



Full wwPDB X-ray Structure Validation Report ⓘ

Dec 18, 2024 – 12:14 PM JST

PDB ID : 9IJL
Title : Structure of wild-type aminotransferase from Mycolicibacterium neoaurum in complex with LLP
Authors : Wei, H.; Cong, L.; You, S.; Liu, W.
Deposited on : 2024-06-24
Resolution : 1.60 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)	:	1.21
EDS	:	3.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.004 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.40

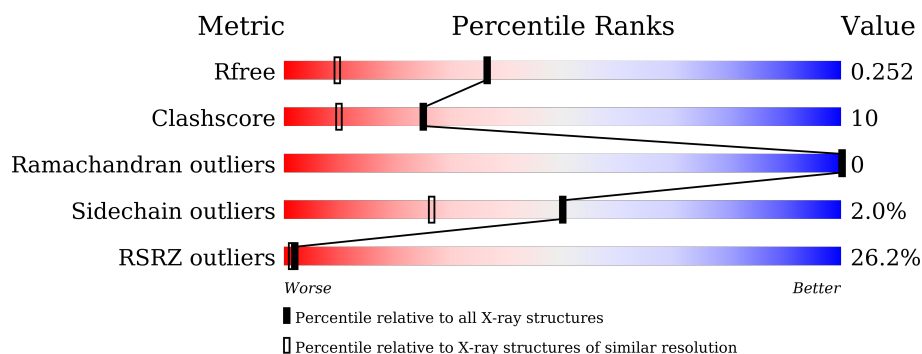
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.60 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	4274 (1.60-1.60)
Clashscore	180529	4682 (1.60-1.60)
Ramachandran outliers	177936	4583 (1.60-1.60)
Sidechain outliers	177891	4582 (1.60-1.60)
RSRZ outliers	164620	4272 (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	335	<div> <div>45%</div> <div>79%</div> <div>16%</div> <div>..</div> </div>
1	B	335	<div> <div>17%</div> <div>84%</div> <div>11%</div> <div>..</div> </div>
1	C	335	<div> <div>15%</div> <div>88%</div> <div>7%</div> <div>..</div> </div>
1	D	335	<div> <div>24%</div> <div>78%</div> <div>17%</div> <div>..</div> </div>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 11367 atoms, of which 0 are hydrogens and 0 are deuteriums.

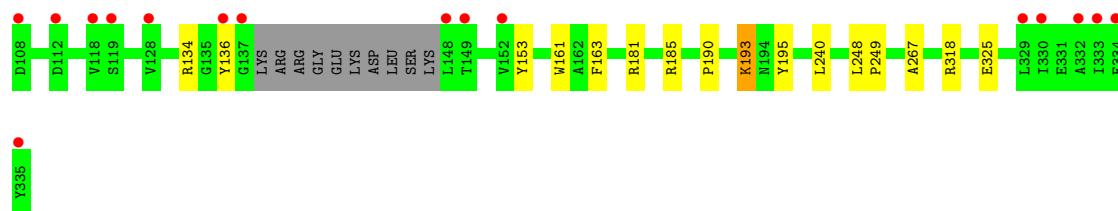
In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Branched-chain amino acid aminotransferase.

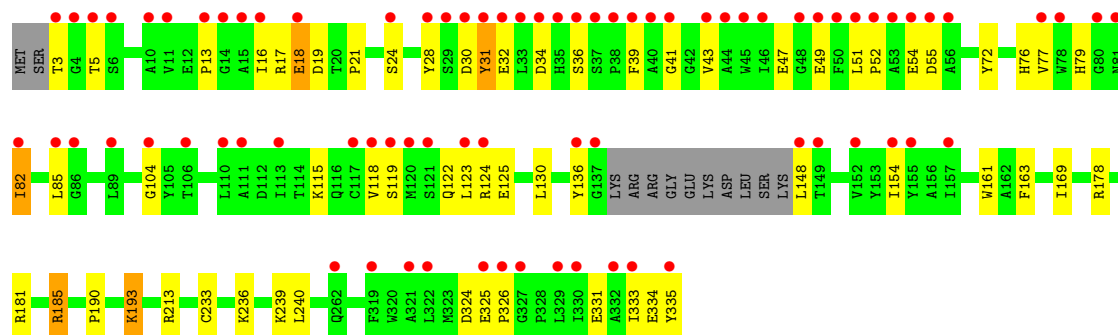
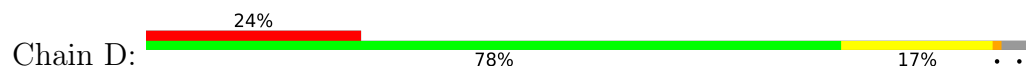
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	323	Total	C	N	O	P	S	0	0	0
			2494	1574	425	486	1	8			
1	B	323	Total	C	N	O	P	S	0	0	0
			2490	1572	425	484	1	8			
1	C	323	Total	C	N	O	P	S	0	0	0
			2494	1574	425	486	1	8			
1	D	323	Total	C	N	O	P	S	0	0	0
			2494	1574	425	486	1	8			

