



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 11:26 AM UTC

PDB ID : 2GD5 / pdb_00002gd5
Title : Structural basis for budding by the ESCRTIII factor CHMP3
Authors : Muziol, T.M.; Pineda-Molina, E.; Ravelli, R.B.; Zamborlini, A.; Usami, Y.;
Gottlinger, H.; Weissenhorn, W.
Deposited on : 2006-03-15
Resolution : 2.80 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

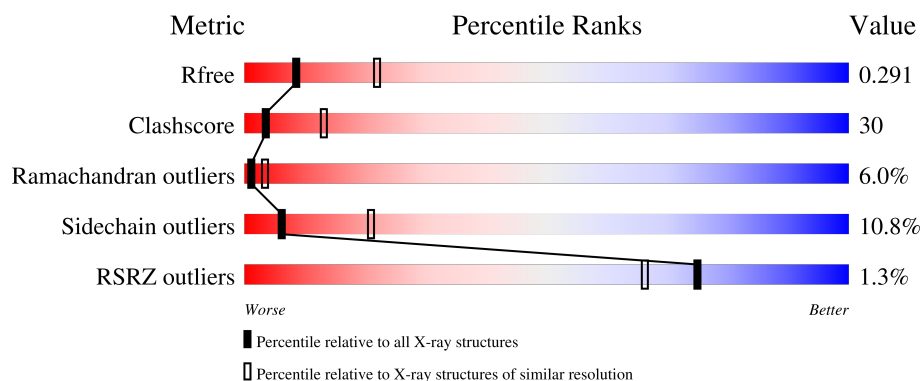
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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	3866 (2.80-2.80)
Clashscore	190562	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)
RSRZ outliers	180081	3869 (2.80-2.80)

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	179	34% 35% 9% • 21%
1	B	179	41% 32% 12% • 13%
1	C	179	38% 36% • • 21%
1	D	179	43% 37% 10% 9%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 4746 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 Charged multivesicular body protein 3.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	142	Total	C	N	O	S	Se	0	0	0
			1134	710	207	205	1	11			
1	B	156	Total	C	N	O	S	Se	0	0	0
			1219	763	223	220	1	12			
1	C	142	Total	C	N	O	S	Se	0	0	0
			1123	703	204	204	1	11			
1	D	162	Total	C	N	O	S	Se	0	0	0
			1270	793	229	234	1	13			

There are 64 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	5	GLY	-	cloning artifact	UNP Q9Y3E7
A	6	ALA	-	cloning artifact	UNP Q9Y3E7
A	7	MSE	-	cloning artifact	UNP Q9Y3E7
A	8	ALA	-	cloning artifact	UNP Q9Y3E7
A	27	MSE	MET	modified residue	UNP Q9Y3E7
A	67	MSE	MET	modified residue	UNP Q9Y3E7
A	84	MSE	MET	modified residue	UNP Q9Y3E7
A	89	MSE	MET	modified residue	UNP Q9Y3E7
A	91	MSE	MET	modified residue	UNP Q9Y3E7
A	111	MSE	MET	modified residue	UNP Q9Y3E7
A	114	MSE	MET	modified residue	UNP Q9Y3E7
A	127	MSE	MET	modified residue	UNP Q9Y3E7
A	134	MSE	MET	modified residue	UNP Q9Y3E7
A	135	MSE	MET	modified residue	UNP Q9Y3E7
A	157	MSE	MET	modified residue	UNP Q9Y3E7
A	163	MSE	MET	modified residue	UNP Q9Y3E7
B	5	GLY	-	cloning artifact	UNP Q9Y3E7
B	6	ALA	-	cloning artifact	UNP Q9Y3E7
B	7	MSE	-	cloning artifact	UNP Q9Y3E7
B	8	ALA	-	cloning artifact	UNP Q9Y3E7
B	27	MSE	MET	modified residue	UNP Q9Y3E7

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Chain	Residue	Modelled	Actual	Comment	Reference
B	67	MSE	MET	modified residue	UNP Q9Y3E7
B	84	MSE	MET	modified residue	UNP Q9Y3E7
B	89	MSE	MET	modified residue	UNP Q9Y3E7
B	91	MSE	MET	modified residue	UNP Q9Y3E7
B	111	MSE	MET	modified residue	UNP Q9Y3E7
B	114	MSE	MET	modified residue	UNP Q9Y3E7
B	127	MSE	MET	modified residue	UNP Q9Y3E7
B	134	MSE	MET	modified residue	UNP Q9Y3E7
B	135	MSE	MET	modified residue	UNP Q9Y3E7
B	157	MSE	MET	modified residue	UNP Q9Y3E7
B	163	MSE	MET	modified residue	UNP Q9Y3E7
C	5	GLY	-	cloning artifact	UNP Q9Y3E7
C	6	ALA	-	cloning artifact	UNP Q9Y3E7
C	7	MSE	-	cloning artifact	UNP Q9Y3E7
C	8	ALA	-	cloning artifact	UNP Q9Y3E7
C	27	MSE	MET	modified residue	UNP Q9Y3E7
C	67	MSE	MET	modified residue	UNP Q9Y3E7
C	84	MSE	MET	modified residue	UNP Q9Y3E7
C	89	MSE	MET	modified residue	UNP Q9Y3E7
C	91	MSE	MET	modified residue	UNP Q9Y3E7
C	111	MSE	MET	modified residue	UNP Q9Y3E7
C	114	MSE	MET	modified residue	UNP Q9Y3E7
C	127	MSE	MET	modified residue	UNP Q9Y3E7
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C	135	MSE	MET	modified residue	UNP Q9Y3E7
C	157	MSE	MET	modified residue	UNP Q9Y3E7
C	163	MSE	MET	modified residue	UNP Q9Y3E7
D	5	GLY	-	cloning artifact	UNP Q9Y3E7
D	6	ALA	-	cloning artifact	UNP Q9Y3E7
D	7	MSE	-	cloning artifact	UNP Q9Y3E7
D	8	ALA	-	cloning artifact	UNP Q9Y3E7
D	27	MSE	MET	modified residue	UNP Q9Y3E7
D	67	MSE	MET	modified residue	UNP Q9Y3E7
D	84	MSE	MET	modified residue	UNP Q9Y3E7
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D	111	MSE	MET	modified residue	UNP Q9Y3E7
D	114	MSE	MET	modified residue	UNP Q9Y3E7
D	127	MSE	MET	modified residue	UNP Q9Y3E7
D	134	MSE	MET	modified residue	UNP Q9Y3E7
D	135	MSE	MET	modified residue	UNP Q9Y3E7
D	157	MSE	MET	modified residue	UNP Q9Y3E7

