



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 02:14 AM UTC

PDB ID : 1C8U / pdb_00001c8u
Title : CRYSTAL STRUCTURE OF THE E.COLI THIOESTERASE II, A HOMOLOGUE OF THE HUMAN NEF-BINDING ENZYME
Authors : Li, J.; Derewenda, Z.S.
Deposited on : 1999-07-29
Resolution : 1.90 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

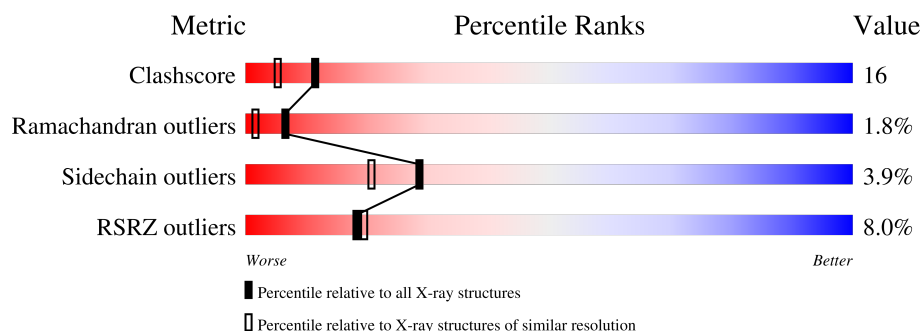
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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))
Clashscore	190562	8410 (1.90-1.90)
Ramachandran outliers	187476	8333 (1.90-1.90)
Sidechain outliers	187428	8333 (1.90-1.90)
RSRZ outliers	180081	7790 (1.90-1.90)

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	285	6% 75% 21% .
1	B	285	9% 69% 26% ..

2 Entry composition [i](#)

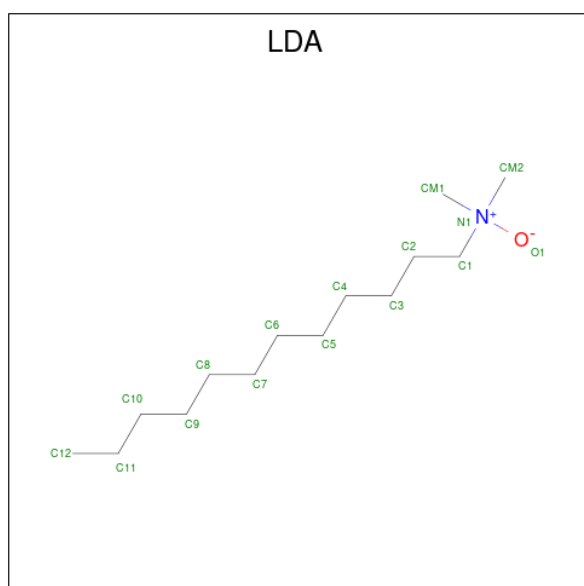
There are 3 unique types of molecules in this entry. The entry contains 5071 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 ACYL-COA THIOESTERASE II.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	285	Total	C	N	O	S	98	0	0
			2253	1438	397	413	5			
1	B	285	Total	C	N	O	S	52	0	0
			2253	1438	397	413	5			

- Molecule 2 is LAURYL DIMETHYLAMINE-N-OXIDE (CCD ID: LDA) (formula: $C_{14}H_{31}NO$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			16	14	1	1		
2	B	1	Total	C	N	O	0	0
			16	14	1	1		

