



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 22, 2025 – 02:10 PM JST

PDB ID : 8H4H / pdb_00008h4h
Title : The apo structure of Aspergillomarasmine A synthetase
Authors : Lu, M.; Zhang, J.; Wang, Z.; Han, L.
Deposited on : 2022-10-10
Resolution : 2.30 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 : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 2.0rc1
EDS : 3.0
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4 : 9.0.006 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.42

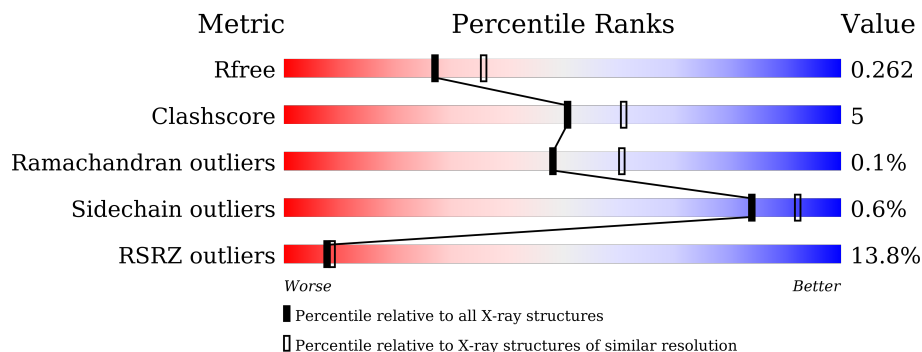
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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}	164625	5963 (2.30-2.30)
Clashscore	180529	6698 (2.30-2.30)
Ramachandran outliers	177936	6640 (2.30-2.30)
Sidechain outliers	177891	6640 (2.30-2.30)
RSRZ outliers	164620	5963 (2.30-2.30)

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	531	<div> <div>10%</div> <div> <div></div> <div>76%</div> <div>13%</div> <div>11%</div> </div> </div>
1	N	531	<div> <div>15%</div> <div> <div></div> <div>82%</div> <div>9%</div> <div>9%</div> </div> </div>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 7466 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 Rhodanese domain-containing protein.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	N	484	Total	C	N	O	P	S	0	0	0
			3751	2372	642	712	1	24			
1	A	475	Total	C	N	O	P	S	0	0	0
			3687	2335	631	696	1	24			

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
N	-5	MET	-	initiating methionine	UNP E3RT21
N	-4	HIS	-	expression tag	UNP E3RT21
N	-3	HIS	-	expression tag	UNP E3RT21
N	-2	HIS	-	expression tag	UNP E3RT21
N	-1	HIS	-	expression tag	UNP E3RT21
N	0	HIS	-	expression tag	UNP E3RT21
N	1	HIS	-	expression tag	UNP E3RT21
A	-5	MET	-	initiating methionine	UNP E3RT21
A	-4	HIS	-	expression tag	UNP E3RT21
A	-3	HIS	-	expression tag	UNP E3RT21
A	-2	HIS	-	expression tag	UNP E3RT21
A	-1	HIS	-	expression tag	UNP E3RT21
A	0	HIS	-	expression tag	UNP E3RT21
A	1	HIS	-	expression tag	UNP E3RT21

