



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 04:57 PM UTC

PDB ID : 8H9C / pdb_00008h9c
Title : Crystal structure of chemically modified E. coli ThrS catalytic domain 4
Authors : Qiao, H.; Xia, M.; Wang, J.; Fang, P.
Deposited on : 2022-10-25
Resolution : 2.15 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

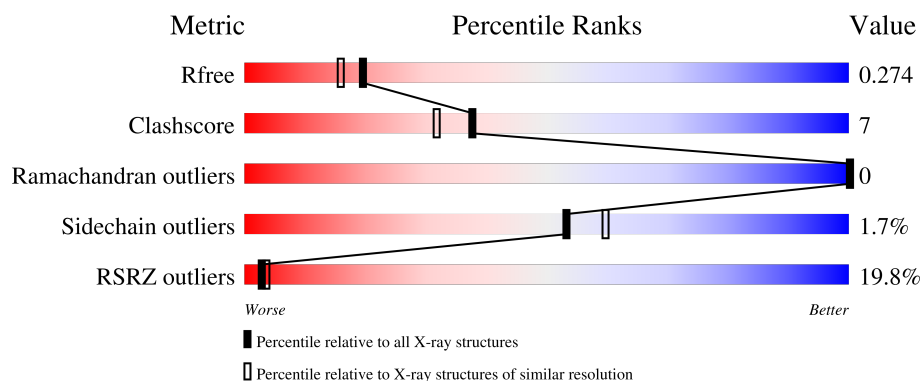
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.15 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	2057 (2.16-2.16)
Clashscore	190562	2159 (2.16-2.16)
Ramachandran outliers	187476	2134 (2.16-2.16)
Sidechain outliers	187428	2133 (2.16-2.16)
RSRZ outliers	180081	2059 (2.16-2.16)

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	410	19% 78% 19% .

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 3455 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.

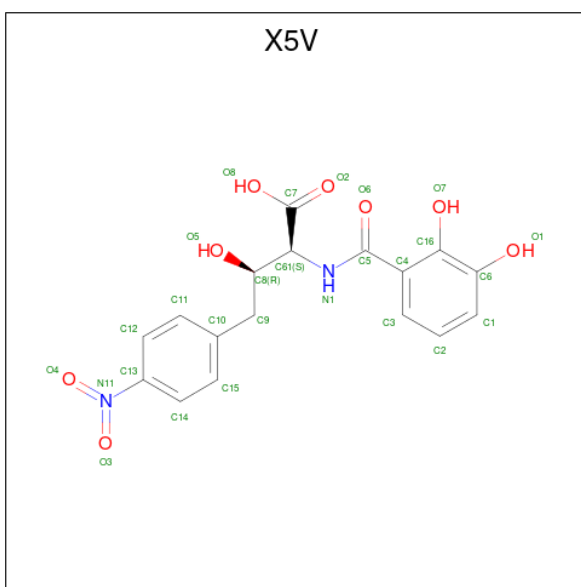
- Molecule 1 is a protein called Threonine-tRNA ligase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	399	Total	C	N	O	S	0	0	0
			3239	2043	575	598	23			

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	241	MET	-	initiating methionine	UNP E2QMS9
A	462	ARG	TYR	engineered mutation	UNP E2QMS9
A	643	LEU	-	expression tag	UNP E2QMS9
A	644	GLU	-	expression tag	UNP E2QMS9
A	645	HIS	-	expression tag	UNP E2QMS9
A	646	HIS	-	expression tag	UNP E2QMS9
A	647	HIS	-	expression tag	UNP E2QMS9
A	648	HIS	-	expression tag	UNP E2QMS9
A	649	HIS	-	expression tag	UNP E2QMS9
A	650	HIS	-	expression tag	UNP E2QMS9

- Molecule 2 is N-(2,3-dihydroxybenzoyl)-4-(4-nitrophenyl)-L-threonine (CCD ID: X5V) (formula: C₁₇H₁₆N₂O₈) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			26	17	2	7		

- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Zn	0	0
			1	1		

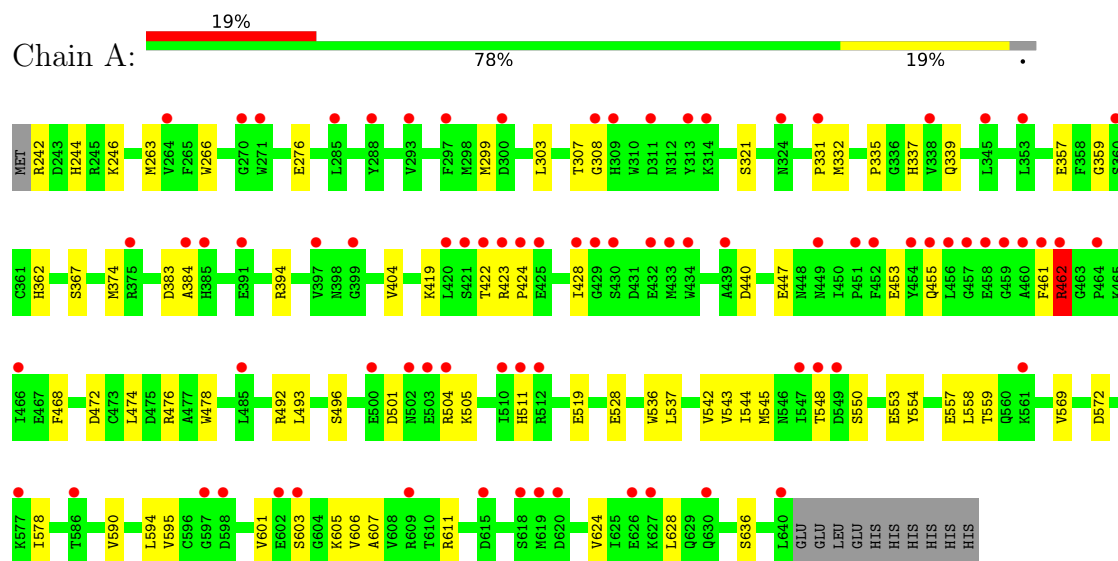
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	189	Total	O	0	0
			189	189		

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: Threonine-tRNA ligase



4 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α , β , γ	92.18Å 92.18Å 120.68Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	48.14 – 2.15 48.14 – 2.15	Depositor EDS
% Data completeness (in resolution range)	39.4 (48.14-2.15) 39.5 (48.14-2.15)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.47 (at 2.16Å)	Xtriage
Refinement program	PHENIX 1.20	Depositor
R, R_{free}	0.226 , 0.276 0.222 , 0.274	Depositor DCC
R_{free} test set	622 reflections (1.87%)	wwPDB-VP
Wilson B-factor (Å ²)	3.9	Xtriage
Anisotropy	0.883	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 29.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.024 for -h,-k,l	Xtriage
F_o, F_c correlation	0.88	EDS
Total number of atoms	3455	wwPDB-VP
Average B, all atoms (Å ²)	18.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.18% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: X5V, ZN

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	0.33	3/3309 (0.1%)	0.41	4/4458 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	462	ARG	NE-CZ	11.33	1.45	1.33
1	A	462	ARG	CZ-NH2	9.85	1.46	1.33
1	A	462	ARG	CZ-NH1	9.20	1.45	1.32

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	462	ARG	NE-CZ-NH1	-12.45	109.05	121.50
1	A	462	ARG	CD-NE-CZ	-10.88	109.17	124.40
1	A	462	ARG	NH1-CZ-NH2	-7.76	109.21	119.30
1	A	462	ARG	NE-CZ-NH2	-6.30	113.53	119.20

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	462	ARG	Sidechain

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	3239	0	3160	45	0
2	A	26	0	0	2	0
3	A	1	0	0	0	0
4	A	189	0	0	4	0
All	All	3455	0	3160	45	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 7.

