



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 11:20 AM UTC

PDB ID : 7I2T / pdb_00007i2t
Title : Group deposition for crystallographic fragment screening of the NS5 RNA-dependent RNA polymerase from Dengue virus serotype 2 – Crystal structure of the NS5 RNA-dependent RNA polymerase from Dengue virus serotype 2 in complex with Z32327641 (DNV2_NS5A-x0781)
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Deposited on : 2025-03-06
Resolution : 1.59 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)

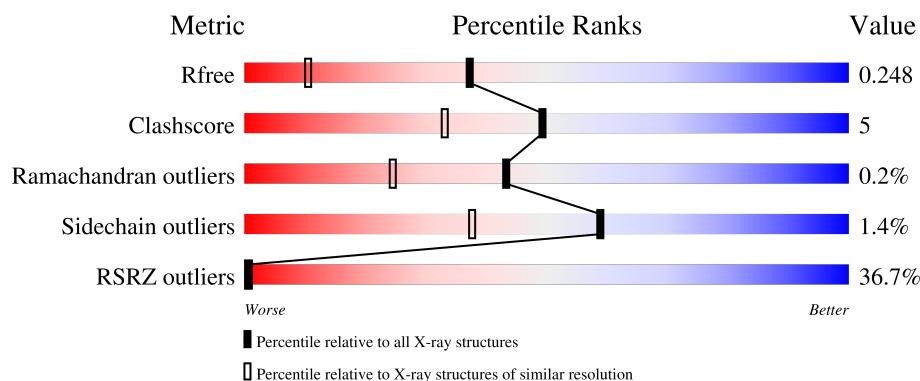
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.59 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	4673 (1.60-1.60)
Clashscore	190562	4931 (1.60-1.60)
Ramachandran outliers	187476	4831 (1.60-1.60)
Sidechain outliers	187428	4830 (1.60-1.60)
RSRZ outliers	180081	4672 (1.60-1.60)

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	637	33% 78% 10% 11%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	PO4	A	1006	-	X	X	-
8	JMM	A	1010	-	-	-	X

2 Entry composition [i](#)

There are 9 unique types of molecules in this entry. The entry contains 5168 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 NS5 RNA-dependent RNA polymerase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	567	Total	C	N	O	S	0	6	0
			4688	2951	840	863	34			

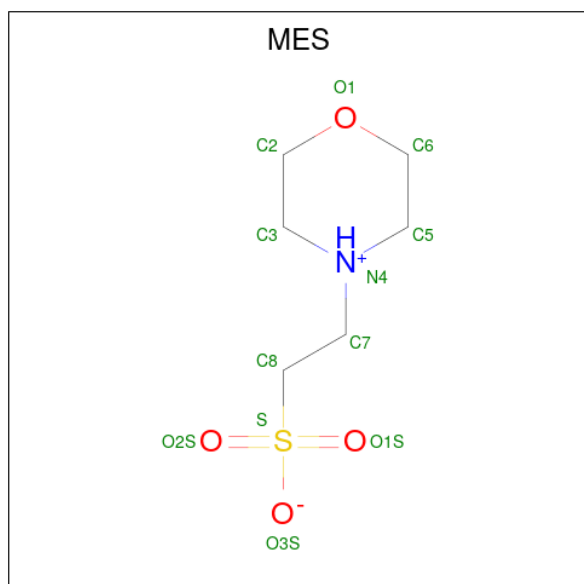
There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	264	GLY	-	expression tag	UNP Q91H74
A	265	PRO	-	expression tag	UNP Q91H74

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

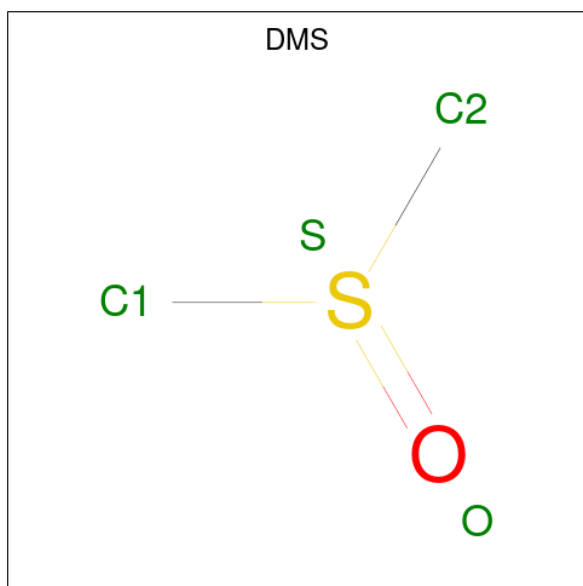
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	2	Total	Zn	0	0
			2	2		

- Molecule 3 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (CCD ID: MES) (formula: C₆H₁₃NO₄S).



