



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 1, 2026 – 11:14 AM UTC

PDB ID : 2B2Y / pdb_00002b2y
Title : Tandem chromodomains of human CHD1
Authors : Flanagan IV, J.F.; Mi, L.-Z.; Chruszcz, M.; Cymborowski, M.; Clines, K.L.;
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Deposited on : 2005-09-19
Resolution : 2.35 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
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

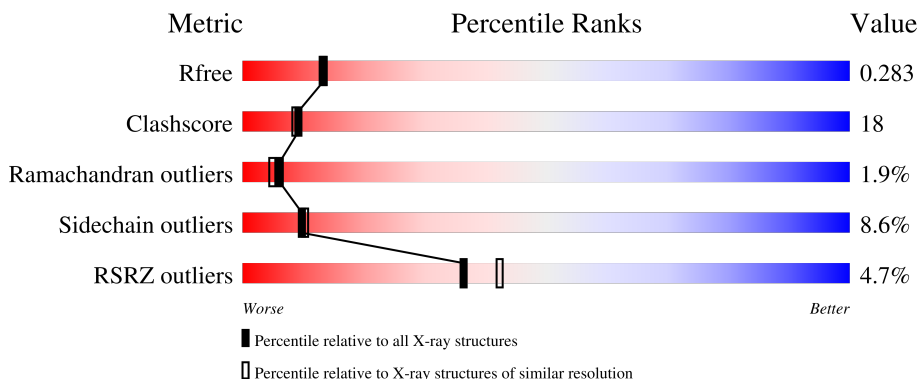
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.35 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	1596 (2.36-2.36)
Clashscore	190562	1663 (2.36-2.36)
Ramachandran outliers	187476	1646 (2.36-2.36)
Sidechain outliers	187428	1646 (2.36-2.36)
RSRZ outliers	180081	1598 (2.36-2.36)

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	187	
1	B	187	
2	C	115	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 3707 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 Chromodomain-helicase-DNA-binding protein 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	175	Total	C	N	O	S	0	0	0
			1438	906	247	278	7			
1	B	169	Total	C	N	O	S	0	0	0
			1383	871	234	271	7			

There are 22 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	cloning artifact	UNP O14646
A	2	LYS	-	cloning artifact	UNP O14646
A	3	LYS	-	cloning artifact	UNP O14646
A	4	HIS	-	expression tag	UNP O14646
A	5	HIS	-	expression tag	UNP O14646
A	6	HIS	-	expression tag	UNP O14646
A	7	HIS	-	expression tag	UNP O14646
A	8	HIS	-	expression tag	UNP O14646
A	9	HIS	-	expression tag	UNP O14646
A	186	LYS	-	cloning artifact	UNP O14646
A	187	LYS	-	cloning artifact	UNP O14646
B	1	MET	-	cloning artifact	UNP O14646
B	2	LYS	-	cloning artifact	UNP O14646
B	3	LYS	-	cloning artifact	UNP O14646
B	4	HIS	-	expression tag	UNP O14646
B	5	HIS	-	expression tag	UNP O14646
B	6	HIS	-	expression tag	UNP O14646
B	7	HIS	-	expression tag	UNP O14646
B	8	HIS	-	expression tag	UNP O14646
B	9	HIS	-	expression tag	UNP O14646
B	186	LYS	-	cloning artifact	UNP O14646
B	187	LYS	-	cloning artifact	UNP O14646

- Molecule 2 is a protein called Chromodomain-helicase-DNA-binding protein 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	86	Total 689	C 433	N 120	O 133	S 3	0	0	0

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	1	MET	-	cloning artifact	UNP O14646
C	2	LYS	-	cloning artifact	UNP O14646
C	3	LYS	-	cloning artifact	UNP O14646
C	4	HIS	-	expression tag	UNP O14646
C	5	HIS	-	expression tag	UNP O14646
C	6	HIS	-	expression tag	UNP O14646
C	7	HIS	-	expression tag	UNP O14646
C	8	HIS	-	expression tag	UNP O14646
C	9	HIS	-	expression tag	UNP O14646

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	100	Total 100	O 100	0	0
3	B	67	Total 67	O 67	0	0
3	C	30	Total 30	O 30	0	0