All (45) 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:359:GLY:HA2	4:A:852:HOH:O	1.85	0.76
1:A:242:ARG:N	4:A:803:HOH:O	2.28	0.66
1:A:263:MET:HE2	1:A:362:HIS:HD2	1.61	0.66
1:A:394:ARG:NH1	1:A:447:GLU:OE2	2.31	0.63
1:A:543:VAL:HG23	1:A:590:VAL:HG11	1.86	0.57
1:A:331:PRO:HG2	1:A:332:MET:HG2	1.86	0.57
1:A:496:SER:HB2	1:A:504:ARG:HD2	1.88	0.56
1:A:266:TRP:HZ2	1:A:519:GLU:HG3	1.71	0.54
1:A:308:GLY:HA3	1:A:492:ARG:HH21	1.74	0.52
1:A:624:VAL:O	1:A:628:LEU:HD12	2.10	0.52
1:A:383:ASP:OD1	1:A:384:ALA:N	2.43	0.52
1:A:548:THR:HG23	1:A:550:SER:H	1.75	0.51
1:A:544:ILE:HG12	1:A:594:LEU:HD12	1.93	0.50
1:A:474:LEU:HB2	1:A:476:ARG:HG3	1.94	0.50
1:A:590:VAL:O	1:A:611:ARG:HB3	2.12	0.49
1:A:542:VAL:HB	1:A:569:VAL:HG23	1.94	0.48
1:A:511:HIS:HB3	2:A:701:X5V:C16	2.44	0.48
1:A:544:ILE:HD13	1:A:558:LEU:HB3	1.95	0.48
1:A:553:GLU:O	1:A:557:GLU:HG3	2.12	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:554:TYR:CD2	1:A:601:VAL:HG22	2.52	0.45
1:A:472:ASP:OD2	1:A:478:TRP:NE1	2.40	0.45
1:A:419:LYS:HB3	1:A:455:GLN:HG3	1.99	0.44
1:A:423:ARG:HA	1:A:424:PRO:HD3	1.89	0.44
1:A:595:VAL:HB	1:A:607:ALA:HB3	2.00	0.43
1:A:394:ARG:HB2	1:A:440:ASP:OD1	2.18	0.43
1:A:594:LEU:HB3	1:A:606:VAL:HG21	2.01	0.43
1:A:603:SER:HB2	1:A:605:LYS:HG3	1.99	0.43
1:A:545:MET:HG2	1:A:572:ASP:HB3	2.01	0.43
1:A:404:VAL:HG11	1:A:468:PHE:CD2	2.54	0.42
1:A:536:TRP:CE2	1:A:537:LEU:HG	2.54	0.42
1:A:246:LYS:NZ	4:A:802:HOH:O	2.26	0.42
1:A:276:GLU:HG2	1:A:536:TRP:O	2.19	0.42
1:A:511:HIS:HB3	2:A:701:X5V:C6	2.49	0.42
1:A:276:GLU:OE1	4:A:801:HOH:O	2.22	0.42
1:A:428:ILE:HD13	1:A:461:PHE:HD2	1.85	0.42
1:A:501:ASP:OD1	1:A:505:LYS:NZ	2.52	0.42
1:A:559:THR:HG23	1:A:569:VAL:HG13	2.03	0.41
1:A:307:THR:HG22	1:A:493:LEU:HD21	2.02	0.41
1:A:335:PRO:O	1:A:339:GLN:HG2	2.21	0.41
1:A:337:HIS:NE2	1:A:357:GLU:OE1	2.45	0.41
1:A:299:MET:HE3	1:A:303:LEU:HD12	2.02	0.41
1:A:504:ARG:HE	1:A:504:ARG:HB3	1.58	0.40
1:A:578:ILE:HD12	1:A:578:ILE:HA	1.93	0.40
1:A:472:ASP:HB2	1:A:528:GLU:OE1	2.21	0.40
1:A:244:HIS:CE1	1:A:374:MET:HE2	2.56	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	397/410 (97%)	393 (99%)	4 (1%)	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	349/365 (96%)	343 (98%)	6 (2%)	53	60

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	321	SER
1	A	367	SER
1	A	422	THR
1	A	453	GLU
1	A	462	ARG
1	A	636	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	622	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 [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 1 is 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
2	X5V	A	701	1,3	25,27,28	2.54	3 (12%)	35,37,39	1.25	4 (11%)

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	X5V	A	701	1,3	-	4/21/22/24	0/2/2/2

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	701	X5V	O4-N11	7.69	1.41	1.22
2	A	701	X5V	O3-N11	7.63	1.40	1.22
2	A	701	X5V	C5-N1	4.87	1.45	1.34

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	701	X5V	C4-C5-N1	3.17	123.53	116.67
2	A	701	X5V	O6-C5-N1	-2.37	117.96	122.47
2	A	701	X5V	C61-N1-C5	-2.37	117.29	121.97
2	A	701	X5V	O2-C7-C61	-2.11	119.29	124.86

There are no chirality outliers.

