



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 06:01 AM UTC

PDB ID : 3HTH / pdb_00003hth
Title : Crystal structure of multidrug binding protein EbrR complexed with proflavin
Authors : Dong, J.; Ni, L.; Schumacher, M.; Brennan, R.
Deposited on : 2009-06-11
Resolution : 2.70 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

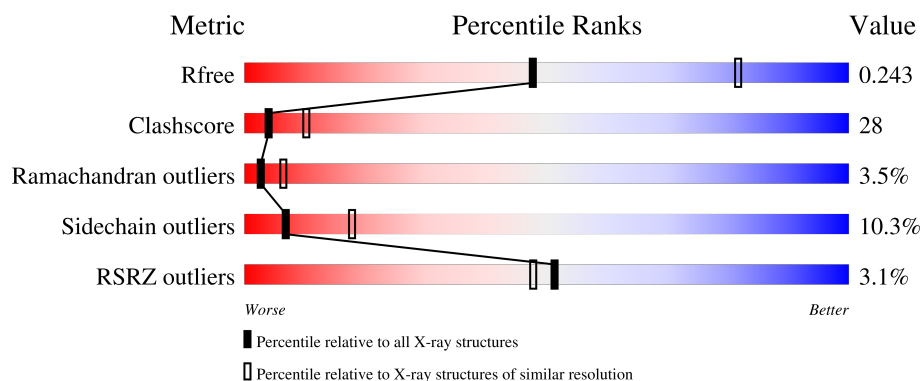
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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	3538 (2.70-2.70)
Clashscore	190562	3843 (2.70-2.70)
Ramachandran outliers	187476	3778 (2.70-2.70)
Sidechain outliers	187428	3778 (2.70-2.70)
RSRZ outliers	180081	3538 (2.70-2.70)

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	217	2% 42% 30% 6% 21%
1	B	217	3% 46% 28% 6% 20%
1	C	217	3% 37% 34% 6% 22%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 4012 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 EbrA repressor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	171	Total	C	N	O	S	0	0	0
			1296	815	233	246	2			
1	B	173	Total	C	N	O	S	0	0	0
			1314	825	237	250	2			
1	C	170	Total	C	N	O	S	0	0	0
			1286	807	232	245	2			

There are 60 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	expression tag	UNP Q79SH7
A	-18	GLY	-	expression tag	UNP Q79SH7
A	-17	SER	-	expression tag	UNP Q79SH7
A	-16	SER	-	expression tag	UNP Q79SH7
A	-15	HIS	-	expression tag	UNP Q79SH7
A	-14	HIS	-	expression tag	UNP Q79SH7
A	-13	HIS	-	expression tag	UNP Q79SH7
A	-12	HIS	-	expression tag	UNP Q79SH7
A	-11	HIS	-	expression tag	UNP Q79SH7
A	-10	HIS	-	expression tag	UNP Q79SH7
A	-9	SER	-	expression tag	UNP Q79SH7
A	-8	SER	-	expression tag	UNP Q79SH7
A	-7	GLY	-	expression tag	UNP Q79SH7
A	-6	LEU	-	expression tag	UNP Q79SH7
A	-5	VAL	-	expression tag	UNP Q79SH7
A	-4	PRO	-	expression tag	UNP Q79SH7
A	-3	ARG	-	expression tag	UNP Q79SH7
A	-2	GLY	-	expression tag	UNP Q79SH7
A	-1	SER	-	expression tag	UNP Q79SH7
A	0	HIS	-	expression tag	UNP Q79SH7
B	-19	MET	-	expression tag	UNP Q79SH7
B	-18	GLY	-	expression tag	UNP Q79SH7
B	-17	SER	-	expression tag	UNP Q79SH7