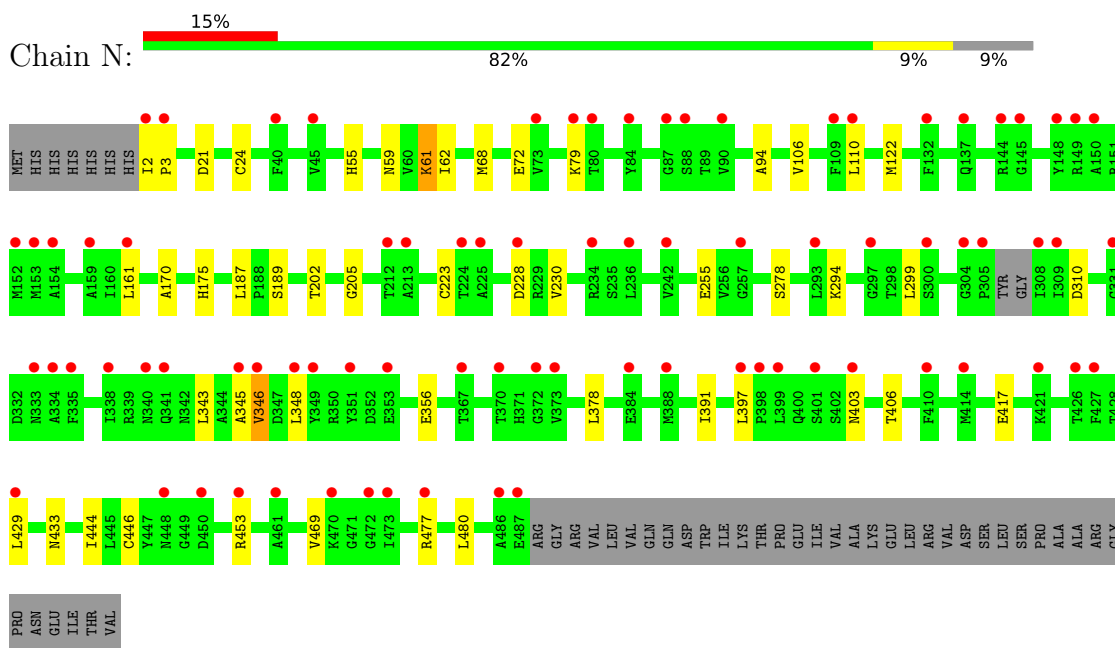
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	N	16	Total	O	0	0
			16	16		
2	A	12	Total	O	0	0
			12	12		

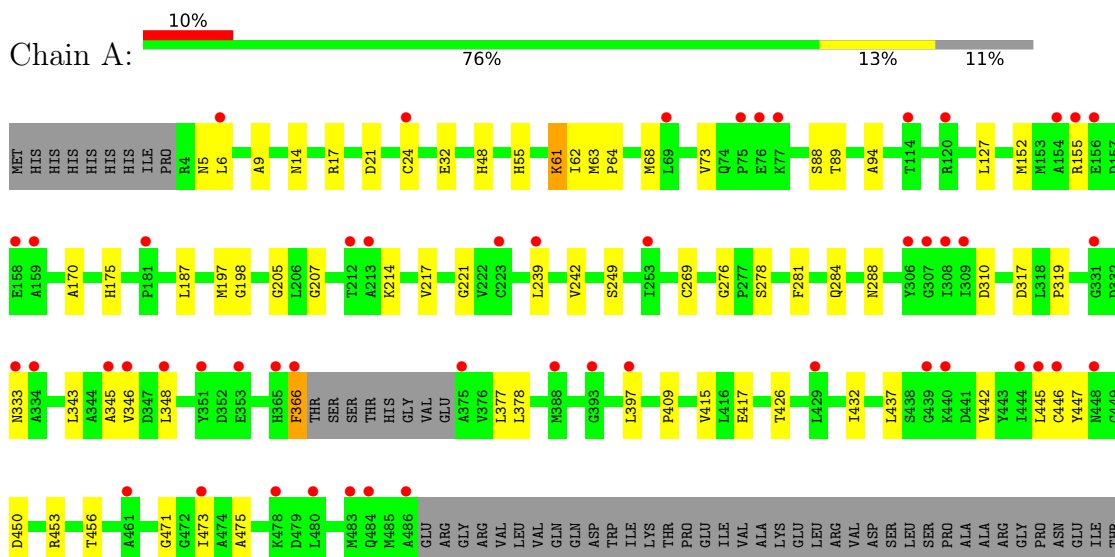
3 Residue-property plots

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: Rhodanese domain-containing protein