All (4) torsion outliers are listed below:

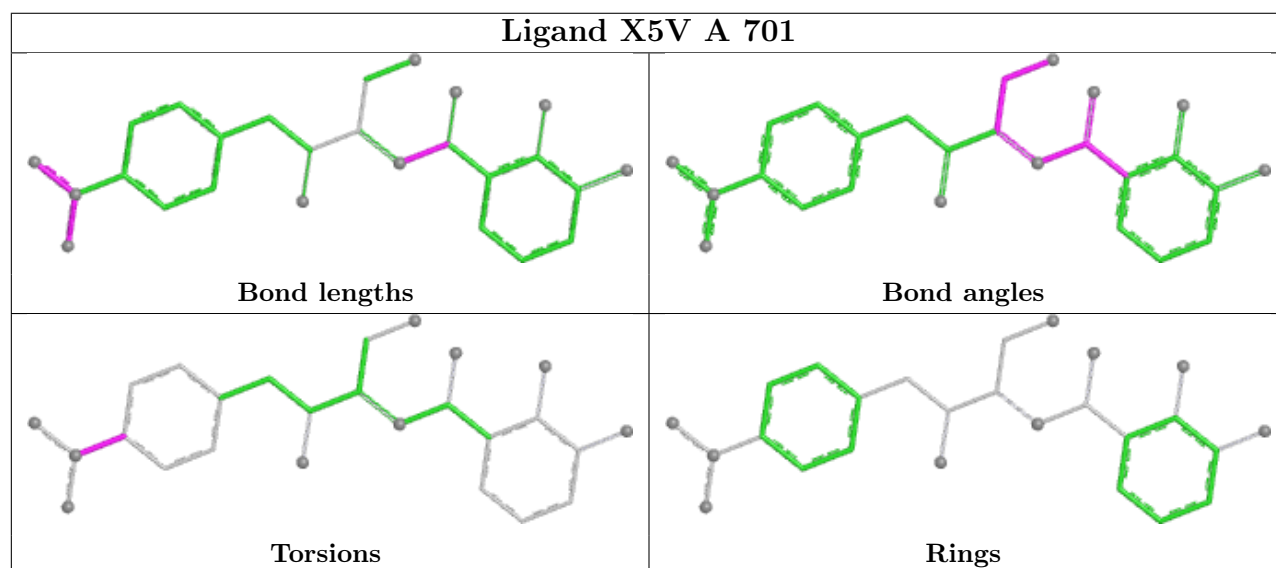
Mol	Chain	Res	Type	Atoms
2	A	701	X5V	C14-C13-N11-O4
2	A	701	X5V	C14-C13-N11-O3
2	A	701	X5V	C12-C13-N11-O4
2	A	701	X5V	C12-C13-N11-O3

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	701	X5V	2	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 [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	399/410 (97%)	1.31	79 (19%) 3 3	9, 18, 30, 37	0

All (79) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	457	GLY	9.1
1	A	456	LEU	7.2
1	A	458	GLU	5.6
1	A	309	HIS	5.5
1	A	615	ASP	5.3
1	A	461	PHE	5.0
1	A	504	ARG	4.8
1	A	285	LEU	4.7
1	A	313	TYR	4.6
1	A	425	GLU	4.5
1	A	434	TRP	4.5
1	A	459	GLY	4.3
1	A	602	GLU	4.3
1	A	460	ALA	4.1
1	A	502	ASN	4.1
1	A	429	GLY	4.1
1	A	432	GLU	4.0
1	A	311	ASP	3.7
1	A	422	THR	3.6
1	A	548	THR	3.6
1	A	449	ASN	3.5
1	A	385	HIS	3.4
1	A	424	PRO	3.4
1	A	420	LEU	3.4
1	A	640	LEU	3.3
1	A	597	GLY	3.3
1	A	455	GLN	3.2