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	356	Total	O	0	0
			356	356		
2	B	370	Total	O	0	0
			370	370		
2	C	358	Total	O	0	0
			358	358		
2	D	311	Total	O	0	0
			311	311		



● Molecule 1: Branched-chain amino acid aminotransferase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	67.18Å 79.28Å 92.21Å 97.20° 108.43° 113.01°	Depositor
Resolution (Å)	41.93 – 1.60 41.93 – 1.60	Depositor EDS
% Data completeness (in resolution range)	89.8 (41.93-1.60) 89.7 (41.93-1.60)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.36 (at 1.60Å)	Xtriage
Refinement program	PHENIX (1.20.1_4487: ???)	Depositor
R, R_{free}	0.204 , 0.232 0.233 , 0.252	Depositor DCC
R_{free} test set	200778 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	18.3	Xtriage
Anisotropy	0.282	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 39.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	11367	wwPDB-VP
Average B, all atoms (Å ²)	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.01% 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: 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	0.67	0/2526	0.78	0/3440
1	B	0.64	0/2522	0.75	0/3435
1	C	0.58	0/2526	0.72	0/3440
1	D	0.72	0/2526	0.80	0/3440
All	All	0.65	0/10100	0.76	0/13755

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 [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	2494	0	2409	65	0
1	B	2490	0	2405	41	0
1	C	2494	0	2409	28	0
1	D	2494	0	2409	71	0
2	A	356	0	0	21	0
2	B	370	0	0	9	0
2	C	358	0	0	9	0
2	D	311	0	0	12	0
All	All	11367	0	9632	189	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 10.

