



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 12:14 PM UTC

PDB ID : 9J0U / pdb_00009j0u
Title : Crystal structure of monomeric PLP-dependent transaminase from *Desulfobacula toluolica* in F 41 3 2 space group
Authors : Matyuta, I.O.; Bakunova, A.K.; Nikolaeva, A.Y.; Rakitina, T.V.; Bezsudnova, E.Y.; Popov, V.O.; Boyko, K.M.
Deposited on : 2024-08-03
Resolution : 2.58 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
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

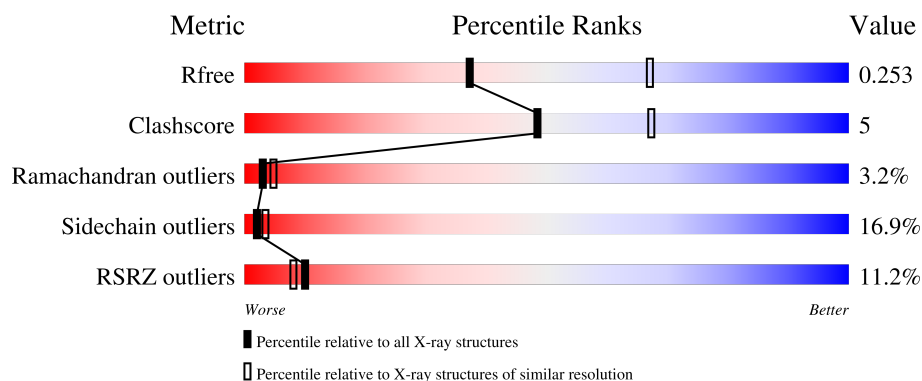
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.58 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	4770 (2.60-2.56)
Clashscore	190562	5124 (2.60-2.56)
Ramachandran outliers	187476	5046 (2.60-2.56)
Sidechain outliers	187428	5046 (2.60-2.56)
RSRZ outliers	180081	4770 (2.60-2.56)

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	286	11% 52% 35% 12%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 2268 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 Dat: predicted D-alanine aminotransferase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	286	Total	C	N	O	P	S	0	0	0
			2253	1431	396	415	1	10			

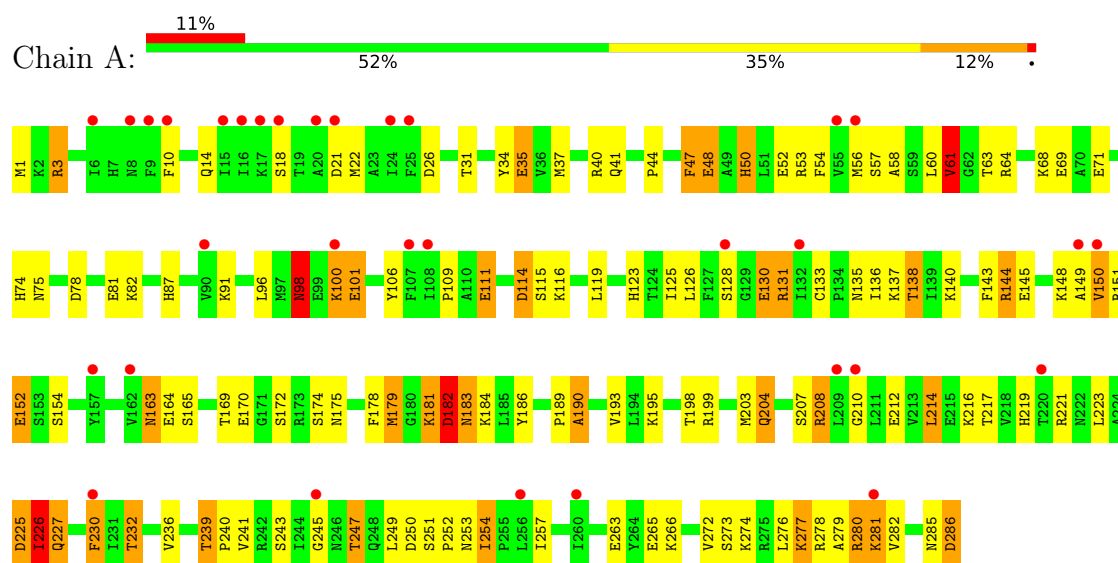
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	15	Total	O	0	0
			15	15		