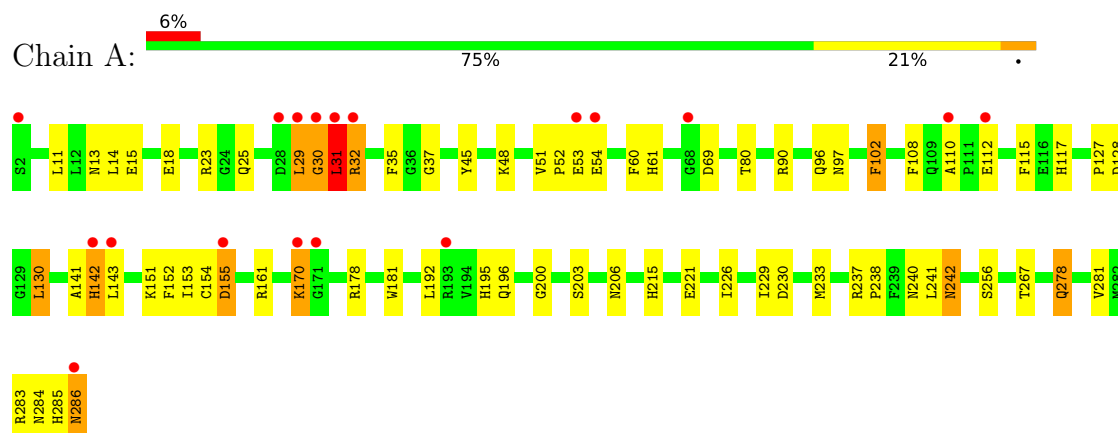
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	274	Total 274	O 274	0	0
3	B	259	Total 259	O 259	0	0

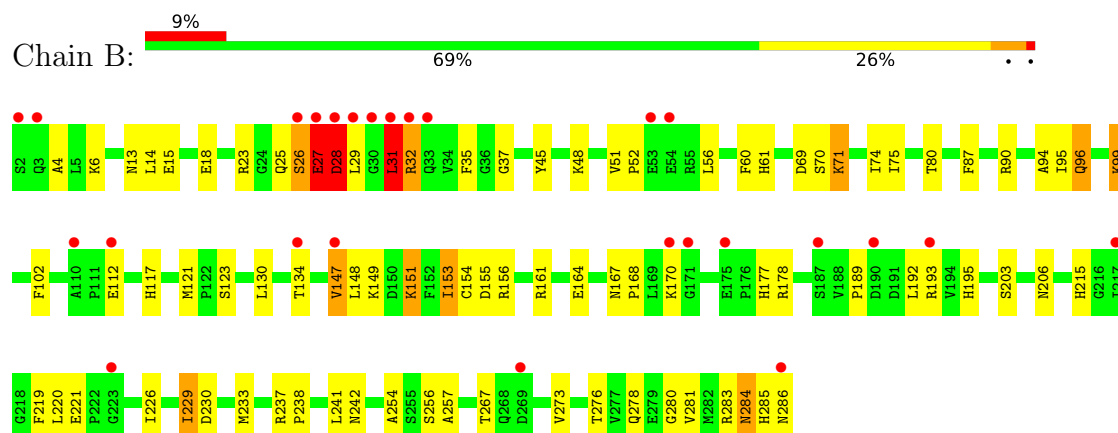
3 Residue-property plots

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: ACYL-COA THIOESTERASE II



• Molecule 1: ACYL-COA THIOESTERASE II



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	95.90Å 119.81Å 165.48Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 1.90 20.00 – 1.90	Depositor EDS
% Data completeness (in resolution range)	99.6 (20.00-1.90) 96.0 (20.00-1.90)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.51 (at 1.90Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.218 , 0.248 0.220 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	22.4	Xtriage
Anisotropy	0.648	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.41 , 59.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	5071	wwPDB-VP
Average B, all atoms (Å ²)	28.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 19.27% 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: LDA

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	0.51	3/2314 (0.1%)	1.00	17/3143 (0.5%)
1	B	0.60	3/2314 (0.1%)	1.21	26/3143 (0.8%)
All	All	0.55	6/4628 (0.1%)	1.11	43/6286 (0.7%)

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	71	LYS	CD-CE	-15.03	1.07	1.52
1	A	32	ARG	CD-NE	-8.87	1.33	1.46
1	A	31	LEU	C-N	6.78	1.42	1.33
1	B	26	SER	C-N	-5.55	1.25	1.33
1	B	28	ASP	N-CA	-5.33	1.39	1.46
1	A	278	GLN	CD-OE1	5.18	1.33	1.23

All (43) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	26	SER	O-C-N	19.47	149.62	122.94
1	B	27	GLU	CA-C-N	16.36	152.79	121.54
1	B	27	GLU	C-N-CA	16.36	152.79	121.54
1	B	27	GLU	O-C-N	14.74	142.20	122.59
1	A	32	ARG	CA-CB-CG	-11.69	90.73	114.10
1	B	71	LYS	CA-CB-CG	10.42	134.94	114.10
1	B	25	GLN	OE1-CD-NE2	-10.35	112.25	122.60
1	B	29	LEU	N-CA-C	10.12	124.75	110.68
1	B	71	LYS	CD-CE-NZ	9.18	141.27	111.90
1	A	31	LEU	CA-C-N	-7.45	110.30	120.44
1	A	31	LEU	C-N-CA	-7.45	110.30	120.44
1	B	27	GLU	CB-CG-CD	6.95	124.42	112.60
1	B	25	GLN	CG-CD-NE2	6.87	126.71	116.40

