



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 11:04 PM UTC

PDB ID : 1SKU / pdb_00001sku
Title : E. coli Aspartate Transcarbamylase 240's Loop Mutant (K244N)
Authors : Alam, N.; Stieglitz, K.A.; Caban, M.D.; Gourinath, S.; Tsuruta, H.;
Kantrowitz, E.R.
Deposited on : 2004-03-05
Resolution : 2.60 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 : 4-5-2 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

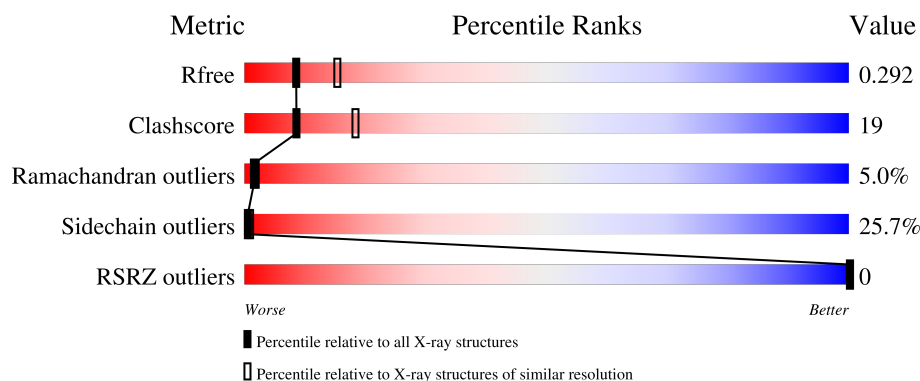
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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}	180053	4008 (2.60-2.60)
Clashscore	190562	4347 (2.60-2.60)
Ramachandran outliers	187476	4277 (2.60-2.60)
Sidechain outliers	187428	4277 (2.60-2.60)
RSRZ outliers	180081	4008 (2.60-2.60)

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	310	
1	C	310	
2	B	153	
2	D	153	

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 7229 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 Aspartate carbamoyltransferase catalytic chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	310	Total	C	N	O	S	0	0	0
			2414	1525	423	457	9			
1	C	310	Total	C	N	O	S	0	0	0
			2414	1525	423	457	9			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	244	ASN	LYS	engineered mutation	UNP P0A786
C	244	ASN	LYS	engineered mutation	UNP P0A786

- Molecule 2 is a protein called Aspartate carbamoyltransferase regulatory chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	148	Total	C	N	O	S	0	0	0
			1160	729	205	221	5			
2	D	148	Total	C	N	O	S	0	0	0
			1159	729	205	220	5			

- Molecule 3 is MALONATE ION (CCD ID: MLI) (formula: C₃H₂O₄).



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

- Molecule 4 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	1	Total	Zn	0	0
			1	1		
4	D	1	Total	Zn	0	0
			1	1		

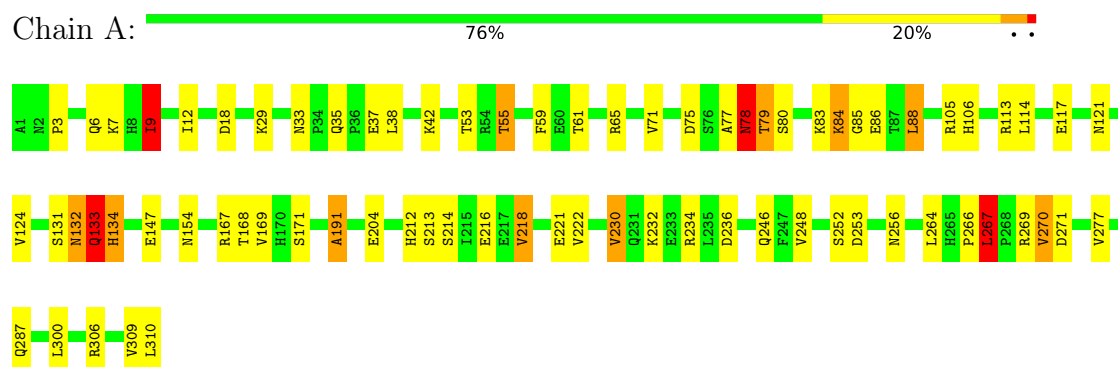
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	22	Total	O	0	0
			22	22		
5	B	10	Total	O	0	0
			10	10		
5	C	27	Total	O	0	0
			27	27		
5	D	7	Total	O	0	0
			7	7		

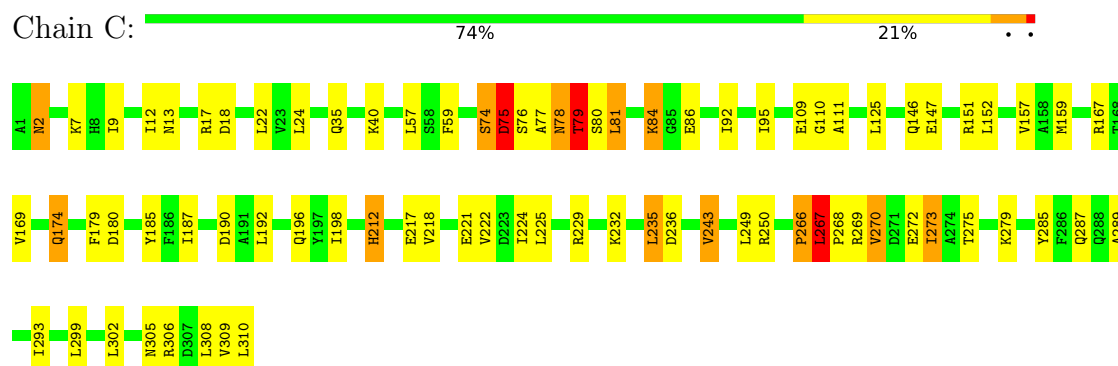
3 Residue-property plots

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.

