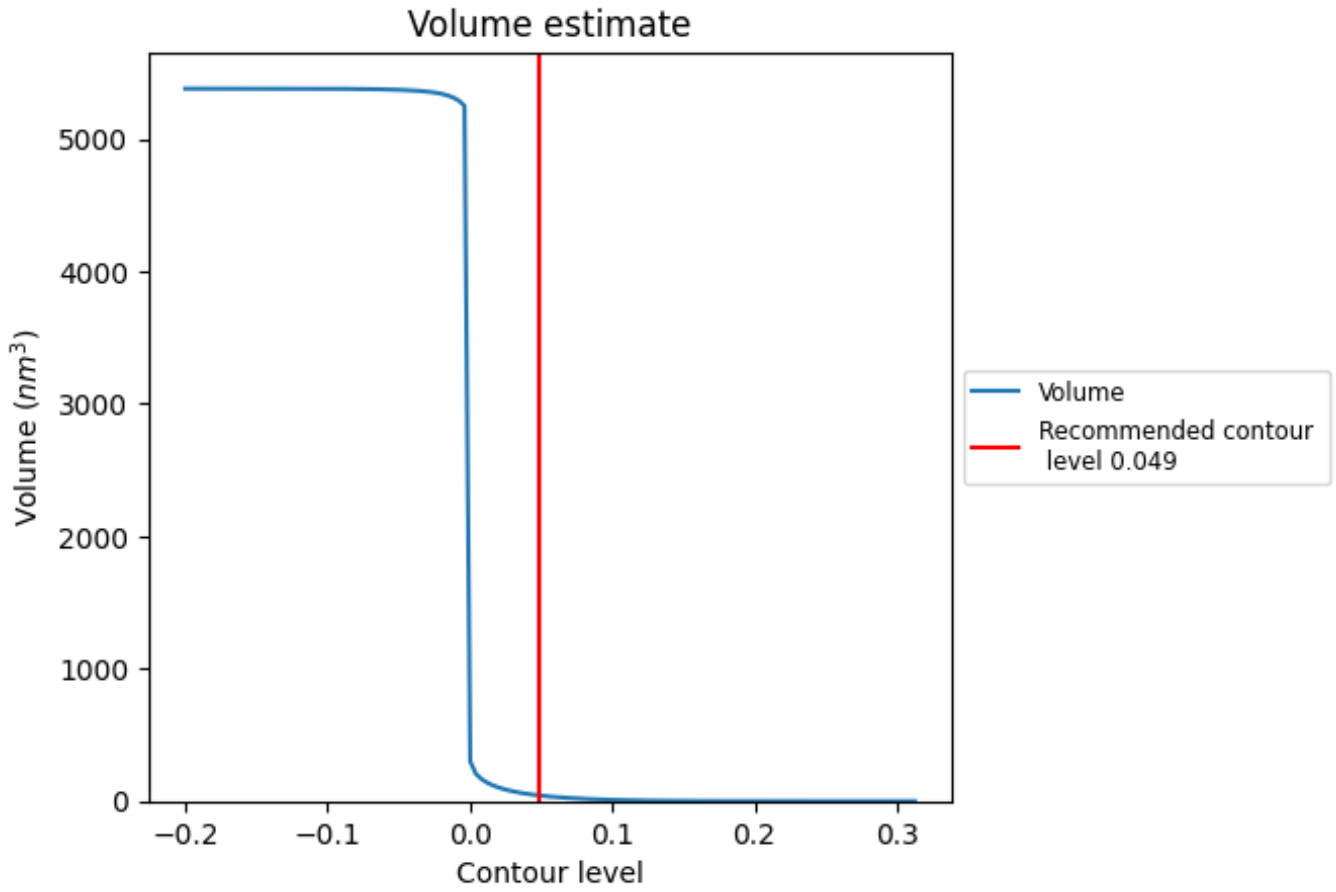
This section contains the results of statistical analysis of the map.

