



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 10:59 AM UTC

PDB ID : 7XPY / pdb_00007xpy
Title : Crystal structure of USP7 in complex with its inhibitor
Authors : Feng, N.; Zeng, K.W.
Deposited on : 2022-05-06
Resolution : 2.35 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

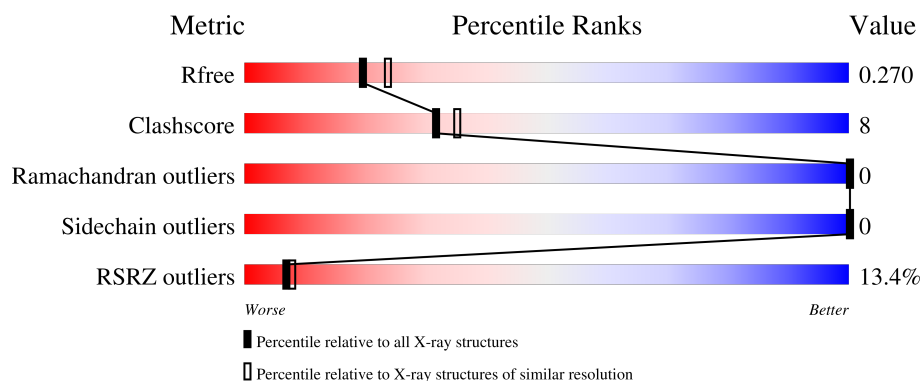
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.35 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	1596 (2.36-2.36)
Clashscore	190562	1663 (2.36-2.36)
Ramachandran outliers	187476	1646 (2.36-2.36)
Sidechain outliers	187428	1646 (2.36-2.36)
RSRZ outliers	180081	1598 (2.36-2.36)

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	548	13% 82% 15% .

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 4400 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.

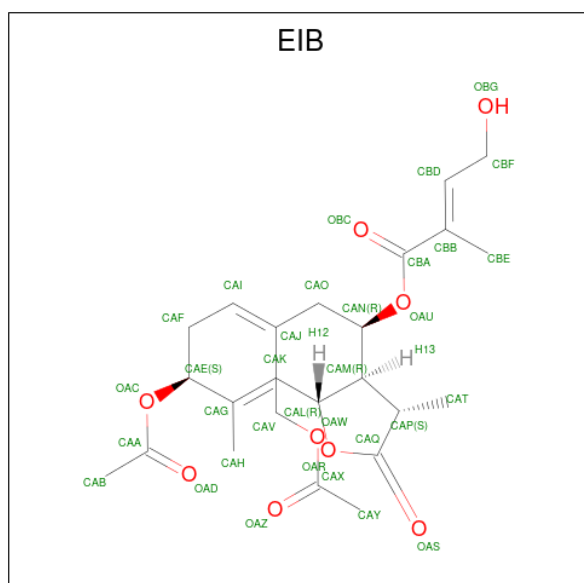
- Molecule 1 is a protein called Ubiquitin carboxyl-terminal hydrolase 7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	528	4338	2762	733	816	27	0	0	0

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	555	GLY	-	expression tag	UNP Q93009
A	556	PRO	-	expression tag	UNP Q93009
A	557	LEU	-	expression tag	UNP Q93009
A	558	GLY	-	expression tag	UNP Q93009
A	559	SER	-	expression tag	UNP Q93009

- Molecule 2 is [(3S,3aR,4R,6Z,9S,10E,11aR)-9-acetyloxy-6-(acetyloxymethyl)-3,10-dimethyl-2-oxidanylidene-3a,4,5,8,9,11a-hexahydro-3H-cyclodeca[b]furan-4-yl] (E)-2-methyl-4-oxidanyl-but-2-enoate (CCD ID: EIB) (formula: C₂₄H₃₂O₉) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			33	24	9		