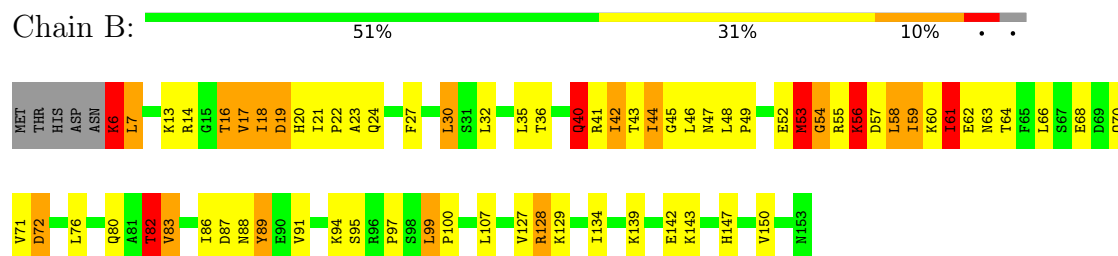
- Molecule 1: Aspartate carbamoyltransferase catalytic chain



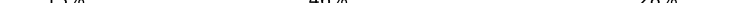
- Molecule 1: Aspartate carbamoyltransferase catalytic chain

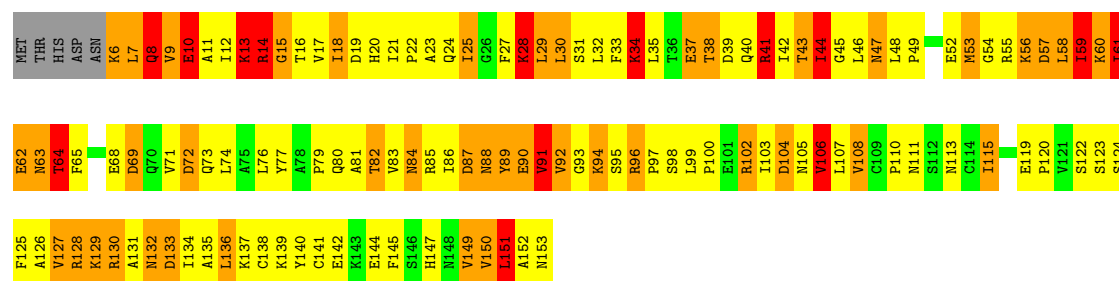


- Molecule 2: Aspartate carbamoyltransferase regulatory chain



- Molecule 2: Aspartate carbamoyltransferase regulatory chain

Chain D:  13% 46% 28% 9% .



4 Data and refinement statistics

Property	Value	Source
Space group	H 3	Depositor
Cell constants a, b, c, α , β , γ	125.67Å 125.67Å 198.20Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	29.55 – 2.60 29.55 – 2.60	Depositor EDS
% Data completeness (in resolution range)	89.4 (29.55-2.60) 89.5 (29.55-2.60)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.80 (at 2.51Å)	Xtriage
Refinement program	REFMAC 5.1.24	Depositor
R, R_{free}	0.201 , 0.231 0.303 , 0.292	Depositor DCC
R_{free} test set	1720 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	46.1	Xtriage
Anisotropy	0.174	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 39.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.480 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	7229	wwPDB-VP
Average B, all atoms (Å ²)	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.80% 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: MLI, ZN

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	0.85	9/2460 (0.4%)	0.91	12/3339 (0.4%)
1	C	0.57	3/2460 (0.1%)	0.88	13/3339 (0.4%)
2	B	0.82	4/1177 (0.3%)	1.22	12/1590 (0.8%)
2	D	0.80	9/1176 (0.8%)	1.19	9/1590 (0.6%)
All	All	0.75	25/7273 (0.3%)	1.00	46/9858 (0.5%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2
1	C	0	1
2	B	0	2
2	D	0	2
All	All	0	7

All (25) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	134	HIS	C-N	23.08	1.62	1.34
1	A	191	ALA	C-N	11.96	1.49	1.33
2	B	83	VAL	C-N	11.81	1.49	1.33
1	C	75	ASP	C-N	-10.97	1.18	1.33
1	A	78	ASN	C-N	-9.88	1.19	1.33
2	D	14	ARG	C-N	-9.49	1.19	1.33
1	A	83	LYS	C-N	-9.46	1.19	1.33
2	D	28	LYS	C-N	-9.35	1.19	1.33
2	D	13	LYS	C-N	9.18	1.45	1.33
1	A	86	GLU	C-N	-9.17	1.20	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	18	ASP	C-N	8.35	1.45	1.33
2	D	61	ILE	C-N	-8.03	1.22	1.33
1	A	80	SER	C-N	7.92	1.45	1.33
1	C	80	SER	C-N	-7.81	1.23	1.33
2	D	15	GLY	C-N	-7.11	1.23	1.33
2	B	6	LYS	C-N	-7.04	1.23	1.33
2	D	62	GLU	C-N	-6.97	1.24	1.33
2	D	44	ILE	C-N	-6.93	1.23	1.33
1	A	9	ILE	C-N	-6.65	1.24	1.33
2	B	89	TYR	C-N	6.44	1.42	1.33
1	C	74	SER	C-N	6.17	1.42	1.33
2	D	59	ILE	CG1-CD1	6.10	1.75	1.51
1	A	131	SER	C-N	5.50	1.40	1.33
2	B	19	ASP	C-N	-5.40	1.25	1.33
2	D	87	ASP	CG-OD1	5.11	1.35	1.25