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	130	LEU	N-CA-C	6.79	118.21	109.72
1	A	154	CYS	N-CA-C	6.52	124.69	110.80
1	B	151	LYS	N-CA-C	-6.49	96.97	110.80
1	A	14	LEU	N-CA-C	6.33	118.97	110.35
1	B	28	ASP	CB-CA-C	6.13	122.61	110.42
1	A	242	ASN	N-CA-C	-6.02	105.42	112.89
1	B	14	LEU	N-CA-C	5.83	118.28	110.35
1	A	32	ARG	NE-CZ-NH2	5.78	124.40	119.20
1	B	242	ASN	N-CA-C	-5.71	105.81	112.89
1	A	229	ILE	N-CA-C	-5.67	106.28	111.67
1	B	229	ILE	N-CA-C	-5.63	106.32	111.67
1	A	267	THR	N-CA-C	-5.62	102.96	110.55
1	B	31	LEU	CA-CB-CG	-5.52	96.98	116.30
1	B	87	PHE	N-CA-C	5.49	118.68	109.95
1	A	32	ARG	O-C-N	-5.45	116.20	122.09
1	A	53	GLU	N-CA-C	5.43	117.90	111.33
1	A	29	LEU	CA-C-N	5.33	131.85	121.41
1	A	29	LEU	C-N-CA	5.33	131.85	121.41
1	B	95	ILE	N-CA-C	5.30	116.11	108.48
1	B	32	ARG	N-CA-C	5.28	117.11	111.36
1	B	27	GLU	CA-C-O	5.20	127.94	120.51
1	B	267	THR	N-CA-C	-5.15	103.60	110.55
1	B	147	VAL	CB-CA-C	-5.13	105.32	112.04
1	B	155	ASP	N-CA-C	-5.13	99.42	108.20
1	B	273	VAL	N-CA-C	5.13	117.01	111.58
1	A	128	ASP	N-CA-C	5.12	119.77	111.37
1	A	155	ASP	N-CA-C	5.12	121.70	110.80
1	A	29	LEU	O-C-N	5.11	129.80	123.01
1	B	31	LEU	CA-C-N	-5.00	113.19	120.29
1	B	31	LEU	C-N-CA	-5.00	113.19	120.29

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	2209	69	0
1	B	2253	0	2208	82	0
2	A	16	0	31	6	0
2	B	16	0	31	2	0
3	A	274	0	0	4	0
3	B	259	0	0	13	0
All	All	5071	0	4479	140	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 16.

All (140) 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:B:32:ARG:HH21	1:B:71:LYS:CG	1.32	1.39
1:B:32:ARG:NH2	1:B:71:LYS:HG3	1.36	1.36
1:B:32:ARG:NH2	1:B:71:LYS:CG	1.97	1.19
1:A:31:LEU:CD1	2:A:800:LDA:H52	1.78	1.13
1:B:27:GLU:HB2	3:B:812:HOH:O	1.55	1.06
1:A:31:LEU:HD12	2:A:800:LDA:H52	1.32	1.04
1:B:32:ARG:HE	1:B:71:LYS:HG2	1.20	1.00
1:B:69:ASP:H	1:B:96:GLN:HE22	1.11	0.98
1:A:195:HIS:HD2	1:A:241:LEU:H	1.16	0.93
1:B:32:ARG:NE	1:B:71:LYS:HG2	1.83	0.92
1:A:69:ASP:H	1:A:96:GLN:HE22	1.18	0.91
1:B:32:ARG:HH21	1:B:71:LYS:HG3	0.76	0.91
1:B:195:HIS:HD2	1:B:241:LEU:H	1.16	0.90
1:B:167:ASN:HB3	1:B:170:LYS:HG2	1.54	0.89
1:B:27:GLU:OE1	3:B:955:HOH:O	1.91	0.88
1:B:32:ARG:HH21	1:B:71:LYS:HG2	1.38	0.86
1:A:32:ARG:HH21	1:A:69:ASP:CG	1.87	0.82
1:A:31:LEU:HD11	2:A:800:LDA:H52	1.59	0.82
1:B:32:ARG:HE	1:B:71:LYS:CG	1.92	0.82
1:B:32:ARG:NE	1:B:71:LYS:CG	2.44	0.81
1:B:32:ARG:NH2	1:B:71:LYS:HG2	1.93	0.79
1:B:32:ARG:CZ	1:B:71:LYS:CG	2.51	0.77
1:B:27:GLU:CB	3:B:812:HOH:O	2.20	0.76
1:A:32:ARG:NH2	1:A:69:ASP:OD1	2.20	0.74
1:A:285:HIS:O	1:A:286:ASN:HB2	1.85	0.74
1:A:170:LYS:HA	1:A:170:LYS:HE2	1.70	0.72
1:A:195:HIS:CD2	1:A:241:LEU:H	2.06	0.72
1:B:203:SER:OG	1:B:233:MET:HE1	1.91	0.71