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: Dat: predicted D-alanine aminotransferase



4 Data and refinement statistics

Property	Value	Source
Space group	F 41 3 2	Depositor
Cell constants a, b, c, α , β , γ	250.09Å 250.09Å 250.09Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	88.58 – 2.58 88.58 – 2.58	Depositor EDS
% Data completeness (in resolution range)	100.0 (88.58-2.58) 100.0 (88.58-2.58)	Depositor EDS
R_{merge}	0.19	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.21 (at 2.58Å)	Xtriage
Refinement program	REFMAC 5.8.0267	Depositor
R, R_{free}	0.209 , 0.253 0.209 , 0.253	Depositor DCC
R_{free} test set	1096 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å ²)	87.9	Xtriage
Anisotropy	0.000	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 50.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	2268	wwPDB-VP
Average B, all atoms (Å ²)	98.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.97% 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	1.26	10/2265 (0.4%)	2.38	147/3054 (4.8%)

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	133	CYS	C-O	9.66	1.28	1.23
1	A	1	MET	N-CA	8.12	1.61	1.46
1	A	50	HIS	CE1-NE2	7.59	1.40	1.32
1	A	219	HIS	CE1-NE2	7.01	1.39	1.32
1	A	74	HIS	CE1-NE2	6.00	1.38	1.32
1	A	281	LYS	CG-CD	5.40	1.68	1.52
1	A	172	SER	CA-CB	-5.25	1.45	1.53
1	A	131	ARG	NE-CZ	5.21	1.38	1.33
1	A	193	VAL	C-O	5.17	1.29	1.23
1	A	190	ALA	C-O	5.05	1.30	1.24

All (147) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	198	THR	CB-CA-C	13.03	134.74	110.11
1	A	152	GLU	CB-CA-C	12.94	130.88	110.96
1	A	40	ARG	CB-CG-CD	-11.68	84.44	111.30
1	A	239	THR	CA-CB-OG1	-11.63	92.15	109.60
1	A	286	ASP	CA-CB-CG	11.52	124.12	112.60
1	A	52	GLU	CB-CA-C	10.80	127.84	110.88
1	A	98	ASN	CA-CB-CG	10.11	122.71	112.60
1	A	68	LYS	CB-CA-C	9.83	129.33	109.76
1	A	217	THR	CB-CA-C	9.50	121.48	109.80
1	A	63	THR	CA-CB-OG1	-9.34	95.59	109.60
1	A	135	ASN	CA-C-N	9.15	138.17	121.70