• Molecule 1: Rhodanese domain-containing protein



VAL

4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	71.89Å 264.10Å 163.37Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	81.68 – 2.30 81.68 – 2.30	Depositor EDS
% Data completeness (in resolution range)	99.2 (81.68-2.30) 88.0 (81.68-2.30)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.20 (at 2.18Å)	Xtriage
Refinement program	PHENIX 1.19.2_4158	Depositor
R, R_{free}	0.240 , 0.260 0.240 , 0.262	Depositor DCC
R_{free} test set	67775 reflections (2.51%)	wwPDB-VP
Wilson B-factor (Å ²)	44.9	Xtriage
Anisotropy	0.828	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 51.6	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	0.95	EDS
Total number of atoms	7466	wwPDB-VP
Average B, all atoms (Å ²)	77.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.08% 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: LLP

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	0.24	0/3747	0.46	0/5085
1	N	0.24	0/3812	0.46	0/5175
All	All	0.24	0/7559	0.46	0/10260

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	3687	0	3637	47	0
1	N	3751	0	3698	28	0
2	A	12	0	0	1	0
2	N	16	0	0	3	0
All	All	7466	0	7335	75	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 5.

All (75) 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:366:PHE:CE2	1:A:377:LEU:HB2	1.97	0.99
1:A:61:LLP:HD3	1:A:89:THR:OG1	1.85	0.76
1:N:346:VAL:HG21	1:N:417:GLU:HG3	1.69	0.75
1:A:366:PHE:HE2	1:A:377:LEU:HB2	1.50	0.74
1:N:446:CYS:SG	2:N:710:HOH:O	2.45	0.74
1:A:152:MET:SD	1:A:155:ARG:NH1	2.63	0.69
1:A:446:CYS:SG	1:A:447:TYR:N	2.67	0.68
1:A:346:VAL:HG21	1:A:417:GLU:HG3	1.75	0.67
1:N:61:LLP:N1	1:N:278:SER:OG	2.27	0.67
1:N:61:LLP:N1	1:N:278:SER:CB	2.58	0.66
1:N:429:LEU:O	1:N:433:ASN:ND2	2.27	0.66
1:A:61:LLP:OP1	1:A:198:GLY:N	2.29	0.65
1:A:397:LEU:HD21	1:A:426:THR:HG21	1.79	0.64
1:A:366:PHE:CE2	1:A:377:LEU:CB	2.79	0.64
1:A:366:PHE:C	2:A:702:HOH:O	2.40	0.60
1:A:61:LLP:N1	1:A:278:SER:OG	2.35	0.58
1:A:94:ALA:HB2	1:A:127:LEU:HD21	1.86	0.57
1:A:345:ALA:HA	1:A:348:LEU:HD21	1.86	0.57
1:N:79:LYS:NZ	2:N:706:HOH:O	2.39	0.56
1:N:343:LEU:HA	1:N:346:VAL:HG12	1.89	0.55
1:A:187:LEU:HD21	1:A:310:ASP:HB3	1.88	0.55
1:A:61:LLP:N1	1:A:278:SER:CB	2.71	0.54
1:N:59:ASN:OD1	1:N:61:LLP:HB3	2.08	0.54
1:N:187:LEU:HD21	1:N:310:ASP:HB3	1.89	0.53
1:A:55:HIS:CE1	1:A:62:ILE:HG12	2.44	0.53