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:60:PHE:CZ	1:A:233:MET:HE3	2.25	0.71
1:B:32:ARG:CZ	1:B:71:LYS:HG2	2.16	0.70
1:B:178:ARG:HH11	1:B:206:ASN:HD22	1.40	0.70
1:B:195:HIS:CD2	1:B:241:LEU:H	2.06	0.70
1:A:170:LYS:O	1:A:221:GLU:OE2	2.11	0.68
1:B:170:LYS:O	1:B:221:GLU:OE2	2.12	0.68
1:A:112:GLU:CD	1:B:283:ARG:HH22	2.03	0.66
1:B:27:GLU:HB3	1:B:28:ASP:CA	2.12	0.63
1:A:32:ARG:NH2	1:A:69:ASP:CG	2.58	0.61
1:A:51:VAL:HG13	1:A:52:PRO:HD2	1.81	0.61
1:A:178:ARG:HH11	1:A:206:ASN:HD22	1.49	0.61
1:A:45:TYR:O	1:A:48:LYS:HG3	2.00	0.60
1:A:11:LEU:CD1	1:A:25:GLN:HB2	2.31	0.60
1:A:29:LEU:CD1	3:A:1048:HOH:O	2.50	0.60
1:A:29:LEU:HD11	3:A:1048:HOH:O	2.02	0.60
1:B:26:SER:O	3:B:812:HOH:O	2.16	0.60
1:B:229:ILE:HG13	1:B:280:GLY:HA2	1.84	0.59
1:A:61:HIS:CE1	1:B:230:ASP:HB2	2.38	0.59
1:A:61:HIS:HE1	1:B:230:ASP:HB2	1.68	0.58
1:B:121:MET:HE3	3:B:1031:HOH:O	2.03	0.58
1:B:56:LEU:HD21	1:B:193:ARG:NH1	2.18	0.58
1:A:256:SER:HA	1:B:112:GLU:O	2.04	0.58
1:B:284:ASN:HD22	1:B:284:ASN:C	2.10	0.58
1:A:29:LEU:HD12	3:A:1024:HOH:O	2.03	0.57
1:A:142:HIS:O	1:A:143:LEU:HG	2.05	0.57
1:A:69:ASP:H	1:A:96:GLN:NE2	1.95	0.57
1:A:60:PHE:CE2	1:A:233:MET:HE3	2.39	0.57
1:A:11:LEU:HD11	1:A:25:GLN:HB2	1.86	0.56
1:B:230:ASP:O	1:B:278:GLN:HG3	2.06	0.56
1:B:60:PHE:CZ	1:B:233:MET:HE3	2.41	0.56
1:A:170:LYS:HE2	1:A:170:LYS:CA	2.37	0.55
1:B:167:ASN:HB3	1:B:170:LYS:CG	2.29	0.55
1:A:226:ILE:HA	1:A:281:VAL:O	2.06	0.55
1:B:15:GLU:OE1	1:B:23:ARG:HD2	2.06	0.55
1:A:237:ARG:HB3	1:A:238:PRO:HD2	1.89	0.55
1:A:31:LEU:HD11	2:A:800:LDA:C7	2.36	0.54
1:A:285:HIS:O	1:A:286:ASN:CB	2.54	0.54
1:A:178:ARG:HH11	1:A:206:ASN:ND2	2.06	0.53
1:A:141:ALA:O	1:A:143:LEU:N	2.41	0.53
1:B:99:LYS:HB2	1:B:99:LYS:NZ	2.23	0.53
1:A:230:ASP:HB2	1:B:61:HIS:HE1	1.74	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:45:TYR:CD1	1:A:48:LYS:HE3	2.43	0.53
1:B:51:VAL:HG13	1:B:52:PRO:HD2	1.90	0.52
1:A:117:HIS:CE1	1:B:254:ALA:HB2	2.45	0.52
1:A:284:ASN:C	1:A:284:ASN:HD22	2.17	0.52
1:B:56:LEU:HD13	1:B:192:LEU:HD23	1.90	0.51
1:A:35:PHE:CE2	1:A:37:GLY:HA3	2.46	0.50
1:A:230:ASP:HB2	1:B:61:HIS:CE1	2.46	0.50
1:B:193:ARG:HD3	3:B:919:HOH:O	2.10	0.50
1:B:164:GLU:HG3	3:B:1005:HOH:O	2.12	0.50
1:A:203:SER:OG	1:A:233:MET:HE1	2.13	0.49
1:A:230:ASP:O	1:A:278:GLN:HG3	2.13	0.49
1:B:75:ILE:N	1:B:75:ILE:HD12	2.27	0.49
1:A:29:LEU:O	1:A:30:GLY:O	2.31	0.49
1:B:35:PHE:CE2	1:B:37:GLY:HA3	2.49	0.48
1:A:80:THR:HA	1:A:90:ARG:HD3	1.95	0.48
1:A:60:PHE:C	1:A:60:PHE:CD1	2.92	0.48
1:A:170:LYS:HE2	1:A:170:LYS:O	2.14	0.47