All (46) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	89	TYR	CA-C-N	-15.38	101.31	123.00
2	B	89	TYR	C-N-CA	-15.38	101.31	123.00
1	C	75	ASP	O-C-N	-10.96	108.01	122.59
2	D	14	ARG	O-C-N	-10.85	107.82	122.36
1	A	78	ASN	O-C-N	-10.74	108.39	122.14
2	D	28	LYS	O-C-N	-10.28	108.92	122.59
2	B	54	GLY	O-C-N	9.86	135.52	122.70
1	C	80	SER	CA-C-N	9.13	135.77	122.08
1	C	80	SER	C-N-CA	9.13	135.77	122.08
1	C	267	LEU	CA-C-N	-9.04	108.54	119.84
1	C	267	LEU	C-N-CA	-9.04	108.54	119.84
1	C	80	SER	O-C-N	-7.85	111.82	122.33
2	D	6	LYS	CA-C-N	-7.71	111.37	123.24
2	D	6	LYS	C-N-CA	-7.71	111.37	123.24
2	B	89	TYR	CA-C-O	7.64	130.29	120.81
2	B	59	ILE	N-CA-C	7.31	118.67	107.99
1	C	268	PRO	CA-N-CD	-7.28	101.80	112.00
2	B	83	VAL	O-C-N	7.27	131.66	122.57
1	A	80	SER	CA-C-N	6.93	131.96	122.19
1	A	80	SER	C-N-CA	6.93	131.96	122.19
1	A	132	ASN	CA-CB-CG	6.82	119.42	112.60
1	A	84	LYS	CA-C-N	6.72	134.59	121.41
1	A	84	LYS	C-N-CA	6.72	134.59	121.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	9	ILE	CA-C-N	6.48	130.03	123.16
1	A	9	ILE	C-N-CA	6.48	130.03	123.16
2	B	88	ASN	CA-CB-CG	6.44	119.04	112.60
1	A	191	ALA	O-C-N	6.38	131.07	122.59
1	A	134	HIS	O-C-N	-6.30	114.08	121.32
1	C	267	LEU	C-N-CD	5.97	149.47	125.00
2	B	40	GLN	O-C-N	-5.94	114.69	122.59
2	B	88	ASN	O-C-N	-5.86	114.79	122.59
2	B	19	ASP	O-C-N	-5.79	114.73	122.14
1	C	267	LEU	CA-C-O	5.68	127.94	120.16
2	D	6	LYS	O-C-N	5.52	131.84	123.00
1	A	84	LYS	N-CA-C	5.46	117.56	109.69
2	D	13	LYS	O-C-N	5.40	129.78	122.59
2	B	89	TYR	CA-CB-CG	5.34	123.52	113.90
2	D	62	GLU	O-C-N	-5.26	115.60	122.59
1	A	132	ASN	OD1-CG-ND2	-5.25	117.35	122.60
2	B	80	GLN	CA-C-O	5.25	127.66	121.78
1	C	266	PRO	CA-C-O	-5.08	111.35	120.60
1	C	77	ALA	O-C-N	-5.04	115.70	122.00
2	D	28	LYS	CA-C-N	5.01	130.74	121.52
2	D	28	LYS	C-N-CA	5.01	130.74	121.52
1	C	266	PRO	CA-C-N	5.00	134.01	121.80
1	C	266	PRO	C-N-CA	5.00	134.01	121.80

There are no chirality outliers.

All (7) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	133	GLN	Mainchain
1	A	78	ASN	Mainchain
2	B	6	LYS	Mainchain
2	B	87	ASP	Mainchain
1	C	75	ASP	Mainchain
2	D	14	ARG	Mainchain
2	D	28	LYS	Mainchain

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	2414	0	2415	23	0
1	C	2414	0	2415	32	0
2	B	1160	0	1185	44	0
2	D	1159	0	1183	189	0
3	A	7	0	2	0	0
3	C	7	0	2	0	0
4	B	1	0	0	0	0
4	D	1	0	0	0	0
5	A	22	0	0	1	0
5	B	10	0	0	3	0
5	C	27	0	0	1	0
5	D	7	0	0	0	0
All	All	7229	0	7202	272	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 19.

All (272) 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)
2:D:59:ILE:CD1	2:D:59:ILE:CG1	1.75	1.61
1:C:267:LEU:HD11	1:C:289:ALA:CB	1.51	1.37
1:A:75:ASP:HB3	1:A:78:ASN:ND2	1.45	1.28
1:C:267:LEU:CD1	1:C:289:ALA:HB2	1.73	1.17
2:D:21:ILE:HB	2:D:57:ASP:O	1.47	1.14
2:D:85:ARG:HB2	2:D:92:VAL:HG23	1.29	1.13
2:B:30:LEU:HD22	2:D:27:PHE:CE2	1.84	1.12
1:C:75:ASP:CG	1:C:79:THR:HB	1.79	1.08
2:B:35:LEU:HB2	2:B:60:LYS:HE3	1.17	1.07
2:D:19:ASP:HA	2:D:58:LEU:HD11	1.31	1.07
2:D:30:LEU:CD1	2:D:59:ILE:HD12	1.88	1.04
2:B:6:LYS:N	2:D:89:TYR:HH	1.54	1.04
2:B:35:LEU:CB	2:B:60:LYS:HE3	1.88	1.03
2:D:30:LEU:HD13	2:D:59:ILE:HD12	1.40	1.03
2:D:20:HIS:HA	2:D:56:LYS:HD3	1.41	1.00
2:D:46:LEU:HA	2:D:57:ASP:HB3	1.43	0.98
1:A:75:ASP:CB	1:A:78:ASN:ND2	2.27	0.98
1:A:75:ASP:HB3	1:A:78:ASN:HD21	0.97	0.97
1:A:75:ASP:CB	1:A:78:ASN:HD21	1.76	0.97
1:C:267:LEU:CD1	1:C:289:ALA:CB	2.40	0.92