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	135	ASN	C-N-CA	9.15	138.17	121.70
1	A	150	VAL	CA-C-N	8.86	132.50	120.54
1	A	150	VAL	C-N-CA	8.86	132.50	120.54
1	A	114	ASP	CA-CB-CG	8.62	121.22	112.60
1	A	280	ARG	CB-CA-C	8.13	123.74	110.90
1	A	281	LYS	N-CA-CB	8.04	122.12	110.06
1	A	135	ASN	CB-CG-OD1	-8.04	104.73	120.80
1	A	163	ASN	CA-CB-CG	7.98	120.58	112.60
1	A	54	PHE	CA-C-N	7.87	130.32	120.72
1	A	54	PHE	C-N-CA	7.87	130.32	120.72
1	A	58	ALA	CA-C-N	7.75	133.51	121.19
1	A	58	ALA	C-N-CA	7.75	133.51	121.19
1	A	149	ALA	CA-C-N	7.73	130.36	120.70
1	A	149	ALA	C-N-CA	7.73	130.36	120.70
1	A	266	LYS	CB-CA-C	7.70	122.97	110.88
1	A	250	ASP	CB-CA-C	7.64	125.63	110.42
1	A	109	PRO	CA-C-N	7.59	133.32	122.09
1	A	109	PRO	C-N-CA	7.59	133.32	122.09
1	A	47	PHE	CB-CA-C	7.57	122.93	110.81
1	A	87	HIS	CA-CB-CG	-7.55	106.25	113.80
1	A	263	GLU	CB-CA-C	7.37	124.27	110.63
1	A	40	ARG	CG-CD-NE	-7.01	96.58	112.00
1	A	225	ASP	CA-CB-CG	6.97	119.57	112.60
1	A	82	LYS	CB-CA-C	6.96	122.35	110.79
1	A	276	LEU	CA-C-N	6.96	129.84	120.65
1	A	276	LEU	C-N-CA	6.96	129.84	120.65
1	A	69	GLU	CB-CG-CD	6.96	124.44	112.60
1	A	212	GLU	CB-CG-CD	6.92	124.37	112.60
1	A	208	ARG	CD-NE-CZ	6.89	134.04	124.40
1	A	208	ARG	CB-CA-C	6.86	122.12	110.74
1	A	277	LYS	CA-C-O	-6.84	113.81	121.00
1	A	138	THR	CA-C-N	6.77	129.64	120.77
1	A	138	THR	C-N-CA	6.77	129.64	120.77
1	A	133	CYS	O-C-N	6.73	124.63	121.53
1	A	281	LYS	CB-CG-CD	6.71	126.74	111.30
1	A	135	ASN	OD1-CG-ND2	6.67	129.26	122.60
1	A	227	GLN	CA-C-N	6.62	127.27	121.58
1	A	227	GLN	C-N-CA	6.62	127.27	121.58
1	A	181	LYS	CA-C-N	6.50	133.96	121.54
1	A	181	LYS	C-N-CA	6.50	133.96	121.54
1	A	203	MET	CA-C-O	-6.45	113.48	121.02
1	A	135	ASN	CB-CG-ND2	6.36	125.93	116.40

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	226	ILE	CA-CB-CG2	6.35	121.30	110.50
1	A	78	ASP	N-CA-CB	6.35	120.12	110.28
1	A	61	VAL	CA-C-N	6.31	130.51	122.00
1	A	61	VAL	C-N-CA	6.31	130.51	122.00
1	A	115	SER	O-C-N	6.29	128.57	122.03
1	A	169	THR	CB-CA-C	6.29	122.93	110.42
1	A	277	LYS	N-CA-CB	6.26	119.05	109.91
1	A	207	SER	CA-C-O	-6.20	114.31	120.82
1	A	145	GLU	CA-C-N	6.18	128.85	120.38
1	A	145	GLU	C-N-CA	6.18	128.85	120.38
1	A	48	GLU	CB-CA-C	6.15	121.00	110.79
1	A	285	ASN	CB-CA-C	6.11	119.38	111.50
1	A	61	VAL	O-C-N	6.11	128.70	121.80
1	A	199	ARG	CG-CD-NE	-6.06	98.67	112.00
1	A	81	GLU	CB-CA-C	6.05	120.33	110.95
1	A	40	ARG	NE-CZ-NH1	-6.04	115.46	121.50
1	A	151	ARG	CB-CG-CD	6.03	125.17	111.30
1	A	91	LYS	CB-CA-C	6.02	120.22	109.38
1	A	278	ARG	CD-NE-CZ	6.02	132.83	124.40
1	A	282	VAL	CB-CA-C	6.01	120.51	112.22
1	A	266	LYS	N-CA-C	-5.93	104.72	111.07
1	A	68	LYS	CA-C-N	5.91	130.58	121.19
1	A	68	LYS	C-N-CA	5.91	130.58	121.19
1	A	277	LYS	CB-CA-C	5.83	119.94	110.96
1	A	74	HIS	CA-C-O	-5.78	114.39	120.63
1	A	276	LEU	O-C-N	5.77	129.36	122.27
1	A	223	LEU	CA-C-N	5.74	127.98	120.28
1	A	223	LEU	C-N-CA	5.74	127.98	120.28
1	A	143	PHE	CB-CA-C	5.70	121.33	110.27
1	A	169	THR	CA-CB-OG1	5.70	118.15	109.60
1	A	210	GLY	CA-C-N	-5.68	114.87	122.42
1	A	210	GLY	C-N-CA	-5.68	114.87	122.42
1	A	135	ASN	O-C-N	5.63	130.24	122.46
1	A	75	ASN	N-CA-CB	5.62	118.23	110.07
1	A	279	ALA	CA-C-N	5.62	128.08	120.44
1	A	279	ALA	C-N-CA	5.62	128.08	120.44
1	A	41	GLN	CB-CG-CD	-5.61	103.07	112.60
1	A	181	LYS	O-C-N	5.61	127.92	122.09
1	A	170	GLU	CA-C-N	5.54	125.37	120.10
1	A	170	GLU	C-N-CA	5.54	125.37	120.10
1	A	53	ARG	CA-C-O	-5.53	115.02	120.82
1	A	183	ASN	CB-CA-C	-5.51	102.37	111.36