## 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.

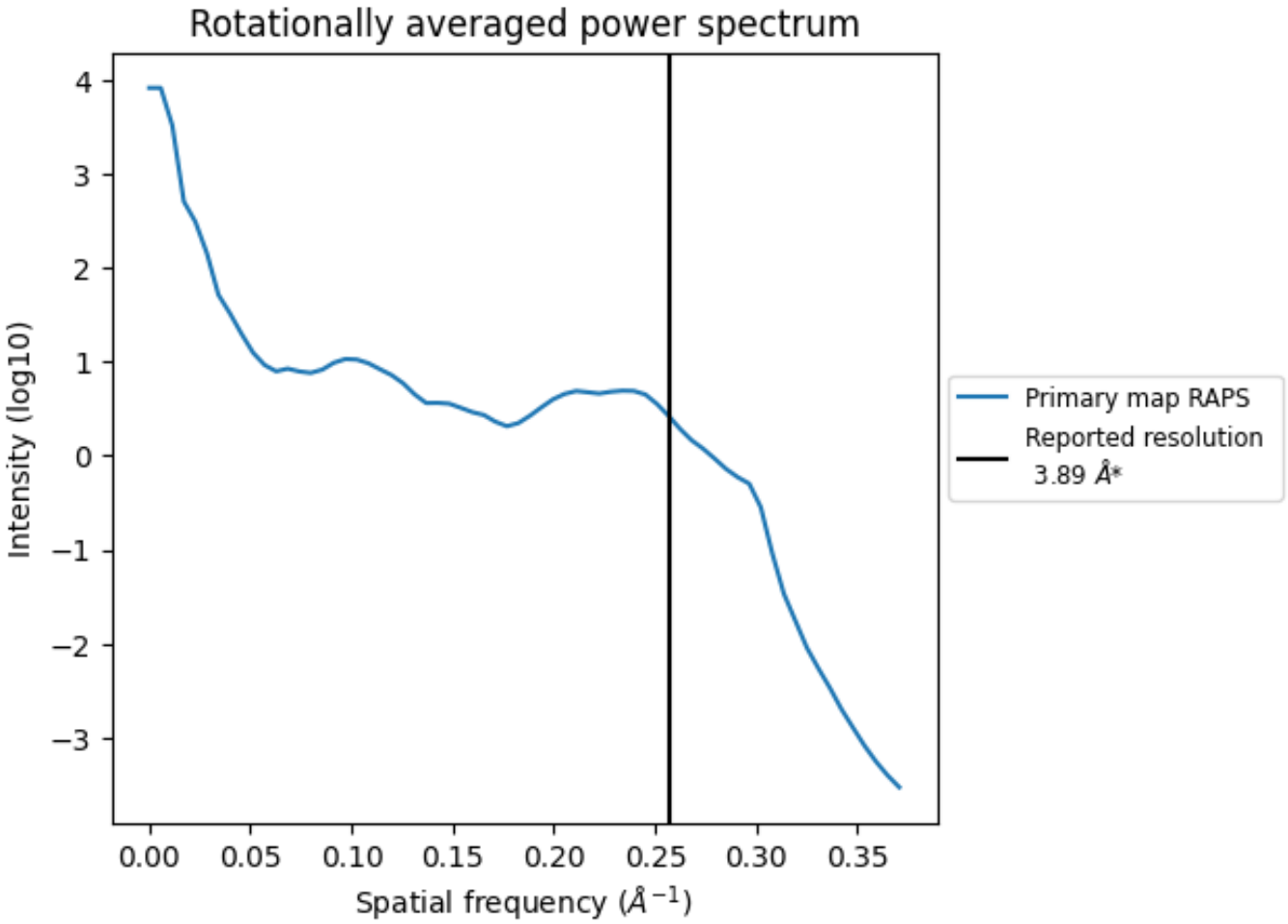
## 7.2 Volume estimate




The volume at the recommended contour level is 43 $nm^3$; this corresponds to an approximate mass of 39 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)