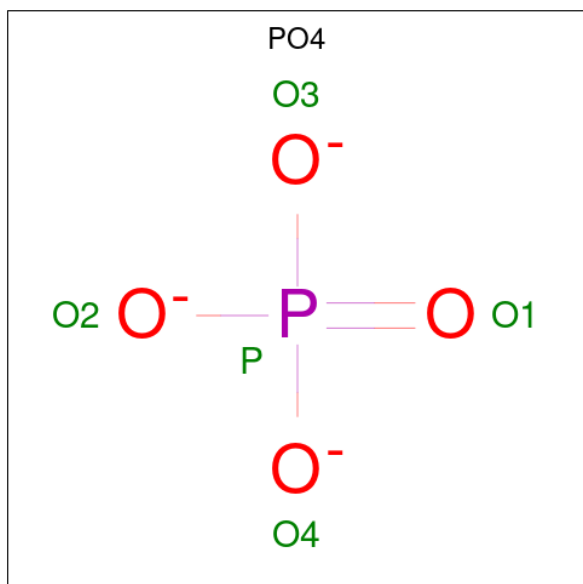
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	S	0	1
			24	12	2	8	2		

- Molecule 4 is DIMETHYL SULFOXIDE (CCD ID: DMS) (formula: C_2H_6OS).



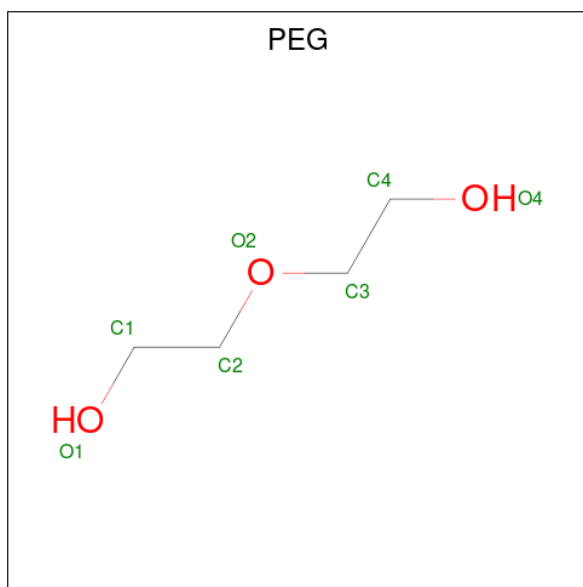
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	O	S	0	0
			4	2	1	1		
4	A	1	Total	C	O	S	0	0
			4	2	1	1		

- Molecule 5 is PHOSPHATE ION (CCD ID: PO4) (formula: O_4P).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	O	P	0	0
			5	4	1		
5	A	1	Total	O	P	0	0
			5	4	1		

- Molecule 6 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: C₄H₁₀O₃).

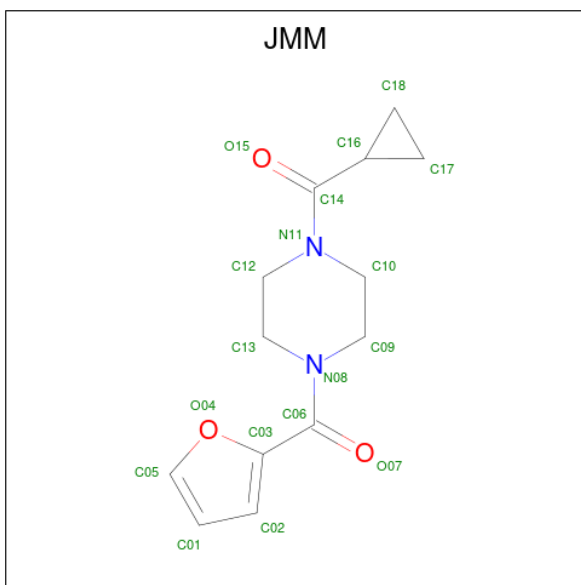


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			7	4	3		

- Molecule 7 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	1	Total	Cl	0	0
			1	1		

- Molecule 8 is [4-(cyclopropanecarbonyl)piperazin-1-yl](furan-2-yl)methanone (CCD ID: JMM) (formula: C₁₃H₁₆N₂O₃) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
8	A	1	Total	C	N	O	0	0
			18	13	2	3		