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	265	GLU	CA-C-N	5.51	127.60	120.44
1	A	265	GLU	C-N-CA	5.51	127.60	120.44
1	A	56	MET	CA-C-O	-5.50	114.72	120.55
1	A	278	ARG	CA-C-N	5.49	127.90	120.38
1	A	278	ARG	C-N-CA	5.49	127.90	120.38
1	A	44	PRO	CB-CA-C	5.48	118.09	111.46
1	A	26	ASP	CA-CB-CG	-5.47	107.13	112.60
1	A	144	ARG	CD-NE-CZ	5.44	132.02	124.40
1	A	21	ASP	CB-CA-C	5.44	120.04	111.77
1	A	71	GLU	CB-CA-C	5.43	120.64	110.70
1	A	208	ARG	CA-CB-CG	5.43	124.97	114.10
1	A	44	PRO	O-C-N	5.43	129.18	123.10
1	A	53	ARG	N-CA-CB	5.43	117.88	110.01
1	A	21	ASP	CA-C-N	-5.36	114.15	122.67
1	A	21	ASP	C-N-CA	-5.36	114.15	122.67
1	A	199	ARG	CA-C-N	5.35	127.77	120.54
1	A	199	ARG	C-N-CA	5.35	127.77	120.54
1	A	279	ALA	O-C-N	5.35	127.79	122.12
1	A	35	GLU	CB-CG-CD	5.32	121.64	112.60
1	A	111	GLU	CB-CA-C	5.32	118.60	109.51
1	A	189	PRO	CA-C-N	5.31	131.68	121.54
1	A	189	PRO	C-N-CA	5.31	131.68	121.54
1	A	163	ASN	CA-C-N	5.25	129.53	121.19
1	A	163	ASN	C-N-CA	5.25	129.53	121.19
1	A	31	THR	CA-CB-OG1	-5.25	101.73	109.60
1	A	285	ASN	CA-C-N	5.22	131.10	121.70
1	A	285	ASN	C-N-CA	5.22	131.10	121.70
1	A	230	PHE	CA-CB-CG	5.22	119.02	113.80
1	A	71	GLU	CB-CG-CD	5.20	121.45	112.60
1	A	131	ARG	CD-NE-CZ	5.20	131.69	124.40
1	A	226	ILE	CB-CA-C	5.18	118.30	110.63
1	A	214	LEU	CA-C-N	5.14	128.63	121.02
1	A	214	LEU	C-N-CA	5.14	128.63	121.02
1	A	115	SER	CA-C-N	5.12	131.33	121.54
1	A	115	SER	C-N-CA	5.12	131.33	121.54
1	A	114	ASP	CA-C-N	5.11	127.40	120.65
1	A	114	ASP	C-N-CA	5.11	127.40	120.65
1	A	272	VAL	O-C-N	5.10	126.90	121.91
1	A	125	ILE	CA-C-N	5.09	129.36	122.19
1	A	125	ILE	C-N-CA	5.09	129.36	122.19
1	A	58	ALA	O-C-N	5.08	127.32	122.03
1	A	273	SER	N-CA-CB	5.08	118.15	110.28

