



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 08:23 PM GMT

PDB ID : 1K3R
Title : Crystal Structure of the Methyltransferase with a Knot from Methanobacterium thermoautotrophicum
Authors : Zarembinski, T.I.; Kim, Y.; Peterson, K.; Christendat, D.; Dharamsi, A.; Arrowsmith, C.H.; Edwards, A.M.; Joachimiak, A.; Midwest Center for Structural Genomics (MCSG)
Deposited on : 2001-10-03
Resolution : 2.30 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

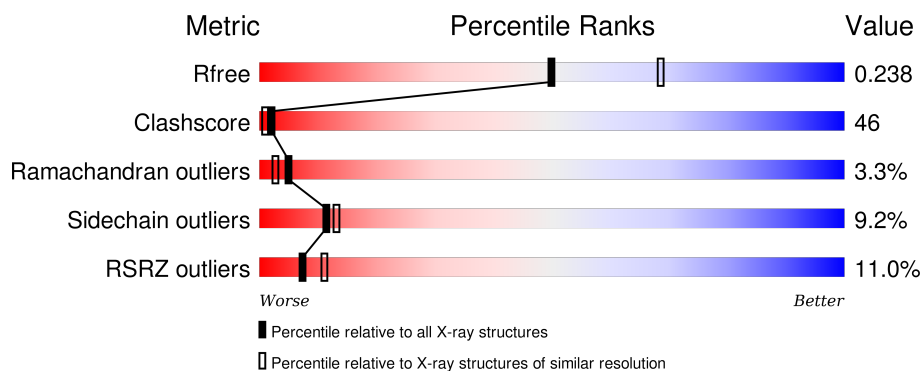
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	3852 (2.30-2.30)
Clashscore	102246	4452 (2.30-2.30)
Ramachandran outliers	100387	4410 (2.30-2.30)
Sidechain outliers	100360	4409 (2.30-2.30)
RSRZ outliers	91569	3857 (2.30-2.30)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	268	 6% 44% 46% 8% .
1	B	268	 16% 46% 43% 10% .

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 4278 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 conserved protein MT0001.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	262	Total	C	N	O	S	0	0	0
			2071	1317	367	379	8			
1	B	264	Total	C	N	O	S	0	0	0
			2087	1327	369	383	8			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	8	LEU	ILE	CONFLICT	UNP O26109
B	8	LEU	ILE	CONFLICT	UNP O26109

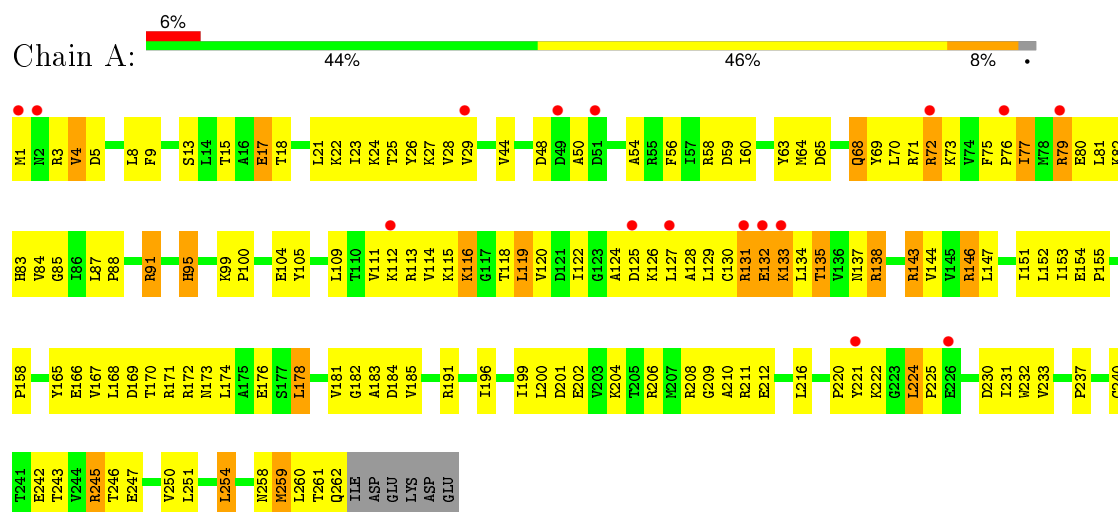
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	71	Total	O	0	0
			71	71		
2	B	49	Total	O	0	0
			49	49		

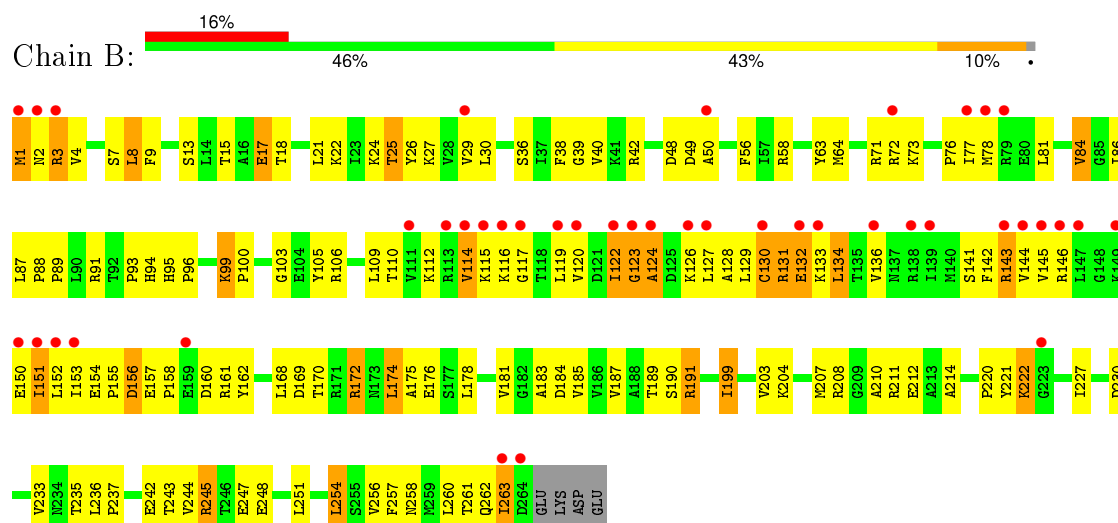
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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 ($\text{RSRZ} > 2$). 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: conserved protein MT0001