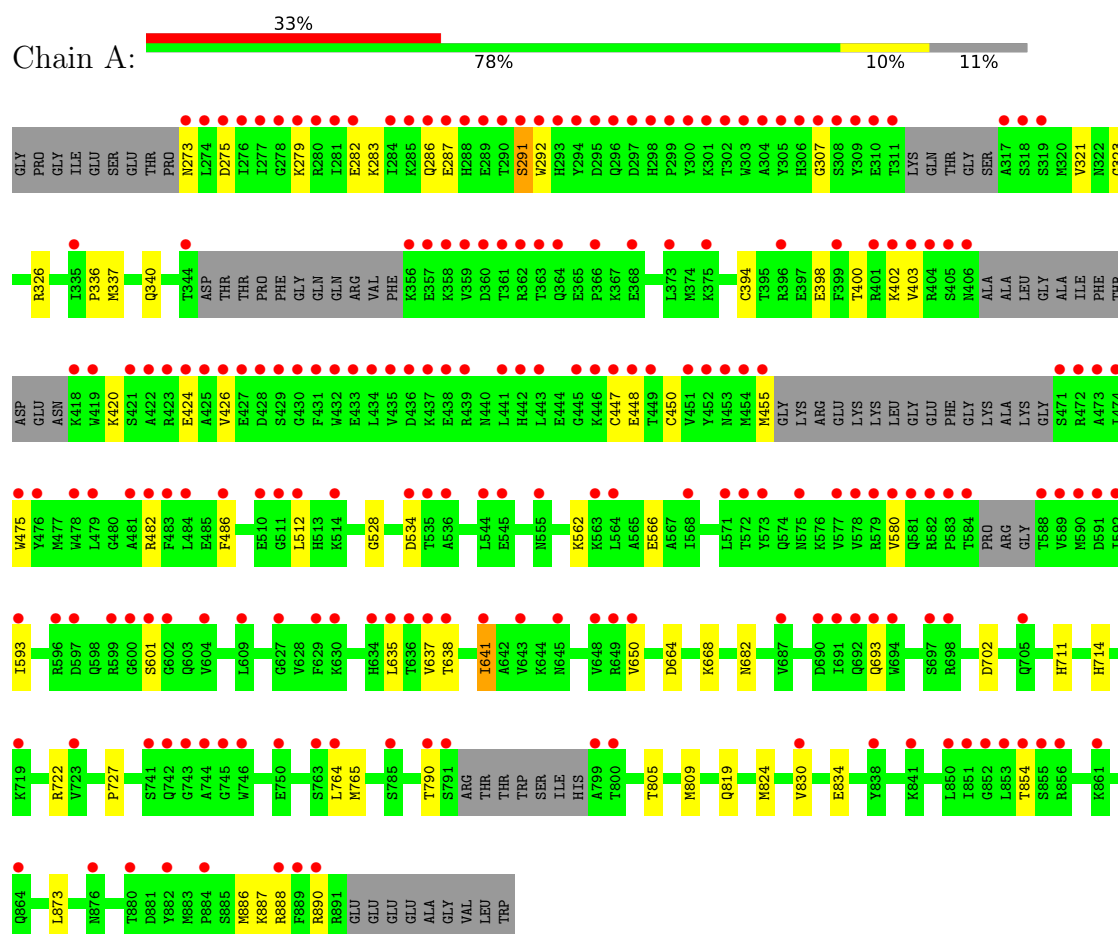
- Molecule 9 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	410	Total	O	0	0
			410	410		

3 Residue-property plots

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: NS5 RNA-dependent RNA polymerase



4 Data and refinement statistics

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	82.34Å 116.21Å 148.02Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	58.11 – 1.59 58.11 – 1.59	Depositor EDS
% Data completeness (in resolution range)	98.8 (58.11-1.59) 98.8 (58.11-1.59)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.97 (at 1.59Å)	Xtriage
Refinement program	REFMAC 5.8.0267	Depositor
R, R_{free}	0.201 , 0.228 0.228 , 0.248	Depositor DCC
R_{free} test set	4838 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å ²)	26.4	Xtriage
Anisotropy	0.269	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 58.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	5168	wwPDB-VP
Average B, all atoms (Å ²)	46.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.39% 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: ZN, MES, DMS, JMM, PEG, CL, PO4

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	1.09	1/4792 (0.0%)	1.29	3/6460 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	714	HIS	CE1-NE2	6.33	1.38	1.32

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	702	ASP	CA-CB-CG	5.55	118.16	112.60
1	A	650	VAL	CA-C-O	-5.17	115.43	119.46
1	A	714	HIS	CE1-NE2-CD2	-5.08	103.92	109.00

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4688	0	4590	48	0
2	A	2	0	0	0	0
3	A	24	0	26	2	0
4	A	8	0	12	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	A	10	0	0	4	0
6	A	7	0	10	0	0
7	A	1	0	0	0	0
8	A	18	0	0	0	0
9	A	410	0	0	11	2
All	All	5168	0	4638	51	2

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 5.