4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	112.27Å 55.03Å 101.55Å 90.00° 112.42° 90.00°	Depositor
Resolution (Å)	15.00 – 2.35 15.00 – 2.35	Depositor EDS
% Data completeness (in resolution range)	75.8 (15.00-2.35) 90.4 (15.00-2.35)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.09	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.95 (at 2.36Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.215 , 0.264 0.235 , 0.283	Depositor DCC
R_{free} test set	1507 reflections (6.88%)	wwPDB-VP
Wilson B-factor (Å ²)	40.7	Xtriage
Anisotropy	0.390	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 49.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	3707	wwPDB-VP
Average B, all atoms (Å ²)	46.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.33% 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

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	0.53	1/1473 (0.1%)	1.36	23/1983 (1.2%)
1	B	0.53	1/1416 (0.1%)	1.03	15/1911 (0.8%)
2	C	0.49	0/704	0.99	3/948 (0.3%)
All	All	0.52	2/3593 (0.1%)	1.17	41/4842 (0.8%)

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	1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	180	ASP	C-N	12.52	1.50	1.33
1	A	186	LYS	C-N	-6.86	1.23	1.33

All (41) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	47	ALA	N-CA-C	19.32	134.71	111.33
1	A	53	LYS	CB-CA-C	-16.57	93.42	109.83
1	A	186	LYS	CB-CA-C	-14.86	84.59	109.55
1	A	186	LYS	N-CA-C	11.98	129.29	113.72
1	A	47	ALA	CB-CA-C	-11.19	91.66	110.68
1	A	33	THR	N-CA-C	-10.37	98.06	113.61
1	A	32	ALA	CB-CA-C	-8.84	92.83	110.42
1	B	136	ILE	N-CA-C	-8.61	95.03	107.77
1	A	186	LYS	O-C-N	-8.42	111.99	122.35
1	A	62	ILE	N-CA-C	8.30	119.72	108.11
1	A	187	LYS	N-CA-CB	8.24	124.50	110.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	106	LYS	CB-CA-C	-8.23	97.17	110.84
1	A	107	ASN	N-CA-C	-7.42	94.99	110.80
2	C	62	ILE	N-CA-C	7.41	118.96	108.36
1	A	52	ASN	N-CA-C	-7.29	90.59	111.00
1	A	33	THR	N-CA-CB	7.22	121.56	110.80
1	A	32	ALA	N-CA-C	7.20	126.13	110.80
1	A	24	ILE	N-CA-C	-6.92	98.48	108.17
1	A	52	ASN	N-CA-CB	6.92	122.26	110.50
1	B	102	LYS	N-CA-C	-6.83	103.89	111.82
1	B	136	ILE	N-CA-CB	6.57	120.76	111.82
1	B	180	ASP	O-C-N	-6.33	114.51	122.17
1	B	135	ARG	CB-CA-C	6.22	122.14	110.95
1	A	187	LYS	N-CA-C	-6.11	93.91	111.00
1	B	154	LYS	N-CA-C	-5.97	99.47	108.96
2	C	13	PHE	N-CA-C	5.94	123.45	110.80
1	B	24	ILE	N-CA-C	-5.76	100.11	108.36
1	A	110	PRO	N-CA-C	-5.67	106.47	113.84
1	B	180	ASP	CA-C-N	5.61	128.07	120.38
1	B	180	ASP	C-N-CA	5.61	128.07	120.38
2	C	13	PHE	CB-CA-C	-5.48	99.51	110.42
1	B	158	LEU	CA-C-N	5.44	125.74	119.92
1	B	158	LEU	C-N-CA	5.44	125.74	119.92
1	A	53	LYS	N-CA-C	5.42	121.75	113.51
1	A	170	LEU	N-CA-C	5.40	117.03	111.03
1	B	38	ALA	N-CA-C	-5.36	105.47	112.23
1	B	44	ASP	CA-C-N	5.33	126.50	119.84
1	B	44	ASP	C-N-CA	5.33	126.50	119.84
1	B	54	GLU	N-CA-C	5.25	112.94	108.22
1	A	56	GLY	N-CA-C	5.22	120.58	112.60
1	A	38	ALA	N-CA-C	-5.17	105.33	111.69

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	186	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	1438	0	1359	33	0
1	B	1383	0	1279	58	0
2	C	689	0	649	39	0
3	A	100	0	0	1	0
3	B	67	0	0	3	0
3	C	30	0	0	3	0
All	All	3707	0	3287	124	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 18.