• Molecule 1: conserved protein MT0001



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	101.31Å 51.35Å 109.25Å 90.00° 94.69° 90.00°	Depositor
Resolution (Å)	500.00 – 2.30 41.65 – 2.30	Depositor EDS
% Data completeness (in resolution range)	(Not available) (500.00-2.30) 95.2 (41.65-2.30)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.07 (at 2.29Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.221 , 0.277 0.241 , 0.238	Depositor DCC
R_{free} test set	2368 reflections (9.85%)	DCC
Wilson B-factor (Å ²)	39.7	Xtriage
Anisotropy	0.142	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 52.4	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	1 of 25123 reflections (0.004%)	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	4278	wwPDB-VP
Average B, all atoms (Å ²)	53.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.04% 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, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

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	0.49	0/2107	0.76	0/2855
1	B	0.48	0/2123	0.71	0/2877
All	All	0.49	0/4230	0.73	0/5732

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2071	0	2154	203	0
1	B	2087	0	2169	196	0
2	A	71	0	0	10	0
2	B	49	0	0	9	0
All	All	4278	0	4323	387	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 46.

All (387) 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:116:LYS:H	1:A:116:LYS:HE3	1.04	1.20

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:26:TYR:O	1:B:29:VAL:HG12	1.45	1.16
1:A:172:ARG:HG2	1:A:176:GLU:HB2	1.22	1.11
1:B:29:VAL:HG23	1:B:64:MET:SD	1.94	1.07
1:B:3:ARG:HH21	1:B:263:ILE:HD12	1.18	1.07
1:B:129:LEU:HD23	1:B:134:LEU:HD21	1.35	1.07
1:A:146:ARG:HH11	1:A:146:ARG:HA	1.18	1.07
1:A:29:VAL:HG11	1:A:87:LEU:HD22	1.07	1.04
1:B:29:VAL:HG21	1:B:88:PRO:HD2	1.38	1.02
1:B:120:VAL:HG21	1:B:153:ILE:HD11	1.38	1.01
1:A:127:LEU:HD22	1:A:153:ILE:HG12	1.40	1.00
1:A:29:VAL:CG1	1:A:87:LEU:HD22	1.91	1.00
1:A:23:ILE:HA	2:A:307:HOH:O	1.63	0.98
1:B:143:ARG:HB2	1:B:143:ARG:HH11	1.26	0.97
1:B:131:ARG:HB3	1:B:134:LEU:HD13	1.50	0.94
1:A:172:ARG:HB2	2:A:306:HOH:O	1.65	0.94
1:B:143:ARG:HB2	1:B:143:ARG:NH1	1.81	0.94
1:A:172:ARG:HG2	1:A:176:GLU:CB	1.98	0.93
1:B:99:LYS:HG3	1:B:100:PRO:HD2	1.51	0.91
1:A:144:VAL:HA	1:A:153:ILE:HG22	1.49	0.91
1:A:127:LEU:HD23	1:A:128:ALA:N	1.87	0.90
1:A:21:LEU:O	1:A:25:THR:HG23	1.72	0.90
1:A:127:LEU:HG	1:A:151:ILE:HB	1.55	0.88
1:A:116:LYS:N	1:A:116:LYS:HE3	1.87	0.88
1:A:129:LEU:HD12	1:A:153:ILE:O	1.73	0.88
1:A:26:TYR:O	1:A:29:VAL:HG22	1.73	0.87
1:A:224:LEU:HD22	1:A:224:LEU:H	1.39	0.86
1:A:116:LYS:H	1:A:116:LYS:CE	1.88	0.84
1:A:127:LEU:HD11	1:A:153:ILE:HG23	1.60	0.84
1:A:3:ARG:HH12	1:A:210:ALA:HB1	1.41	0.84
1:A:143:ARG:HH11	1:A:143:ARG:HG3	1.44	0.82
1:B:122:ILE:HG23	1:B:123:GLY:N	1.95	0.82
1:B:127:LEU:HB3	1:B:151:ILE:HG23	1.62	0.81
1:B:8:LEU:HD21	1:B:40:VAL:HG21	1.62	0.81
1:A:72:ARG:H	1:A:72:ARG:HD3	1.46	0.81
1:B:106:ARG:HD3	1:B:122:ILE:HG13	1.63	0.81
1:B:3:ARG:HH21	1:B:263:ILE:CD1	1.94	0.80