All (189) 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:D:51:LEU:HD23	1:D:52:PRO:N	1.48	1.27
1:D:51:LEU:HD23	1:D:52:PRO:CD	1.76	1.15
1:A:57:LYS:HE3	2:A:579:HOH:O	1.51	1.09
1:D:51:LEU:HD21	1:D:55:ASP:HB2	1.30	1.08
1:D:51:LEU:CD2	1:D:52:PRO:HD2	1.83	1.08
1:A:38:PRO:HD3	2:A:460:HOH:O	1.58	1.00
1:D:51:LEU:CD2	1:D:55:ASP:HB2	1.93	0.99
1:D:51:LEU:CD2	1:D:52:PRO:CD	2.42	0.94
1:A:17:ARG:NH2	1:A:31:TYR:O	2.00	0.94
1:B:51:LEU:HD23	1:B:55:ASP:HB2	1.51	0.92
1:A:51:LEU:HD23	1:A:55:ASP:HB2	1.51	0.90
1:A:18:GLU:HG3	2:A:424:HOH:O	1.76	0.86
1:B:116:GLN:HB2	2:B:428:HOH:O	1.75	0.85
1:D:16:ILE:HD11	1:D:31:TYR:OH	1.78	0.83
1:B:17:ARG:NH1	1:B:29:SER:O	2.13	0.82
1:A:17:ARG:NH1	1:A:29:SER:O	2.13	0.82
1:A:51:LEU:CD2	1:A:55:ASP:HB2	2.10	0.80
1:B:51:LEU:CD2	1:B:55:ASP:HB2	2.10	0.80
1:D:51:LEU:HD21	1:D:55:ASP:CB	2.11	0.79
1:D:51:LEU:CD2	1:D:52:PRO:N	2.40	0.77
1:A:18:GLU:CG	2:A:424:HOH:O	2.32	0.77
1:A:335:TYR:HB3	2:A:637:HOH:O	1.84	0.77
1:A:335:TYR:OXT	2:A:401:HOH:O	2.05	0.74
1:A:38:PRO:CD	2:A:460:HOH:O	2.25	0.73
1:A:45:TRP:CZ3	2:A:572:HOH:O	2.41	0.72
1:D:16:ILE:CD1	1:D:123:LEU:CD2	2.68	0.72
1:D:16:ILE:CD1	1:D:123:LEU:HD23	2.19	0.72
1:B:167:GLU:OE2	1:B:213:ARG:HD3	1.89	0.72
1:A:167:GLU:OE2	1:A:213:ARG:HD3	1.89	0.71
1:D:325:GLU:HG3	2:D:480:HOH:O	1.88	0.71
1:D:34:ASP:H	1:D:122:GLN:HE22	1.38	0.71
1:D:51:LEU:HD21	1:D:52:PRO:HD2	1.71	0.71
1:C:181:ARG:NH1	2:C:402:HOH:O	2.24	0.70
1:A:45:TRP:CH2	2:A:572:HOH:O	2.46	0.69
1:A:3:THR:O	2:A:402:HOH:O	2.11	0.68
1:A:129:ASN:ND2	2:A:408:HOH:O	2.25	0.67
1:D:148:LEU:N	2:D:404:HOH:O	2.28	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:66:GLY:HA2	1:C:195:TYR:CD2	2.32	0.65
1:D:16:ILE:HD12	1:D:123:LEU:CD2	2.26	0.64
1:B:17:ARG:NH2	1:B:31:TYR:O	2.30	0.64
1:D:16:ILE:HD12	1:D:123:LEU:HD22	1.80	0.64
1:A:3:THR:HG23	1:A:5:THR:H	1.63	0.64
1:A:181:ARG:NH2	1:D:181:ARG:NH2	2.46	0.64
1:D:51:LEU:HD23	1:D:52:PRO:CA	2.25	0.64
1:B:3:THR:HG23	1:B:5:THR:H	1.63	0.63
1:B:47:GLU:N	2:B:405:HOH:O	2.30	0.63
1:D:3:THR:HG22	1:D:5:THR:H	1.64	0.62
1:D:233:CYS:HB3	1:D:240:LEU:HD11	1.81	0.62
1:A:95:GLY:HA3	2:A:564:HOH:O	1.99	0.62
1:D:51:LEU:HD23	1:D:52:PRO:HD2	1.52	0.61
1:D:51:LEU:CD2	1:D:52:PRO:O	2.48	0.61
1:C:181:ARG:HG3	2:C:402:HOH:O	1.99	0.61
1:C:72:TYR:CE1	1:C:193:LLP:HG3	2.36	0.60
1:C:181:ARG:CD	2:C:402:HOH:O	2.49	0.60
1:D:115:LYS:HE3	2:D:417:HOH:O	2.00	0.60
1:D:77:VAL:HG12	1:D:124:ARG:O	2.00	0.59
1:A:214:THR:OG1	1:A:215:ALA:N	2.33	0.58
1:D:51:LEU:CG	1:D:52:PRO:CD	2.81	0.58
1:B:233:CYS:HB3	1:B:240:LEU:HD11	1.86	0.58
1:C:134:ARG:NH2	2:C:406:HOH:O	2.37	0.57
1:B:214:THR:OG1	1:B:215:ALA:N	2.33	0.57
1:A:56:ALA:O	2:A:403:HOH:O	2.17	0.57
1:D:34:ASP:OD1	1:D:36:SER:OG	2.23	0.57
1:B:181:ARG:NH2	1:C:181:ARG:NH2	2.52	0.57
1:A:58:ILE:O	1:C:58:ILE:N	2.32	0.56
1:D:51:LEU:HD23	1:D:51:LEU:C	2.21	0.56
1:A:51:LEU:CD2	1:A:55:ASP:CB	2.83	0.56
1:D:51:LEU:HD22	1:D:55:ASP:HB2	1.87	0.56
1:D:104:GLY:N	2:D:405:HOH:O	2.28	0.56
1:A:233:CYS:HB3	1:A:240:LEU:HD11	1.86	0.55
1:B:51:LEU:CD2	1:B:55:ASP:CB	2.83	0.55
1:D:41:GLY:O	1:D:123:LEU:HD11	2.07	0.55
1:D:213:ARG:HB3	1:D:213:ARG:CZ	2.37	0.55
1:D:185:ARG:HA	1:D:190:PRO:HD2	1.88	0.55
1:D:239:LYS:NZ	2:D:410:HOH:O	2.39	0.55
1:B:51:LEU:HD23	1:B:55:ASP:CB	2.33	0.54
1:B:39:PHE:HB3	1:B:43:VAL:HG22	1.89	0.54
1:B:39:PHE:HB3	1:B:43:VAL:CG2	2.38	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:18:GLU:HG2	1:D:19:ASP:N	2.22	0.54
1:A:39:PHE:HB3	1:A:43:VAL:HG22	1.89	0.54
1:A:39:PHE:HB3	1:A:43:VAL:CG2	2.38	0.53
1:A:51:LEU:HD23	1:A:55:ASP:CB	2.33	0.53
1:D:51:LEU:HG	1:D:52:PRO:CD	2.39	0.52
1:D:72:TYR:CE1	1:D:193:LLP:HG3	2.44	0.52
1:C:12:GLU:HG3	2:C:527:HOH:O	2.07	0.52
1:C:95:GLY:HA3	2:C:530:HOH:O	2.10	0.51
1:D:115:LYS:CE	2:D:417:HOH:O	2.57	0.51
1:D:51:LEU:CG	1:D:52:PRO:HD2	2.39	0.51
1:A:195:TYR:CD2	1:C:66:GLY:HA2	2.45	0.51
1:B:116:GLN:CB	2:B:428:HOH:O	2.46	0.51
1:D:324:ASP:O	1:D:326:PRO:HD3	2.10	0.51
1:D:16:ILE:HD13	1:D:123:LEU:HD23	1.91	0.51
1:D:13:PRO:HA	2:D:429:HOH:O	2.11	0.51
1:A:63:THR:HB	1:A:134:ARG:HB3	1.93	0.50
1:A:239:LYS:HE2	2:A:666:HOH:O	2.11	0.50
1:C:11:VAL:HG12	1:C:11:VAL:O	2.12	0.50
1:B:14:GLY:O	1:B:158:PRO:HG2	2.11	0.50
1:B:63:THR:HB	1:B:134:ARG:HB3	1.93	0.50
1:D:119:SER:OG	1:D:334:GLU:O	2.21	0.50
1:B:116:GLN:CA	2:B:428:HOH:O	2.59	0.49
1:A:66:GLY:HA2	1:C:195:TYR:CE2	2.47	0.49