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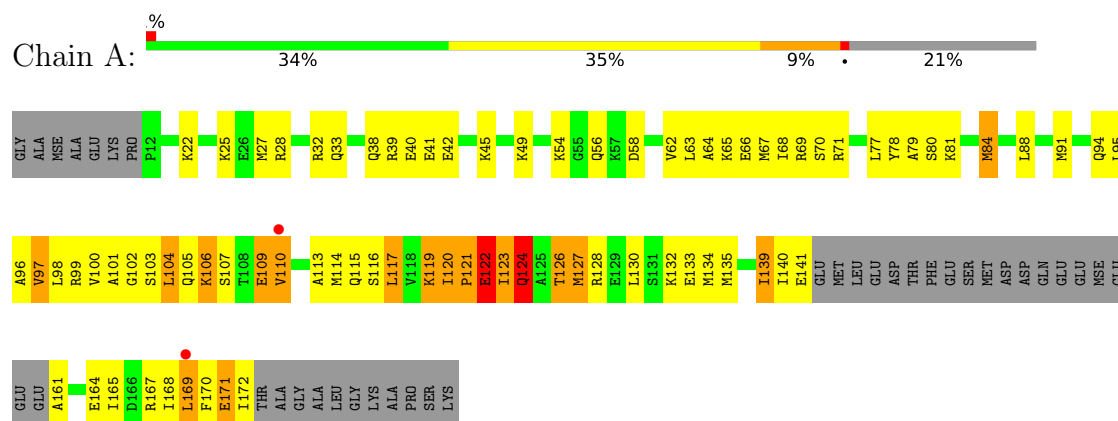
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Chain	Residue	Modelled	Actual	Comment	Reference
D	163	MSE	MET	modified residue	UNP Q9Y3E7

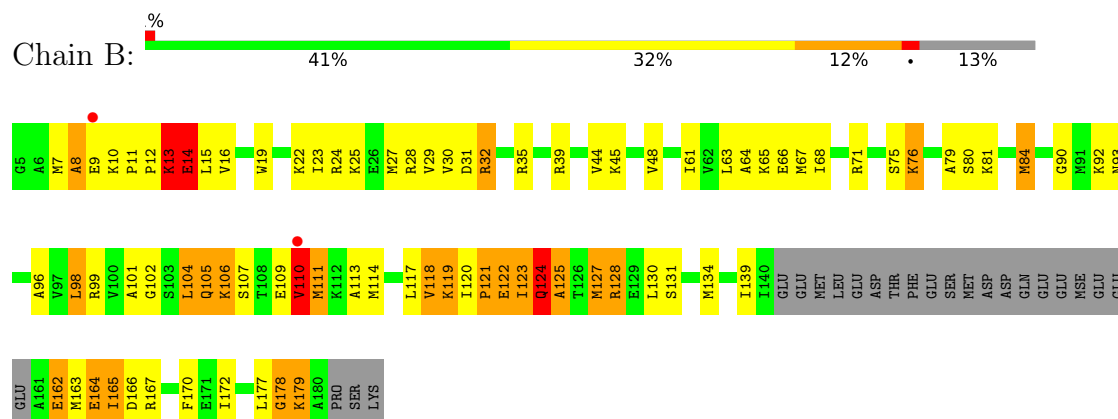
3 Residue-property plots [i](#)

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.

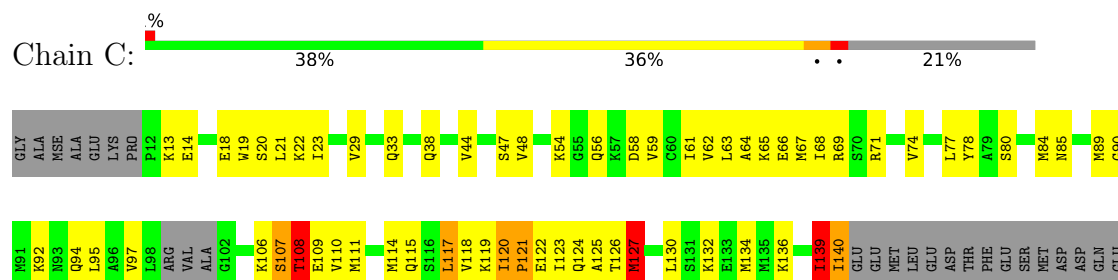
• Molecule 1: Charged multivesicular body protein 3