All (51) 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:664:ASP:OD1	5:A:1006:PO4:O4	2.01	0.79
4:A:1004:DMS:H11	9:A:1279:HOH:O	1.84	0.78
1:A:534:ASP:OD1	5:A:1006:PO4:O4	2.01	0.77
1:A:400:THR:HG23	1:A:426:VAL:HG11	1.72	0.71
1:A:323:GLY:HA3	3:A:1003[B]:MES:H71	1.76	0.67
1:A:664:ASP:OD1	5:A:1006:PO4:P	2.53	0.66
4:A:1004:DMS:H12	9:A:1293:HOH:O	1.96	0.65
1:A:638:THR:HA	1:A:641:ILE:HG22	1.82	0.61
1:A:400:THR:HG23	1:A:426:VAL:CG1	2.36	0.56
1:A:400:THR:O	1:A:403:VAL:HG22	2.07	0.55
1:A:447:CYS:SG	1:A:450:CYS:HB2	2.47	0.55
1:A:512[A]:LEU:HD21	1:A:711:HIS:NE2	2.22	0.54
1:A:398:GLU:O	1:A:402:LYS:HG3	2.08	0.54
1:A:873:LEU:HD13	3:A:1003[B]:MES:H62	1.90	0.53
1:A:764:LEU:HG	1:A:765:MET:CE	2.38	0.52
1:A:279:LYS:HE3	1:A:448:GLU:HB2	1.92	0.52
1:A:834:GLU:OE2	1:A:890:ARG:NE	2.39	0.51
1:A:764:LEU:HG	1:A:765:MET:HE3	1.91	0.51
1:A:534:ASP:OD1	5:A:1006:PO4:P	2.68	0.51
1:A:886:MET:HE1	9:A:1130:HOH:O	2.11	0.51
1:A:562:LYS:HE3	1:A:566:GLU:OE2	2.11	0.51
1:A:580:VAL:HG21	1:A:593:ILE:HD11	1.94	0.49
1:A:475:TRP:CD1	1:A:475:TRP:N	2.78	0.49
1:A:528:GLY:O	1:A:668:LYS:HE3	2.15	0.47
1:A:764:LEU:O	1:A:765:MET:HE2	2.14	0.47
1:A:638:THR:O	1:A:641:ILE:HG22	2.15	0.47
1:A:819:GLN:NE2	9:A:1108:HOH:O	2.35	0.46
1:A:283:LYS:HG2	1:A:287:GLU:OE1	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:637:VAL:HG13	9:A:1442:HOH:O	2.15	0.45
1:A:273:ASN:N	1:A:275:ASP:OD1	2.50	0.45
1:A:282:GLU:O	1:A:286:GLN:HG3	2.16	0.45
1:A:886:MET:CE	9:A:1130:HOH:O	2.65	0.44
1:A:275:ASP:OD1	1:A:275:ASP:N	2.51	0.44
1:A:580:VAL:CG2	1:A:593:ILE:HD11	2.48	0.44
1:A:512[A]:LEU:HG	1:A:727:PRO:CB	2.48	0.44
1:A:321:VAL:HG11	1:A:326:ARG:CZ	2.48	0.43
1:A:722:ARG:HB3	1:A:824:MET:SD	2.58	0.43
1:A:888:ARG:NH2	9:A:1106:HOH:O	2.33	0.43
1:A:682:ASN:ND2	1:A:693:GLN:HG2	2.34	0.42
1:A:291:SER:O	1:A:292:TRP:C	2.62	0.42
1:A:336:PRO:O	1:A:340:GLN:HG2	2.19	0.42
1:A:337:MET:HG2	9:A:1359:HOH:O	2.19	0.42
4:A:1004:DMS:C1	9:A:1279:HOH:O	2.56	0.42
1:A:805:THR:HG23	1:A:809:MET:HE1	2.01	0.42
1:A:420:LYS:HB3	1:A:424:GLU:CD	2.45	0.41
1:A:790:THR:HG21	9:A:1451:HOH:O	2.20	0.41
1:A:764:LEU:C	1:A:765:MET:HE2	2.44	0.41
1:A:854:THR:HG22	9:A:1103:HOH:O	2.20	0.41
1:A:475:TRP:N	1:A:475:TRP:HD1	2.18	0.41
1:A:394:CYS:HB3	1:A:486:PHE:CE2	2.56	0.41
1:A:292:TRP:CZ2	1:A:307:GLY:HA3	2.56	0.40