1:B:120:VAL:CG2	1:B:153:ILE:HD11	2.10	0.80
1:A:72:ARG:HH12	1:A:73:LYS:HG3	1.47	0.79
1:A:221:TYR:HD1	1:A:222:LYS:H	1.31	0.78
1:A:184:ASP:CG	1:A:211:ARG:HB2	2.04	0.78
1:A:79:ARG:HG3	1:A:82:LYS:NZ	1.97	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:133:LYS:HG3	1:A:133:LYS:O	1.83	0.77
1:B:127:LEU:CB	1:B:151:ILE:HG23	2.15	0.77
1:A:122:ILE:CD1	1:A:127:LEU:HD12	2.15	0.77
1:A:183:ALA:HB1	1:A:212:GLU:O	1.84	0.77
1:B:29:VAL:CG2	1:B:88:PRO:HD2	2.15	0.76
1:B:99:LYS:HE2	1:B:124:ALA:HB2	1.66	0.76
1:A:224:LEU:HD22	1:A:224:LEU:N	2.01	0.76
1:A:245:ARG:HG2	1:A:245:ARG:HH11	1.51	0.76
1:B:58:ARG:HD3	1:B:169:ASP:HB2	1.67	0.76
1:A:127:LEU:HD22	1:A:153:ILE:CG1	2.15	0.75
1:B:247:GLU:OE1	2:B:309:HOH:O	2.03	0.75
1:A:127:LEU:HD23	1:A:128:ALA:H	1.50	0.74
1:A:224:LEU:H	1:A:224:LEU:CD2	2.00	0.74
1:B:145:VAL:HB	1:B:152:LEU:CD1	2.18	0.74
1:B:129:LEU:HD23	1:B:134:LEU:CD2	2.17	0.73
1:B:25:THR:HG21	2:B:283:HOH:O	1.87	0.73
1:A:172:ARG:CG	1:A:176:GLU:HB2	2.12	0.73
1:B:29:VAL:HG21	1:B:88:PRO:CD	2.18	0.73
1:B:106:ARG:HB2	1:B:122:ILE:HD11	1.71	0.73
1:B:174:LEU:HD22	2:B:284:HOH:O	1.87	0.73
1:B:94:HIS:C	1:B:96:PRO:HD3	2.09	0.72
1:A:127:LEU:CD2	1:A:153:ILE:HG12	2.16	0.72
1:B:122:ILE:HB	1:B:127:LEU:HD21	1.71	0.72
1:A:120:VAL:HG11	1:A:153:ILE:HD11	1.71	0.72
1:B:13:SER:HB3	2:B:280:HOH:O	1.89	0.72
1:A:242:GLU:HG2	1:B:91:ARG:HB2	1.72	0.71
1:A:111:VAL:HG12	1:A:112:LYS:HG2	1.73	0.71
1:A:199:ILE:HG22	1:A:199:ILE:O	1.89	0.70
1:A:68:GLN:H	1:A:68:GLN:CD	1.93	0.70
1:A:25:THR:O	1:A:29:VAL:HG13	1.90	0.70
1:A:127:LEU:CD1	1:A:153:ILE:HG23	2.21	0.70
1:B:199:ILE:O	1:B:203:VAL:HG23	1.91	0.70
1:A:174:LEU:HD23	1:A:225:PRO:HD2	1.73	0.70
1:A:129:LEU:HD11	1:A:154:GLU:HA	1.73	0.70
1:A:184:ASP:OD2	1:A:211:ARG:HB2	1.90	0.70
1:B:4:VAL:HG13	1:B:210:ALA:CB	2.21	0.70
1:A:99:LYS:NZ	1:A:124:ALA:HB1	2.07	0.69
1:B:144:VAL:HA	1:B:153:ILE:HG22	1.73	0.69
1:A:25:THR:HG21	2:A:271:HOH:O	1.93	0.69
1:B:1:MET:HB2	1:B:261:THR:OG1	1.93	0.69
1:B:29:VAL:CG2	1:B:64:MET:SD	2.79	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:21:LEU:O	1:B:25:THR:HG23	1.92	0.68
1:B:120:VAL:HG11	1:B:142:PHE:CZ	2.28	0.68
1:B:145:VAL:HB	1:B:152:LEU:HD12	1.76	0.68
1:B:105:TYR:CD2	1:B:158:PRO:HD3	2.28	0.68
1:B:42:ARG:HH21	1:B:181:VAL:HG22	1.59	0.68
1:A:220:PRO:HB3	1:A:243:THR:OG1	1.94	0.68
1:B:27:LYS:HB2	1:B:27:LYS:NZ	2.09	0.68
1:A:245:ARG:HG2	1:A:245:ARG:NH1	2.09	0.68
1:B:27:LYS:HB2	1:B:27:LYS:HZ2	1.59	0.68
1:A:114:VAL:HB	1:A:116:LYS:NZ	2.09	0.67
1:B:172:ARG:HD2	1:B:172:ARG:N	2.09	0.67
1:A:129:LEU:CD1	1:A:154:GLU:HA	2.24	0.67
1:B:191:ARG:HD3	1:B:191:ARG:H	1.58	0.66
1:B:3:ARG:NH2	1:B:263:ILE:HD12	2.01	0.66
1:A:58:ARG:NH1	1:A:59:ASP:OD1	2.29	0.66
1:B:15:THR:HB	1:B:24:LYS:HG3	1.77	0.66
1:B:29:VAL:HB	1:B:87:LEU:CD2	2.25	0.65
1:B:29:VAL:HB	1:B:87:LEU:HD22	1.78	0.65
1:A:146:ARG:NH1	1:A:146:ARG:HA	2.03	0.65
1:B:110:THR:CG2	1:B:136:VAL:HA	2.26	0.65
1:B:17:GLU:OE1	1:B:18:THR:HG23	1.97	0.65
1:B:141:SER:OG	1:B:157:GLU:HB3	1.97	0.65
1:A:181:VAL:HA	2:A:309:HOH:O	1.96	0.64
1:B:130:CYS:SG	1:B:131:ARG:N	2.70	0.64
1:A:29:VAL:HG11	1:A:87:LEU:CD2	2.04	0.64