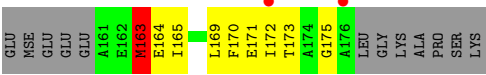


• Molecule 1: Charged multivesicular body protein 3

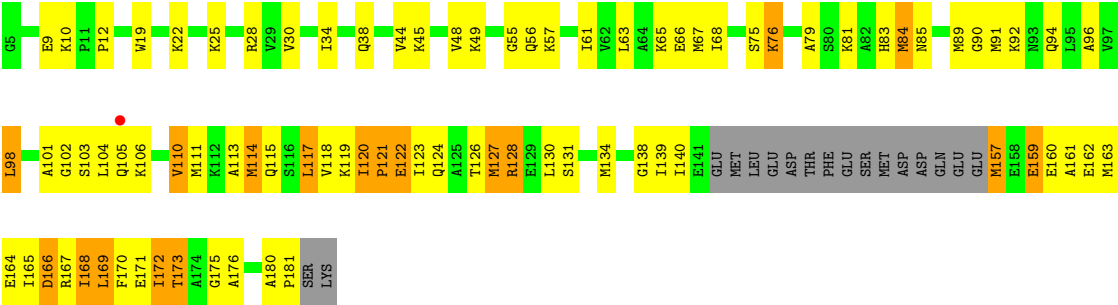


• Molecule 1: Charged multivesicular body protein 3





● Molecule 1: Charged multivesicular body protein 3



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	33.58Å 72.57Å 89.23Å 68.68° 83.61° 76.70°	Depositor
Resolution (Å)	20.00 – 2.80 20.00 – 2.80	Depositor EDS
% Data completeness (in resolution range)	95.7 (20.00-2.80) 95.4 (20.00-2.80)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.63 (at 2.81Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.259 , 0.301 0.252 , 0.291	Depositor DCC
R_{free} test set	914 reflections (4.88%)	wwPDB-VP
Wilson B-factor (Å ²)	62.6	Xtriage
Anisotropy	0.714	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 61.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	4746	wwPDB-VP
Average B, all atoms (Å ²)	59.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 13.63% 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](#)

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	0.91	1/1128 (0.1%)	1.10	2/1476 (0.1%)
1	B	0.93	1/1213 (0.1%)	1.09	5/1589 (0.3%)
1	C	0.89	1/1116 (0.1%)	1.05	4/1459 (0.3%)
1	D	0.94	2/1265 (0.2%)	1.09	4/1659 (0.2%)
All	All	0.92	5/4722 (0.1%)	1.08	15/6183 (0.2%)

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	84	MSE	SE-CE	-7.47	1.73	1.95
1	D	84	MSE	SE-CE	-6.55	1.75	1.95
1	D	114	MSE	SE-CE	-5.67	1.78	1.95
1	C	127	MSE	SE-CE	-5.56	1.78	1.95
1	B	84	MSE	SE-CE	-5.11	1.80	1.95

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	14	GLU	N-CA-C	-8.35	102.11	113.30
1	B	163	MSE	N-CA-C	-7.04	102.72	112.30
1	C	120	ILE	CA-C-N	6.74	128.26	119.84
1	C	120	ILE	C-N-CA	6.74	128.26	119.84
1	D	169	LEU	N-CA-C	-6.45	103.16	111.02
1	C	115	GLN	N-CA-C	-6.38	106.08	114.31
1	D	120	ILE	CA-C-N	6.33	127.75	119.84
1	D	120	ILE	C-N-CA	6.33	127.75	119.84
1	B	125	ALA	N-CA-C	-6.17	104.82	112.90
1	C	92	LYS	N-CA-C	-5.74	104.93	111.07
1	A	171	GLU	N-CA-C	-5.38	99.35	110.80
1	A	126	THR	N-CA-C	-5.18	105.33	110.97
1	D	161	ALA	N-CA-C	-5.13	106.99	113.20
1	B	111	MSE	N-CA-C	-5.12	107.10	113.55
1	B	24	ARG	N-CA-C	-5.06	105.68	111.14

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	1134	0	1232	83	0
1	B	1219	0	1325	84	0
1	C	1123	0	1218	76	0
1	D	1270	0	1365	69	0
All	All	4746	0	5140	293	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 30.