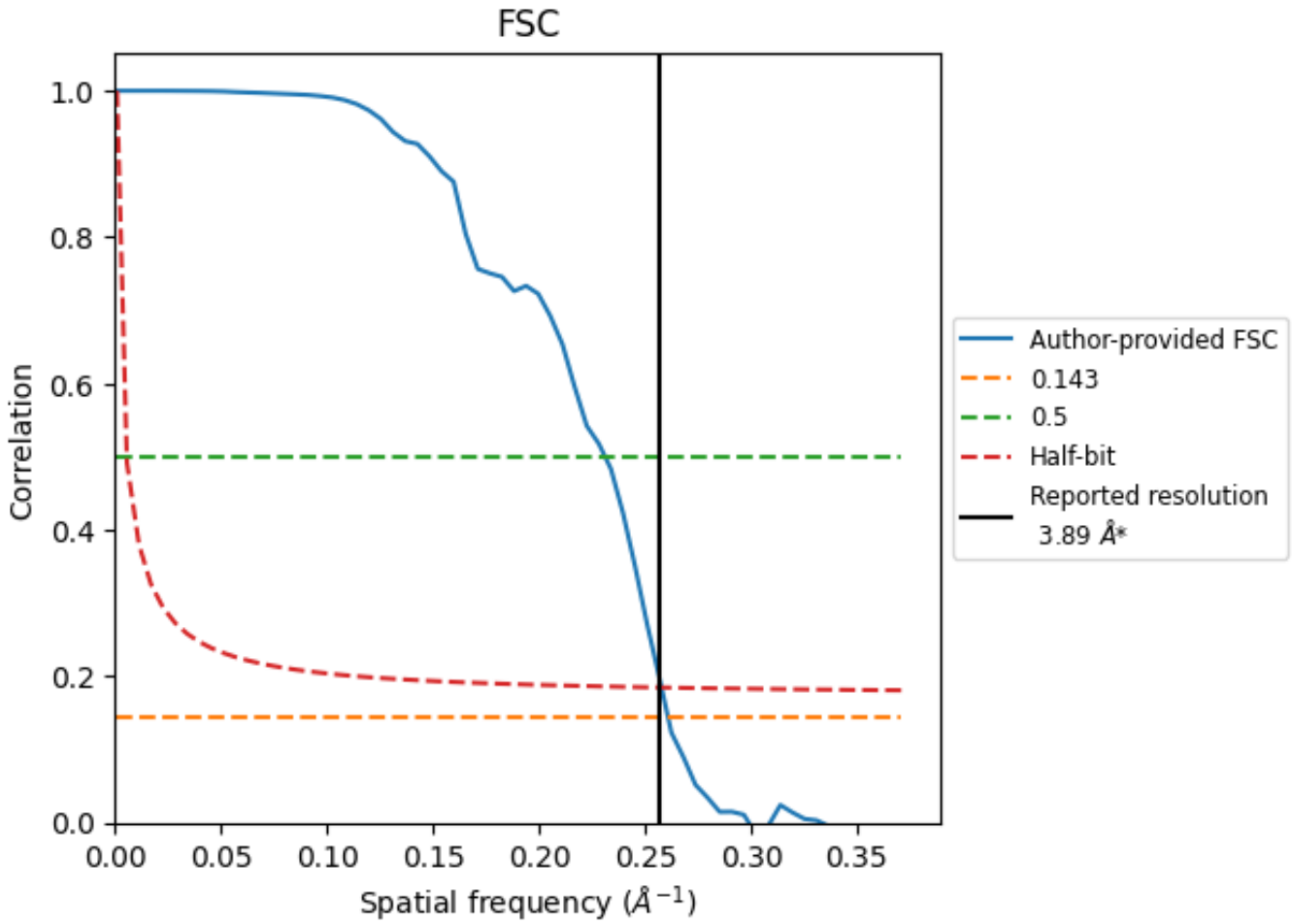



*Reported resolution corresponds to spatial frequency of 0.257 Å$^{-1}$

# 8 Fourier-Shell correlation

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

## 8.1 FSC




*Reported resolution corresponds to spatial frequency of 0.257 Å$^{-1}$

## 8.2 Resolution estimates (i)

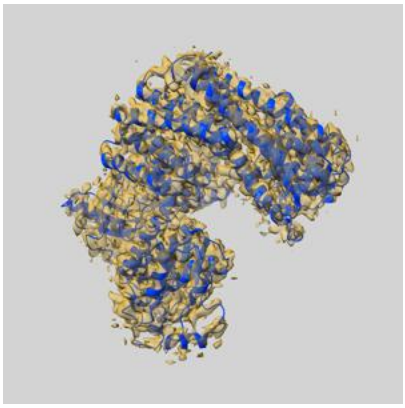
| Resolution estimate (Å) | Estimation criterion (FSC cut-off) | | |
|---|---|---|---|
| | 0.143 | 0.5 | Half-bit |
| Reported by author | 3.89 | - | - |
| Author-provided FSC curve | 3.83 | 4.33 | 3.88 |
| Unmasked-calculated* | - | - | - |

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

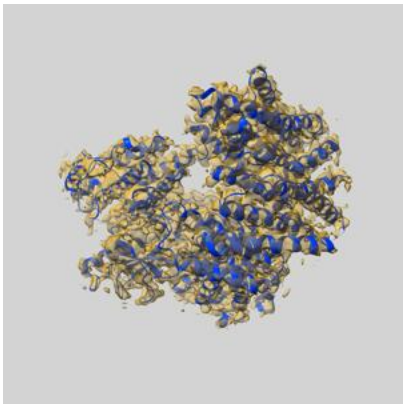
# 9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-23815 and PDB model 7MFF. Per-residue inclusion information can be found in section 3 on page 5.