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:13:LYS:HD2	2:D:14:ARG:H	1.32	0.92
2:D:44:ILE:HG23	2:D:59:ILE:HB	1.50	0.92
2:B:30:LEU:HD22	2:D:27:PHE:HE2	1.28	0.91
1:C:75:ASP:OD2	1:C:79:THR:HB	1.69	0.90
2:D:20:HIS:CA	2:D:56:LYS:HE2	2.02	0.90
2:D:20:HIS:HA	2:D:56:LYS:CD	2.01	0.90
2:D:13:LYS:HG3	2:D:62:GLU:HB2	1.53	0.89
2:D:20:HIS:HA	2:D:56:LYS:HE2	1.53	0.89
2:D:82:THR:HA	2:D:96:ARG:HA	1.56	0.88
2:D:7:LEU:O	2:D:8:GLN:HG2	1.74	0.88
2:D:20:HIS:CB	2:D:56:LYS:HE2	2.04	0.87
1:C:267:LEU:HD11	1:C:289:ALA:HB2	0.88	0.85
1:C:78:ASN:O	1:C:79:THR:O	1.96	0.84
2:D:20:HIS:HA	2:D:56:LYS:CE	2.08	0.83
2:D:13:LYS:HE2	2:D:63:ASN:OD1	1.80	0.82
2:D:72:ASP:O	2:D:100:PRO:HD3	1.77	0.82
2:D:19:ASP:CA	2:D:58:LEU:HD11	2.09	0.82
2:D:30:LEU:CD1	2:D:59:ILE:CD1	2.57	0.81
2:D:82:THR:HG22	2:D:96:ARG:HG2	1.60	0.81
1:A:133:GLN:NE2	1:A:168:THR:HA	1.95	0.80
2:D:13:LYS:HD2	2:D:14:ARG:N	1.96	0.80
2:B:36:THR:HG21	2:D:27:PHE:CD2	2.17	0.79
1:C:75:ASP:OD2	1:C:79:THR:CB	2.30	0.79
2:D:152:ALA:O	2:D:153:ASN:CG	2.25	0.79
2:D:38:THR:OG1	2:D:42:ILE:HD11	1.84	0.77
2:D:20:HIS:HB2	2:D:81:ALA:HA	1.67	0.77
2:D:21:ILE:CB	2:D:57:ASP:O	2.32	0.76
2:D:21:ILE:O	2:D:56:LYS:HG2	1.85	0.75
2:D:23:ALA:HA	2:D:57:ASP:OD1	1.87	0.75
2:D:59:ILE:CD1	2:D:59:ILE:CB	2.66	0.72
2:D:65:PHE:HB2	2:D:85:ARG:HH12	1.54	0.72
2:D:34:LYS:O	2:D:35:LEU:HD23	1.89	0.72
2:B:36:THR:HG21	2:D:27:PHE:CG	2.25	0.71
2:B:71:VAL:HG21	2:B:83:VAL:HG21	1.73	0.71
1:A:133:GLN:HE21	1:A:168:THR:HA	1.55	0.70
2:D:87:ASP:C	2:D:87:ASP:OD2	2.36	0.69
2:B:53:MET:HE2	2:B:53:MET:HA	1.73	0.69
2:D:41:ARG:NH1	2:D:43:THR:HG22	2.08	0.68
2:D:18:ILE:HB	2:D:82:THR:O	1.93	0.68
2:D:44:ILE:HG22	2:D:58:LEU:O	1.92	0.68
2:D:110:PRO:HD3	2:D:150:VAL:HG13	1.74	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:10:GLU:C	2:D:12:ILE:HD12	2.19	0.67
2:D:23:ALA:HB2	2:D:55:ARG:HB2	1.75	0.67
2:D:13:LYS:NZ	2:D:63:ASN:HD21	1.93	0.67
2:D:17:VAL:HG13	2:D:60:LYS:HA	1.77	0.66
2:D:9:VAL:O	2:D:10:GLU:HB2	1.96	0.65
2:D:83:VAL:HB	2:D:95:SER:O	1.97	0.65
2:D:49:PRO:HB3	2:D:54:GLY:O	1.98	0.64
2:D:128:ARG:HG3	2:D:128:ARG:O	1.97	0.64
2:D:45:GLY:N	2:D:58:LEU:O	2.31	0.63
2:B:27:PHE:HZ	2:D:31:SER:HB3	1.63	0.63
1:C:267:LEU:HD11	1:C:289:ALA:HB1	1.72	0.63
1:C:109:GLU:OE1	2:D:111:ASN:ND2	2.28	0.63
1:C:192:LEU:HD21	1:C:235:LEU:HD21	1.80	0.62
2:B:30:LEU:CD2	2:D:27:PHE:CE2	2.75	0.62
2:D:19:ASP:HA	2:D:58:LEU:CD1	2.21	0.62
1:A:133:GLN:CG	1:A:167:ARG:O	2.48	0.62
2:D:89:TYR:O	2:D:90:GLU:HB2	2.00	0.62
2:D:15:GLY:HA2	2:D:64:THR:H	1.65	0.61
2:D:84:ASN:HD22	2:D:94:LYS:HB3	1.66	0.61
2:D:10:GLU:OE2	2:D:10:GLU:HA	2.00	0.61
2:D:14:ARG:O	2:D:62:GLU:HA	2.01	0.60
2:B:6:LYS:N	2:D:89:TYR:OH	2.30	0.60
2:D:102:ARG:HG3	2:D:104:ASP:OD1	2.01	0.60
2:D:13:LYS:CG	2:D:62:GLU:HB2	2.29	0.60
2:D:71:VAL:O	2:D:74:LEU:HD12	2.01	0.60
2:D:135:ALA:HA	2:D:145:PHE:O	2.01	0.60
2:D:18:ILE:HD11	2:D:21:ILE:CG1	2.32	0.60
2:D:110:PRO:HG2	2:D:145:PHE:CG	2.37	0.59
2:D:125:PHE:HD2	2:D:136:LEU:HB2	1.64	0.59
1:A:133:GLN:OE1	1:A:171:SER:HB2	2.02	0.59
1:A:61:THR:HG23	5:A:5216:HOH:O	2.03	0.59
2:D:126:ALA:O	2:D:136:LEU:HA	2.02	0.59
2:D:20:HIS:HB3	2:D:56:LYS:HE2	1.85	0.59
2:D:107:LEU:HD13	2:D:136:LEU:HD13	1.83	0.59
2:B:35:LEU:HD13	2:B:60:LYS:HG3	1.84	0.59
2:D:84:ASN:HB3	2:D:94:LYS:HB3	1.83	0.59
2:D:17:VAL:HG13	2:D:59:ILE:O	2.03	0.59
2:D:73:GLN:HE22	2:D:103:ILE:HG12	1.68	0.59
2:B:35:LEU:CB	2:B:60:LYS:CE	2.76	0.58
2:D:22:PRO:HB2	2:D:25:ILE:HG13	1.84	0.58
2:B:71:VAL:HG21	2:B:83:VAL:CG2	2.32	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:21:ILE:HG22	2:D:57:ASP:HB2	1.85	0.58
2:D:125:PHE:CD2	2:D:136:LEU:HB2	2.38	0.58
2:D:35:LEU:O	2:D:38:THR:HG23	2.03	0.58
2:D:62:GLU:O	2:D:63:ASN:C	2.44	0.57