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-16	SER	-	expression tag	UNP Q79SH7
B	-15	HIS	-	expression tag	UNP Q79SH7
B	-14	HIS	-	expression tag	UNP Q79SH7
B	-13	HIS	-	expression tag	UNP Q79SH7
B	-12	HIS	-	expression tag	UNP Q79SH7
B	-11	HIS	-	expression tag	UNP Q79SH7
B	-10	HIS	-	expression tag	UNP Q79SH7
B	-9	SER	-	expression tag	UNP Q79SH7
B	-8	SER	-	expression tag	UNP Q79SH7
B	-7	GLY	-	expression tag	UNP Q79SH7
B	-6	LEU	-	expression tag	UNP Q79SH7
B	-5	VAL	-	expression tag	UNP Q79SH7
B	-4	PRO	-	expression tag	UNP Q79SH7
B	-3	ARG	-	expression tag	UNP Q79SH7
B	-2	GLY	-	expression tag	UNP Q79SH7
B	-1	SER	-	expression tag	UNP Q79SH7
B	0	HIS	-	expression tag	UNP Q79SH7
C	-19	MET	-	expression tag	UNP Q79SH7
C	-18	GLY	-	expression tag	UNP Q79SH7
C	-17	SER	-	expression tag	UNP Q79SH7
C	-16	SER	-	expression tag	UNP Q79SH7
C	-15	HIS	-	expression tag	UNP Q79SH7
C	-14	HIS	-	expression tag	UNP Q79SH7
C	-13	HIS	-	expression tag	UNP Q79SH7
C	-12	HIS	-	expression tag	UNP Q79SH7
C	-11	HIS	-	expression tag	UNP Q79SH7
C	-10	HIS	-	expression tag	UNP Q79SH7
C	-9	SER	-	expression tag	UNP Q79SH7
C	-8	SER	-	expression tag	UNP Q79SH7
C	-7	GLY	-	expression tag	UNP Q79SH7
C	-6	LEU	-	expression tag	UNP Q79SH7
C	-5	VAL	-	expression tag	UNP Q79SH7
C	-4	PRO	-	expression tag	UNP Q79SH7
C	-3	ARG	-	expression tag	UNP Q79SH7
C	-2	GLY	-	expression tag	UNP Q79SH7
C	-1	SER	-	expression tag	UNP Q79SH7
C	0	HIS	-	expression tag	UNP Q79SH7

- Molecule 2 is NICKEL (II) ION (CCD ID: NI) (formula: Ni).

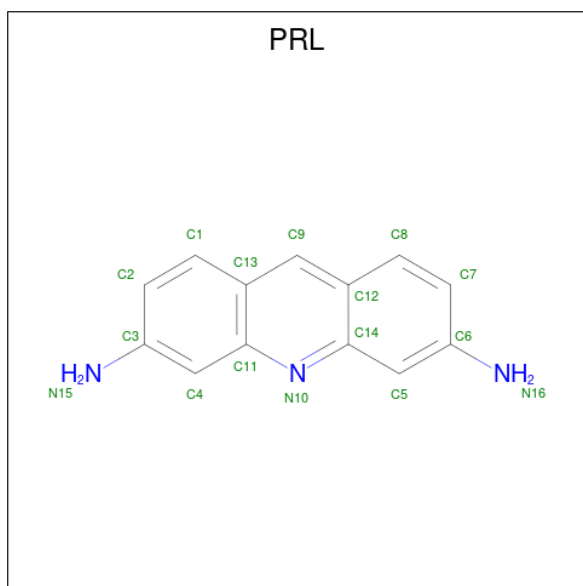
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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	2	Total Ni 2 2	0	0
2	C	1	Total Ni 1 1	0	0

- Molecule 3 is PROFLAVIN (CCD ID: PRL) (formula: C₁₃H₁₁N₃).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C N 16 13 3	0	0
3	B	1	Total C N 16 13 3	0	0