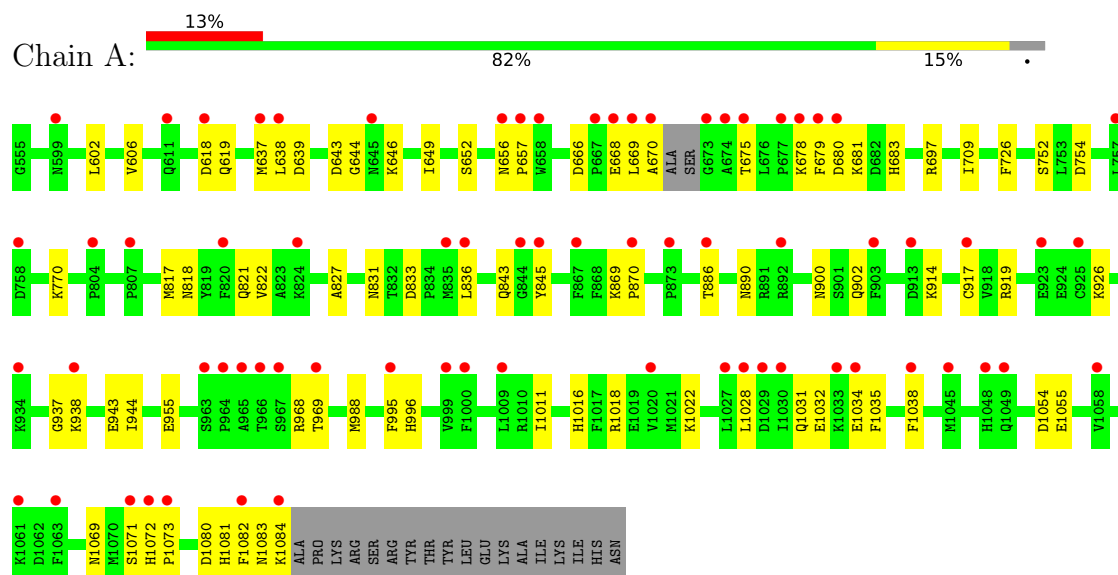
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	29	Total	O	0	0
			29	29		

3 Residue-property plots [i](#)

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

- Molecule 1: Ubiquitin carboxyl-terminal hydrolase 7



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	78.00Å 80.17Å 150.86Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	38.74 – 2.35 38.74 – 2.35	Depositor EDS
% Data completeness (in resolution range)	99.7 (38.74-2.35) 99.7 (38.74-2.35)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.53 (at 2.34Å)	Xtriage
Refinement program	PHENIX 1.14 _3260	Depositor
R, R_{free}	0.224 , 0.266 0.227 , 0.270	Depositor DCC
R_{free} test set	2012 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	60.9	Xtriage
Anisotropy	0.579	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 45.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.016 for k,h,-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	4400	wwPDB-VP
Average B, all atoms (Å ²)	80.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.06% 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: EIB