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Mol	Chain	Res	Type	RSRZ
1	A	485	LEU	3.2
1	A	451	PRO	3.1
1	A	609	ARG	3.0
1	A	384	ALA	3.0
1	A	510	ILE	3.0
1	A	324	ASN	2.9
1	A	620	ASP	2.9
1	A	462	ARG	2.8
1	A	288	TYR	2.8
1	A	300	ASP	2.8
1	A	264	VAL	2.8
1	A	549	ASP	2.8
1	A	454	TYR	2.7
1	A	466	ILE	2.7
1	A	428	ILE	2.7
1	A	500	GLU	2.6
1	A	421	SER	2.6
1	A	619	MET	2.6
1	A	297	PHE	2.5
1	A	293	VAL	2.5
1	A	314	LYS	2.5
1	A	586	THR	2.4
1	A	430	SER	2.4
1	A	603	SER	2.3
1	A	331	PRO	2.3
1	A	561	LYS	2.3
1	A	503	GLU	2.3
1	A	626	GLU	2.3
1	A	308	GLY	2.3
1	A	433	MET	2.2
1	A	618	SER	2.2
1	A	271	TRP	2.2
1	A	270	GLY	2.2
1	A	345	LEU	2.2
1	A	360	SER	2.2
1	A	598	ASP	2.2
1	A	391	GLU	2.1
1	A	547	ILE	2.1
1	A	397	VAL	2.1
1	A	375	ARG	2.1
1	A	512	ARG	2.1
1	A	353	LEU	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	627	LYS	2.1
1	A	511	HIS	2.1
1	A	338	VAL	2.1
1	A	577	LYS	2.1
1	A	423	ARG	2.1
1	A	464	PRO	2.1
1	A	439	ALA	2.1
1	A	452	PHE	2.0
1	A	630	GLN	2.0
1	A	399	GLY	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](#)

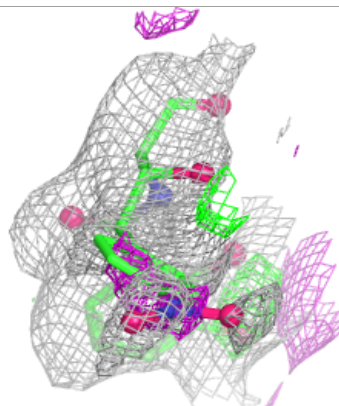
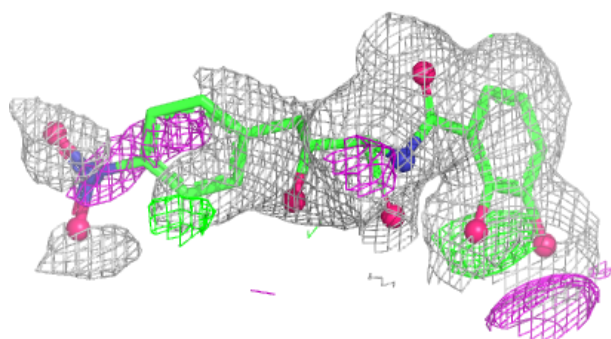
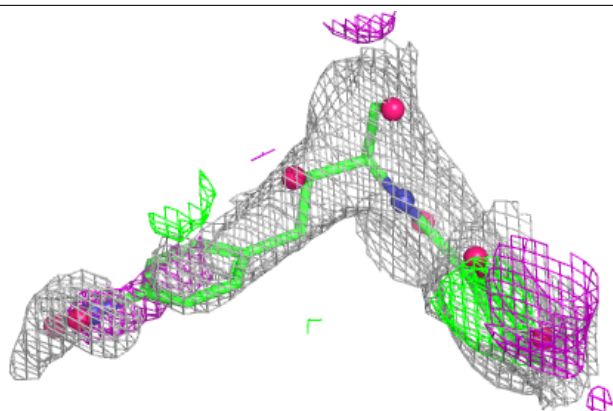
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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	X5V	A	701	26/27	0.70	0.20	27,31,32,32	0
3	ZN	A	702	1/1	0.79	0.13	24,24,24,24	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 X5V A 701:

$2mF_o - DF_c$ (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.