All (293) 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:169:LEU:O	1:D:173:THR:HG22	1.37	1.20
1:C:33:GLN:HE22	1:C:122:GLU:HG2	1.16	1.09
1:C:33:GLN:NE2	1:C:122:GLU:HG2	1.74	1.00
1:D:160:GLU:HB3	1:D:163:MSE:HE2	1.40	1.00
1:C:71:ARG:NH2	1:D:101:ALA:HB2	1.77	0.99
1:C:71:ARG:HH22	1:D:101:ALA:HB2	1.25	0.96
1:C:172:ILE:HD12	1:C:173:THR:HG22	1.46	0.96
1:C:139:ILE:HD13	1:C:139:ILE:H	1.27	0.94
1:D:165:ILE:HD12	1:D:166:ASP:N	1.82	0.93
1:C:58:ASP:O	1:C:62:VAL:HG23	1.67	0.93
1:D:165:ILE:HD12	1:D:166:ASP:H	1.34	0.92
1:C:33:GLN:HE22	1:C:122:GLU:CG	1.84	0.89
1:A:120:ILE:HG13	1:A:121:PRO:HD2	1.54	0.88
1:A:101:ALA:HB2	1:B:71:ARG:HH22	1.39	0.87
1:A:116:SER:HA	1:A:119:LYS:HE2	1.56	0.85
1:D:124:GLN:O	1:D:128:ARG:HB2	1.77	0.84
1:A:38:GLN:HE22	1:B:96:ALA:HB1	1.43	0.83
1:A:164:GLU:HA	1:A:167:ARG:HB2	1.61	0.82
1:C:172:ILE:CD1	1:C:173:THR:HG22	2.09	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:45:LYS:HA	1:A:67:MSE:HE1	1.61	0.81
1:B:98:LEU:HD23	1:B:102:GLY:HA2	1.65	0.79
1:A:67:MSE:HE3	1:B:172:ILE:HD13	1.66	0.78
1:D:169:LEU:C	1:D:173:THR:HG22	2.08	0.78
1:A:71:ARG:NH2	1:B:101:ALA:HB2	1.99	0.78
1:B:166:ASP:HB3	1:B:179:LYS:HA	1.63	0.77
1:C:139:ILE:H	1:C:139:ILE:CD1	1.98	0.76
1:B:125:ALA:HA	1:B:128:ARG:HH12	1.50	0.76
1:A:27:MSE:HG2	1:A:84:MSE:HE3	1.66	0.76
1:D:111:MSE:HG3	1:D:140:ILE:HG23	1.67	0.76
1:A:71:ARG:HH22	1:B:101:ALA:HB2	1.50	0.74
1:A:68:ILE:HG13	1:A:69:ARG:N	2.01	0.73
1:A:114:MSE:HE2	1:A:134:MSE:SE	2.39	0.73
1:B:128:ARG:HH11	1:B:128:ARG:HB2	1.52	0.73
1:D:123:ILE:HD12	1:D:127:MSE:HE2	1.71	0.73
1:C:48:VAL:HG11	1:D:172:ILE:HD11	1.68	0.73
1:B:113:ALA:O	1:B:117:LEU:HB2	1.88	0.72
1:C:169:LEU:O	1:C:172:ILE:HG13	1.90	0.72
1:C:172:ILE:HD12	1:C:173:THR:CG2	2.20	0.72
1:B:125:ALA:HA	1:B:128:ARG:NH1	2.04	0.72
1:B:162:GLU:OE1	1:B:165:ILE:HD12	1.90	0.72
1:D:157:MSE:HG3	1:D:159:GLU:HB2	1.71	0.71
1:A:117:LEU:O	1:A:120:ILE:HG22	1.91	0.71
1:C:139:ILE:HD13	1:C:139:ILE:N	2.03	0.71
1:C:29:VAL:O	1:C:33:GLN:HG3	1.90	0.71
1:B:119:LYS:HD3	1:B:119:LYS:C	2.16	0.70
1:D:106:LYS:HG3	1:D:138:GLY:O	1.91	0.70
1:B:120:ILE:HG23	1:B:121:PRO:HD3	1.74	0.69
1:A:109:GLU:OE2	1:A:109:GLU:HA	1.90	0.69
1:C:111:MSE:SE	1:C:140:ILE:HB	2.43	0.69
1:B:76:LYS:HB2	1:B:76:LYS:NZ	2.08	0.69
1:C:170:PHE:O	1:C:172:ILE:N	2.26	0.68
1:B:25:LYS:HA	1:B:28:ARG:NH1	2.09	0.68
1:D:94:GLN:HE22	1:D:105:GLN:H	1.41	0.68
1:B:165:ILE:HD13	1:B:166:ASP:H	1.59	0.67
1:C:111:MSE:SE	1:C:140:ILE:HD13	2.45	0.67
1:C:63:LEU:O	1:C:66:GLU:HB3	1.95	0.67
1:D:122:GLU:CD	1:D:122:GLU:H	2.03	0.66
1:A:94:GLN:NE2	1:A:94:GLN:HA	2.11	0.65
1:D:157:MSE:CG	1:D:159:GLU:HB2	2.26	0.65
1:A:45:LYS:CA	1:A:67:MSE:HE1	2.25	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:161:ALA:O	1:A:165:ILE:HG23	1.97	0.65
1:B:25:LYS:HA	1:B:28:ARG:HH11	1.62	0.65
1:B:118:VAL:HG12	1:B:127:MSE:HB3	1.79	0.64
1:C:107:SER:H	1:C:139:ILE:HG22	1.63	0.64
1:D:63:LEU:O	1:D:66:GLU:HB3	1.98	0.64
1:A:168:ILE:C	1:A:170:PHE:H	2.05	0.63
1:B:11:PRO:HB2	1:B:15:LEU:HD11	1.81	0.63
1:A:101:ALA:HB2	1:B:71:ARG:NH2	2.12	0.63
1:B:32:ARG:HG3	1:B:32:ARG:HH11	1.64	0.63
1:B:114:MSE:HE2	1:B:134:MSE:SE	2.49	0.62
1:C:22:LYS:HD2	1:C:130:LEU:HD21	1.81	0.62
1:B:128:ARG:HB2	1:B:128:ARG:NH1	2.15	0.62
1:A:22:LYS:HD2	1:A:130:LEU:HD21	1.82	0.62
1:D:76:LYS:HB2	1:D:76:LYS:NZ	2.14	0.61
1:C:65:LYS:O	1:C:68:ILE:HG12	2.00	0.61
1:B:11:PRO:HB2	1:B:15:LEU:CD1	2.31	0.60
1:D:114:MSE:HE2	1:D:134:MSE:SE	2.51	0.60
1:B:29:VAL:O	1:B:32:ARG:HB3	2.01	0.60
1:A:123:ILE:HD12	1:A:124:GLN:N	2.17	0.60
1:B:63:LEU:O	1:B:66:GLU:HB3	2.01	0.60
1:B:109:GLU:OE2	1:B:109:GLU:HA	2.01	0.60
1:C:106:LYS:HA	1:C:139:ILE:HA	1.83	0.60
1:B:105:GLN:OE1	1:B:106:LYS:O	2.19	0.60
1:C:33:GLN:HE22	1:C:122:GLU:CD	2.09	0.60
1:B:9:GLU:O	1:B:9:GLU:HG2	2.02	0.59
1:C:71:ARG:HH22	1:D:101:ALA:CB	2.09	0.59
1:C:94:GLN:HA	1:C:94:GLN:NE2	2.17	0.59
1:C:56:GLN:HB3	1:C:59:VAL:HG23	1.84	0.59
1:D:164:GLU:HG3	1:D:167:ARG:NH1	2.18	0.59
1:D:169:LEU:O	1:D:172:ILE:HG12	2.03	0.59
1:A:67:MSE:HE3	1:B:172:ILE:CD1	2.33	0.59
1:C:68:ILE:HG13	1:C:69:ARG:N	2.17	0.58
1:C:61:ILE:O	1:C:64:ALA:HB3	2.04	0.58
1:A:63:LEU:O	1:A:64:ALA:C	2.44	0.58
1:B:122:GLU:C	1:B:124:GLN:H	2.11	0.58
1:A:33:GLN:HE22	1:A:122:GLU:CD	2.12	0.57
1:B:104:LEU:HD13	1:B:139:ILE:HD11	1.86	0.57
1:D:79:ALA:O	1:D:83:HIS:HD2	1.87	0.57