2:D:20:HIS:CG	2:D:56:LYS:HE2	2.39	0.57
2:D:72:ASP:HA	2:D:98:SER:H	1.70	0.57
1:C:75:ASP:OD2	1:C:79:THR:CG2	2.53	0.57
1:A:78:ASN:O	1:A:79:THR:CB	2.51	0.57
2:D:20:HIS:CA	2:D:56:LYS:HD3	2.26	0.56
2:D:15:GLY:HA3	2:D:62:GLU:O	2.05	0.56
2:D:47:ASN:H	2:D:57:ASP:CG	2.13	0.56
2:D:18:ILE:HD11	2:D:21:ILE:HG12	1.88	0.56
1:A:212:HIS:CD2	1:A:218:VAL:HG12	2.40	0.56
2:D:43:THR:O	2:D:60:LYS:HG3	2.05	0.56
2:D:21:ILE:CG2	2:D:57:ASP:HB2	2.36	0.56
2:D:46:LEU:O	2:D:48:LEU:HD12	2.05	0.56
2:D:44:ILE:HA	2:D:59:ILE:HA	1.87	0.55
2:B:128:ARG:HG3	5:B:5194:HOH:O	2.06	0.55
2:B:55:ARG:O	2:B:56:LYS:HB2	2.07	0.55
2:D:83:VAL:O	2:D:94:LYS:HA	2.05	0.55
2:D:19:ASP:OD1	2:D:58:LEU:HD21	2.06	0.55
1:C:2:ASN:HD21	1:C:302:LEU:HD12	1.72	0.54
2:B:16:THR:O	2:B:17:VAL:HG12	2.08	0.54
2:D:77:TYR:O	2:D:79:PRO:HD3	2.07	0.54
2:D:85:ARG:CB	2:D:92:VAL:HG23	2.19	0.54
2:D:10:GLU:O	2:D:12:ILE:HD12	2.08	0.53
2:D:13:LYS:HZ1	2:D:63:ASN:HD21	1.55	0.53
2:D:41:ARG:HB2	2:D:62:GLU:OE2	2.09	0.53
2:B:47:ASN:HA	2:B:56:LYS:HG2	1.91	0.53
2:D:43:THR:O	2:D:43:THR:OG1	2.24	0.53
2:D:62:GLU:O	2:D:64:THR:N	2.42	0.53
2:D:104:ASP:O	2:D:105:ASN:HB2	2.09	0.53
2:D:61:ILE:HG23	2:D:64:THR:HB	1.90	0.53
2:D:59:ILE:HG21	2:D:59:ILE:HD13	1.92	0.52
2:D:18:ILE:HD13	2:D:59:ILE:HG23	1.92	0.52
2:D:90:GLU:O	2:D:91:VAL:HG23	2.09	0.52
2:D:84:ASN:HB3	2:D:94:LYS:CB	2.40	0.52
2:D:135:ALA:HB1	2:D:144:GLU:CG	2.40	0.52
2:D:79:PRO:HB2	2:D:80:GLN:HE22	1.74	0.51
2:D:83:VAL:O	2:D:83:VAL:HG12	2.10	0.51
2:D:85:ARG:HB2	2:D:92:VAL:CG2	2.20	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:104:ASP:HB3	2:D:123:SER:O	2.11	0.51
2:D:141:CYS:O	2:D:142:GLU:HB2	2.08	0.51
2:D:130:ARG:HG2	2:D:133:ASP:O	2.09	0.51
2:D:129:LYS:HG3	2:D:134:ILE:HD13	1.93	0.51
2:D:9:VAL:O	2:D:10:GLU:CB	2.57	0.50
1:A:133:GLN:HG3	1:A:167:ARG:O	2.10	0.50
2:D:15:GLY:O	2:D:16:THR:HB	2.11	0.50
2:B:60:LYS:O	2:B:61:ILE:HB	2.10	0.50
1:C:75:ASP:O	1:C:76:SER:C	2.52	0.50
1:A:132:ASN:HD21	2:B:142:GLU:CD	2.19	0.50
2:D:152:ALA:O	2:D:153:ASN:OD1	2.29	0.50
2:B:6:LYS:HD2	2:B:6:LYS:C	2.36	0.50
2:B:35:LEU:HB3	2:B:60:LYS:HD2	1.95	0.49
2:D:7:LEU:O	2:D:8:GLN:CG	2.53	0.49
2:D:136:LEU:HD11	2:D:150:VAL:HB	1.95	0.49
2:D:52:GLU:OE1	2:D:56:LYS:NZ	2.45	0.49
2:D:64:THR:O	2:D:64:THR:HG22	2.12	0.49
1:C:157:VAL:HG12	1:C:224:ILE:HD13	1.93	0.49
2:D:20:HIS:HB3	2:D:80:GLN:O	2.12	0.49
2:D:119:GLU:OE1	2:D:120:PRO:HD2	2.13	0.49
2:B:18:ILE:HG21	2:B:82:THR:H	1.77	0.49
1:C:110:GLY:HA3	2:D:140:TYR:HB3	1.94	0.49
1:C:266:PRO:O	5:C:5170:HOH:O	2.20	0.49
2:D:19:ASP:CG	2:D:58:LEU:HD21	2.37	0.49
2:D:28:LYS:HA	2:D:31:SER:OG	2.13	0.48
2:D:61:ILE:CG2	2:D:64:THR:HB	2.42	0.48
1:A:75:ASP:CG	1:A:78:ASN:HD21	2.20	0.48
1:C:267:LEU:CD1	1:C:289:ALA:HB1	2.35	0.48
2:B:35:LEU:HB3	2:B:60:LYS:CD	2.43	0.48
2:B:59:ILE:HG12	2:B:60:LYS:HG2	1.96	0.48
2:D:17:VAL:CG2	2:D:60:LYS:HB3	2.43	0.48
2:D:47:ASN:O	2:D:48:LEU:HG	2.14	0.48
2:D:108:VAL:O	2:D:150:VAL:HG12	2.14	0.48
2:D:73:GLN:NE2	2:D:103:ILE:HG12	2.29	0.48
2:D:41:ARG:NH1	2:D:42:ILE:N	2.62	0.48
2:D:19:ASP:O	2:D:20:HIS:HB2	2.14	0.47
2:D:29:LEU:CD2	2:D:33:PHE:CD1	2.98	0.47
1:C:185:TYR:CG	1:C:218:VAL:HG21	2.50	0.47
2:B:30:LEU:HD23	2:B:36:THR:HG23	1.96	0.47
2:D:30:LEU:HD22	2:D:44:ILE:CD1	2.44	0.47
2:B:40:GLN:OE1	2:B:63:ASN:HB3	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:23:ALA:O	2:D:24:GLN:HB2	2.13	0.47
2:B:107:LEU:HD22	2:B:150:VAL:HG11	1.97	0.47
2:D:59:ILE:CD1	2:D:59:ILE:HG21	2.44	0.46
2:D:79:PRO:HG2	2:D:80:GLN:NE2	2.30	0.46
2:D:81:ALA:O	2:D:82:THR:HG23	2.14	0.46
1:A:266:PRO:O	1:A:267:LEU:HB2	2.15	0.46
1:C:78:ASN:C	1:C:79:THR:O	2.58	0.46
2:D:20:HIS:CA	2:D:56:LYS:CE	2.78	0.46
2:D:125:PHE:CD2	2:D:136:LEU:HD12	2.51	0.46