1:B:168:PRO:HB3	1:B:219:PHE:CE1	2.49	0.47
1:B:56:LEU:HD21	1:B:193:ARG:HH11	1.79	0.47
1:A:31:LEU:HD11	2:A:800:LDA:C5	2.38	0.47
1:A:31:LEU:HD11	2:A:800:LDA:H72	1.96	0.47
1:B:56:LEU:CD2	1:B:193:ARG:HH11	2.27	0.47
1:B:285:HIS:O	1:B:286:ASN:HB2	2.14	0.47
1:B:178:ARG:HH11	1:B:206:ASN:ND2	2.10	0.47
1:B:226:ILE:HA	1:B:281:VAL:O	2.15	0.46
1:A:127:PRO:HB3	1:A:181:TRP:CG	2.51	0.46
1:B:45:TYR:O	1:B:48:LYS:HG3	2.16	0.46
1:A:102:PHE:CD2	1:A:102:PHE:C	2.94	0.46
1:B:134:THR:HG21	3:B:894:HOH:O	2.15	0.45
1:B:130:LEU:O	1:B:161:ARG:HD3	2.15	0.45
1:B:94:ALA:HB3	1:B:102:PHE:HB3	1.98	0.45
1:A:69:ASP:N	1:A:96:GLN:HE22	2.00	0.45
1:B:80:THR:HA	1:B:90:ARG:HD3	1.98	0.45
1:B:256:SER:O	1:B:257:ALA:HB3	2.16	0.44
1:A:11:LEU:HD12	1:A:25:GLN:HB2	1.99	0.44
1:A:15:GLU:OE1	1:A:23:ARG:HD2	2.17	0.44
1:B:148:LEU:O	1:B:149:LYS:C	2.61	0.44
1:A:115:PHE:CZ	1:B:284:ASN:HB2	2.53	0.44
1:A:200:GLY:HA2	1:A:233:MET:HE1	2.00	0.44
1:B:74:ILE:C	1:B:75:ILE:HD12	2.42	0.44
1:B:237:ARG:HB3	1:B:238:PRO:HD2	1.99	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:75:ILE:N	1:B:75:ILE:CD1	2.81	0.43
1:B:32:ARG:O	1:B:70:SER:OG	2.35	0.43
1:A:192:LEU:O	1:A:196:GLN:HG3	2.17	0.43
1:B:189:PRO:O	1:B:195:HIS:HE1	2.01	0.43
2:B:801:LDA:HM13	3:B:825:HOH:O	2.19	0.42
1:A:117:HIS:ND1	1:B:215:HIS:HE1	2.17	0.42
1:A:32:ARG:O	1:A:32:ARG:HG2	2.10	0.42
1:A:112:GLU:OE1	1:B:283:ARG:NH2	2.48	0.42
1:A:283:ARG:HH22	1:B:112:GLU:CD	2.27	0.42
1:B:177:HIS:HD2	3:B:994:HOH:O	2.03	0.42
1:B:60:PHE:HZ	1:B:233:MET:HE3	1.85	0.42
1:B:60:PHE:CD1	1:B:60:PHE:C	2.98	0.41
1:B:69:ASP:H	1:B:96:GLN:NE2	1.95	0.41
1:B:123:SER:HA	3:B:1031:HOH:O	2.19	0.41
1:B:220:LEU:HD23	1:B:220:LEU:HA	1.85	0.41
1:A:115:PHE:HZ	1:B:284:ASN:HB2	1.85	0.41
1:A:240:ASN:OD1	1:A:242:ASN:HB2	2.19	0.41
1:B:156:ARG:HD2	3:B:849:HOH:O	2.19	0.41
1:B:220:LEU:HD11	2:B:801:LDA:H61	2.02	0.41
1:B:284:ASN:C	1:B:284:ASN:ND2	2.75	0.41
1:A:96:GLN:O	1:A:97:ASN:HB2	2.20	0.41
1:A:215:HIS:HD2	3:A:930:HOH:O	2.04	0.41
1:A:54:GLU:HG2	1:A:110:ALA:HB1	2.02	0.41
1:A:142:HIS:O	1:A:143:LEU:CG	2.69	0.41
1:B:4:ALA:HB3	3:B:881:HOH:O	2.20	0.41
1:B:117:HIS:CD2	1:B:117:HIS:C	2.98	0.41
1:B:233:MET:HG3	1:B:276:THR:HG22	2.03	0.40
1:A:108:PHE:CD1	1:A:108:PHE:N	2.89	0.40
1:A:130:LEU:O	1:A:161:ARG:HD3	2.20	0.40
1:B:27:GLU:HB3	1:B:28:ASP:HA	2.00	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	283/285 (99%)	271 (96%)	7 (2%)	5 (2%)	6	1
1	B	283/285 (99%)	273 (96%)	5 (2%)	5 (2%)	6	1
All	All	566/570 (99%)	544 (96%)	12 (2%)	10 (2%)	6	1