1:D:124:GLN:HG2	1:D:128:ARG:CZ	2.34	0.57
1:C:54:LYS:HD2	1:C:56:GLN:HE22	1.68	0.57
1:A:81:LYS:HA	1:A:84:MSE:CE	2.34	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:22:LYS:HD2	1:B:130:LEU:HD21	1.84	0.57
1:B:120:ILE:CG2	1:B:121:PRO:HD3	2.35	0.57
1:D:34:ILE:O	1:D:38:GLN:HG2	2.04	0.57
1:D:157:MSE:HE3	1:D:157:MSE:HA	1.87	0.57
1:A:58:ASP:O	1:A:62:VAL:HG23	2.04	0.56
1:B:123:ILE:C	1:B:125:ALA:H	2.13	0.56
1:C:74:VAL:O	1:C:77:LEU:HB2	2.06	0.56
1:C:170:PHE:C	1:C:172:ILE:H	2.13	0.56
1:A:167:ARG:O	1:A:170:PHE:HB2	2.06	0.56
1:B:30:VAL:HG21	1:B:84:MSE:HE1	1.88	0.56
1:C:173:THR:HG23	1:C:175:GLY:H	1.71	0.56
1:A:169:LEU:O	1:A:172:ILE:HG12	2.06	0.55
1:B:123:ILE:O	1:B:125:ALA:N	2.33	0.55
1:A:120:ILE:HG13	1:A:121:PRO:CD	2.33	0.55
1:A:38:GLN:HE22	1:B:96:ALA:CB	2.17	0.55
1:D:44:VAL:O	1:D:48:VAL:HG23	2.06	0.54
1:A:68:ILE:HG13	1:A:69:ARG:H	1.73	0.54
1:A:122:GLU:O	1:A:124:GLN:HG3	2.08	0.54
1:A:65:LYS:O	1:A:68:ILE:HG12	2.08	0.54
1:C:134:MSE:HB3	1:C:139:ILE:HG12	1.90	0.54
1:B:93:ASN:O	1:B:96:ALA:HB3	2.08	0.54
1:D:25:LYS:HA	1:D:28:ARG:NH1	2.22	0.53
1:B:7:MSE:O	1:B:8:ALA:O	2.26	0.53
1:B:45:LYS:HA	1:B:67:MSE:HE1	1.90	0.53
1:B:170:PHE:HD2	1:B:178:GLY:HA2	1.73	0.53
1:C:54:LYS:HD2	1:C:56:GLN:NE2	2.24	0.53
1:C:71:ARG:NH2	1:D:101:ALA:CB	2.62	0.53
1:D:45:LYS:HE2	1:D:49:LYS:HE3	1.90	0.53
1:D:157:MSE:HA	1:D:157:MSE:CE	2.38	0.53
1:C:106:LYS:O	1:C:106:LYS:HG3	2.09	0.53
1:A:105:GLN:O	1:A:107:SER:N	2.41	0.53
1:A:140:ILE:HG22	1:A:141:GLU:N	2.24	0.53
1:B:81:LYS:HA	1:B:84:MSE:HE3	1.90	0.53
1:D:115:GLN:HE21	1:D:119:LYS:HE2	1.74	0.53
1:D:118:VAL:HG12	1:D:127:MSE:HB3	1.91	0.52
1:A:45:LYS:HA	1:A:67:MSE:CE	2.38	0.52
1:B:76:LYS:HB2	1:B:76:LYS:HZ3	1.74	0.52
1:B:121:PRO:O	1:B:122:GLU:HB2	2.10	0.52
1:C:120:ILE:HD13	1:C:123:ILE:HD11	1.92	0.52
1:C:78:TYR:CZ	1:D:92:LYS:HG2	2.44	0.52
1:B:12:PRO:O	1:B:14:GLU:N	2.33	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:15:LEU:HB3	1:B:19:TRP:CZ2	2.45	0.52
1:C:140:ILE:HD12	1:C:140:ILE:H	1.75	0.52
1:A:54:LYS:HB2	1:A:56:GLN:HE21	1.75	0.51
1:A:104:LEU:HB3	1:A:139:ILE:HG22	1.93	0.51
1:B:119:LYS:HD2	1:B:124:GLN:HG2	1.93	0.51
1:B:61:ILE:O	1:B:64:ALA:HB3	2.10	0.51
1:C:80:SER:OG	1:C:120:ILE:HG12	2.11	0.51
1:D:79:ALA:O	1:D:83:HIS:CD2	2.64	0.51
1:D:84:MSE:HG3	1:D:117:LEU:HD21	1.92	0.51
1:C:23:ILE:HD11	1:C:114:MSE:HE1	1.93	0.51
1:B:44:VAL:O	1:B:48:VAL:HG23	2.11	0.51
1:D:127:MSE:O	1:D:131:SER:HB2	2.11	0.51
1:A:49:LYS:HE2	1:B:172:ILE:O	2.09	0.51
1:C:68:ILE:CG1	1:C:69:ARG:N	2.74	0.51
1:B:13:LYS:N	1:B:13:LYS:HE2	2.25	0.51
1:C:38:GLN:NE2	1:D:96:ALA:HB1	2.26	0.51
1:B:162:GLU:C	1:B:162:GLU:CD	2.80	0.50
1:C:90:GLY:HA3	1:C:110:VAL:HG11	1.92	0.50
1:B:23:ILE:O	1:B:27:MSE:HG3	2.12	0.50
1:D:45:LYS:HA	1:D:67:MSE:HE1	1.92	0.50
1:D:103:SER:O	1:D:105:GLN:NE2	2.43	0.50
1:D:165:ILE:CD1	1:D:166:ASP:H	2.17	0.50
1:A:67:MSE:O	1:A:68:ILE:C	2.55	0.49
1:A:117:LEU:HG	1:A:127:MSE:HE3	1.93	0.49
1:D:157:MSE:HG3	1:D:159:GLU:H	1.77	0.49
1:A:67:MSE:O	1:A:70:SER:HB2	2.12	0.49
1:A:40:GLU:OE2	1:A:40:GLU:HA	2.13	0.49
1:C:120:ILE:O	1:C:124:GLN:N	2.38	0.49
1:C:90:GLY:HA3	1:C:110:VAL:CG1	2.42	0.49
1:D:89:MSE:O	1:D:90:GLY:C	2.56	0.49
1:A:164:GLU:O	1:A:168:ILE:HG13	2.13	0.49
1:B:121:PRO:O	1:B:122:GLU:CB	2.60	0.49
1:A:168:ILE:C	1:A:170:PHE:N	2.71	0.49
1:A:139:ILE:O	1:A:139:ILE:HG13	2.12	0.48
1:D:30:VAL:HG21	1:D:84:MSE:HE1	1.95	0.48
1:D:159:GLU:O	1:D:162:GLU:HG2	2.13	0.48
1:C:44:VAL:O	1:C:48:VAL:HG23	2.13	0.48
1:A:99:ARG:HA	1:A:99:ARG:CZ	2.44	0.48
1:D:139:ILE:O	1:D:139:ILE:HG22	2.13	0.48
1:D:173:THR:OG1	1:D:176:ALA:HB3	2.14	0.48
1:D:169:LEU:C	1:D:173:THR:CG2	2.85	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:81:LYS:HA	1:D:84:MSE:HE3	1.96	0.48
1:D:98:LEU:HA	1:D:102:GLY:H	1.79	0.48
1:D:180:ALA:HB3	1:D:181:PRO:HD3	1.95	0.47
1:B:107:SER:HB3	1:B:110:VAL:HG22	1.96	0.47
1:C:48:VAL:HG11	1:D:172:ILE:CD1	2.42	0.47
1:A:41:GLU:CD	1:A:70:SER:HB3	2.40	0.47
1:B:13:LYS:HE2	1:B:13:LYS:CA	2.44	0.47
1:D:170:PHE:CE1	1:D:175:GLY:HA2	2.49	0.47
1:B:15:LEU:N	1:B:15:LEU:HD12	2.30	0.47
1:D:120:ILE:O	1:D:124:GLN:HB2	2.14	0.47
1:A:88:LEU:O	1:A:91:MSE:HB2	2.14	0.47
1:C:84:MSE:HG3	1:C:117:LEU:HD21	1.96	0.47
1:D:110:VAL:HG23	1:D:110:VAL:O	2.14	0.46
1:A:113:ALA:C	1:A:115:GLN:H	2.24	0.46
1:C:107:SER:O	1:C:109:GLU:N	2.49	0.46