1:D:16:ILE:HG13	1:D:16:ILE:O	2.11	0.49
1:D:31:TYR:CE2	1:D:124:ARG:HD3	2.47	0.49
1:C:161:TRP:HB3	1:C:163:PHE:O	2.12	0.49
1:A:239:LYS:CE	2:A:666:HOH:O	2.60	0.49
1:C:49:GLU:HG2	1:C:51:LEU:HG	1.94	0.49
1:D:331:GLU:OE2	2:D:401:HOH:O	2.20	0.49
1:A:33:LEU:CD2	1:A:122:GLN:HB2	2.43	0.48
1:C:181:ARG:HD2	2:C:402:HOH:O	2.13	0.48
1:B:3:THR:HG22	1:B:208:LYS:NZ	2.28	0.48
1:A:3:THR:HG22	1:A:208:LYS:NZ	2.29	0.48
1:B:331:GLU:HB2	2:B:418:HOH:O	2.12	0.48
1:C:181:ARG:CZ	2:C:402:HOH:O	2.61	0.48
1:D:79:HIS:ND1	1:D:324:ASP:OD1	2.34	0.48
1:D:77:VAL:O	1:D:125:GLU:HA	2.15	0.47
1:A:151:GLN:OE1	2:A:404:HOH:O	2.20	0.47
1:A:161:TRP:HB3	1:A:163:PHE:O	2.15	0.47
1:B:3:THR:HG22	1:B:208:LYS:HZ1	1.80	0.47
1:D:16:ILE:HG13	2:D:416:HOH:O	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:161:TRP:HB3	1:B:163:PHE:O	2.15	0.46
1:D:82:ILE:HG23	2:D:464:HOH:O	2.14	0.46
1:B:137:GLY:O	2:B:401:HOH:O	2.20	0.46
1:A:181:ARG:NH2	1:D:181:ARG:CZ	2.79	0.46
1:D:47:GLU:OE1	1:D:136:TYR:OH	2.34	0.46
1:D:130:LEU:HG	1:D:154:ILE:HG12	1.97	0.46
1:B:17:ARG:HH12	1:B:31:TYR:H	1.64	0.46
1:A:207:ALA:CB	1:A:214:THR:O	2.64	0.46
1:B:207:ALA:CB	1:B:214:THR:O	2.64	0.46
1:D:115:LYS:HE2	1:D:331:GLU:OE1	2.16	0.46
1:A:181:ARG:CZ	1:D:181:ARG:NH2	2.79	0.45
1:A:148:LEU:CD1	2:A:469:HOH:O	2.63	0.45
1:A:324:ASP:HB2	2:A:448:HOH:O	2.17	0.45
1:C:185:ARG:HA	1:C:190:PRO:HD2	1.99	0.45
1:A:15:ALA:O	1:A:158:PRO:HB3	2.17	0.45
1:A:181:ARG:HH21	1:D:181:ARG:HH21	1.64	0.45
1:B:213:ARG:NH2	2:B:413:HOH:O	2.49	0.44
1:D:21:PRO:HG2	1:D:169:ILE:HG13	1.99	0.44
1:A:136:TYR:C	1:A:136:TYR:CD1	2.91	0.44
1:B:207:ALA:HB2	1:B:214:THR:O	2.18	0.44
1:D:39:PHE:HD1	1:D:43:VAL:HG22	1.82	0.44
1:A:207:ALA:HB2	1:A:214:THR:O	2.18	0.44
1:C:47:GLU:OE1	1:C:136:TYR:OH	2.34	0.44
1:A:17:ARG:HH22	1:A:31:TYR:C	2.15	0.43
1:C:248:LEU:HD12	1:C:249:PRO:HD2	2.00	0.43
1:A:181:ARG:HH21	1:D:181:ARG:NH2	2.16	0.43
1:B:181:ARG:HH21	1:C:181:ARG:HH21	1.65	0.43
1:A:43:VAL:HG21	1:A:120:MET:HB2	2.01	0.43
1:A:278:TYR:CZ	1:D:178:ARG:HD3	2.52	0.43
1:A:58:ILE:N	1:C:58:ILE:O	2.36	0.43
1:D:213:ARG:HB3	1:D:213:ARG:NH1	2.34	0.43
1:D:236:LYS:NZ	2:D:421:HOH:O	2.49	0.43
1:B:51:LEU:HD21	1:B:55:ASP:CB	2.49	0.43
1:B:136:TYR:CD1	1:B:136:TYR:C	2.91	0.43
1:A:33:LEU:HD22	1:A:40:ALA:HB1	2.01	0.42
1:B:116:GLN:O	1:B:120:MET:HG3	2.19	0.42
1:B:43:VAL:HG21	1:B:120:MET:HB2	2.01	0.42
1:B:72:TYR:CE1	1:B:193:LLP:HG3	2.54	0.42
1:A:72:TYR:CE1	1:A:193:LLP:HG3	2.53	0.42
1:A:116:GLN:O	1:A:120:MET:HG3	2.19	0.42
1:D:161:TRP:HB3	1:D:163:PHE:O	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:51:LEU:HD21	1:A:55:ASP:CB	2.49	0.42
1:A:14:GLY:O	1:A:158:PRO:HG2	2.19	0.42
1:A:148:LEU:HD13	2:A:469:HOH:O	2.20	0.42
1:B:64:GLY:O	1:B:68:SER:HA	2.20	0.42
1:C:325:GLU:OE2	2:C:401:HOH:O	2.21	0.42
1:D:17:ARG:HA	1:D:28:TYR:CE2	2.55	0.42
1:D:30:ASP:OD1	1:D:30:ASP:C	2.59	0.42
1:D:122:GLN:HA	1:D:335:TYR:HD2	1.84	0.41
1:A:97:ARG:NE	2:A:410:HOH:O	2.30	0.41
1:A:185:ARG:HA	1:A:190:PRO:HD2	2.02	0.41
1:D:118:VAL:CG1	1:D:333:ILE:HG13	2.50	0.41
1:B:185:ARG:HA	1:B:190:PRO:HD2	2.02	0.41
1:D:51:LEU:HD23	1:D:52:PRO:O	2.19	0.41
1:A:60:ILE:CD1	1:C:153:TYR:HB3	2.50	0.41
1:A:21:PRO:HA	1:A:22:PRO:HD3	1.94	0.41
1:A:195:TYR:CD1	1:C:66:GLY:O	2.74	0.41
1:C:318:ARG:HA	1:C:318:ARG:HD2	1.87	0.41
1:A:64:GLY:O	1:A:68:SER:HA	2.20	0.41
1:D:85:LEU:HD23	2:D:417:HOH:O	2.20	0.41
1:A:8:LEU:O	2:A:405:HOH:O	2.22	0.41
1:B:112:ASP:OD1	2:B:402:HOH:O	2.22	0.41
1:A:51:LEU:HD21	1:A:55:ASP:HB2	2.01	0.40
1:B:326:PRO:HA	1:B:330:ILE:HD11	2.03	0.40
1:B:51:LEU:HD21	1:B:55:ASP:HB2	2.01	0.40
1:B:181:ARG:HH21	1:C:181:ARG:NH2	2.19	0.40
1:C:240:LEU:O	1:C:267:ALA:HA	2.21	0.40
1:D:122:GLN:HA	1:D:335:TYR:CD2	2.56	0.40
1:B:220:SER:HA	2:B:581:HOH:O	2.20	0.40
1:D:51:LEU:HD22	1:D:52:PRO:O	2.20	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	318/335 (95%)	310 (98%)	8 (2%)	0	100	100
1	B	318/335 (95%)	310 (98%)	8 (2%)	0	100	100
1	C	318/335 (95%)	308 (97%)	10 (3%)	0	100	100
1	D	318/335 (95%)	309 (97%)	9 (3%)	0	100	100
All	All	1272/1340 (95%)	1237 (97%)	35 (3%)	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	259/270 (96%)	255 (98%)	4 (2%)	60	39
1	B	258/270 (96%)	253 (98%)	5 (2%)	52	29
1	C	259/270 (96%)	256 (99%)	3 (1%)	67	50
1	D	259/270 (96%)	250 (96%)	9 (4%)	31	10
All	All	1035/1080 (96%)	1014 (98%)	21 (2%)	50	26