All (124) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:137:ILE:HD11	1:B:152:TYR:HD2	1.09	1.15
1:B:103:ARG:O	1:B:106:LYS:HD2	1.56	1.02
1:A:132:ILE:HG13	1:A:156:GLN:HG3	1.40	1.00
1:B:137:ILE:HD11	1:B:152:TYR:CD2	1.98	0.98
1:B:76:THR:HG23	1:B:79:THR:H	1.35	0.91
1:B:136:ILE:HD13	1:B:178:CYS:HB3	1.51	0.90
2:C:54:GLU:HA	2:C:55:PRO:C	2.01	0.86
1:B:181:GLU:O	1:B:185:ARG:HG3	1.77	0.84
1:A:52:ASN:O	1:A:53:LYS:HB2	1.77	0.84
1:B:135:ARG:HH22	1:B:185:ARG:NH1	1.78	0.80
1:B:181:GLU:OE1	3:B:254:HOH:O	2.01	0.78
1:A:103:ARG:O	1:A:106:LYS:HG3	1.83	0.77
1:B:171:ILE:HD12	1:B:172:SER:N	2.00	0.76
1:B:176:GLN:HE22	1:B:179:ILE:HD11	1.51	0.76
2:C:24:ILE:O	2:C:24:ILE:HD12	1.87	0.73
2:C:22:CYS:SG	2:C:58:ILE:HD11	2.28	0.73
1:B:99:GLN:O	1:B:103:ARG:HB2	1.92	0.69
1:A:159:PRO:HB3	1:B:123:THR:HG21	1.74	0.69
2:C:50:GLU:HA	2:C:50:GLU:OE1	1.92	0.68
1:B:176:GLN:NE2	1:B:179:ILE:HD11	2.07	0.68
1:B:137:ILE:C	1:B:137:ILE:HD12	2.21	0.66
2:C:36:ILE:O	2:C:36:ILE:HD13	1.96	0.66
2:C:16:ILE:HD13	2:C:62:ILE:HG23	1.77	0.65
2:C:54:GLU:HA	2:C:55:PRO:O	1.97	0.65
1:B:62:ILE:HD13	1:B:73:THR:O	1.98	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:122:LEU:O	1:B:126:LEU:HD22	1.97	0.63
1:B:106:LYS:HD3	1:B:107:ASN:H	1.64	0.61
1:B:106:LYS:HD3	1:B:107:ASN:N	2.15	0.61
2:C:27:LYS:HB2	2:C:55:PRO:HA	1.83	0.61
1:B:62:ILE:HD13	1:B:62:ILE:H	1.65	0.60
2:C:22:CYS:HG	2:C:58:ILE:HD11	1.66	0.59
1:A:152:TYR:OH	1:B:97:LYS:HE2	2.01	0.59
2:C:51:LYS:HB2	2:C:51:LYS:NZ	2.19	0.58
1:B:133:VAL:HG11	1:B:136:ILE:CD1	2.33	0.58
1:B:136:ILE:CD1	1:B:178:CYS:HB3	2.28	0.57
2:C:62:ILE:HD12	2:C:80:LEU:HD11	1.87	0.57
1:B:176:GLN:O	1:B:179:ILE:HG12	2.05	0.56
2:C:58:ILE:HD13	2:C:59:GLN:N	2.21	0.56
2:C:49:PHE:CG	2:C:50:GLU:N	2.74	0.56
2:C:77:GLU:HG2	2:C:91:LEU:HD11	1.88	0.56
1:A:24:ILE:CG2	1:A:56:GLY:HA3	2.37	0.55
2:C:13:PHE:HB2	2:C:86:ARG:NH1	2.22	0.54
1:B:106:LYS:HE3	1:B:107:ASN:OD1	2.08	0.54
1:B:62:ILE:HD11	1:B:64:TRP:CZ2	2.43	0.54
1:B:171:ILE:HD12	1:B:171:ILE:C	2.33	0.54
1:A:151:TYR:HD1	1:A:171:ILE:HD11	1.73	0.54
1:B:15:THR:CG2	1:B:65:LYS:HE2	2.38	0.54
1:A:104:TRP:HA	1:A:104:TRP:CE3	2.42	0.53
2:C:27:LYS:HB3	2:C:55:PRO:HB3	1.89	0.53
1:A:126:LEU:HD13	3:A:201:HOH:O	2.07	0.53
1:A:37:TYR:CD1	1:A:170:LEU:HD21	2.43	0.53
1:A:77:GLU:HG3	1:A:91:LEU:HD21	1.90	0.53
1:A:57:GLU:O	1:A:59:GLN:HG3	2.08	0.53
1:B:83:GLN:O	1:B:84:ASN:HB2	2.09	0.53
2:C:54:GLU:CA	2:C:55:PRO:C	2.80	0.53
1:A:36:ILE:HD13	1:A:36:ILE:O	2.08	0.52
1:B:135:ARG:HH22	1:B:185:ARG:HH11	1.55	0.52
1:B:134:GLY:O	1:B:135:ARG:HB2	2.08	0.52
1:A:171:ILE:H	1:A:171:ILE:HD13	1.76	0.51
1:B:92:ASP:OD1	1:B:92:ASP:N	2.42	0.51
1:B:96:LYS:HD2	2:C:50:GLU:OE2	2.09	0.51
2:C:58:ILE:HD12	2:C:60:TYR:CZ	2.46	0.51
1:B:133:VAL:HG11	1:B:136:ILE:HD12	1.92	0.50
1:B:135:ARG:NH2	1:B:185:ARG:NH1	2.55	0.50