1:B:174:LEU:HD13	2:B:284:HOH:O	1.95	0.64
1:B:29:VAL:HG11	1:B:88:PRO:HD2	1.79	0.64
1:A:146:ARG:NH1	1:A:147:LEU:H	1.96	0.64
1:A:72:ARG:NH1	1:A:72:ARG:HB2	2.11	0.64
1:B:120:VAL:O	1:B:127:LEU:HD23	1.97	0.64
1:B:110:THR:HG22	1:B:136:VAL:HA	1.79	0.64
1:B:2:ASN:ND2	1:B:3:ARG:HD3	2.13	0.64
1:A:129:LEU:HD22	1:A:134:LEU:HD11	1.80	0.63
1:A:79:ARG:HG3	1:A:82:LYS:HZ2	1.63	0.63
1:B:29:VAL:CG2	1:B:87:LEU:HD22	2.28	0.63
1:B:42:ARG:HH21	1:B:181:VAL:CG2	2.10	0.63
1:B:129:LEU:HD12	1:B:130:CYS:H	1.63	0.63
1:B:143:ARG:CB	1:B:143:ARG:HH11	2.06	0.63
1:B:191:ARG:HG2	1:B:191:ARG:HH11	1.64	0.62
1:A:15:THR:HB	1:A:24:LYS:HG3	1.82	0.62
1:B:106:ARG:HD3	1:B:122:ILE:CG1	2.29	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:63:TYR:CZ	1:B:71:ARG:HD3	2.35	0.62
1:A:185:VAL:HA	1:A:230:ASP:OD2	1.99	0.62
1:A:120:VAL:CG1	1:A:153:ILE:HD11	2.29	0.62
1:B:129:LEU:CD2	1:B:155:PRO:HD3	2.30	0.61
1:B:58:ARG:HG2	1:B:58:ARG:HH11	1.64	0.61
1:B:127:LEU:HD23	1:B:127:LEU:H	1.64	0.61
1:A:122:ILE:HD11	1:A:127:LEU:HD12	1.83	0.61
1:A:3:ARG:CZ	1:A:3:ARG:HB2	2.30	0.61
1:A:122:ILE:HD13	1:A:127:LEU:HD12	1.83	0.60
1:A:200:LEU:HD11	1:A:260:LEU:HD21	1.84	0.60
1:A:127:LEU:HD13	1:A:153:ILE:HD13	1.84	0.60
1:A:72:ARG:H	1:A:72:ARG:HH11	1.50	0.60
1:B:127:LEU:HD12	1:B:151:ILE:HG12	1.84	0.60
1:A:72:ARG:N	1:A:72:ARG:HH11	2.00	0.60
1:B:184:ASP:OD1	1:B:211:ARG:HB3	2.02	0.59
1:A:3:ARG:HH22	1:A:210:ALA:HB2	1.67	0.59
1:A:143:ARG:HH11	1:A:143:ARG:CG	2.15	0.59
1:B:106:ARG:HE	1:B:123:GLY:CA	2.14	0.59
1:A:172:ARG:HG3	1:A:173:ASN:N	2.18	0.59
1:B:122:ILE:HG23	1:B:123:GLY:H	1.68	0.59
1:A:261:THR:O	1:A:261:THR:HG22	2.03	0.59
1:B:122:ILE:HG22	1:B:127:LEU:HD22	1.84	0.58
1:B:152:LEU:HD12	1:B:152:LEU:O	2.02	0.58
1:A:178:LEU:HD21	1:A:216:LEU:HD11	1.85	0.58
1:B:117:GLY:HA3	1:B:130:CYS:O	2.03	0.58
1:B:220:PRO:HB2	1:B:243:THR:HB	1.85	0.58
1:B:172:ARG:HB3	1:B:176:GLU:HB3	1.84	0.58
1:B:72:ARG:HH11	1:B:73:LYS:HG2	1.69	0.58
1:A:172:ARG:HG3	1:A:173:ASN:H	1.69	0.57
1:A:26:TYR:HB3	2:A:307:HOH:O	2.03	0.57
1:A:146:ARG:CA	1:A:146:ARG:HH11	2.07	0.57
1:A:242:GLU:HG2	1:B:91:ARG:CB	2.34	0.57
1:A:77:ILE:O	1:A:77:ILE:HG13	2.04	0.57
1:A:17:GLU:CD	1:A:17:GLU:H	2.07	0.57
1:B:84:VAL:HG22	1:B:87:LEU:HD12	1.86	0.57
1:A:58:ARG:HH11	1:A:58:ARG:HG2	1.69	0.57
1:B:122:ILE:CG2	1:B:123:GLY:N	2.67	0.56
1:A:79:ARG:HG3	1:A:82:LYS:HZ1	1.68	0.56
1:B:4:VAL:HG13	1:B:210:ALA:HB3	1.87	0.56
1:A:119:LEU:HG	1:A:126:LYS:HG2	1.87	0.56
1:A:204:LYS:O	1:A:208:ARG:HG2	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:68:GLN:H	1:A:68:GLN:NE2	2.03	0.56
1:A:69:TYR:CD1	1:A:70:LEU:HG	2.41	0.56
1:B:42:ARG:HG2	1:B:42:ARG:HH11	1.70	0.56
1:A:58:ARG:HD3	1:A:169:ASP:HB2	1.86	0.56
1:A:125:ASP:OD1	1:A:126:LYS:N	2.38	0.56
1:B:76:PRO:HD2	1:B:78:MET:HE1	1.88	0.56
1:A:122:ILE:HD13	1:A:127:LEU:CD1	2.36	0.56
1:A:221:TYR:CD1	1:A:222:LYS:HG2	2.41	0.56
1:B:221:TYR:HB2	1:B:222:LYS:HD2	1.88	0.56
1:A:105:TYR:CD2	1:A:158:PRO:HG3	2.41	0.56
1:A:127:LEU:HG	1:A:151:ILE:CB	2.33	0.56
1:A:84:VAL:O	1:A:87:LEU:HG	2.05	0.55
1:B:29:VAL:CB	1:B:87:LEU:HD22	2.36	0.55