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	51	LEU
1	A	76	HIS
1	A	136	TYR
1	A	213	ARG
1	B	16	ILE
1	B	51	LEU
1	B	76	HIS
1	B	136	TYR
1	B	213	ARG
1	C	12	GLU
1	C	17	ARG
1	C	76	HIS
1	D	18	GLU

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Mol	Chain	Res	Type
1	D	24	SER
1	D	31	TYR
1	D	32	GLU
1	D	49	GLU
1	D	54	GLU
1	D	76	HIS
1	D	82	ILE
1	D	185	ARG

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	116	GLN
1	A	151	GLN
1	B	116	GLN
1	D	122	GLN
1	D	262	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

4 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	C	193	1	23,24,25	0.84	1 (4%)	25,32,34	1.03	2 (8%)
1	LLP	B	193	1	23,24,25	0.76	0	25,32,34	1.04	3 (12%)
1	LLP	A	193	1	23,24,25	0.76	0	25,32,34	1.03	4 (16%)
1	LLP	D	193	1	23,24,25	0.88	2 (8%)	25,32,34	1.08	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
1	LLP	C	193	1	-	3/16/17/19	0/1/1/1
1	LLP	B	193	1	-	3/16/17/19	0/1/1/1
1	LLP	A	193	1	-	3/16/17/19	0/1/1/1
1	LLP	D	193	1	-	3/16/17/19	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	193	LLP	P-OP2	-2.25	1.46	1.54
1	D	193	LLP	O-C	2.19	1.28	1.19
1	D	193	LLP	P-OP2	-2.05	1.46	1.54