1:B:128:ARG:HH11	1:B:128:ARG:CB	2.25	0.46
1:A:117:LEU:C	1:A:119:LYS:H	2.23	0.46
1:C:109:GLU:HA	1:C:109:GLU:OE2	2.16	0.46
1:C:117:LEU:O	1:C:120:ILE:HD12	2.16	0.46
1:A:78:TYR:O	1:A:79:ALA:C	2.56	0.46
1:A:140:ILE:CG2	1:A:141:GLU:N	2.79	0.46
1:B:30:VAL:CG2	1:B:84:MSE:HE1	2.46	0.46
1:B:170:PHE:CD2	1:B:178:GLY:HA2	2.51	0.45
1:D:168:ILE:O	1:D:169:LEU:C	2.60	0.45
1:A:25:LYS:HA	1:A:28:ARG:NH1	2.31	0.45
1:B:12:PRO:C	1:B:14:GLU:H	2.19	0.45
1:D:65:LYS:O	1:D:68:ILE:HG12	2.17	0.45
1:B:170:PHE:CD2	1:B:179:LYS:HG2	2.51	0.45
1:C:67:MSE:O	1:C:68:ILE:C	2.58	0.45
1:B:90:GLY:HA3	1:B:110:VAL:CG1	2.46	0.45
1:D:61:ILE:O	1:D:65:LYS:HG3	2.17	0.45
1:A:63:LEU:O	1:A:66:GLU:HB3	2.17	0.45
1:A:139:ILE:O	1:A:140:ILE:HD13	2.17	0.45
1:C:33:GLN:NE2	1:C:122:GLU:OE2	2.50	0.44
1:C:13:LYS:HZ3	1:C:95:LEU:HD21	1.83	0.44
1:D:98:LEU:HG	1:D:102:GLY:HA2	1.98	0.44
1:C:122:GLU:CD	1:C:122:GLU:H	2.13	0.44
1:C:19:TRP:O	1:C:20:SER:C	2.58	0.44
1:D:55:GLY:O	1:D:57:LYS:N	2.49	0.44
1:A:78:TYR:OH	1:B:92:LYS:HG2	2.17	0.44
1:A:81:LYS:HA	1:A:84:MSE:HE2	1.97	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:14:GLU:C	1:B:16:VAL:N	2.72	0.44
1:C:173:THR:HG23	1:C:175:GLY:N	2.32	0.44
1:A:94:GLN:O	1:A:95:LEU:C	2.61	0.44
1:B:109:GLU:C	1:B:111:MSE:H	2.25	0.44
1:A:63:LEU:O	1:A:66:GLU:N	2.51	0.44
1:B:35:ARG:HG2	1:B:39:ARG:HH21	1.83	0.44
1:D:89:MSE:O	1:D:92:LYS:N	2.51	0.44
1:D:22:LYS:HD2	1:D:130:LEU:HD21	2.00	0.44
1:C:114:MSE:HE2	1:C:134:MSE:SE	2.68	0.43
1:A:97:VAL:HG12	1:A:103:SER:O	2.17	0.43
1:A:105:GLN:HE22	1:A:167:ARG:HH12	1.67	0.43
1:C:77:LEU:HD23	1:C:77:LEU:HA	1.86	0.43
1:A:22:LYS:CD	1:A:130:LEU:HD21	2.47	0.43
1:A:121:PRO:HB2	1:A:122:GLU:H	1.60	0.43
1:A:124:GLN:HE21	1:A:128:ARG:HH22	1.67	0.43
1:B:65:LYS:O	1:B:68:ILE:HG12	2.19	0.43
1:B:164:GLU:OE1	1:B:167:ARG:NH2	2.52	0.43
1:A:39:ARG:HA	1:A:42:GLU:OE1	2.19	0.43
1:A:124:GLN:NE2	1:A:128:ARG:HH22	2.16	0.43
1:A:95:LEU:O	1:A:98:LEU:HB2	2.19	0.43
1:A:96:ALA:C	1:A:98:LEU:N	2.76	0.43
1:C:77:LEU:O	1:C:80:SER:HB2	2.19	0.43
1:D:114:MSE:CE	1:D:134:MSE:SE	3.16	0.43
1:C:117:LEU:C	1:C:119:LYS:H	2.27	0.42
1:B:13:LYS:HG3	1:B:98:LEU:HD21	2.01	0.42
1:B:76:LYS:O	1:B:79:ALA:HB3	2.19	0.42
1:C:18:GLU:O	1:C:21:LEU:HB2	2.19	0.42
1:B:122:GLU:C	1:B:124:GLN:N	2.77	0.42
1:B:130:LEU:O	1:B:131:SER:C	2.63	0.42
1:C:54:LYS:HB2	1:C:56:GLN:HE21	1.85	0.42
1:A:94:GLN:CA	1:A:94:GLN:HE21	2.32	0.42
1:A:106:LYS:HB2	1:A:106:LYS:HE3	1.82	0.42
1:C:122:GLU:OE1	1:C:122:GLU:N	2.27	0.42
1:D:12:PRO:HB3	1:D:104:LEU:HG	2.02	0.42
1:A:99:ARG:HA	1:A:99:ARG:NH1	2.35	0.42
1:B:81:LYS:HA	1:B:84:MSE:CE	2.50	0.42
1:C:85:ASN:O	1:C:89:MSE:HG2	2.20	0.42
1:B:75:SER:O	1:B:76:LYS:C	2.63	0.42
1:D:139:ILE:O	1:D:139:ILE:CG2	2.68	0.42
1:A:77:LEU:O	1:A:80:SER:HB2	2.19	0.41
1:C:109:GLU:C	1:C:111:MSE:H	2.26	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:80:SER:O	1:A:81:LYS:C	2.61	0.41
1:C:107:SER:C	1:C:109:GLU:N	2.77	0.41
1:D:76:LYS:HB2	1:D:76:LYS:HZ2	1.86	0.41
1:D:120:ILE:HA	1:D:121:PRO:HD2	1.63	0.41
1:A:135:MSE:HA	1:A:140:ILE:HB	2.02	0.41
1:C:121:PRO:HA	1:C:124:GLN:OE1	2.20	0.41
1:A:65:LYS:HA	1:A:68:ILE:HG12	2.03	0.41
1:A:81:LYS:HA	1:A:84:MSE:HE3	2.02	0.41
1:A:123:ILE:HD12	1:A:123:ILE:C	2.45	0.41
1:B:110:VAL:HG23	1:B:110:VAL:O	2.19	0.41
1:D:113:ALA:O	1:D:117:LEU:HB2	2.21	0.41
1:D:19:TRP:HE3	1:D:91:MSE:SE	2.54	0.41
1:A:94:GLN:HA	1:A:94:GLN:HE21	1.80	0.41
1:C:126:THR:O	1:C:127:MSE:C	2.64	0.41
1:C:132:LYS:HE3	1:C:132:LYS:HB2	1.84	0.41
1:B:30:VAL:O	1:B:31:ASP:C	2.65	0.40
1:B:165:ILE:CD1	1:B:166:ASP:H	2.30	0.40
1:C:56:GLN:HB3	1:C:59:VAL:CG2	2.50	0.40
1:C:106:LYS:O	1:C:108:THR:N	2.55	0.40
1:C:163:MSE:O	1:C:164:GLU:C	2.63	0.40
1:A:38:GLN:NE2	1:B:96:ALA:HB1	2.22	0.40
1:A:110:VAL:O	1:A:110:VAL:HG23	2.21	0.40
1:A:132:LYS:O	1:A:133:GLU:C	2.64	0.40
1:B:79:ALA:O	1:B:80:SER:C	2.65	0.40
1:B:114:MSE:HE2	1:B:134:MSE:CE	2.51	0.40
1:B:177:LEU:O	1:B:178:GLY:O	2.40	0.40
1:C:172:ILE:HD12	1:C:173:THR:CB	2.52	0.40
1:A:54:LYS:HD2	1:A:56:GLN:NE2	2.36	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	138/179 (77%)	118 (86%)	12 (9%)	8 (6%)	1	4
1	B	152/179 (85%)	121 (80%)	20 (13%)	11 (7%)	1	2
1	C	136/179 (76%)	108 (79%)	16 (12%)	12 (9%)	0	1
1	D	158/179 (88%)	143 (90%)	11 (7%)	4 (2%)	4	16
All	All	584/716 (82%)	490 (84%)	59 (10%)	35 (6%)	1	3