1:A:99:LYS:HZ1	1:A:124:ALA:HB1	1.70	0.55
1:B:49:ASP:HB2	2:B:280:HOH:O	2.06	0.55
1:A:127:LEU:CD1	1:A:153:ILE:CG2	2.84	0.55
1:B:27:LYS:HG3	1:B:247:GLU:OE2	2.07	0.55
1:B:204:LYS:HE2	1:B:260:LEU:HD22	1.88	0.55
1:B:127:LEU:HD11	1:B:153:ILE:HD13	1.87	0.55
1:B:190:SER:HB2	2:B:314:HOH:O	2.07	0.55
1:A:3:ARG:HH22	1:A:210:ALA:CB	2.19	0.55
1:B:245:ARG:NH1	1:B:245:ARG:HG3	2.22	0.55
1:A:129:LEU:HD23	1:A:134:LEU:HG	1.90	0.54
1:A:199:ILE:HG22	1:A:202:GLU:HB3	1.89	0.54
1:A:184:ASP:OD1	1:A:211:ARG:HB2	2.07	0.54
1:B:1:MET:HE2	1:B:38:PHE:O	2.06	0.54
1:B:25:THR:HG22	1:B:56:PHE:HZ	1.73	0.54
1:B:112:LYS:HD2	1:B:119:LEU:HD12	1.89	0.54
1:A:127:LEU:CG	1:A:151:ILE:HB	2.33	0.54
1:A:127:LEU:HD11	1:A:153:ILE:CG2	2.36	0.54
1:A:100:PRO:HA	1:A:104:GLU:OE1	2.07	0.54
1:B:29:VAL:HG11	1:B:88:PRO:CD	2.38	0.53
1:A:130:CYS:O	1:A:132:GLU:N	2.41	0.53
1:B:27:LYS:HD3	1:B:247:GLU:OE1	2.09	0.53
1:B:122:ILE:HG13	1:B:123:GLY:H	1.72	0.53
1:B:95:HIS:N	1:B:96:PRO:HD3	2.23	0.53
1:A:245:ARG:NH2	1:B:89:PRO:HD2	2.23	0.53
1:B:170:THR:O	1:B:170:THR:OG1	2.25	0.53
1:A:259:MET:HE2	1:B:256:VAL:HG13	1.91	0.53
1:A:99:LYS:CE	1:A:124:ALA:HB1	2.39	0.52
1:B:1:MET:HE2	1:B:38:PHE:HB3	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:127:LEU:HB2	1:B:151:ILE:HG23	1.89	0.52
1:B:129:LEU:HD13	1:B:153:ILE:O	2.09	0.52
1:A:75:PHE:C	1:A:77:ILE:H	2.12	0.52
1:A:3:ARG:NH1	1:A:3:ARG:HB2	2.25	0.52
1:B:129:LEU:HD13	1:B:154:GLU:HA	1.92	0.52
1:A:109:LEU:HA	1:A:138:ARG:O	2.10	0.51
1:B:144:VAL:HG22	1:B:151:ILE:HD11	1.92	0.51
1:B:129:LEU:CD1	1:B:155:PRO:HD3	2.41	0.51
1:B:208:ARG:C	1:B:210:ALA:H	2.13	0.51
1:B:2:ASN:ND2	1:B:3:ARG:CD	2.73	0.51
1:A:258:ASN:ND2	1:B:237:PRO:HD2	2.25	0.51
1:A:196:ILE:HD12	1:A:233:VAL:HG11	1.91	0.51
1:A:114:VAL:HB	1:A:116:LYS:HZ2	1.76	0.51
1:A:143:ARG:NH1	1:A:143:ARG:HG3	2.21	0.51
1:A:129:LEU:CD2	1:A:134:LEU:HD11	2.40	0.50
1:B:222:LYS:HD2	1:B:222:LYS:N	2.26	0.50
1:B:189:THR:HA	1:B:233:VAL:O	2.12	0.50
1:B:48:ASP:CG	1:B:49:ASP:H	2.15	0.50
1:B:26:TYR:CE2	1:B:30:LEU:HD21	2.47	0.50
1:A:221:TYR:CD1	1:A:222:LYS:N	2.72	0.50
1:B:181:VAL:HG13	1:B:181:VAL:O	2.12	0.50
1:A:54:ALA:HB3	1:A:171:ARG:NH1	2.27	0.50
1:A:3:ARG:NH1	1:A:210:ALA:HB1	2.19	0.50
1:A:200:LEU:HD11	1:A:260:LEU:CD2	2.40	0.50
1:B:76:PRO:HD2	1:B:78:MET:CE	2.41	0.50
1:A:83:HIS:C	1:A:85:GLY:N	2.65	0.50
1:A:25:THR:HG22	1:A:56:PHE:HZ	1.77	0.50
1:A:63:TYR:CZ	1:A:71:ARG:HD3	2.47	0.50
1:A:105:TYR:CG	1:A:158:PRO:HG3	2.47	0.49
1:A:137:ASN:C	1:A:138:ARG:HD2	2.33	0.49
1:A:129:LEU:HD11	1:A:155:PRO:CD	2.42	0.49
1:A:99:LYS:HD2	1:A:100:PRO:HD2	1.95	0.49
1:A:246:THR:O	1:A:250:VAL:HG23	2.11	0.49
1:A:72:ARG:HD3	1:A:72:ARG:N	2.21	0.49
1:B:29:VAL:HG22	1:B:64:MET:HE1	1.94	0.49
1:B:106:ARG:CB	1:B:122:ILE:HD11	2.39	0.49
1:A:25:THR:HG22	1:A:56:PHE:CZ	2.48	0.49
1:B:58:ARG:NH1	1:B:58:ARG:HG2	2.28	0.49
1:B:48:ASP:CG	1:B:49:ASP:N	2.66	0.49
1:B:245:ARG:HG3	1:B:245:ARG:HH11	1.78	0.49
1:B:122:ILE:HB	1:B:127:LEU:CD2	2.40	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:127:LEU:HB2	1:B:151:ILE:O	2.13	0.49
1:A:259:MET:CE	1:B:256:VAL:HG13	2.43	0.49