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	193	LLP	OP4-C5'-C5	2.51	114.13	109.35
1	A	193	LLP	OP4-C5'-C5	2.50	114.11	109.35
1	A	193	LLP	OP3-P-OP2	2.27	116.31	107.64
1	B	193	LLP	OP3-P-OP2	2.27	116.30	107.64
1	C	193	LLP	OP4-C5'-C5	2.24	113.61	109.35
1	B	193	LLP	OP3-P-OP4	-2.17	100.97	106.73
1	A	193	LLP	OP3-P-OP4	-2.15	101.02	106.73
1	C	193	LLP	OP3-P-OP4	-2.03	101.33	106.73
1	A	193	LLP	OP2-P-OP4	-2.00	101.41	106.73

There are no chirality outliers.

All (12) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	193	LLP	C4-C4'-NZ-CE
1	A	193	LLP	CG-CD-CE-NZ
1	B	193	LLP	C4-C4'-NZ-CE
1	B	193	LLP	CG-CD-CE-NZ
1	C	193	LLP	C4-C4'-NZ-CE
1	D	193	LLP	C4-C4'-NZ-CE
1	C	193	LLP	CG-CD-CE-NZ
1	D	193	LLP	CG-CD-CE-NZ

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Mol	Chain	Res	Type	Atoms
1	A	193	LLP	C3-C4-C4'-NZ
1	B	193	LLP	C3-C4-C4'-NZ
1	C	193	LLP	C3-C4-C4'-NZ
1	D	193	LLP	C3-C4-C4'-NZ

There are no ring outliers.

4 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	C	193	LLP	1	0
1	B	193	LLP	1	0
1	A	193	LLP	1	0
1	D	193	LLP	1	0

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	322/335 (96%)	2.05	152 (47%) 0 0	11, 21, 43, 58	0
1	B	322/335 (96%)	0.76	58 (18%) 4 3	11, 21, 43, 55	0
1	C	322/335 (96%)	0.84	49 (15%) 6 5	12, 25, 44, 54	0
1	D	322/335 (96%)	1.14	79 (24%) 2 2	11, 24, 49, 64	0
All	All	1288/1340 (96%)	1.20	338 (26%) 2 1	11, 23, 46, 64	0

All (338) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	326	PRO	8.0
1	A	53	ALA	7.3
1	B	3	THR	6.7
1	A	45	TRP	6.5
1	A	41	GLY	6.4
1	A	39	PHE	6.4
1	A	3	THR	6.3
1	A	38	PRO	6.2
1	A	333	ILE	6.2
1	B	39	PHE	6.2
1	A	51	LEU	6.1
1	B	45	TRP	5.9
1	A	50	PHE	5.7
1	A	43	VAL	5.7
1	A	136	TYR	5.6
1	A	52	PRO	5.6
1	A	330	ILE	5.5
1	A	135	GLY	5.5
1	A	335	TYR	5.4
1	C	3	THR	5.3
1	A	119	SER	5.3

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Mol	Chain	Res	Type	RSRZ
1	A	105	TYR	5.2
1	B	43	VAL	5.1
1	D	16	ILE	5.1
1	C	4	GLY	5.1
1	B	50	PHE	5.1
1	B	51	LEU	5.0
1	D	3	THR	5.0
1	A	16	ILE	4.9
1	A	46	ILE	4.9
1	C	12	GLU	4.8
1	D	39	PHE	4.8
1	D	15	ALA	4.8
1	D	14	GLY	4.7
1	A	121	SER	4.6
1	A	40	ALA	4.6
1	A	31	TYR	4.6
1	D	51	LEU	4.6
1	A	48	GLY	4.4
1	A	149	THR	4.4
1	A	117	CYS	4.4
1	D	53	ALA	4.4
1	D	137	GLY	4.3
1	D	45	TRP	4.3
1	A	60	ILE	4.3
1	A	61	PHE	4.3
1	A	44	ALA	4.3
1	B	148	LEU	4.3
1	A	104	GLY	4.2
1	A	157	ILE	4.2
1	A	302	ALA	4.2
1	D	327	GLY	4.1
1	A	214	THR	4.1
1	A	49	GLU	4.1
1	A	113	ILE	4.1
1	B	46	ILE	4.1
1	A	148	LEU	4.1
1	D	31	TYR	4.0
1	A	154	ILE	4.0
1	B	52	PRO	4.0
1	D	41	GLY	4.0
1	A	118	VAL	4.0
1	A	42	GLY	4.0