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:1134:HOH:O	9:A:1134:HOH:O[2_445]	1.69	0.51
9:A:1318:HOH:O	9:A:1418:HOH:O[2_545]	2.10	0.10

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	559/637 (88%)	543 (97%)	15 (3%)	1 (0%)	43	24

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	291	SER

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	505/554 (91%)	498 (99%)	7 (1%)	59	38

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	455	MET
1	A	482	ARG
1	A	601	SER
1	A	635	LEU
1	A	641	ILE
1	A	830	VAL
1	A	887	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	273	ASN
1	A	298	HIS
1	A	513	HIS
1	A	603	GLN
1	A	618	GLN
1	A	634	HIS

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Mol	Chain	Res	Type
1	A	705	GLN
1	A	801	HIS

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 11 ligands modelled in this entry, 3 are monoatomic - leaving 8 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$
5	PO4	A	1006	-	4,4,4	5.27	4 (100%)	6,6,6	0.45	0
5	PO4	A	1007	-	4,4,4	1.45	1 (25%)	6,6,6	0.55	0
3	MES	A	1003[A]	-	12,12,12	0.76	0	15,16,16	0.63	0
8	JMM	A	1010	-	20,20,20	0.22	0	27,28,28	0.64	1 (3%)
4	DMS	A	1004	-	3,3,3	0.76	0	3,3,3	0.56	0
3	MES	A	1003[B]	-	12,12,12	0.71	0	15,16,16	0.29	0
4	DMS	A	1005	-	3,3,3	0.33	0	3,3,3	0.15	0
6	PEG	A	1008	-	6,6,6	0.15	0	5,5,5	0.17	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
8	JMM	A	1010	-	-	2/16/28/28	0/3/3/3
3	MES	A	1003[B]	-	-	0/6/14/14	0/1/1/1
3	MES	A	1003[A]	-	-	0/6/14/14	0/1/1/1
6	PEG	A	1008	-	-	2/4/4/4	-

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	1006	PO4	P-O1	8.60	1.70	1.50
5	A	1006	PO4	P-O2	5.09	1.69	1.54
5	A	1007	PO4	P-O1	2.74	1.57	1.50
5	A	1006	PO4	P-O3	2.48	1.61	1.54
5	A	1006	PO4	P-O4	-2.26	1.48	1.54

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	A	1010	JMM	C12-N11-C10	2.08	116.92	112.68

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
8	A	1010	JMM	N11-C14-C16-C17
8	A	1010	JMM	O15-C14-C16-C17
6	A	1008	PEG	O2-C3-C4-O4
6	A	1008	PEG	O1-C1-C2-O2

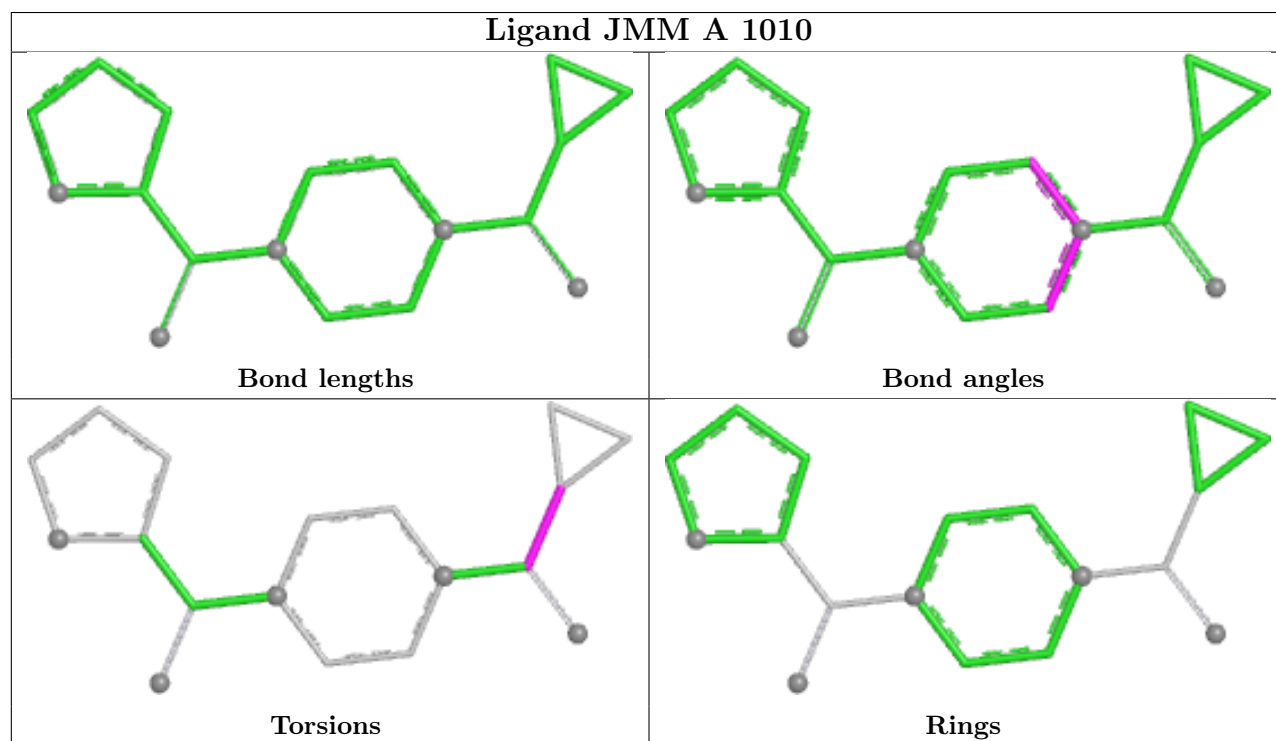
There are no ring outliers.