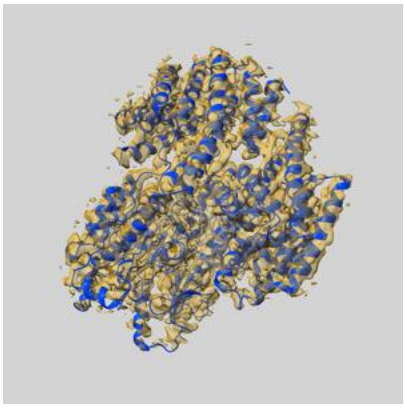
## 9.1 Map-model overlay



X



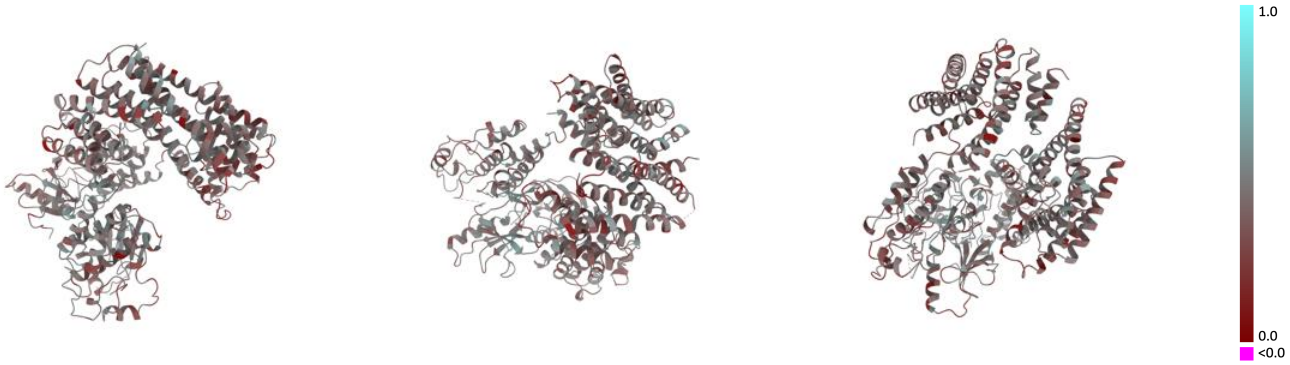
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.049 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.

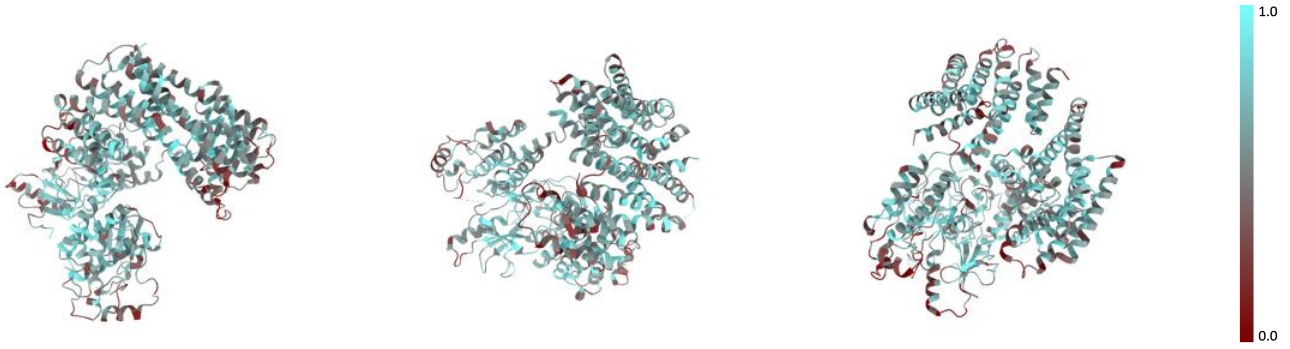
## 9.2 Q-score mapped to coordinate model




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.