1:N:55:HIS:CE1	1:N:62:ILE:HG12	2.44	0.52
1:A:14:ASN:HB3	1:A:17:ARG:HE	1.77	0.50
1:A:445:LEU:HD21	1:A:473:ILE:HD13	1.92	0.50
1:A:409:PRO:HD2	1:A:450:ASP:HB3	1.94	0.50
1:A:63:MET:HB2	1:A:64:PRO:HD3	1.93	0.49
1:A:284:GLN:NE2	1:A:288:ASN:OD1	2.37	0.49
1:A:366:PHE:CZ	1:A:377:LEU:N	2.81	0.49
1:A:152:MET:HE1	1:A:155:ARG:HH22	1.77	0.49
1:A:471:GLY:HA3	1:A:475:ALA:HB2	1.94	0.48
1:A:5:ASN:ND2	1:A:9:ALA:O	2.37	0.48
1:A:207:GLY:HA3	1:A:249:SER:HB3	1.95	0.47
1:A:453:ARG:O	1:A:456:THR:HG22	2.14	0.47
1:A:432:ILE:HG23	1:A:437:LEU:HB2	1.96	0.46
1:A:61:LLP:HG2	1:A:88:SER:HB3	1.97	0.46
1:A:61:LLP:OP2	1:A:61:LLP:NZ	2.48	0.46
1:A:343:LEU:HA	1:A:346:VAL:HG12	1.98	0.46
1:N:175:HIS:HB2	1:N:205:GLY:HA3	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:175:HIS:CD2	1:N:202:THR:HA	2.52	0.45
1:A:21:ASP:HB3	1:A:24:CYS:HB3	1.97	0.45
1:A:197:MET:HE1	1:A:221:GLY:HA3	1.99	0.45
1:N:294:LYS:HB2	1:N:299:LEU:HD22	1.99	0.45
1:N:356:GLU:HB2	1:N:453:ARG:HD3	1.98	0.45
1:A:276:GLY:N	1:A:317:ASP:O	2.50	0.45
1:N:378:LEU:HD22	1:N:397:LEU:HD13	1.99	0.44
1:A:278:SER:HA	1:A:281:PHE:HB3	1.99	0.44
1:A:32:GLU:HA	1:A:48:HIS:HA	1.99	0.44
1:N:345:ALA:HA	1:N:348:LEU:HD21	1.99	0.44
1:A:68:MET:HG2	1:A:170:ALA:HB3	2.00	0.44
1:A:378:LEU:HD13	1:A:442:VAL:HG13	1.98	0.44
1:N:21:ASP:HB3	1:N:24:CYS:HB2	2.00	0.44
1:N:68:MET:HG2	1:N:170:ALA:HB3	1.99	0.44
1:N:110:LEU:HD11	1:N:122:MET:HG3	1.99	0.44
1:A:269:CYS:SG	1:A:319:PRO:HG3	2.58	0.44
1:N:403:ASN:HB2	1:N:406:THR:HG23	1.99	0.44
1:N:189:SER:OG	1:N:310:ASP:OD2	2.26	0.43
1:A:61:LLP:HG2	1:A:88:SER:CB	2.47	0.43
1:A:366:PHE:HZ	1:A:377:LEU:N	2.16	0.43
1:A:366:PHE:HE2	1:A:377:LEU:CB	2.26	0.43
1:N:72:GLU:HB3	1:N:161:LEU:HD11	2.02	0.41
1:A:239:LEU:O	1:A:242:VAL:HG22	2.20	0.41
1:A:175:HIS:HB2	1:A:205:GLY:HA3	2.01	0.41
1:A:333:ASN:OD1	1:A:333:ASN:N	2.50	0.41
1:N:444:ILE:O	1:N:469:VAL:HG22	2.21	0.41
1:N:477:ARG:NH1	2:N:708:HOH:O	2.53	0.41
1:A:6:LEU:H	1:A:6:LEU:HD12	1.85	0.41
1:A:214:LYS:HG2	1:A:217:VAL:HG23	2.02	0.41
1:N:94:ALA:HA	1:N:106:VAL:HG21	2.03	0.41
1:N:2:ILE:HB	1:N:3:PRO:HD3	2.02	0.40
1:N:223:CYS:O	1:N:255:GLU:HA	2.21	0.40
1:N:391:ILE:HD13	1:N:480:LEU:HD21	2.02	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	470/531 (88%)	457 (97%)	13 (3%)	0	100	100
1	N	479/531 (90%)	459 (96%)	19 (4%)	1 (0%)	44	55
All	All	949/1062 (89%)	916 (96%)	32 (3%)	1 (0%)	48	60