2:C:27:LYS:CB	2:C:55:PRO:HB3	2.41	0.50
2:C:49:PHE:CD1	2:C:50:GLU:N	2.80	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:76:THR:HG22	2:C:77:GLU:N	2.26	0.50
2:C:43:GLY:N	3:C:129:HOH:O	2.41	0.49
2:C:13:PHE:CZ	2:C:84:ASN:HB3	2.47	0.49
1:A:171:ILE:HD13	1:A:171:ILE:N	2.27	0.49
2:C:36:ILE:HD13	2:C:40:GLU:HG3	1.93	0.49
1:B:181:GLU:O	1:B:185:ARG:CG	2.56	0.49
1:A:104:TRP:HA	1:A:104:TRP:HE3	1.78	0.48
2:C:58:ILE:HD13	2:C:58:ILE:C	2.37	0.48
2:C:76:THR:HG22	2:C:78:GLU:H	1.77	0.48
1:A:139:HIS:CE1	3:C:129:HOH:O	2.65	0.48
1:B:109:SER:O	1:B:113:VAL:HG23	2.13	0.48
2:C:49:PHE:O	2:C:50:GLU:HB2	2.13	0.48
2:C:27:LYS:HB2	2:C:55:PRO:CA	2.42	0.48
1:A:69:HIS:HA	1:A:72:ASN:OD1	2.14	0.48
2:C:63:LYS:NZ	2:C:69:HIS:CE1	2.81	0.48
1:B:76:THR:CG2	1:B:79:THR:HG23	2.44	0.48
1:B:133:VAL:HG11	1:B:136:ILE:HD11	1.96	0.47
1:B:151:TYR:CD1	1:B:171:ILE:HD11	2.49	0.47
1:A:92:ASP:O	1:A:96:LYS:HG3	2.15	0.47
1:A:151:TYR:CD1	1:A:171:ILE:HD11	2.50	0.47
1:B:15:THR:HG23	1:B:65:LYS:HE2	1.97	0.47
2:C:51:LYS:HB2	2:C:51:LYS:HZ1	1.80	0.46
1:A:170:LEU:C	1:A:170:LEU:HD13	2.41	0.46
1:B:36:ILE:O	1:B:40:GLU:HG3	2.16	0.46
1:B:50:GLU:O	1:B:51:LYS:C	2.58	0.45
1:B:97:LYS:O	1:B:101:THR:HG23	2.16	0.45
2:C:40:GLU:C	3:C:129:HOH:O	2.60	0.45
1:A:74:TRP:C	1:A:75:GLU:HG2	2.42	0.45
1:B:137:ILE:O	1:B:138:ALA:HB2	2.16	0.44
1:B:44:ASP:HA	1:B:45:PRO:HD3	1.79	0.44
1:A:77:GLU:HG3	1:A:91:LEU:CD2	2.48	0.44
1:B:98:ASP:O	1:B:102:LYS:HG2	2.17	0.44
1:A:154:LYS:HD3	1:A:154:LYS:C	2.44	0.43
1:B:154:LYS:HE2	1:B:158:LEU:O	2.18	0.43
1:A:171:ILE:H	1:A:171:ILE:CD1	2.30	0.43
1:B:23:ARG:HG2	1:B:74:TRP:CZ3	2.54	0.43
1:B:84:ASN:HA	3:B:189:HOH:O	2.19	0.43
1:B:141:ASN:HA	3:B:234:HOH:O	2.18	0.43
1:B:15:THR:HG21	1:B:65:LYS:HE2	2.01	0.43
2:C:87:GLY:O	2:C:90:LYS:HG2	2.19	0.43
1:A:97:LYS:HE3	1:B:152:TYR:OH	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:168:GLY:HA2	1:A:171:ILE:HD11	2.00	0.42
1:A:168:GLY:HA2	1:A:171:ILE:CD1	2.49	0.42
1:B:76:THR:C	1:B:78:GLU:N	2.78	0.42
1:B:107:ASN:CB	2:C:36:ILE:HG13	2.50	0.42
1:B:95:LYS:O	1:B:99:GLN:HG3	2.20	0.41
1:A:89:LYS:HD2	1:A:89:LYS:HA	1.92	0.41
1:B:62:ILE:HD13	1:B:62:ILE:N	2.33	0.41
2:C:46:ASN:O	2:C:47:ALA:C	2.62	0.41
2:C:13:PHE:HD2	2:C:86:ARG:CG	2.33	0.41
2:C:24:ILE:O	2:C:24:ILE:CD1	2.65	0.41
1:A:81:LYS:HG3	1:A:88:MET:HE2	2.03	0.41
1:A:97:LYS:CE	1:B:152:TYR:OH	2.69	0.41
1:A:154:LYS:HE3	1:A:155:TRP:O	2.20	0.41
1:B:137:ILE:C	1:B:137:ILE:CD1	2.90	0.40
2:C:16:ILE:CD1	2:C:62:ILE:HG23	2.49	0.40
2:C:62:ILE:CD1	2:C:80:LEU:HD11	2.50	0.40
1:A:168:GLY:O	1:A:171:ILE:HD13	2.22	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	171/187 (91%)	159 (93%)	9 (5%)	3 (2%)	6	5
1	B	163/187 (87%)	151 (93%)	11 (7%)	1 (1%)	21	24
2	C	84/115 (73%)	72 (86%)	8 (10%)	4 (5%)	2	0
All	All	418/489 (86%)	382 (91%)	28 (7%)	8 (2%)	6	5