3 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	1006	PO4	4	0
4	A	1004	DMS	3	0
3	A	1003[B]	MES	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	567/637 (89%)	2.48	208 (36%) 1 0	5, 34, 89, 133	79 (13%)

All (208) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	303	TRP	15.9
1	A	512[A]	LEU	15.0
1	A	426	VAL	14.6
1	A	853	LEU	14.2
1	A	851	ILE	14.1
1	A	431	PHE	14.0
1	A	580	VAL	14.0
1	A	335	ILE	13.9
1	A	435	VAL	13.7
1	A	304	ALA	13.5
1	A	719[A]	LYS	13.3
1	A	281	ILE	13.2
1	A	425	ALA	13.1
1	A	609	LEU	13.1
1	A	838	TYR	13.0
1	A	850	LEU	12.8
1	A	434	LEU	12.6
1	A	305	TYR	12.0
1	A	403	VAL	11.6
1	A	854	THR	11.4
1	A	307	GLY	11.3
1	A	311	THR	11.2
1	A	852	GLY	11.2
1	A	589	VAL	11.1
1	A	573	TYR	10.9
1	A	600	GLY	10.8
1	A	405	SER	10.2

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Mol	Chain	Res	Type	RSRZ
1	A	855	SER	10.2
1	A	317	ALA	10.1
1	A	430	GLY	9.9
1	A	406	ASN	9.7
1	A	864[A]	GLN	9.7
1	A	697	SER	9.6
1	A	308	SER	9.6
1	A	511	GLY	9.5
1	A	743	GLY	9.3
1	A	741[A]	SER	9.2
1	A	588	THR	9.2
1	A	856	ARG	9.1
1	A	601	SER	9.0
1	A	584	THR	8.8
1	A	437	LYS	8.7
1	A	292	TRP	8.6
1	A	306	HIS	8.6
1	A	449	THR	8.5
1	A	301	LYS	8.3
1	A	429	SER	8.3
1	A	785[A]	SER	8.3
1	A	861	LYS	8.3
1	A	475	TRP	8.2
1	A	514	LYS	8.2
1	A	698	ARG	8.2
1	A	763[A]	SER	8.1
1	A	841	LYS	8.0
1	A	439	ARG	8.0
1	A	438	GLU	7.9
1	A	474	ILE	7.9
1	A	582	ARG	7.8
1	A	591	ASP	7.7
1	A	396	ARG	7.6
1	A	404	ARG	7.6
1	A	319	SER	7.5
1	A	581	GLN	7.4
1	A	599	ARG	7.4
1	A	436	ASP	7.3
1	A	583	PRO	7.3
1	A	590	MET	7.2
1	A	423	ARG	7.2
1	A	705	GLN	7.1