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	204	GLN	CB-CA-C	-5.07	102.07	110.68
1	A	101	GLU	CA-C-N	5.06	130.44	122.70
1	A	101	GLU	C-N-CA	5.06	130.44	122.70
1	A	34	TYR	CA-C-O	5.05	127.44	121.58
1	A	266	LYS	CA-C-N	5.05	127.35	120.54
1	A	266	LYS	C-N-CA	5.05	127.35	120.54
1	A	3	ARG	CG-CD-NE	-5.03	100.94	112.00
1	A	175	ASN	CB-CA-C	5.03	118.71	109.46
1	A	100	LYS	CA-C-N	5.02	129.52	122.09
1	A	100	LYS	C-N-CA	5.02	129.52	122.09

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	2253	0	2299	25	0
2	A	15	0	0	0	0
All	All	2268	0	2299	25	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 (25) 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:37:MET:HE1	1:A:47:PHE:HA	1.45	0.98
1:A:35:GLU:OE1	1:A:50:HIS:HD2	1.57	0.88
1:A:96:LEU:HD12	1:A:101:GLU:HB3	1.64	0.79
1:A:57:SER:O	1:A:61:VAL:HG13	1.92	0.68
1:A:3:ARG:HG2	1:A:22:MET:HB3	1.80	0.64
1:A:136:ILE:HG22	1:A:138:THR:HG23	1.85	0.59
1:A:35:GLU:OE1	1:A:50:HIS:CD2	2.49	0.58
1:A:37:MET:CE	1:A:47:PHE:HA	2.25	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:37:MET:HE3	1:A:50:HIS:HB2	1.89	0.55
1:A:251:SER:N	1:A:252:PRO:HD2	2.25	0.52
1:A:123:HIS:HD2	1:A:243:SER:OG	1.94	0.51
1:A:174:SER:HB2	1:A:232:THR:O	2.12	0.48
1:A:178:PHE:HB2	1:A:186:TYR:HB2	1.98	0.46
1:A:10:PHE:HB2	1:A:106:TYR:HB3	1.97	0.45
1:A:37:MET:HE1	1:A:47:PHE:CD1	2.53	0.44
1:A:277:LYS:HG2	1:A:280:ARG:NH1	2.32	0.44
1:A:230:PHE:HA	1:A:241:VAL:HG23	2.00	0.44
1:A:226:ILE:HG23	1:A:249:LEU:HD21	1.99	0.43
1:A:179:MET:HE2	1:A:183:ASN:HB3	2.02	0.42
1:A:254:ILE:HG22	1:A:257:ILE:H	1.85	0.42
1:A:123:HIS:CD2	1:A:243:SER:OG	2.72	0.41
1:A:130:GLU:OE2	1:A:163:ASN:HB2	2.20	0.41
1:A:182:ASP:HB2	1:A:184:LYS:HG2	2.03	0.41
1:A:57:SER:HB3	1:A:136:ILE:HD12	2.03	0.41
1:A:186:TYR:HA	1:A:214:LEU:O	2.22	0.40

There are no symmetry-related clashes.