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	N	346	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	399/449 (89%)	396 (99%)	3 (1%)	79	89
1	N	408/449 (91%)	406 (100%)	2 (0%)	86	93
All	All	807/898 (90%)	802 (99%)	5 (1%)	84	92

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	N	228	ASP
1	N	230	VAL
1	A	73	VAL
1	A	366	PHE
1	A	415	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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
1	LLP	N	61	1	23,24,25	1.84	4 (17%)	25,32,34	3.01	4 (16%)
1	LLP	A	61	1	23,24,25	1.86	4 (17%)	25,32,34	1.56	3 (12%)

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
1	LLP	N	61	1	-	4/16/17/19	0/1/1/1
1	LLP	A	61	1	-	8/16/17/19	0/1/1/1

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	N	61	LLP	C4-C5	-4.76	1.36	1.42
1	A	61	LLP	C4-C5	-4.72	1.36	1.42
1	A	61	LLP	C4'-NZ	3.96	1.40	1.27
1	N	61	LLP	C4'-NZ	3.74	1.39	1.27
1	N	61	LLP	C4-C4'	3.41	1.53	1.46
1	A	61	LLP	C4-C4'	3.41	1.53	1.46
1	A	61	LLP	C4-C3	-3.28	1.35	1.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	N	61	LLP	C4-C3	-3.22	1.36	1.40

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	N	61	LLP	CE-NZ-C4'	13.06	159.00	118.90
1	A	61	LLP	C4-C4'-NZ	6.08	152.22	124.31
1	N	61	LLP	C4-C4'-NZ	5.98	151.76	124.31
1	A	61	LLP	C5-C6-N1	-2.28	120.03	123.82
1	N	61	LLP	C5-C6-N1	-2.25	120.08	123.82
1	A	61	LLP	C3-C4-C5	2.14	119.91	118.26
1	N	61	LLP	C3-C4-C5	2.11	119.88	118.26

There are no chirality outliers.

All (12) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	N	61	LLP	C5-C4-C4'-NZ
1	N	61	LLP	C4-C4'-NZ-CE
1	A	61	LLP	C4-C4'-NZ-CE
1	A	61	LLP	C5'-OP4-P-OP1
1	A	61	LLP	C5'-OP4-P-OP2
1	A	61	LLP	C5'-OP4-P-OP3
1	N	61	LLP	CA-CB-CG-CD
1	N	61	LLP	C3-C4-C4'-NZ
1	A	61	LLP	C3-C4-C4'-NZ
1	A	61	LLP	CG-CD-CE-NZ
1	A	61	LLP	C5-C4-C4'-NZ
1	A	61	LLP	CA-CB-CG-CD

There are no ring outliers.

2 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	N	61	LLP	3	0
1	A	61	LLP	7	0

5.5 Carbohydrates

There are no oligosaccharides in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

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	474/531 (89%)	0.95	51 (10%)	12 13	59, 76, 97, 126	0
1	N	483/531 (90%)	1.12	81 (16%)	5 6	51, 76, 100, 120	0
All	All	957/1062 (90%)	1.04	132 (13%)	8 8	51, 76, 99, 126	0

All (132) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	366	PHE	6.6
1	A	486	ALA	6.6
1	N	305	PRO	6.5
1	N	2	ILE	5.7
1	A	307	GLY	5.1
1	N	334	ALA	4.9
1	N	388	MET	4.7
1	A	6	LEU	4.6
1	A	213	ALA	4.4
1	A	346	VAL	4.4
1	N	341	GLN	4.3
1	N	414	MET	4.2
1	N	346	VAL	4.1
1	N	429	LEU	4.1
1	A	334	ALA	4.0
1	N	448	ASN	4.0
1	A	375	ALA	3.9
1	N	331	GLY	3.7
1	N	373	VAL	3.7
1	N	213	ALA	3.7
1	N	487	GLU	3.7
1	A	365	HIS	3.6
1	N	461	ALA	3.6
1	A	446	CYS	3.5