2:D:18:ILE:HD11	2:D:21:ILE:HG13	1.96	0.46
2:D:37:GLU:H	2:D:37:GLU:HG2	1.43	0.46
2:D:69:ASP:O	2:D:73:GLN:HG2	2.16	0.46
1:A:75:ASP:CG	1:A:78:ASN:ND2	2.74	0.45
2:B:35:LEU:HB3	2:B:60:LYS:HE3	1.90	0.45
2:B:48:LEU:HD23	2:B:49:PRO:HD2	1.97	0.45
2:D:147:HIS:O	2:D:151:LEU:HB2	2.16	0.45
1:C:2:ASN:HD21	1:C:302:LEU:CD1	2.30	0.45
2:D:52:GLU:HG2	2:D:53:MET:N	2.32	0.45
1:C:75:ASP:OD2	1:C:79:THR:HG21	2.16	0.45
2:D:130:ARG:NH1	2:D:133:ASP:OD1	2.49	0.45
2:B:44:ILE:HG23	2:B:45:GLY:N	2.31	0.45
2:B:59:ILE:CG1	2:B:60:LYS:HG2	2.47	0.45
1:C:9:ILE:HG21	1:C:299:LEU:HD21	1.98	0.45
1:C:269:ARG:HD3	1:C:273:ILE:HB	1.98	0.45
2:D:73:GLN:OE1	2:D:102:ARG:O	2.34	0.45
2:D:100:PRO:O	2:D:127:VAL:HG11	2.16	0.45
2:B:17:VAL:HG21	2:B:59:ILE:O	2.17	0.45
2:D:82:THR:CG2	2:D:96:ARG:HG2	2.38	0.45
1:C:110:GLY:O	2:D:115:ILE:HG21	2.17	0.45
2:D:83:VAL:O	2:D:95:SER:N	2.50	0.45
2:D:19:ASP:OD2	2:D:20:HIS:ND1	2.50	0.45
2:D:57:ASP:OD1	2:D:57:ASP:N	2.50	0.45
2:D:59:ILE:CD1	2:D:59:ILE:CG2	2.94	0.45
1:A:84:LYS:HD3	1:A:84:LYS:HA	1.86	0.45
2:D:41:ARG:HH11	2:D:42:ILE:N	2.15	0.45
1:C:152:LEU:HD13	1:C:179:PHE:CZ	2.53	0.44
2:D:41:ARG:HH11	2:D:41:ARG:C	2.24	0.44
2:B:139:LYS:NZ	5:B:5185:HOH:O	2.50	0.44
2:B:72:ASP:O	2:B:100:PRO:HD3	2.18	0.44
2:D:40:GLN:O	2:D:42:ILE:HD12	2.18	0.44
2:B:23:ALA:HA	2:B:56:LYS:HD3	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:111:ALA:HA	2:D:115:ILE:HG12	2.00	0.44
1:A:133:GLN:HG2	1:A:167:ARG:C	2.42	0.44
1:C:13:ASN:HD21	1:C:174:GLN:NE2	2.16	0.44
2:D:22:PRO:O	2:D:57:ASP:OD1	2.36	0.44
2:D:105:ASN:O	2:D:106:VAL:HG13	2.18	0.43
2:B:19:ASP:HB3	2:B:58:LEU:HG	2.01	0.43
2:D:17:VAL:HG13	2:D:60:LYS:CA	2.45	0.43
2:D:74:LEU:HB2	2:D:97:PRO:HB3	2.00	0.43
2:D:41:ARG:CZ	2:D:43:THR:HG22	2.48	0.43
2:D:138:CYS:HB3	2:D:141:CYS:SG	2.58	0.43
2:D:13:LYS:NZ	2:D:63:ASN:ND2	2.65	0.43
1:A:133:GLN:HG2	1:A:167:ARG:HB2	1.99	0.43
2:B:30:LEU:HD22	2:D:27:PHE:CD2	2.45	0.43
2:D:27:PHE:H	2:D:46:LEU:HD13	1.83	0.43
2:D:61:ILE:HG21	2:D:64:THR:CG2	2.48	0.43
2:D:18:ILE:CD1	2:D:59:ILE:HG23	2.49	0.43
2:D:19:ASP:O	2:D:81:ALA:HA	2.19	0.43
2:D:84:ASN:HA	2:D:94:LYS:HA	2.00	0.43
1:A:113:ARG:HB2	5:B:5213:HOH:O	2.18	0.42
2:B:20:HIS:O	2:B:20:HIS:ND1	2.49	0.42
1:C:212:HIS:ND1	1:C:212:HIS:N	2.68	0.42
2:D:18:ILE:O	2:D:58:LEU:CD1	2.68	0.42
2:D:17:VAL:HG22	2:D:60:LYS:HB3	2.01	0.42
2:D:40:GLN:OE1	2:D:62:GLU:OE1	2.37	0.42
2:D:103:ILE:CG2	2:D:106:VAL:HG23	2.50	0.42
2:B:55:ARG:O	2:B:56:LYS:CB	2.67	0.42
1:C:81:LEU:HB3	1:C:86:GLU:HG2	2.02	0.42
1:C:125:LEU:HD23	1:C:299:LEU:HD23	2.02	0.42
2:D:102:ARG:NE	2:D:124:SER:OG	2.50	0.42
1:A:88:LEU:CD2	1:A:106:HIS:HE2	2.33	0.41
1:A:133:GLN:HG2	1:A:167:ARG:O	2.20	0.41
2:D:149:VAL:HG12	2:D:150:VAL:N	2.35	0.41
1:C:109:GLU:CD	2:D:113:ASN:HD22	2.28	0.41
2:D:87:ASP:O	2:D:88:ASN:HB2	2.19	0.41
2:D:10:GLU:O	2:D:12:ILE:CD1	2.69	0.41
2:D:72:ASP:CG	2:D:98:SER:O	2.64	0.41
2:D:35:LEU:O	2:D:38:THR:CG2	2.67	0.41
2:B:30:LEU:CD2	2:B:36:THR:HG23	2.51	0.41
2:D:73:GLN:HE22	2:D:103:ILE:CG1	2.32	0.41
2:D:129:LYS:HB2	2:D:129:LYS:HE3	1.81	0.41
1:A:55:THR:HG21	1:A:134:HIS:CE1	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:30:LEU:CD1	2:D:59:ILE:HD11	2.48	0.41
2:D:11:ALA:C	2:D:12:ILE:HD12	2.46	0.40
2:D:132:ASN:ND2	2:D:132:ASN:N	2.69	0.40
2:B:30:LEU:HB3	2:D:27:PHE:CE2	2.57	0.40
2:B:42:ILE:HG23	2:B:43:THR:N	2.36	0.40
2:D:25:ILE:HD12	2:D:77:TYR:O	2.21	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	308/310 (99%)	276 (90%)	22 (7%)	10 (3%)	3	5
1	C	308/310 (99%)	283 (92%)	18 (6%)	7 (2%)	5	9
2	B	146/153 (95%)	104 (71%)	30 (20%)	12 (8%)	0	0
2	D	146/153 (95%)	102 (70%)	28 (19%)	16 (11%)	0	0
All	All	908/926 (98%)	765 (84%)	98 (11%)	45 (5%)	1	2