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	30	GLY
1	B	27	GLU
1	B	153	ILE
1	A	142	HIS
1	A	155	ASP
1	B	151	LYS
1	B	28	ASP
1	B	31	LEU
1	A	31	LEU
1	A	151	LYS

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	242/242 (100%)	235 (97%)	7 (3%)	37	31
1	B	242/242 (100%)	230 (95%)	12 (5%)	22	14
All	All	484/484 (100%)	465 (96%)	19 (4%)	28	21

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	13	ASN
1	A	18	GLU
1	A	102	PHE

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	152	PHE
1	A	153	ILE
1	A	170	LYS
1	A	286	ASN
1	B	6	LYS
1	B	13	ASN
1	B	18	GLU
1	B	27	GLU
1	B	28	ASP
1	B	31	LEU
1	B	96	GLN
1	B	99	LYS
1	B	147	VAL
1	B	153	ILE
1	B	154	CYS
1	B	284	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (21) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	3	GLN
1	A	7	ASN
1	A	33	GLN
1	A	85	ASN
1	A	96	GLN
1	A	177	HIS
1	A	195	HIS
1	A	206	ASN
1	A	215	HIS
1	A	268	GLN
1	A	284	ASN
1	B	3	GLN
1	B	7	ASN
1	B	33	GLN
1	B	85	ASN
1	B	96	GLN
1	B	195	HIS
1	B	206	ASN
1	B	215	HIS
1	B	268	GLN
1	B	284	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