1:B:129:LEU:HD21	1:B:155:PRO:HD3	1.95	0.49
1:B:109:LEU:HD12	1:B:110:THR:N	2.28	0.49
1:A:137:ASN:O	1:A:138:ARG:HD2	2.13	0.49
1:A:129:LEU:CD2	1:A:155:PRO:HD3	2.43	0.48
1:B:207:MET:O	1:B:210:ALA:HB2	2.12	0.48
1:A:72:ARG:CZ	1:A:72:ARG:HB2	2.43	0.48
1:B:64:MET:O	1:B:95:HIS:HE1	1.96	0.48
1:B:126:LYS:HD3	1:B:127:LEU:H	1.78	0.48
1:A:143:ARG:NH1	1:A:143:ARG:CG	2.75	0.48
1:A:131:ARG:HB2	2:A:279:HOH:O	2.13	0.48
1:B:29:VAL:CG1	1:B:88:PRO:HD2	2.43	0.48
1:A:29:VAL:HB	1:A:64:MET:SD	2.54	0.48
1:A:129:LEU:HD21	1:A:155:PRO:HD3	1.96	0.48
1:B:132:GLU:CD	1:B:132:GLU:H	2.16	0.48
1:B:235:THR:HG21	1:B:257:PHE:HE1	1.79	0.48
1:A:146:ARG:NH1	1:A:147:LEU:N	2.60	0.48
1:B:150:GLU:O	1:B:150:GLU:HG3	2.14	0.48
1:B:9:PHE:CE1	1:B:214:ALA:HB1	2.49	0.47
1:A:18:THR:HB	1:A:27:LYS:NZ	2.29	0.47
1:A:1:MET:H1	1:A:261:THR:HB	1.79	0.47
1:B:247:GLU:HG2	1:B:248:GLU:N	2.30	0.47
1:A:83:HIS:C	1:A:85:GLY:H	2.16	0.47
1:A:129:LEU:HD11	1:A:155:PRO:HD3	1.96	0.47
1:B:185:VAL:HA	1:B:230:ASP:OD1	2.14	0.47
1:A:24:LYS:HG2	1:A:56:PHE:CE2	2.48	0.47
1:A:65:ASP:O	1:A:95:HIS:HE1	1.97	0.47
1:B:127:LEU:HD23	1:B:127:LEU:N	2.27	0.47
1:A:115:LYS:N	1:A:116:LYS:HE3	2.30	0.47
1:A:118:THR:OG1	1:A:134:LEU:HB2	2.15	0.47
1:B:42:ARG:NH2	1:B:181:VAL:HG22	2.28	0.47
1:B:81:LEU:HD12	1:B:81:LEU:O	2.15	0.47
1:A:3:ARG:O	1:A:4:VAL:C	2.53	0.47
1:A:113:ARG:HH21	1:A:135:THR:HA	1.79	0.47
1:B:211:ARG:HG3	1:B:212:GLU:HG3	1.97	0.47
1:A:221:TYR:CE1	1:A:222:LYS:HG2	2.50	0.46
1:A:1:MET:N	1:A:261:THR:O	2.43	0.46
1:A:91:ARG:HG2	1:A:91:ARG:HH11	1.80	0.46
1:A:131:ARG:C	2:A:301:HOH:O	2.53	0.46
1:A:13:SER:HB3	2:A:318:HOH:O	2.14	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:27:LYS:CB	1:B:27:LYS:NZ	2.78	0.46
1:A:230:ASP:C	1:A:231:ILE:HG13	2.36	0.46
1:A:127:LEU:HD21	1:A:153:ILE:N	2.31	0.46
1:B:158:PRO:HB2	1:B:160:ASP:OD1	2.15	0.46
1:A:166:GLU:OE1	1:A:168:LEU:HD21	2.16	0.46
1:B:86:ILE:HD12	1:B:86:ILE:C	2.36	0.46
1:A:127:LEU:HD21	1:A:152:LEU:C	2.37	0.46
1:A:8:LEU:HD11	1:A:254:LEU:HD11	1.98	0.46
1:B:220:PRO:HB3	1:B:244:VAL:O	2.16	0.45
1:B:29:VAL:HG23	1:B:87:LEU:HD22	1.98	0.45
1:A:138:ARG:HH11	1:A:138:ARG:HG2	1.82	0.45
1:A:127:LEU:HD22	1:A:153:ILE:CD1	2.45	0.45
1:A:80:GLU:OE2	1:A:80:GLU:HA	2.16	0.45
1:A:65:ASP:HB2	1:A:165:TYR:CZ	2.52	0.45
1:B:18:THR:HG21	1:B:27:LYS:HZ1	1.82	0.45
1:A:251:LEU:HD23	1:B:251:LEU:HD23	1.99	0.45
1:A:237:PRO:HB2	1:B:262:GLN:NE2	2.32	0.45
1:A:22:LYS:HD2	1:B:22:LYS:HD2	1.98	0.45
1:B:114:VAL:HG13	1:B:116:LYS:H	1.81	0.45
1:B:103:GLY:HA2	1:B:143:ARG:HH22	1.81	0.45
1:B:183:ALA:HB1	1:B:212:GLU:O	2.17	0.45
1:B:106:ARG:HE	1:B:123:GLY:N	2.15	0.45
1:A:240:CYS:HB2	1:B:36:SER:O	2.17	0.45
1:B:106:ARG:HH21	1:B:123:GLY:CA	2.30	0.45
1:B:78:MET:HE3	1:B:81:LEU:HD21	1.98	0.45
1:A:58:ARG:NH1	1:A:58:ARG:HG2	2.32	0.44
1:B:106:ARG:NE	1:B:123:GLY:HA3	2.32	0.44
1:B:126:LYS:HD3	1:B:127:LEU:N	2.33	0.44
1:A:129:LEU:CD1	1:A:155:PRO:HD3	2.48	0.44
1:A:208:ARG:C	1:A:210:ALA:N	2.69	0.44
1:A:199:ILE:CG2	1:A:202:GLU:HB3	2.48	0.44
1:A:208:ARG:HH21	1:A:262:GLN:N	2.14	0.44
1:A:220:PRO:HD2	1:A:221:TYR:CE2	2.52	0.44