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	0.25	0/4437	0.51	0/5988

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	A	4338	0	4253	67	0
2	A	33	0	0	6	0
3	A	29	0	0	2	0
All	All	4400	0	4253	70	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 (70) 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:968:ARG:HB2	1:A:968:ARG:NH1	1.93	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:639:ASP:OD1	1:A:681:LYS:HE3	1.83	0.77
1:A:678:LYS:HG2	1:A:679:PHE:N	2.00	0.74
1:A:678:LYS:HG2	1:A:679:PHE:H	1.54	0.73
1:A:968:ARG:HB2	1:A:968:ARG:HH11	1.54	0.71
1:A:944:ILE:HB	1:A:969:THR:HG23	1.74	0.69
1:A:869:LYS:HD3	1:A:870:PRO:HD2	1.76	0.68
1:A:666:ASP:CG	2:A:1201:EIB:OAD	2.38	0.66
1:A:1038:PHE:HB2	1:A:1080:ASP:O	1.96	0.65
1:A:656:ASN:HB3	1:A:657:PRO:HD3	1.80	0.64
1:A:1038:PHE:HB3	1:A:1081:HIS:HB3	1.80	0.64
1:A:1054:ASP:O	1:A:1055:GLU:HG3	1.99	0.63
1:A:668:GLU:HA	1:A:668:GLU:OE1	1.99	0.62
1:A:666:ASP:CB	2:A:1201:EIB:OAD	2.49	0.60
1:A:968:ARG:HH11	1:A:968:ARG:CB	2.14	0.60
1:A:1016:HIS:NE2	1:A:1055:GLU:HA	2.17	0.60
1:A:618:ASP:O	1:A:675:THR:HB	2.01	0.60
1:A:697:ARG:NH2	3:A:1302:HOH:O	2.32	0.59
1:A:1018:ARG:O	1:A:1022:LYS:HG2	2.02	0.59
1:A:643:ASP:HB3	1:A:646:LYS:HD3	1.83	0.59
1:A:817:MET:HE2	1:A:821:GLN:HB3	1.84	0.59
1:A:1016:HIS:CE1	1:A:1055:GLU:HA	2.38	0.59
1:A:902:GLN:NE2	1:A:902:GLN:H	2.01	0.58
1:A:926:LYS:NZ	1:A:937:GLY:O	2.37	0.57
1:A:1038:PHE:CB	1:A:1081:HIS:HB3	2.35	0.57
1:A:666:ASP:C	1:A:668:GLU:N	2.63	0.56
1:A:1031:GLN:HB3	1:A:1034:GLU:HB2	1.87	0.56
1:A:919:ARG:HB2	1:A:955:GLU:HB3	1.87	0.56
1:A:666:ASP:HB2	2:A:1201:EIB:OAD	2.05	0.55
2:A:1201:EIB:CAJ	2:A:1201:EIB:CAK	2.84	0.55
1:A:666:ASP:C	1:A:668:GLU:H	2.13	0.55
2:A:1201:EIB:CAK	2:A:1201:EIB:CAI	2.85	0.54
1:A:833:ASP:HB3	1:A:836:LEU:HG	1.90	0.54
1:A:1016:HIS:ND1	1:A:1018:ARG:HG3	2.23	0.54
2:A:1201:EIB:CAF	2:A:1201:EIB:CAB	2.85	0.53
1:A:996:HIS:ND1	1:A:1081:HIS:O	2.34	0.52
1:A:669:LEU:HD12	1:A:669:LEU:N	2.24	0.52
1:A:602:LEU:HB3	1:A:644:GLY:HA2	1.92	0.51
1:A:827:ALA:O	1:A:831:ASN:N	2.44	0.51
1:A:669:LEU:N	1:A:669:LEU:CD1	2.72	0.51
1:A:619:GLN:HE22	1:A:670:ALA:CB	2.25	0.50
1:A:697:ARG:NE	3:A:1302:HOH:O	2.43	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:902:GLN:NE2	1:A:902:GLN:N	2.60	0.49
1:A:752:SER:OG	1:A:754:ASP:OD1	2.30	0.49
1:A:943:GLU:CD	1:A:968:ARG:HD3	2.38	0.49
1:A:1016:HIS:HE2	1:A:1055:GLU:HA	1.76	0.48
1:A:818:ASN:O	1:A:822:VAL:HG12	2.14	0.48
1:A:917:CYS:SG	1:A:919:ARG:HB3	2.55	0.47
1:A:1028:LEU:HD23	1:A:1028:LEU:HA	1.72	0.47
1:A:649:ILE:HA	1:A:652:SER:HB3	1.97	0.47
1:A:637:MET:HE3	1:A:637:MET:HB3	1.79	0.46
1:A:1069:ASN:OD1	1:A:1071:SER:HB3	2.16	0.46
1:A:726:PHE:CE1	1:A:770:LYS:HG3	2.51	0.45
1:A:709:ILE:CG2	1:A:754:ASP:HB3	2.46	0.45
1:A:995:PHE:O	1:A:1080:ASP:HA	2.17	0.45
1:A:843:GLN:OE1	1:A:845:TYR:HB2	2.17	0.45
1:A:602:LEU:O	1:A:606:VAL:HG23	2.17	0.44
1:A:938:LYS:HD2	1:A:938:LYS:HA	1.70	0.44
1:A:890:ASN:O	1:A:914:LYS:HE3	2.19	0.43
1:A:680:ASP:OD1	1:A:683:HIS:ND1	2.52	0.43
1:A:1031:GLN:OE1	1:A:1032:GLU:N	2.51	0.43
1:A:1083:ASN:CG	1:A:1084:LYS:H	2.25	0.43
1:A:638:LEU:HD12	1:A:638:LEU:HA	1.64	0.42
1:A:886:THR:O	1:A:890:ASN:ND2	2.52	0.42
1:A:1072:HIS:ND1	1:A:1073:PRO:HD3	2.34	0.42
1:A:900:ASN:CG	1:A:902:GLN:HE21	2.28	0.41
1:A:683:HIS:O	1:A:709:ILE:HG12	2.19	0.41
1:A:988:MET:HE3	1:A:1011:ILE:HD11	2.03	0.41
1:A:1081:HIS:HB2	1:A:1082:PHE:H	1.55	0.40
1:A:1035:PHE:HA	1:A:1038:PHE:CE2	2.57	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	524/548 (96%)	494 (94%)	30 (6%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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	484/501 (97%)	484 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	619	GLN
1	A	654	ASN
1	A	700	ASN
1	A	838	GLN
1	A	902	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