All (35) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	121	PRO
1	A	122	GLU
1	B	8	ALA
1	B	122	GLU
1	B	124	GLN
1	C	107	SER
1	C	136	LYS
1	C	163	MSE
1	C	171	GLU
1	A	106	LYS
1	A	124	GLN
1	A	171	GLU
1	B	13	LYS
1	C	118	VAL
1	C	125	ALA
1	C	127	MSE
1	C	165	ILE
1	D	171	GLU
1	B	104	LEU
1	B	118	VAL
1	C	108	THR
1	D	56	GLN
1	A	169	LEU
1	A	100	VAL
1	B	123	ILE
1	B	178	GLY
1	C	121	PRO
1	C	139	ILE
1	B	106	LYS
1	A	102	GLY
1	B	110	VAL
1	B	121	PRO
1	D	172	ILE

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Mol	Chain	Res	Type
1	C	97	VAL
1	D	121	PRO

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	126/142 (89%)	112 (89%)	14 (11%)	6	20
1	B	132/142 (93%)	115 (87%)	17 (13%)	4	14
1	C	124/142 (87%)	116 (94%)	8 (6%)	15	43
1	D	138/142 (97%)	121 (88%)	17 (12%)	4	16
All	All	520/568 (92%)	464 (89%)	56 (11%)	6	21