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	283/286 (99%)	244 (86%)	30 (11%)	9 (3%)	3 5

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	195	LYS
1	A	245	GLY
1	A	182	ASP
1	A	190	ALA

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	154	SER
1	A	98	ASN
1	A	247	THR
1	A	116	LYS
1	A	236	VAL

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	242/246 (98%)	201 (83%)	41 (17%)	2 3

All (41) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	14	GLN
1	A	18	SER
1	A	48	GLU
1	A	60	LEU
1	A	61	VAL
1	A	64	ARG
1	A	98	ASN
1	A	100	LYS
1	A	111	GLU
1	A	114	ASP
1	A	119	LEU
1	A	126	LEU
1	A	128	SER
1	A	130	GLU
1	A	131	ARG
1	A	140	LYS
1	A	144	ARG
1	A	148	LYS
1	A	150	VAL
1	A	152	GLU
1	A	164	GLU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	165	SER
1	A	179	MET
1	A	181	LYS
1	A	182	ASP
1	A	204	GLN
1	A	208	ARG
1	A	216	LYS
1	A	221	ARG
1	A	225	ASP
1	A	226	ILE
1	A	227	GLN
1	A	232	THR
1	A	239	THR
1	A	240	PRO
1	A	247	THR
1	A	253	ASN
1	A	254	ILE
1	A	274	LYS
1	A	281	LYS
1	A	286	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	7	HIS
1	A	13	ASN
1	A	50	HIS
1	A	74	HIS
1	A	89	ASN
1	A	123	HIS
1	A	253	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

1 non-standard protein/DNA/RNA residue 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$
1	LLP	A	137	1	23,24,25	1.33	3 (13%)	25,32,34	2.11	6 (24%)

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	A	137	1	-	5/16/17/19	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	137	LLP	C3-C2	4.41	1.45	1.41
1	A	137	LLP	O3-C3	2.69	1.43	1.36
1	A	137	LLP	P-OP1	2.51	1.58	1.50

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	137	LLP	C4-C3-C2	-5.15	117.24	120.14
1	A	137	LLP	OP4-P-OP1	4.47	118.53	106.44
1	A	137	LLP	OP3-P-OP4	-3.87	96.57	106.67
1	A	137	LLP	C2'-C2-C3	3.30	124.66	120.80
1	A	137	LLP	C5'-C5-C6	-2.81	114.78	119.36
1	A	137	LLP	CD-CE-NZ	2.45	117.32	110.83

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	137	LLP	C4-C4'-NZ-CE
1	A	137	LLP	O-C-CA-CB
1	A	137	LLP	CE-CD-CG-CB

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms
1	A	137	LLP	CD-CE-NZ-C4'
1	A	137	LLP	C3-C4-C4'-NZ

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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	285/286 (99%)	0.55	32 (11%) 10 8	66, 95, 131, 165	0

All (32) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	9	PHE	6.3
1	A	16	ILE	5.0
1	A	24	ILE	5.0
1	A	245	GLY	4.0
1	A	210	GLY	3.9
1	A	21	ASP	3.8
1	A	162	VAL	3.5
1	A	100	LYS	3.5
1	A	128	SER	3.4
1	A	107	PHE	3.3
1	A	20	ALA	3.3
1	A	220	THR	3.3
1	A	8	ASN	3.3
1	A	209	LEU	3.3
1	A	15	ILE	3.3
1	A	256	LEU	3.2
1	A	18	SER	3.0
1	A	90	VAL	2.8
1	A	157	TYR	2.8
1	A	260	ILE	2.7
1	A	230	PHE	2.6
1	A	149	ALA	2.6
1	A	108	ILE	2.4
1	A	25	PHE	2.4
1	A	10	PHE	2.4
1	A	56	MET	2.2
1	A	150	VAL	2.2

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	6	ILE	2.1
1	A	132	ILE	2.0
1	A	55	VAL	2.0
1	A	17	LYS	2.0
1	A	281	LYS	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($\text{\AA}^2$)	Q<0.9
1	LLP	A	137	24/25	0.97	0.08	63,76,83,87	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides 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.