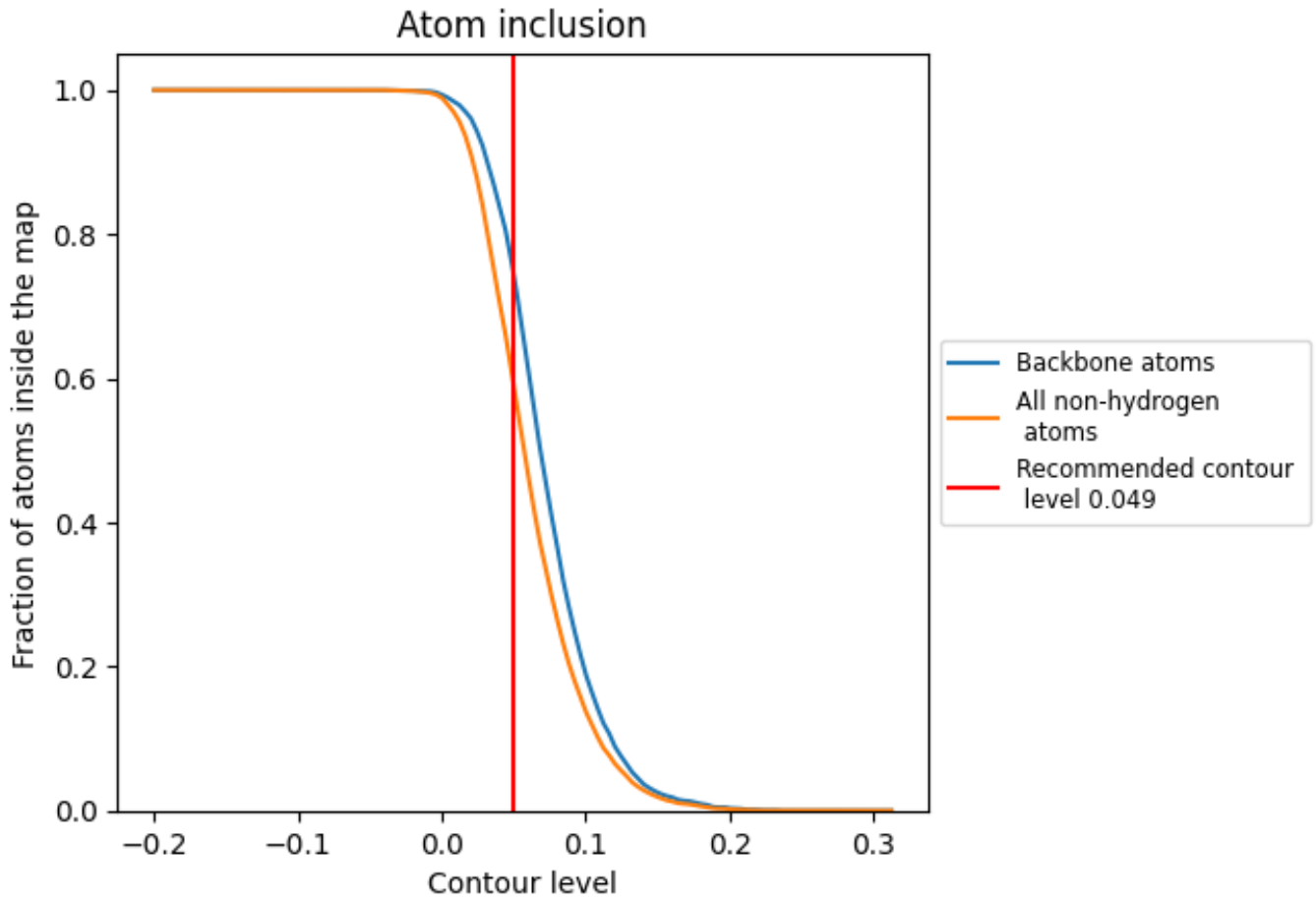
## 9.3 Atom inclusion mapped to coordinate model




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 (0.049).

## 9.4 Atom inclusion (i)




At the recommended contour level, 75% of all backbone atoms, 60% of all non-hydrogen atoms, are inside the map.

## 9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.049) and Q-score for the entire model and for each chain.


| Chain | Atom inclusion | Q-score |
|---|---|---|
| All | 0.6009 | 0.4070 |
| A | 0.6308 | 0.4310 |
| B | 0.5689 | 0.4030 |
| C | 0.6153 | 0.4010 |
| D | 0.5892 | 0.3860 |