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	31	GLY
1	A	32	ALA
1	B	47	ALA
2	C	47	ALA
2	C	55	PRO
1	A	108	ALA
2	C	51	LYS
2	C	50	GLU

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	150/164 (92%)	139 (93%)	11 (7%)	13	14
1	B	143/164 (87%)	133 (93%)	10 (7%)	14	15
2	C	69/101 (68%)	59 (86%)	10 (14%)	3	2
All	All	362/429 (84%)	331 (91%)	31 (9%)	10	10

All (31) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	36	ILE
1	A	50	GLU
1	A	54	GLU
1	A	80	LEU
1	A	105	LEU
1	A	126	LEU
1	A	137	ILE
1	A	154	LYS
1	A	171	ILE
1	A	173	LYS
1	A	184	SER
1	B	15	THR
1	B	58	ILE
1	B	62	ILE
1	B	76	THR

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Mol	Chain	Res	Type
1	B	80	LEU
1	B	89	LYS
1	B	92	ASP
1	B	101	THR
1	B	106	LYS
1	B	126	LEU
2	C	16	ILE
2	C	18	ARG
2	C	24	ILE
2	C	36	ILE
2	C	51	LYS
2	C	54	GLU
2	C	55	PRO
2	C	58	ILE
2	C	80	LEU
2	C	91	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	129	GLN
1	A	141	ASN
1	A	142	GLN
1	B	46	ASN
2	C	69	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

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	175/187 (93%)	0.20	6 (3%)	48	55	20, 39, 64, 81	0
1	B	169/187 (90%)	0.48	5 (2%)	52	59	28, 51, 66, 78	0
2	C	86/115 (74%)	0.53	9 (10%)	11	13	28, 43, 81, 88	0
All	All	430/489 (87%)	0.37	20 (4%)	36	42	20, 44, 68, 88	0

All (20) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	C	55	PRO	5.6
2	C	52	ASN	4.5
1	A	52	ASN	3.9
1	A	32	ALA	3.4
1	B	179	ILE	3.3
2	C	13	PHE	3.3
1	A	50	GLU	3.3
2	C	54	GLU	2.9
1	B	125	ASP	2.8
2	C	47	ALA	2.8
1	A	54	GLU	2.8
1	B	62	ILE	2.7
2	C	50	GLU	2.5
2	C	53	LYS	2.5
2	C	96	LYS	2.2
2	C	84	ASN	2.2
1	A	118	CYS	2.2
1	A	31	GLY	2.1
1	B	55	PRO	2.1
1	B	47	ALA	2.1

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.