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Mol	Chain	Res	Type	RSRZ
1	A	153	TYR	4.0
1	C	31	TYR	3.9
1	D	333	ILE	3.9
1	A	334	GLU	3.9
1	A	137	GLY	3.9
1	A	152	VAL	3.9
1	C	136	TYR	3.9
1	A	156	ALA	3.9
1	A	262	GLN	3.9
1	B	330	ILE	3.9
1	A	332	ALA	3.9
1	D	43	VAL	3.9
1	A	58	ILE	3.8
1	D	5	THR	3.8
1	A	103	ALA	3.8
1	B	4	GLY	3.8
1	A	331	GLU	3.8
1	A	77	VAL	3.7
1	D	35	HIS	3.7
1	D	80	GLY	3.7
1	A	111	ALA	3.7
1	A	120	MET	3.7
1	A	56	ALA	3.6
1	A	106	THR	3.6
1	D	52	PRO	3.6
1	A	155	TYR	3.6
1	D	325	GLU	3.6
1	D	330	ILE	3.5
1	D	54	GLU	3.5
1	A	319	PHE	3.5
1	C	11	VAL	3.5
1	B	333	ILE	3.5
1	D	136	TYR	3.5
1	A	23	GLY	3.5
1	C	33	LEU	3.5
1	A	30	ASP	3.5
1	B	31	TYR	3.4
1	A	124	ARG	3.4
1	D	37	SER	3.4
1	B	40	ALA	3.4
1	A	78	TRP	3.4
1	C	32	GLU	3.4

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Mol	Chain	Res	Type	RSRZ
1	D	152	VAL	3.4
1	A	28	TYR	3.4
1	C	51	LEU	3.4
1	D	111	ALA	3.4
1	D	332	ALA	3.4
1	B	214	THR	3.4
1	A	122	GLN	3.4
1	A	128	VAL	3.3
1	A	82	ILE	3.3
1	D	82	ILE	3.3
1	C	45	TRP	3.3
1	C	104	GLY	3.3
1	D	117	CYS	3.3
1	A	5	THR	3.3
1	B	334	GLU	3.3
1	A	47	GLU	3.2
1	D	46	ILE	3.2
1	A	64	GLY	3.2
1	D	50	PHE	3.2
1	A	123	LEU	3.2
1	A	18	GLU	3.2
1	A	213	ARG	3.2
1	D	4	GLY	3.2
1	B	16	ILE	3.2
1	A	65	PHE	3.2
1	A	110	LEU	3.2
1	A	29	SER	3.2
1	A	37	SER	3.2
1	A	161	TRP	3.2
1	B	42	GLY	3.2
1	A	102	ASP	3.2
1	A	159	TYR	3.2
1	B	5	THR	3.2
1	A	59	SER	3.1
1	D	335	TYR	3.1
1	C	39	PHE	3.1
1	A	20	THR	3.1
1	A	114	THR	3.1
1	D	118	VAL	3.1
1	C	5	THR	3.1
1	D	262	GLN	3.1
1	B	332	ALA	3.1

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Mol	Chain	Res	Type	RSRZ
1	D	49	GLU	3.1
1	A	112	ASP	3.1
1	A	33	LEU	3.0
1	A	158	PRO	3.0
1	B	33	LEU	3.0
1	C	148	LEU	3.0
1	C	137	GLY	3.0
1	D	124	ARG	3.0
1	D	44	ALA	3.0
1	C	119	SER	3.0
1	D	33	LEU	3.0
1	C	334	GLU	3.0
1	A	57	LYS	3.0
1	A	329	LEU	3.0
1	A	17	ARG	3.0
1	B	136	TYR	3.0
1	A	35	HIS	3.0
1	A	15	ALA	3.0
1	A	131	THR	2.9
1	B	335	TYR	2.9
1	B	119	SER	2.9
1	A	211	GLY	2.9
1	B	41	GLY	2.9
1	A	160	LEU	2.9
1	A	36	SER	2.9
1	C	35	HIS	2.9
1	A	170	PHE	2.9
1	A	300	GLY	2.9
1	D	321	ALA	2.9
1	B	118	VAL	2.9
1	D	104	GLY	2.9
1	C	16	ILE	2.8
1	A	322	LEU	2.8
1	D	18	GLU	2.8
1	D	89	LEU	2.8
1	A	25	VAL	2.8
1	D	106	THR	2.8
1	B	32	GLU	2.8
1	A	151	GLN	2.8
1	B	14	GLY	2.8
1	A	34	ASP	2.8
1	D	38	PRO	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	63	THR	2.8
1	A	54	GLU	2.8
1	B	48	GLY	2.8
1	D	85	LEU	2.7
1	B	53	ALA	2.7
1	D	77	VAL	2.7
1	D	30	ASP	2.7
1	A	132	VAL	2.7
1	A	320	TRP	2.7
1	A	80	GLY	2.7
1	C	108	ASP	2.7
1	D	319	PHE	2.7
1	D	110	LEU	2.7
1	B	120	MET	2.7
1	A	328	PRO	2.7
1	D	13	PRO	2.7
1	A	195	TYR	2.7
1	D	36	SER	2.7
1	B	123	LEU	2.6
1	A	21	PRO	2.6
1	A	303	ILE	2.6
1	B	15	ALA	2.6
1	C	40	ALA	2.6
1	D	113	ILE	2.6
1	A	305	ASN	2.6
1	B	38	PRO	2.6
1	C	38	PRO	2.6
1	A	321	ALA	2.6
1	C	36	SER	2.6
1	C	43	VAL	2.6
1	B	55	ASP	2.6
1	C	53	ALA	2.6
1	B	117	CYS	2.6
1	A	116	GLN	2.6
1	A	22	PRO	2.6
1	C	48	GLY	2.6
1	A	127	PHE	2.5
1	A	75	ALA	2.5
1	A	325	GLU	2.5
1	B	34	ASP	2.5
1	B	106	THR	2.5
1	C	50	PHE	2.5