2 ligands 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
2	LDA	B	801	-	13,15,15	2.32	2 (15%)	14,17,17	1.88	5 (35%)
2	LDA	A	800	-	13,15,15	2.12	1 (7%)	14,17,17	1.82	4 (28%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	LDA	B	801	-	-	8/13/13/13	-
2	LDA	A	800	-	-	8/13/13/13	-

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	801	LDA	O1-N1	-7.86	1.22	1.42

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	800	LDA	O1-N1	-7.15	1.24	1.42
2	B	801	LDA	C1-N1	-2.04	1.49	1.51

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	801	LDA	CM2-N1-C1	3.66	117.92	110.23
2	A	800	LDA	CM2-N1-C1	3.43	117.44	110.23
2	A	800	LDA	O1-N1-C1	3.19	117.09	109.27
2	B	801	LDA	O1-N1-C1	2.97	116.57	109.27
2	A	800	LDA	CM1-N1-C1	-2.64	104.70	110.23
2	B	801	LDA	C9-C8-C7	-2.59	101.30	114.37
2	B	801	LDA	C6-C5-C4	-2.32	102.65	114.37
2	A	800	LDA	C9-C8-C7	-2.31	102.71	114.37
2	B	801	LDA	CM1-N1-C1	-2.06	105.91	110.23

There are no chirality outliers.

All (16) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	801	LDA	C2-C1-N1-CM1
2	B	801	LDA	C2-C1-N1-CM2
2	B	801	LDA	C4-C5-C6-C7
2	B	801	LDA	C11-C10-C9-C8
2	A	800	LDA	C4-C5-C6-C7
2	A	800	LDA	C6-C7-C8-C9
2	B	801	LDA	C1-C2-C3-C4
2	A	800	LDA	C2-C3-C4-C5
2	B	801	LDA	C2-C3-C4-C5
2	B	801	LDA	C9-C10-C11-C12
2	A	800	LDA	C11-C10-C9-C8
2	A	800	LDA	C1-C2-C3-C4
2	A	800	LDA	C2-C1-N1-CM1
2	A	800	LDA	C2-C1-N1-CM2
2	A	800	LDA	C2-C1-N1-O1
2	B	801	LDA	C2-C1-N1-O1

There are no ring outliers.

2 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	801	LDA	2	0
2	A	800	LDA	6	0

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	273/285 (95%)	0.33	18 (6%) 24 26	16, 25, 40, 59	1 (0%)
1	B	279/285 (97%)	0.43	26 (9%) 14 15	16, 25, 45, 77	1 (0%)
All	All	552/570 (96%)	0.38	44 (7%) 18 19	16, 25, 42, 77	2 (0%)

All (44) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	29	LEU	10.5
1	A	29	LEU	6.3
1	B	170	LYS	5.4
1	B	32	ARG	5.3
1	A	143	LEU	5.2
1	A	31	LEU	4.9
1	B	2	SER	4.8
1	A	155	ASP	4.7
1	A	170	LYS	4.6
1	A	2	SER	4.4
1	B	28	ASP	4.3
1	A	286	ASN	3.9
1	B	31	LEU	3.7
1	A	30	GLY	3.6
1	B	147	VAL	3.5
1	A	142	HIS	3.5
1	A	193	ARG	3.4
1	B	27	GLU	3.3
1	B	286	ASN	3.2
1	B	223	GLY	3.1
1	B	190	ASP	3.1
1	B	26	SER	3.1
1	A	32	ARG	3.0
1	B	175	GLU	2.9

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	B	30	GLY	2.8
1	A	54	GLU	2.8
1	B	171	GLY	2.7
1	A	68	GLY	2.6
1	B	54	GLU	2.5
1	B	112	GLU	2.5
1	B	110	ALA	2.4
1	B	269	ASP	2.4
1	A	110	ALA	2.4
1	B	217	ILE	2.4
1	B	193	ARG	2.3
1	B	134	THR	2.3
1	A	53	GLU	2.3
1	A	112	GLU	2.3
1	A	28	ASP	2.2
1	B	33	GLN	2.2
1	B	3	GLN	2.1
1	A	171	GLY	2.1
1	B	53	GLU	2.1
1	B	187	SER	2.1

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	LDA	A	800	16/16	0.60	0.22	45,49,54,55	0
2	LDA	B	801	16/16	0.67	0.33	72,75,80,81	0

6.5 Other polymers ⓘ

There are no such residues in this entry.