1 ligand is 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	EIB	A	1201	1	34,34,34	3.27	10 (29%)	40,47,47	2.83	14 (35%)

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	EIB	A	1201	1	-	15/41/57/57	1/2/2/2

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1201	EIB	CBD-CBB	9.61	1.53	1.33
2	A	1201	EIB	CAL-CAK	-7.84	1.37	1.49
2	A	1201	EIB	CAP-CAQ	-7.00	1.39	1.51
2	A	1201	EIB	CAH-CAG	-6.15	1.39	1.50
2	A	1201	EIB	CAE-CAG	-4.87	1.39	1.51
2	A	1201	EIB	CAV-CAJ	-4.82	1.39	1.50
2	A	1201	EIB	CAF-CAI	-4.81	1.41	1.50
2	A	1201	EIB	CAP-CAM	-3.37	1.49	1.53
2	A	1201	EIB	CAI-CAJ	3.07	1.39	1.32
2	A	1201	EIB	CAK-CAG	2.59	1.39	1.33

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1201	EIB	CAL-OAR-CAQ	-7.24	102.97	110.32
2	A	1201	EIB	CBF-CBD-CBB	-7.23	114.87	126.61
2	A	1201	EIB	OAS-CAQ-CAP	-6.29	120.94	128.62

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1201	EIB	CAM-CAL-CAK	-5.09	107.79	114.12
2	A	1201	EIB	CAN-OAU-CBA	-4.51	109.91	117.59
2	A	1201	EIB	CAT-CAP-CAM	-4.30	107.43	117.20
2	A	1201	EIB	CAV-OAW-CAX	-4.12	108.86	116.10
2	A	1201	EIB	OAR-CAQ-CAP	4.06	115.13	110.42
2	A	1201	EIB	CAF-CAI-CAJ	-3.85	121.12	127.29
2	A	1201	EIB	CAE-OAC-CAA	-3.52	111.76	117.00
2	A	1201	EIB	CAH-CAG-CAE	2.84	121.35	114.94
2	A	1201	EIB	OAR-CAL-CAK	2.73	114.30	108.97
2	A	1201	EIB	OAC-CAA-CAB	2.46	115.47	111.09
2	A	1201	EIB	OAR-CAQ-OAS	2.15	123.92	121.26

There are no chirality outliers.

All (15) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1201	EIB	OAD-CAA-OAC-CAE
2	A	1201	EIB	CAG-CAE-CAF-CAI
2	A	1201	EIB	OAC-CAE-CAF-CAI
2	A	1201	EIB	CAG-CAK-CAL-CAM
2	A	1201	EIB	CAG-CAK-CAL-OAR
2	A	1201	EIB	CAP-CAM-CAN-OAU
2	A	1201	EIB	CBB-CBA-OAU-CAN
2	A	1201	EIB	CAB-CAA-OAC-CAE
2	A	1201	EIB	CAY-CAX-OAW-CAV
2	A	1201	EIB	OBC-CBA-OAU-CAN
2	A	1201	EIB	OAZ-CAX-OAW-CAV
2	A	1201	EIB	CAO-CAJ-CAV-OAW
2	A	1201	EIB	CAI-CAJ-CAV-OAW
2	A	1201	EIB	CAL-CAM-CAN-OAU
2	A	1201	EIB	CBB-CBD-CBF-OBG

