



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 12:45 AM UTC

PDB ID : 5I3Q / pdb_00005i3q
Title : DENGUE SEROTYPE 3 RNA-DEPENDENT RNA POLYMERASE BOUND
TO COMPOUND 29
Authors : Noble, C.G.
Deposited on : 2016-02-10
Resolution : 1.88 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

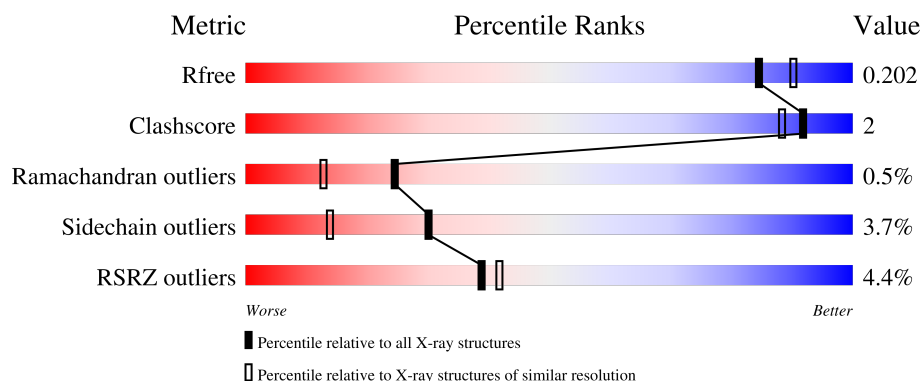
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.88 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}	180053	1220 (1.88-1.88)
Clashscore	190562	1234 (1.88-1.88)
Ramachandran outliers	187476	1222 (1.88-1.88)
Sidechain outliers	187428	1222 (1.88-1.88)
RSRZ outliers	180081	1220 (1.88-1.88)

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

Mol	Chain	Length	Quality of chain
1	A	635	4% 83% 9% 8%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 5412 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 Genome polyprotein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	585	Total	C	N	O	S	0	5	0
			4788	3025	856	876	31			

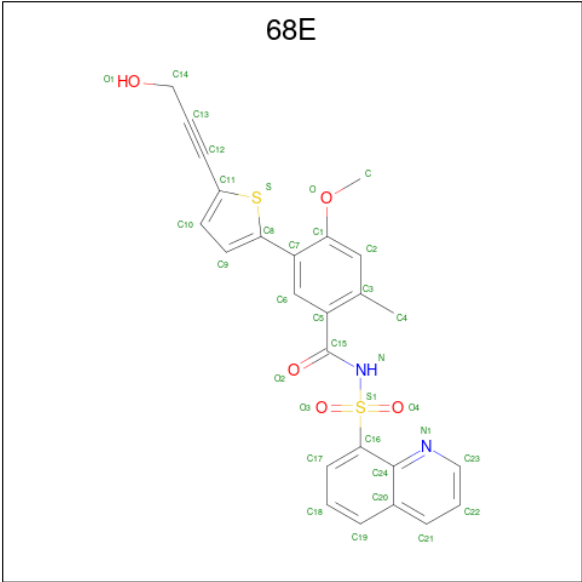
There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	266	GLY	-	expression tag	UNP Q6DLV0
A	267	SER	-	expression tag	UNP Q6DLV0
A	268	HIS	-	expression tag	UNP Q6DLV0
A	269	MET	-	expression tag	UNP Q6DLV0
A	270	LEU	-	expression tag	UNP Q6DLV0
A	271	ASP	-	expression tag	UNP Q6DLV0
A	374	GLU	GLY	variant	UNP Q6DLV0

- Molecule 2 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	2	Total	Zn	0	0
			2	2		

- Molecule 3 is 5-[5-(3-hydroxyprop-1-yn-1-yl)thiophen-2-yl]-4-methoxy-2-methyl-N-[(quinolin-8-yl)sulfonyl]benzamide (CCD ID: 68E) (formula: C₂₅H₂₀N₂O₅S₂).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	S	0	0
			34	25	2	5	2		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	588	Total	O	0	0
			588	588		

4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	161.14Å 175.90Å 57.79Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	27.53 – 1.88 27.53 – 1.88	Depositor EDS
% Data completeness (in resolution range)	98.9 (27.53-1.88) 98.8 (27.53-1.88)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.19 (at 1.88Å)	Xtriage
Refinement program	BUSTER-TNT 2.11.4	Depositor
R, R_{free}	0.176 , 0.202 0.177 , 0.202	Depositor DCC
R_{free} test set	3375 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å ²)	29.3	Xtriage
Anisotropy	0.528	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 59.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	5412	wwPDB-VP
Average B, all atoms (Å ²)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.67% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, 68E

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.86	2/4924 (0.0%)	1.16	12/6669 (0.2%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	809	MET	SD-CE	-6.80	1.62	1.79
1	A	863	ILE	CA-C	5.25	1.58	1.52