All (45) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	85	GLY
1	A	133	GLN
2	B	17	VAL
2	B	56	LYS
1	C	79	THR
1	C	243	VAL
1	C	267	LEU
2	D	9	VAL
2	D	10	GLU

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Mol	Chain	Res	Type
2	D	41	ARG
2	D	63	ASN
2	D	88	ASN
2	D	90	GLU
2	D	131	ALA
1	A	191	ALA
2	B	53	MET
2	B	61	ILE
2	B	62	GLU
1	C	84	LYS
1	C	270	VAL
2	D	8	GLN
2	D	13	LYS
2	D	34	LYS
2	D	91	VAL
1	A	79	THR
1	A	270	VAL
1	C	249	LEU
1	A	77	ALA
2	B	82	THR
2	B	99	LEU
1	C	2	ASN
2	D	64	THR
2	D	89	TYR
2	D	151	LEU
1	A	3	PRO
2	B	54	GLY
2	B	7	LEU
2	B	57	ASP
2	B	97	PRO
2	D	106	VAL
1	A	230	VAL
2	B	22	PRO
1	A	267	LEU
1	A	9	ILE
2	D	93	GLY

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	261/261 (100%)	209 (80%)	52 (20%)	1	2
1	C	261/261 (100%)	208 (80%)	53 (20%)	1	2
2	B	132/137 (96%)	93 (70%)	39 (30%)	0	0
2	D	132/137 (96%)	74 (56%)	58 (44%)	0	0
All	All	786/796 (99%)	584 (74%)	202 (26%)	0	1

All (202) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	6	GLN
1	A	7	LYS
1	A	9	ILE
1	A	12	ILE
1	A	29	LYS
1	A	33	ASN
1	A	35	GLN
1	A	37	GLU
1	A	38	LEU
1	A	42	LYS
1	A	53	THR
1	A	55	THR
1	A	59	PHE
1	A	65	ARG
1	A	71	VAL
1	A	88	LEU
1	A	105	ARG
1	A	114	LEU
1	A	117	GLU
1	A	121	ASN
1	A	124	VAL
1	A	133	GLN
1	A	147	GLU
1	A	154	ASN
1	A	169	VAL
1	A	204	GLU
1	A	213	SER
1	A	214	SER
1	A	216	GLU
1	A	218	VAL

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Mol	Chain	Res	Type
1	A	221	GLU
1	A	222	VAL
1	A	230	VAL
1	A	232	LYS
1	A	234	ARG
1	A	236	ASP
1	A	246	GLN
1	A	248	VAL
1	A	252	SER
1	A	253	ASP
1	A	256	ASN
1	A	264	LEU
1	A	267	LEU
1	A	269	ARG
1	A	270	VAL
1	A	271	ASP
1	A	277	VAL
1	A	287	GLN
1	A	300	LEU
1	A	306	ARG
1	A	309	VAL
1	A	310	LEU
2	B	6	LYS
2	B	7	LEU
2	B	13	LYS
2	B	14	ARG
2	B	16	THR
2	B	18	ILE
2	B	21	ILE
2	B	24	GLN
2	B	30	LEU
2	B	32	LEU
2	B	40	GLN
2	B	41	ARG
2	B	42	ILE
2	B	44	ILE
2	B	46	LEU
2	B	52	GLU
2	B	53	MET
2	B	56	LYS
2	B	58	LEU
2	B	61	ILE