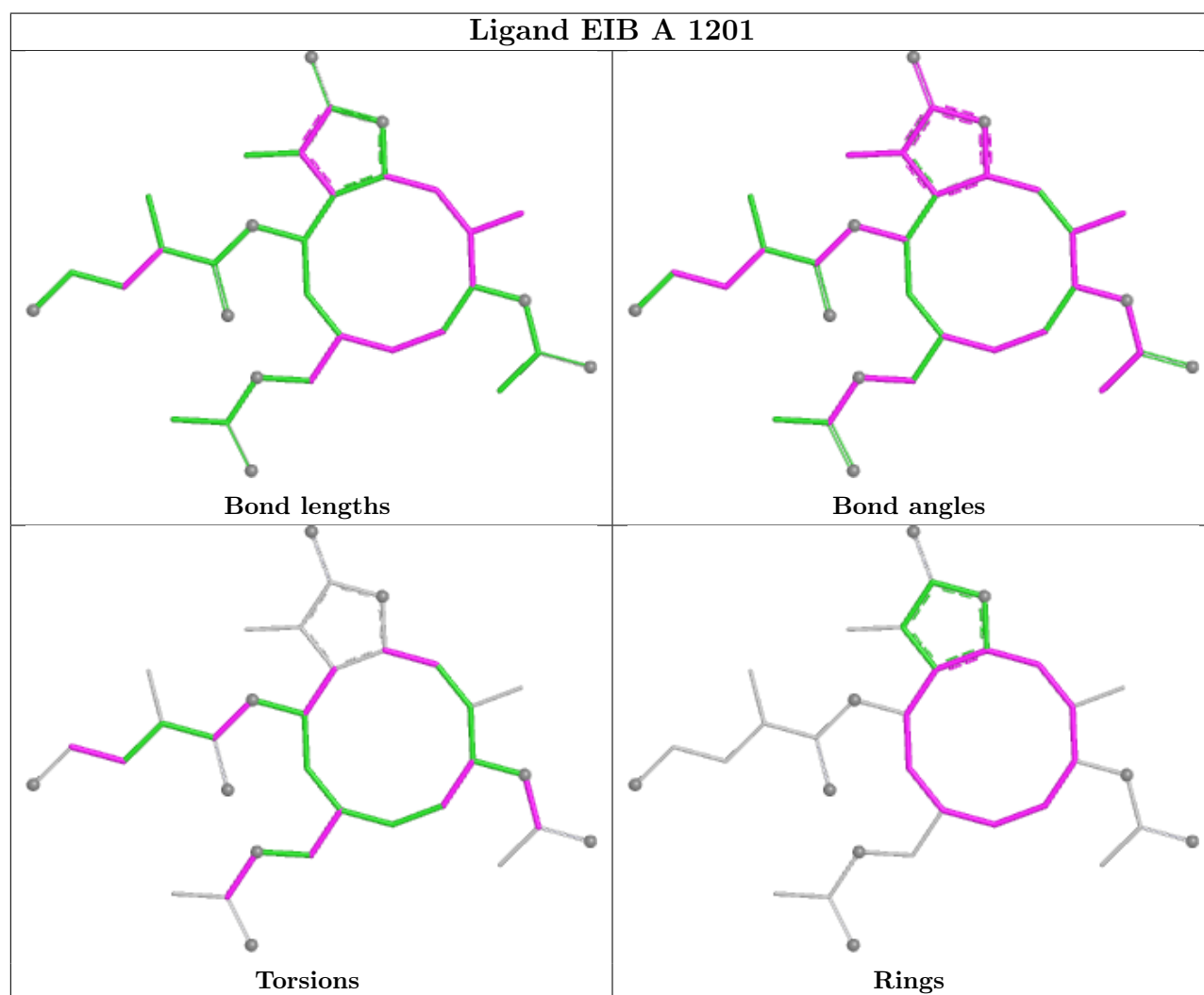
All (1) ring outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1201	EIB	CAE-CAF-CAG-CAI-CAJ-CAK-CAL-CAM-CAN-CAO

1 monomer is involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1201	EIB	6	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 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 ⓘ

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, 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	528/548 (96%)	1.06	71 (13%) 7 8	46, 77, 117, 143	0

All (71) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	966	THR	5.7
1	A	1027	LEU	5.0
1	A	845	TYR	5.0
1	A	670	ALA	4.9
1	A	674	ALA	4.8
1	A	656	ASN	4.6
1	A	1000	PHE	4.6
1	A	967	SER	4.4
1	A	1072	HIS	4.4
1	A	637	MET	4.4
1	A	757	LEU	4.2
1	A	638	LEU	4.1
1	A	669	LEU	4.0
1	A	673	GLY	3.9
1	A	1030	ILE	3.6
1	A	758	ASP	3.6
1	A	1071	SER	3.5
1	A	804	PRO	3.5
1	A	678	LYS	3.4
1	A	965	ALA	3.4
1	A	1048	HIS	3.3
1	A	963	SER	3.2
1	A	1082	PHE	3.2
1	A	667	PRO	3.2
1	A	1029	ASP	3.1
1	A	1049	GLN	3.1
1	A	1084	LYS	3.1