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Mol	Chain	Res	Type	RSRZ
1	N	308	ILE	3.5
1	A	429	LEU	3.5
1	N	370	THR	3.4
1	N	153	MET	3.3
1	A	308	ILE	3.3
1	A	75	PRO	3.2
1	N	399	LEU	3.2
1	N	426	THR	3.2
1	N	473	ILE	3.2
1	A	253	ILE	3.2
1	A	159	ALA	3.2
1	A	306	TYR	3.1
1	N	403	ASN	3.1
1	N	398	PRO	3.1
1	N	453	ARG	3.0
1	N	145	GLY	3.0
1	N	297	GLY	3.0
1	N	450	ASP	3.0
1	N	242	VAL	3.0
1	N	152	MET	2.9
1	A	348	LEU	2.9
1	A	120	ARG	2.9
1	A	473	ILE	2.9
1	N	257	GLY	2.9
1	N	486	ALA	2.8
1	A	76	GLU	2.8
1	A	331	GLY	2.8
1	N	472	GLY	2.8
1	A	77	LYS	2.8
1	N	159	ALA	2.8
1	N	149	ARG	2.7
1	N	87	GLY	2.7
1	A	223	CYS	2.7
1	N	80	THR	2.7
1	N	293	LEU	2.7
1	A	448	ASN	2.7
1	A	158	GLU	2.7
1	A	388	MET	2.7
1	N	421	LYS	2.7
1	N	410	PHE	2.6
1	N	372	GLY	2.6
1	N	225	ALA	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	351	TYR	2.6
1	N	367	THR	2.6
1	N	3	PRO	2.6
1	N	304	GLY	2.6
1	N	397	LEU	2.6
1	N	340	ASN	2.6
1	N	40	PHE	2.5
1	N	150	ALA	2.5
1	N	333	ASN	2.5
1	A	212	THR	2.5
1	N	351	TYR	2.5
1	N	154	ALA	2.5
1	A	154	ALA	2.5
1	N	148	TYR	2.5
1	N	353	GLU	2.5
1	A	478	LYS	2.5
1	N	348	LEU	2.5
1	A	155	ARG	2.5
1	N	309	ILE	2.4
1	N	45	VAL	2.4
1	N	90	VAL	2.4
1	N	88	SER	2.4
1	N	477	ARG	2.4
1	N	427	PHE	2.4
1	A	445	LEU	2.4
1	N	84	TYR	2.4
1	A	397	LEU	2.4
1	N	161	LEU	2.3
1	N	73	VAL	2.3
1	A	114	THR	2.3
1	A	181	PRO	2.3
1	N	335	PHE	2.3
1	N	234	ARG	2.3
1	A	484	GLN	2.3
1	N	110	LEU	2.2
1	N	345	ALA	2.2
1	A	345	ALA	2.2
1	N	338	ILE	2.2
1	A	156	GLU	2.2
1	N	224	THR	2.2
1	N	228	ASP	2.2
1	A	333	ASN	2.2

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Mol	Chain	Res	Type	RSRZ
1	N	79	LYS	2.2
1	N	109	PHE	2.2
1	N	470	LYS	2.2
1	N	300	SER	2.1
1	N	401	SER	2.1
1	A	444	ILE	2.1
1	A	461	ALA	2.1
1	A	439	GLY	2.1
1	N	137	GLN	2.1
1	N	212	THR	2.1
1	A	353	GLU	2.1
1	N	144	ARG	2.1
1	A	24	CYS	2.1
1	A	440	LYS	2.1
1	N	349	TYR	2.1
1	N	132	PHE	2.1
1	N	236	LEU	2.1
1	N	384	GLU	2.0
1	A	393	GLY	2.0
1	A	309	ILE	2.0
1	A	480	LEU	2.0
1	A	69	LEU	2.0
1	A	239	LEU	2.0
1	A	483	MET	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [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(\AA^2)	Q<0.9
1	LLP	A	61	24/25	0.75	0.26	64,79,91,96	0
1	LLP	N	61	24/25	0.87	0.18	52,69,76,78	0

6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.