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Mol	Chain	Res	Type
2	B	64	THR
2	B	66	LEU
2	B	68	GLU
2	B	70	GLN
2	B	72	ASP
2	B	76	LEU
2	B	82	THR
2	B	86	ILE
2	B	89	TYR
2	B	91	VAL
2	B	94	LYS
2	B	95	SER
2	B	99	LEU
2	B	127	VAL
2	B	128	ARG
2	B	129	LYS
2	B	134	ILE
2	B	143	LYS
2	B	147	HIS
1	C	7	LYS
1	C	12	ILE
1	C	17	ARG
1	C	18	ASP
1	C	22	LEU
1	C	24	LEU
1	C	35	GLN
1	C	40	LYS
1	C	57	LEU
1	C	59	PHE
1	C	74	SER
1	C	78	ASN
1	C	79	THR
1	C	81	LEU
1	C	84	LYS
1	C	92	ILE
1	C	95	ILE
1	C	146	GLN
1	C	147	GLU
1	C	151	ARG
1	C	159	MET
1	C	167	ARG
1	C	169	VAL

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Mol	Chain	Res	Type
1	C	174	GLN
1	C	180	ASP
1	C	187	ILE
1	C	190	ASP
1	C	196	GLN
1	C	198	ILE
1	C	212	HIS
1	C	217	GLU
1	C	221	GLU
1	C	222	VAL
1	C	225	LEU
1	C	229	ARG
1	C	232	LYS
1	C	235	LEU
1	C	236	ASP
1	C	243	VAL
1	C	250	ARG
1	C	270	VAL
1	C	272	GLU
1	C	273	ILE
1	C	275	THR
1	C	279	LYS
1	C	285	TYR
1	C	287	GLN
1	C	293	ILE
1	C	305	ASN
1	C	306	ARG
1	C	308	LEU
1	C	309	VAL
1	C	310	LEU
2	D	6	LYS
2	D	7	LEU
2	D	8	GLN
2	D	10	GLU
2	D	13	LYS
2	D	14	ARG
2	D	18	ILE
2	D	25	ILE
2	D	28	LYS
2	D	29	LEU
2	D	30	LEU
2	D	32	LEU

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Mol	Chain	Res	Type
2	D	34	LYS
2	D	37	GLU
2	D	38	THR
2	D	39	ASP
2	D	41	ARG
2	D	43	THR
2	D	44	ILE
2	D	47	ASN
2	D	53	MET
2	D	56	LYS
2	D	57	ASP
2	D	58	LEU
2	D	59	ILE
2	D	60	LYS
2	D	61	ILE
2	D	64	THR
2	D	68	GLU
2	D	69	ASP
2	D	72	ASP
2	D	76	LEU
2	D	82	THR
2	D	84	ASN
2	D	86	ILE
2	D	91	VAL
2	D	92	VAL
2	D	94	LYS
2	D	96	ARG
2	D	99	LEU
2	D	102	ARG
2	D	104	ASP
2	D	106	VAL
2	D	108	VAL
2	D	115	ILE
2	D	122	SER
2	D	127	VAL
2	D	128	ARG
2	D	129	LYS
2	D	130	ARG
2	D	132	ASN
2	D	133	ASP
2	D	136	LEU
2	D	137	LYS

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Mol	Chain	Res	Type
2	D	139	LYS
2	D	149	VAL
2	D	150	VAL
2	D	151	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (27) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	2	ASN
1	A	8	HIS
1	A	78	ASN
1	A	132	ASN
1	A	146	GLN
1	A	182	ASN
1	A	212	HIS
1	A	305	ASN
2	B	47	ASN
2	B	63	ASN
2	B	73	GLN
1	C	13	ASN
1	C	41	HIS
1	C	108	GLN
1	C	126	ASN
1	C	133	GLN
1	C	196	GLN
1	C	231	GLN
1	C	244	ASN
1	C	297	GLN
2	D	40	GLN
2	D	63	ASN
2	D	73	GLN
2	D	80	GLN
2	D	84	ASN
2	D	113	ASN
2	D	147	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	MLI	C	312	-	6,6,6	2.27	2 (33%)	7,7,7	1.02	0
3	MLI	A	311	-	6,6,6	1.96	2 (33%)	7,7,7	1.22	1 (14%)

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
3	MLI	C	312	-	-	4/4/4/4	-
3	MLI	A	311	-	-	2/4/4/4	-

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	312	MLI	C1-C2	3.80	1.57	1.51
3	A	311	MLI	C1-C3	3.06	1.55	1.51
3	C	312	MLI	C1-C3	2.79	1.55	1.51
3	A	311	MLI	C1-C2	2.77	1.55	1.51

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	311	MLI	O7-C2-C1	2.09	120.98	114.51

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	C	312	MLI	C3-C1-C2-O7
3	C	312	MLI	C3-C1-C2-O6
3	C	312	MLI	C2-C1-C3-O9
3	A	311	MLI	C2-C1-C3-O9
3	C	312	MLI	C2-C1-C3-O8
3	A	311	MLI	C2-C1-C3-O8

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	3
2	D	2
1	C	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	134:HIS	C	135:PRO	N	1.62
1	A	78:ASN	C	79:THR	N	1.19
1	A	83:LYS	C	84:LYS	N	1.19
1	D	14:ARG	C	15:GLY	N	1.19
1	D	28:LYS	C	29:LEU	N	1.19
1	C	75:ASP	C	76:SER	N	1.18

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	310/310 (100%)	-1.51	0 100 100	2, 19, 55, 79	0
1	C	310/310 (100%)	-1.48	0 100 100	4, 22, 55, 104	0
2	B	148/153 (96%)	-1.15	0 100 100	3, 55, 119, 151	0
2	D	148/153 (96%)	-1.21	0 100 100	2, 49, 95, 107	0
All	All	916/926 (98%)	-1.39	0 100 100	2, 25, 87, 151	0

There are no RSRZ outliers to report.

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	MLI	C	312	7/7	0.98	0.06	68,72,73,74	0
3	MLI	A	311	7/7	0.99	0.06	55,61,63,66	0
4	ZN	B	315	1/1	1.00	0.03	84,84,84,84	0
4	ZN	D	314	1/1	1.00	0.01	59,59,59,59	0

6.5 Other polymers [i](#)

There are no such residues in this entry.