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Mol	Chain	Res	Type	RSRZ
1	A	356	LYS	6.9
1	A	579	ARG	6.8
1	A	318	SER	6.8
1	A	693	GLN	6.7
1	A	418	LYS	6.7
1	A	742	GLN	6.6
1	A	359	VAL	6.4
1	A	298	HIS	6.3
1	A	424	GLU	6.3
1	A	290	THR	6.2
1	A	479	LEU	6.2
1	A	690	ASP	6.0
1	A	363	THR	5.7
1	A	433	GLU	5.7
1	A	510	GLU	5.7
1	A	889	PHE	5.7
1	A	294	TYR	5.6
1	A	357	GLU	5.4
1	A	799	ALA	5.4
1	A	362	ARG	5.3
1	A	422	ALA	5.2
1	A	286	GLN	5.1
1	A	419	TRP	5.1
1	A	441	LEU	5.1
1	A	452	TYR	5.0
1	A	293	HIS	5.0
1	A	478	TRP	4.8
1	A	284	ILE	4.8
1	A	744	ALA	4.8
1	A	597	ASP	4.8
1	A	310	GLU	4.7
1	A	476	TYR	4.7
1	A	637	VAL	4.7
1	A	534	ASP	4.6
1	A	432	TRP	4.6
1	A	746	TRP	4.6
1	A	361	THR	4.5
1	A	571	LEU	4.5
1	A	309	TYR	4.5
1	A	302	THR	4.5
1	A	275	ASP	4.3
1	A	300	TYR	4.2

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Mol	Chain	Res	Type	RSRZ
1	A	274	LEU	4.2
1	A	399	PHE	4.2
1	A	299	PRO	4.2
1	A	277	ILE	4.2
1	A	287	GLU	4.1
1	A	800	THR	4.1
1	A	471	SER	4.1
1	A	453	ASN	4.0
1	A	273	ASN	3.9
1	A	473	ALA	3.9
1	A	544	LEU	3.9
1	A	882	TYR	3.8
1	A	641	ILE	3.7
1	A	282	GLU	3.7
1	A	880	THR	3.7
1	A	360	ASP	3.6
1	A	443	LEU	3.6
1	A	291	SER	3.5
1	A	596	ARG	3.5
1	A	279	LYS	3.5
1	A	428	ASP	3.4
1	A	288	HIS	3.4
1	A	634	HIS	3.4
1	A	635	LEU	3.4
1	A	593	ILE	3.4
1	A	344	THR	3.4
1	A	448	GLU	3.4
1	A	447	CYS	3.3
1	A	745	GLY	3.3
1	A	455	MET	3.3
1	A	445	GLY	3.2
1	A	278	GLY	3.2
1	A	289	GLU	3.2
1	A	451	VAL	3.2
1	A	790	THR	3.1
1	A	446	LYS	3.1
1	A	285	LYS	3.0
1	A	358	LYS	3.0
1	A	564	LEU	3.0
1	A	402	LYS	3.0
1	A	296	GLN	2.9
1	A	577	VAL	2.9

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Mol	Chain	Res	Type	RSRZ
1	A	276	ILE	2.9
1	A	592	ILE	2.9
1	A	484	LEU	2.9
1	A	536	ALA	2.9
1	A	295	ASP	2.9
1	A	578	VAL	2.9
1	A	694	TRP	2.8
1	A	401	ARG	2.8
1	A	648	VAL	2.8
1	A	750	GLU	2.8
1	A	563	LYS	2.8
1	A	888	ARG	2.8
1	A	649	ARG	2.7
1	A	638	THR	2.7
1	A	791	SER	2.7
1	A	604	VAL	2.6
1	A	427	GLU	2.5
1	A	876	ASN	2.5
1	A	454	MET	2.5
1	A	602	GLY	2.4
1	A	364	GLN	2.4
1	A	368	GLU	2.4
1	A	572	THR	2.4
1	A	297	ASP	2.4
1	A	630	LYS	2.4
1	A	627	GLY	2.4
1	A	483	PHE	2.4
1	A	643	VAL	2.3
1	A	472	ARG	2.3
1	A	890	ARG	2.3
1	A	442	HIS	2.3
1	A	555	ASN	2.2
1	A	692	GLN	2.2
1	A	535	THR	2.2
1	A	830	VAL	2.2
1	A	366	PRO	2.2
1	A	482	ARG	2.2
1	A	650	VAL	2.2
1	A	884	PRO	2.1
1	A	568	ILE	2.1
1	A	575	ASN	2.1
1	A	486	PHE	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	687	VAL	2.1
1	A	373	LEU	2.1
1	A	481	ALA	2.1
1	A	545	GLU	2.1
1	A	280	ARG	2.1
1	A	421	SER	2.1
1	A	375	LYS	2.0
1	A	629	PHE	2.0
1	A	636	THR	2.0
1	A	764	LEU	2.0
1	A	691	ILE	2.0
1	A	723	VAL	2.0
1	A	645	ASN	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.