1:B:199:ILE:HG13	1:B:203:VAL:CG2	2.48	0.44
1:A:231:ILE:HG22	1:A:232:TRP:N	2.33	0.44
1:A:129:LEU:CD1	1:A:153:ILE:O	2.55	0.44
1:A:208:ARG:O	1:A:209:GLY:C	2.55	0.44
1:B:106:ARG:NH2	1:B:123:GLY:HA3	2.33	0.44
1:B:7:SER:HB3	1:B:42:ARG:NH1	2.32	0.44
1:B:122:ILE:CG2	1:B:127:LEU:HD22	2.47	0.44
1:A:243:THR:HG22	2:B:269:HOH:O	2.16	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:78:MET:CE	1:B:81:LEU:HD21	2.48	0.44
1:A:58:ARG:HD3	1:A:169:ASP:CB	2.48	0.43
1:B:115:LYS:HG2	1:B:115:LYS:H	1.54	0.43
1:B:4:VAL:HG13	1:B:210:ALA:HB1	2.00	0.43
1:B:245:ARG:CG	1:B:245:ARG:HH11	2.29	0.43
1:B:39:GLY:HA2	1:B:162:TYR:CE1	2.54	0.43
1:B:99:LYS:HE2	1:B:124:ALA:CB	2.41	0.43
1:A:68:GLN:N	1:A:68:GLN:CD	2.66	0.43
1:B:203:VAL:O	1:B:207:MET:HG2	2.17	0.43
1:B:119:LEU:HD23	1:B:128:ALA:HB2	1.99	0.43
1:A:184:ASP:OD2	1:A:184:ASP:N	2.48	0.43
1:A:199:ILE:O	1:A:199:ILE:CG2	2.61	0.43
1:B:141:SER:CB	1:B:157:GLU:HB3	2.47	0.43
1:A:9:PHE:CE2	1:A:44:VAL:HG11	2.54	0.43
1:A:170:THR:O	1:A:170:THR:OG1	2.36	0.43
1:A:113:ARG:CB	1:A:113:ARG:NH1	2.82	0.43
1:A:83:HIS:O	1:A:85:GLY:N	2.51	0.43
1:A:91:ARG:HG2	1:A:91:ARG:NH1	2.34	0.43
1:B:132:GLU:HG2	1:B:133:LYS:N	2.34	0.43
1:A:91:ARG:NH1	1:B:242:GLU:OE2	2.52	0.43
1:B:174:LEU:HD13	1:B:178:LEU:CD2	2.48	0.42
1:B:133:LYS:HB2	2:B:278:HOH:O	2.19	0.42
1:A:91:ARG:HB3	1:B:242:GLU:HB2	2.01	0.42
1:A:29:VAL:HG21	1:A:88:PRO:CD	2.50	0.42
1:B:18:THR:HG21	1:B:27:LYS:HE2	2.01	0.42
1:A:58:ARG:CZ	1:A:59:ASP:OD1	2.67	0.42
1:A:69:TYR:CE1	1:A:70:LEU:HG	2.54	0.42
1:B:9:PHE:HE1	1:B:214:ALA:HB1	1.83	0.42
1:B:38:PHE:HE1	1:B:251:LEU:CD1	2.32	0.42
1:B:114:VAL:HG12	1:B:117:GLY:H	1.85	0.42
1:B:143:ARG:HG2	1:B:156:ASP:HB3	2.02	0.42
1:B:1:MET:HE3	1:B:258:ASN:OD1	2.19	0.42
1:A:119:LEU:HD12	1:A:119:LEU:HA	1.80	0.42
1:A:127:LEU:HD13	1:A:153:ILE:CG2	2.50	0.41
1:B:58:ARG:HD3	1:B:169:ASP:CB	2.46	0.41
1:B:89:PRO:HG2	1:B:91:ARG:NH1	2.35	0.41
1:B:145:VAL:HB	1:B:152:LEU:HD11	1.99	0.41
1:A:100:PRO:CD	1:A:124:ALA:HB2	2.50	0.41
1:B:168:LEU:HA	1:B:168:LEU:HD23	1.90	0.41
1:B:208:ARG:C	1:B:210:ALA:N	2.73	0.41
1:B:175:ALA:HB2	1:B:227:ILE:HD13	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:116:LYS:CE	1:A:116:LYS:N	2.65	0.41
1:A:127:LEU:HD21	1:A:152:LEU:CA	2.51	0.41
1:B:254:LEU:HD12	1:B:254:LEU:HA	1.87	0.41
1:A:63:TYR:CE2	1:A:84:VAL:HG22	2.55	0.41
1:A:5:ASP:O	1:A:212:GLU:HA	2.20	0.41
1:B:191:ARG:HG2	1:B:191:ARG:NH1	2.33	0.41
1:B:187:VAL:HG11	1:B:257:PHE:CZ	2.56	0.41
1:A:173:ASN:HB2	2:A:319:HOH:O	2.21	0.40
1:A:48:ASP:HB3	2:A:318:HOH:O	2.21	0.40
1:B:93:PRO:HB3	1:B:161:ARG:HD3	2.03	0.40
1:A:28:VAL:HG11	1:A:60:ILE:HB	2.03	0.40
1:A:60:ILE:HD13	1:A:81:LEU:HD22	2.03	0.40
1:B:120:VAL:O	1:B:127:LEU:CD2	2.68	0.40
1:B:145:VAL:HG12	1:B:146:ARG:HG3	2.03	0.40
1:B:78:MET:HB2	1:B:81:LEU:HG	2.03	0.40
1:A:127:LEU:HD13	1:A:153:ILE:HG21	2.04	0.40
1:A:127:LEU:CD2	1:A:151:ILE:O	2.69	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	260/268 (97%)	232 (89%)	20 (8%)	8 (3%)	5	3
1	B	262/268 (98%)	226 (86%)	27 (10%)	9 (3%)	5	2
All	All	522/536 (97%)	458 (88%)	47 (9%)	17 (3%)	5	3