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	283	ILE	CA-C-N	5.86	128.45	120.54
1	A	283	ILE	C-N-CA	5.86	128.45	120.54
1	A	332	ASP	N-CA-C	-5.82	105.07	111.82
1	A	840	GLY	N-CA-C	-5.73	105.34	111.93
1	A	533	ASP	CA-CB-CG	5.62	118.22	112.60
1	A	497	PHE	CA-CB-CG	-5.51	108.29	113.80
1	A	860	ALA	CA-C-N	5.39	127.50	120.28
1	A	860	ALA	C-N-CA	5.39	127.50	120.28
1	A	274	ASP	CA-CB-CG	5.30	117.90	112.60
1	A	600	SER	N-CA-C	5.29	117.04	111.28
1	A	574	ASN	N-CA-C	-5.04	100.13	108.75
1	A	672	ASP	CA-CB-CG	-5.02	107.58	112.60

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4788	0	4687	15	0
2	A	2	0	0	0	0
3	A	34	0	0	0	0
4	A	588	0	0	0	0
All	All	5412	0	4687	15	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 2.

All (15) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:802:GLN:H	1:A:802:GLN:HE21	1.21	0.86
1:A:375:ILE:HD11	1:A:640:GLU:HG2	1.77	0.65
1:A:716:LEU:HD21	1:A:839:LEU:HD23	1.86	0.58
1:A:372:VAL:HG21	1:A:628:LEU:HD11	1.86	0.57
1:A:385:GLY:HA3	1:A:555:GLN:HE22	1.70	0.57
1:A:802:GLN:H	1:A:802:GLN:NE2	1.98	0.54
1:A:543:GLU:O	1:A:547[A]:HIS:HD2	1.92	0.52
1:A:764[B]:LEU:HG	1:A:765:MET:HE2	1.95	0.48
1:A:627:VAL:HG21	1:A:646:TRP:CD1	2.53	0.44
1:A:805:THR:CG2	1:A:809:MET:HE1	2.48	0.44
1:A:380:LEU:HD11	1:A:614:MET:HE2	2.01	0.42
1:A:320:ILE:HD11	1:A:341:ALA:HB1	2.01	0.42
1:A:768:HIS:HA	1:A:838:TYR:HA	2.02	0.41
1:A:452:ASN:HD21	1:A:578:LYS:HD2	1.86	0.41
1:A:548:ASN:HD22	1:A:551:LYS:HE2	1.86	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	584/635 (92%)	571 (98%)	10 (2%)	3 (0%)	24 13

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	343	THR
1	A	342	MET
1	A	333	VAL

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	515/552 (93%)	496 (96%)	19 (4%)	30 14

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	296	GLU
1	A	313	THR
1	A	319	MET
1	A	326	LEU
1	A	350	GLN
1	A	400	LYS
1	A	425	VAL
1	A	443	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	473	ILE
1	A	481	ARG
1	A	533	ASP
1	A	638	LEU
1	A	664	ASP
1	A	676	ASN
1	A	742	GLN
1	A	785	VAL
1	A	797	ILE
1	A	802	GLN
1	A	842	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	272	ASN
1	A	287	HIS
1	A	339	GLN
1	A	452	ASN
1	A	548	ASN
1	A	555	GLN
1	A	617	GLN
1	A	621	GLN
1	A	645	GLN
1	A	676	ASN
1	A	682	ASN
1	A	704	GLN
1	A	768	HIS
1	A	802	GLN
1	A	835	ASN
1	A	869	GLN

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 oligosaccharides in this entry.

5.6 Ligand geometry

Of 3 ligands modelled in this entry, 2 are monoatomic - leaving 1 for Mogul analysis.

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	68E	A	1003	-	37,37,37	0.27	0	51,53,53	0.62	1 (1%)

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	68E	A	1003	-	-	2/23/25/25	0/4/4/4

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1003	68E	C16-S1-N	-3.30	101.92	107.28

There are no chirality outliers.