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Mol	Chain	Res	Type	RSRZ
1	A	999	VAL	3.1
1	A	1038	PHE	3.0
1	A	886	THR	3.0
1	A	645	ASN	3.0
1	A	675	THR	2.9
1	A	836	LEU	2.9
1	A	938	LYS	2.8
1	A	1033	LYS	2.8
1	A	657	PRO	2.8
1	A	668	GLU	2.8
1	A	867	PHE	2.7
1	A	1020	VAL	2.7
1	A	835	MET	2.6
1	A	1063	PHE	2.6
1	A	844	GLY	2.6
1	A	892	ARG	2.5
1	A	870	PRO	2.4
1	A	1061	LYS	2.4
1	A	1009	LEU	2.4
1	A	1034	GLU	2.3
1	A	807	PRO	2.3
1	A	1073	PRO	2.3
1	A	903	PHE	2.3
1	A	934	LYS	2.3
1	A	679	PHE	2.3
1	A	618	ASP	2.3
1	A	913	ASP	2.3
1	A	611	GLN	2.3
1	A	824	LYS	2.2
1	A	680	ASP	2.2
1	A	677	PRO	2.2
1	A	923	GLU	2.2
1	A	873	PRO	2.2
1	A	1045	MET	2.2
1	A	658	TRP	2.1
1	A	969	THR	2.1
1	A	820	PHE	2.1
1	A	917	CYS	2.1
1	A	925	CYS	2.1
1	A	1058	VAL	2.1
1	A	599	ASN	2.0
1	A	995	PHE	2.0

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Mol	Chain	Res	Type	RSRZ
1	A	1028	LEU	2.0
1	A	964	PRO	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](#)

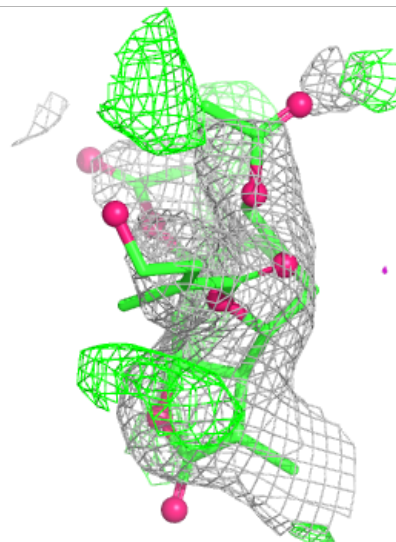
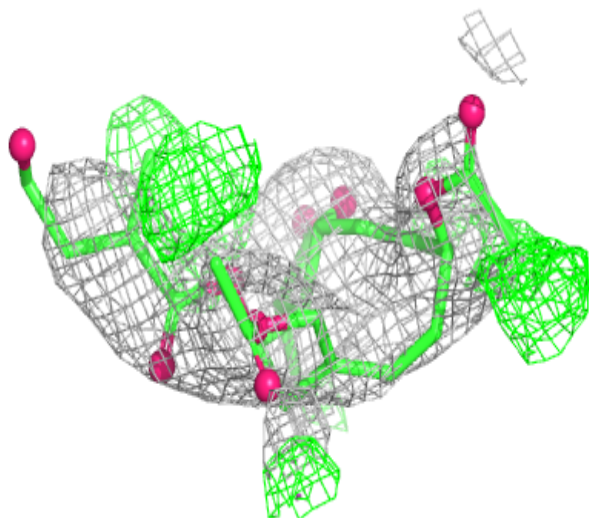
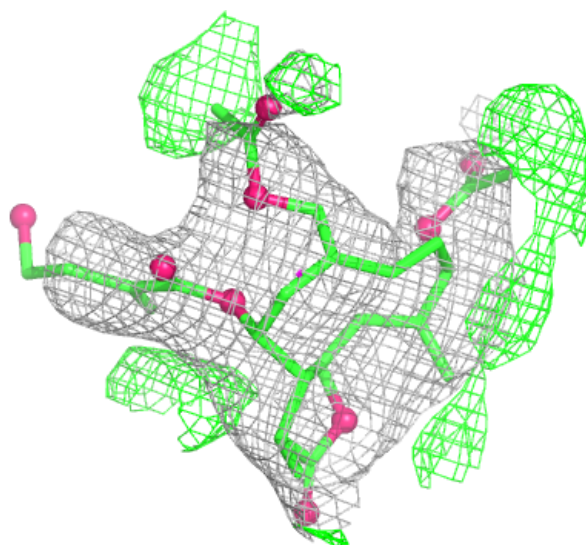
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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
2	EIB	A	1201	33/33	0.78	0.26	76,91,109,119	33

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 EIB A 1201:

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



6.5 Other polymers [i](#)

There are no such residues in this entry.