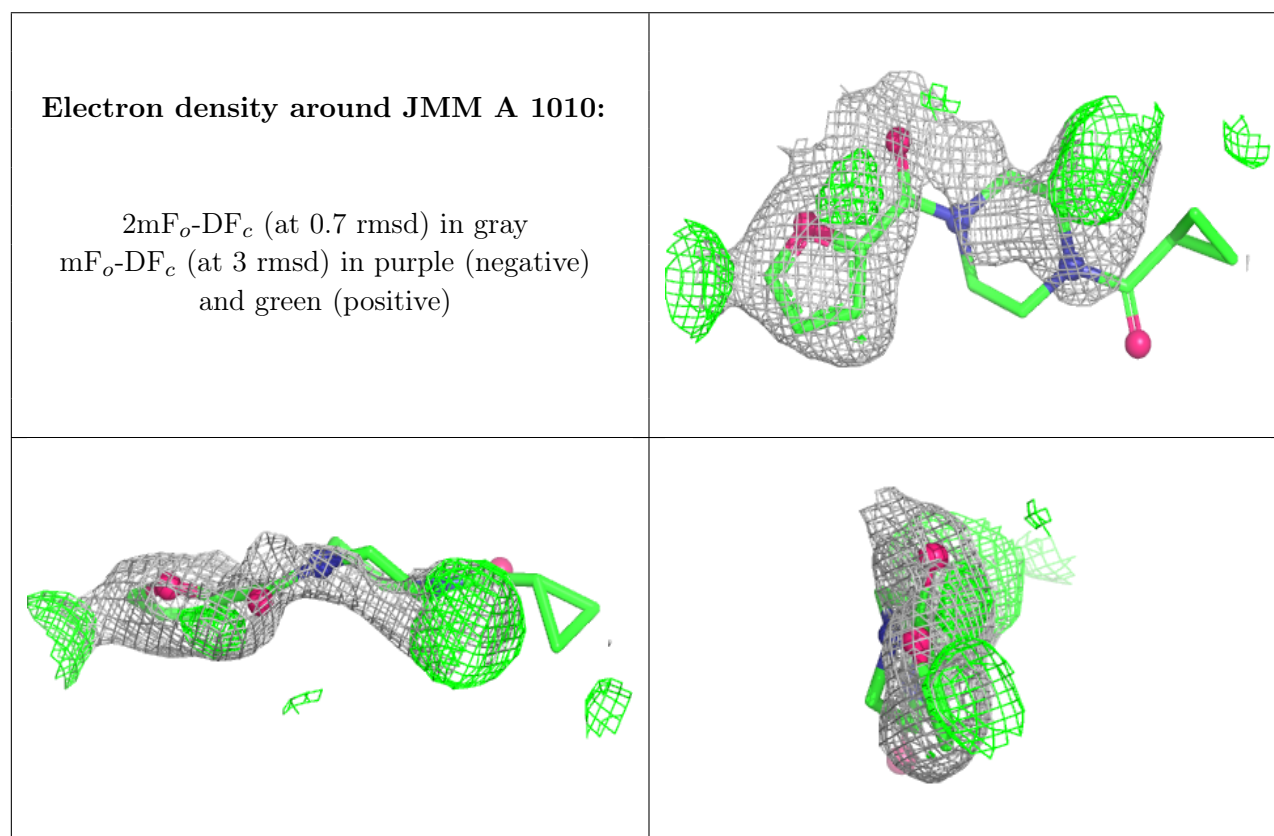
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
8	JMM	A	1010	18/18	0.57	0.43	56,61,63,63	18
5	PO4	A	1007	5/5	0.67	0.14	57,69,76,91	0
5	PO4	A	1006	5/5	0.76	0.15	32,32,50,55	0
4	DMS	A	1005	4/4	0.82	0.22	67,83,91,99	0
6	PEG	A	1008	7/7	0.83	0.16	59,67,74,74	0
4	DMS	A	1004	4/4	0.94	0.12	39,40,40,41	0
2	ZN	A	1002	1/1	0.98	0.04	49,49,49,49	0
3	MES	A	1003[A]	12/12	0.98	0.32	20,24,30,30	12
3	MES	A	1003[B]	12/12	0.98	0.32	586,602,646,652	12
7	CL	A	1009	1/1	0.99	0.04	36,36,36,36	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	ZN	A	1001	1/1	1.00	0.02	20,20,20,20	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.



6.5 Other polymers [i](#)

There are no such residues in this entry.