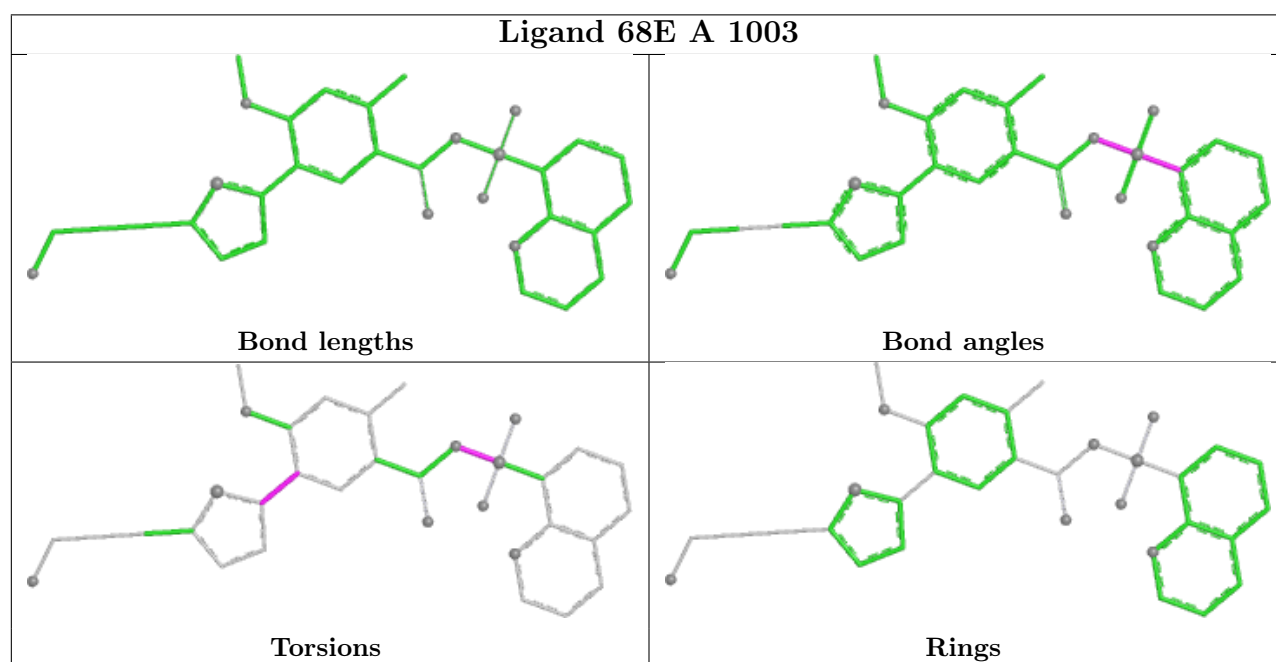
All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	1003	68E	C15-N-S1-O3
3	A	1003	68E	C1-C7-C8-C9

There are no ring outliers.

No monomer is involved in short contacts.

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 than 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.



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2		OWAB(Å ²)	Q<0.9
1	A	585/635 (92%)	0.11	26 (4%)	39 42	15, 35, 70, 107	5 (0%)

All (26) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	743	GLY	5.6
1	A	585	THR	4.1
1	A	333	VAL	4.1
1	A	744	ALA	3.9
1	A	601	GLY	3.8
1	A	745	GLY	3.4
1	A	406	ALA	3.3
1	A	357	LYS	3.2
1	A	404	THR	3.1
1	A	407	ALA	3.0
1	A	470	SER	2.6
1	A	742	GLN	2.6
1	A	746	TRP	2.5
1	A	473	ILE	2.5
1	A	453	MET	2.5
1	A	353	VAL	2.4
1	A	343	THR	2.3
1	A	348	PHE	2.2
1	A	313	THR	2.2
1	A	310	VAL	2.2
1	A	293	TYR	2.1
1	A	795	TRP	2.1
1	A	883	MET	2.1
1	A	405	ASN	2.1
1	A	319	MET	2.0
1	A	350	GLN	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

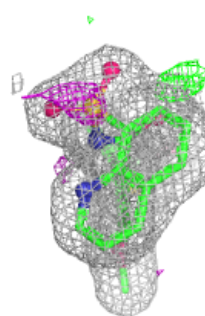
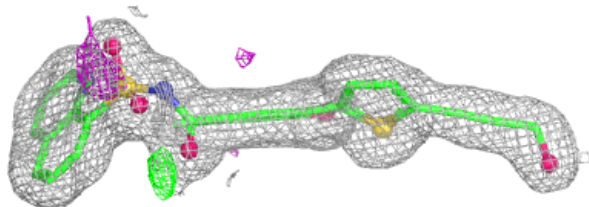
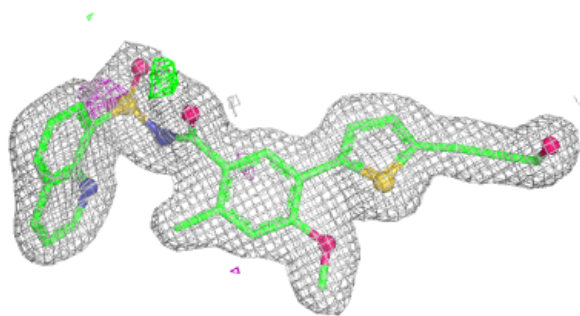
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	68E	A	1003	34/34	0.98	0.05	21,27,36,38	0
2	ZN	A	1002	1/1	0.99	0.02	34,34,34,34	0
2	ZN	A	1001	1/1	1.00	0.03	25,25,25,25	0

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

Electron density around 68E A 1003:

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



6.5 Other polymers ⓘ

There are no such residues in this entry.