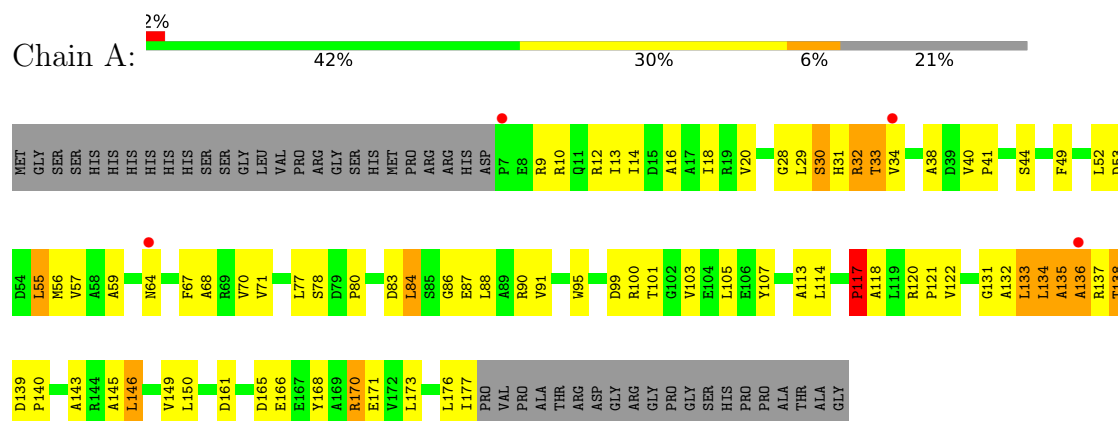
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	27	Total O 27 27	0	0
4	B	27	Total O 27 27	0	0
4	C	27	Total O 27 27	0	0

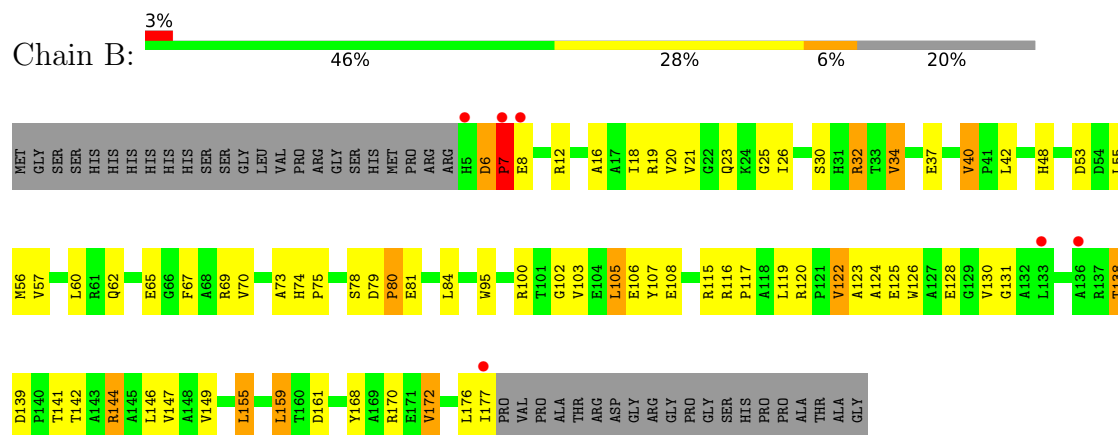
3 Residue-property plots [i](#)

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.