All (17) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	4	VAL

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Mol	Chain	Res	Type
1	A	79	ARG
1	A	132	GLU
1	A	131	ARG
1	A	182	GLY
1	B	50	ALA
1	B	123	GLY
1	A	50	ALA
1	B	124	ALA
1	B	134	LEU
1	B	122	ILE
1	B	131	ARG
1	B	156	ASP
1	A	76	PRO
1	A	77	ILE
1	B	99	LYS
1	B	199	ILE

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	227/233 (97%)	205 (90%)	22 (10%)	10	12
1	B	229/233 (98%)	209 (91%)	20 (9%)	13	15
All	All	456/466 (98%)	414 (91%)	42 (9%)	11	13

All (42) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	17	GLU
1	A	68	GLN
1	A	72	ARG
1	A	91	ARG
1	A	95	HIS
1	A	116	LYS
1	A	119	LEU

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Mol	Chain	Res	Type
1	A	133	LYS
1	A	135	THR
1	A	138	ARG
1	A	143	ARG
1	A	146	ARG
1	A	167	VAL
1	A	178	LEU
1	A	191	ARG
1	A	201	ASP
1	A	206	ARG
1	A	224	LEU
1	A	245	ARG
1	A	247	GLU
1	A	254	LEU
1	A	259	MET
1	B	1	MET
1	B	3	ARG
1	B	8	LEU
1	B	17	GLU
1	B	25	THR
1	B	77	ILE
1	B	84	VAL
1	B	114	VAL
1	B	130	CYS
1	B	132	GLU
1	B	143	ARG
1	B	151	ILE
1	B	172	ARG
1	B	174	LEU
1	B	191	ARG
1	B	222	LYS
1	B	236	LEU
1	B	245	ARG
1	B	254	LEU
1	B	263	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	47	HIS
1	A	68	GLN
1	B	2	ASN

5.3.3 RNA [i](#)

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 carbohydrates 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	262/268 (97%)	0.37	16 (6%)	25 33	17, 43, 91, 119	0
1	B	264/268 (98%)	0.87	42 (15%)	3 4	21, 54, 100, 135	0
All	All	526/536 (98%)	0.62	58 (11%)	7 11	17, 47, 97, 135	0

All (58) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	133	LYS	9.0
1	A	2	ASN	7.2
1	A	1	MET	7.0
1	A	132	GLU	6.4
1	B	1	MET	6.4
1	B	127	LEU	6.3
1	B	119	LEU	5.9
1	B	263	ILE	5.5
1	B	130	CYS	5.5
1	B	124	ALA	4.5
1	B	114	VAL	4.5
1	B	117	GLY	4.4
1	B	113	ARG	4.3
1	B	150	GLU	4.2
1	B	2	ASN	4.1
1	B	29	VAL	4.1
1	B	153	ILE	4.1
1	A	133	LYS	3.7
1	B	143	ARG	3.7
1	B	115	LYS	3.7
1	B	122	ILE	3.5
1	A	221	TYR	3.5
1	A	226	GLU	3.5
1	B	72	ARG	3.4

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Mol	Chain	Res	Type	RSRZ
1	A	112	LYS	3.4
1	B	116	LYS	3.4
1	B	149	LYS	3.1
1	A	125	ASP	3.1
1	B	3	ARG	3.1
1	A	49	ASP	3.0
1	B	264	ASP	3.0
1	B	126	LYS	2.9
1	B	152	LEU	2.9
1	A	79	ARG	2.8
1	A	127	LEU	2.8
1	A	51	ASP	2.8
1	B	138	ARG	2.8
1	B	79	ARG	2.8
1	B	145	VAL	2.7
1	B	123	GLY	2.6
1	B	111	VAL	2.6
1	A	72	ARG	2.6
1	B	147	LEU	2.6
1	B	136	VAL	2.5
1	B	159	GLU	2.5
1	B	151	ILE	2.5
1	B	77	ILE	2.5
1	B	132	GLU	2.4
1	B	144	VAL	2.3
1	A	131	ARG	2.3
1	A	29	VAL	2.3
1	A	76	PRO	2.2
1	B	223	GLY	2.2
1	B	50	ALA	2.2
1	B	78	MET	2.1
1	B	139	ILE	2.1
1	B	120	VAL	2.1
1	B	146	ARG	2.1

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

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

6.3 Carbohydrates [i](#)

There are no carbohydrates 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.