All (56) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	32	ARG
1	A	97	VAL
1	A	104	LEU
1	A	109	GLU
1	A	110	VAL
1	A	117	LEU
1	A	119	LYS
1	A	120	ILE
1	A	122	GLU
1	A	123	ILE
1	A	124	GLN
1	A	126	THR
1	A	127	MSE
1	A	139	ILE
1	B	10	LYS
1	B	13	LYS
1	B	14	GLU
1	B	32	ARG
1	B	76	LYS

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Mol	Chain	Res	Type
1	B	98	LEU
1	B	99	ARG
1	B	105	GLN
1	B	110	VAL
1	B	119	LYS
1	B	124	GLN
1	B	127	MSE
1	B	128	ARG
1	B	162	GLU
1	B	164	GLU
1	B	165	ILE
1	B	179	LYS
1	C	14	GLU
1	C	47	SER
1	C	108	THR
1	C	117	LEU
1	C	127	MSE
1	C	139	ILE
1	C	140	ILE
1	C	163	MSE
1	D	9	GLU
1	D	10	LYS
1	D	75	SER
1	D	76	LYS
1	D	85	ASN
1	D	98	LEU
1	D	110	VAL
1	D	117	LEU
1	D	122	GLU
1	D	126	THR
1	D	127	MSE
1	D	128	ARG
1	D	157	MSE
1	D	159	GLU
1	D	166	ASP
1	D	168	ILE
1	D	173	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	33	GLN

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Mol	Chain	Res	Type
1	A	38	GLN
1	A	56	GLN
1	A	93	ASN
1	A	94	GLN
1	A	105	GLN
1	A	124	GLN
1	B	38	GLN
1	B	93	ASN
1	B	94	GLN
1	C	94	GLN
1	D	17	ASN
1	D	83	HIS
1	D	94	GLN
1	D	115	GLN

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 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 [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	131/179 (73%)	-0.15	2 (1%) 72 63	23, 56, 90, 93	0
1	B	144/179 (80%)	-0.12	2 (1%) 73 64	38, 58, 82, 90	0
1	C	131/179 (73%)	-0.07	2 (1%) 72 63	34, 61, 92, 98	0
1	D	149/179 (83%)	-0.31	1 (0%) 84 77	29, 55, 71, 82	0
All	All	555/716 (77%)	-0.17	7 (1%) 75 66	23, 58, 88, 98	0

All (7) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	9	GLU	3.7
1	C	172	ILE	2.7
1	A	110	VAL	2.6
1	D	105	GLN	2.4
1	A	169	LEU	2.4
1	C	176	ALA	2.2
1	B	110	VAL	2.0

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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.