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Mol	Chain	Res	Type	RSRZ
1	B	30	ASP	2.5
1	A	26	ILE	2.5
1	D	48	GLY	2.5
1	D	322	LEU	2.5
1	D	32	GLU	2.5
1	C	46	ILE	2.5
1	D	120	MET	2.5
1	D	149	THR	2.5
1	C	335	TYR	2.5
1	D	28	TYR	2.5
1	A	19	ASP	2.5
1	A	306	GLY	2.4
1	B	122	GLN	2.4
1	B	13	PRO	2.4
1	C	13	PRO	2.4
1	A	115	LYS	2.4
1	A	207	ALA	2.4
1	A	92	LEU	2.4
1	C	329	LEU	2.4
1	D	148	LEU	2.4
1	D	329	LEU	2.4
1	A	304	GLY	2.4
1	A	133	THR	2.4
1	A	74	VAL	2.4
1	D	11	VAL	2.4
1	A	10	ALA	2.4
1	D	40	ALA	2.4
1	B	37	SER	2.4
1	D	123	LEU	2.4
1	A	108	ASP	2.4
1	C	149	THR	2.3
1	D	121	SER	2.3
1	C	54	GLU	2.3
1	A	85	LEU	2.3
1	A	79	HIS	2.3
1	B	35	HIS	2.3
1	A	259	ILE	2.3
1	D	24	SER	2.3
1	D	157	ILE	2.3
1	A	166	ALA	2.3
1	B	103	ALA	2.3
1	A	86	GLY	2.3

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Mol	Chain	Res	Type	RSRZ
1	C	41	GLY	2.3
1	C	118	VAL	2.3
1	A	125	GLU	2.3
1	A	326	PRO	2.3
1	A	81	ASN	2.3
1	A	307	ALA	2.3
1	B	56	ALA	2.3
1	D	10	ALA	2.3
1	D	56	ALA	2.3
1	A	324	ASP	2.2
1	C	102	ASP	2.2
1	A	83	PHE	2.2
1	C	330	ILE	2.2
1	D	154	ILE	2.2
1	A	327	GLY	2.2
1	D	86	GLY	2.2
1	A	8	LEU	2.2
1	A	13	PRO	2.2
1	B	49	GLU	2.2
1	A	150	HIS	2.2
1	B	154	ILE	2.2
1	B	44	ALA	2.2
1	C	15	ALA	2.2
1	D	29	SER	2.2
1	C	17	ARG	2.2
1	D	55	ASP	2.2
1	A	32	GLU	2.2
1	B	156	ALA	2.2
1	D	34	ASP	2.2
1	C	28	TYR	2.2
1	A	290	GLY	2.2
1	B	6	SER	2.1
1	A	107	LYS	2.1
1	C	14	GLY	2.1
1	C	128	VAL	2.1
1	B	17	ARG	2.1
1	A	6	SER	2.1
1	D	119	SER	2.1
1	C	30	ASP	2.1
1	D	78	TRP	2.1
1	A	68	SER	2.1
1	A	70	LEU	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	99	LEU	2.1
1	A	130	LEU	2.1
1	A	55	ASP	2.1
1	B	112	ASP	2.1
1	A	169	ILE	2.1
1	B	157	ILE	2.1
1	C	333	ILE	2.1
1	B	104	GLY	2.1
1	D	6	SER	2.1
1	A	212	ALA	2.0
1	C	56	ALA	2.0
1	C	332	ALA	2.0
1	C	106	THR	2.0
1	B	213	ARG	2.0
1	B	108	ASP	2.0
1	D	81	ASN	2.0
1	B	153	TYR	2.0
1	C	152	VAL	2.0
1	D	155	TYR	2.0
1	B	149	THR	2.0
1	A	4	GLY	2.0
1	A	14	GLY	2.0
1	C	112	ASP	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(Å ²)	Q<0.9
1	LLP	A	193	24/25	0.91	0.13	13,17,25,36	0
1	LLP	D	193	24/25	0.93	0.11	14,19,28,34	0
1	LLP	C	193	24/25	0.94	0.11	15,19,29,36	0
1	LLP	B	193	24/25	0.95	0.09	13,17,25,36	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.