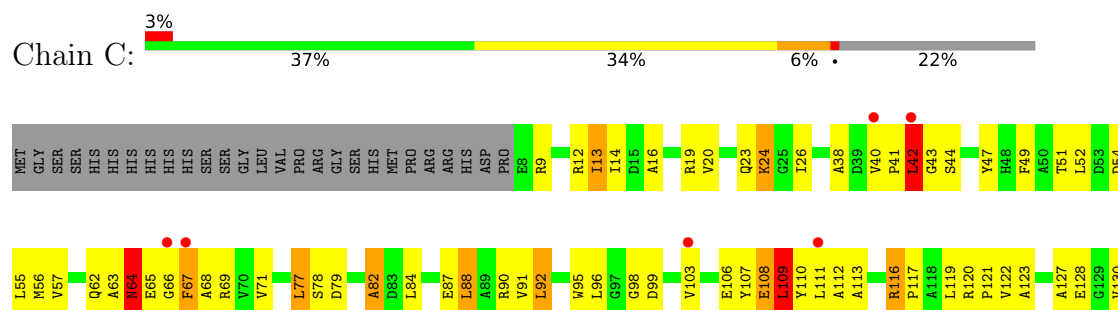
• Molecule 1: EbrA repressor



• Molecule 1: EbrA repressor



• Molecule 1: EbrA repressor



L133	L134	R137	T138	D139	P140	T141	T142	A143	L146	V147	A148	V149	L150	D151	L155	L158	L159	T160	D161	T162	P163	Y164	D165	E166	E167	Y168	I177	PRO	VAL	PRO	PRO	ALA	THR	ARG	ASP	GLY	ARG	GLY	PRO	GLY	SER	HIS	PRO	PRO	ALA	THR	ALA	GLY
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4 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α , β , γ	99.72Å 99.72Å 133.73Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	86.39 – 2.70 86.36 – 2.70	Depositor EDS
% Data completeness (in resolution range)	100.0 (86.39-2.70) 100.0 (86.36-2.70)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.90 (at 2.69Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.228 , 0.277 0.239 , 0.243	Depositor DCC
R_{free} test set	1108 reflections (5.12%)	wwPDB-VP
Wilson B-factor (Å ²)	66.1	Xtriage
Anisotropy	0.418	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 53.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.036 for -h,-k,l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	4012	wwPDB-VP
Average B, all atoms (Å ²)	74.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.28% 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: NI, PRL

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	0.46	0/1317	0.95	3/1796 (0.2%)
1	B	0.94	8/1336 (0.6%)	0.98	7/1823 (0.4%)
1	C	0.51	0/1306	1.05	7/1781 (0.4%)
All	All	0.67	8/3959 (0.2%)	1.00	17/5400 (0.3%)

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	B	0	1

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	8	GLU	CA-C	-15.16	1.32	1.52
1	B	8	GLU	C-O	-13.51	1.06	1.24
1	B	8	GLU	CA-CB	-11.46	1.35	1.53
1	B	8	GLU	N-CA	-9.35	1.34	1.46
1	B	8	GLU	C-N	-7.78	1.23	1.33
1	B	8	GLU	CB-CG	-6.75	1.32	1.52
1	B	7	PRO	C-N	-6.32	1.24	1.33
1	B	8	GLU	CG-CD	-5.16	1.39	1.52

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	108	GLU	N-CA-C	-8.91	102.92	113.88
1	B	131	GLY	N-CA-C	-8.16	104.54	114.66

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	109	LEU	N-CA-C	-7.93	102.59	111.07
1	C	82	ALA	N-CA-C	-7.59	99.22	110.46
1	B	7	PRO	O-C-N	-7.05	113.12	122.64
1	A	30	SER	N-CA-C	6.75	120.76	111.71
1	B	74	HIS	CA-C-N	6.58	128.07	119.84
1	B	74	HIS	C-N-CA	6.58	128.07	119.84
1	A	166	GLU	N-CA-C	5.74	117.21	111.07
1	C	116	ARG	CA-C-N	5.68	126.94	119.84
1	C	116	ARG	C-N-CA	5.68	126.94	119.84
1	B	40	VAL	N-CA-C	-5.56	101.78	108.45
1	A	135	ALA	N-CA-C	-5.55	105.54	112.93
1	B	123	ALA	N-CA-C	-5.51	104.68	111.40
1	B	34	VAL	N-CA-C	-5.39	105.28	110.72
1	C	168	TYR	N-CA-C	-5.12	104.63	111.24
1	C	63	ALA	N-CA-C	-5.05	107.07	113.43

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	7	PRO	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	1296	0	1307	76	0
1	B	1314	0	1317	64	0
1	C	1286	0	1290	86	0
2	A	2	0	0	0	0
2	C	1	0	0	0	0
3	A	16	0	11	0	0
3	B	16	0	11	2	0
4	A	27	0	0	0	0
4	B	27	0	0	1	0
4	C	27	0	0	5	0
All	All	4012	0	3936	220	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 28.

All (220) 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:C:42:LEU:HD12	1:C:42:LEU:H	1.29	0.95
1:C:164:TYR:HB2	4:C:327:HOH:O	1.71	0.89
1:C:84:LEU:HD22	1:C:137:ARG:HG2	1.56	0.87
1:C:56:MET:HE1	1:C:116:ARG:HE	1.38	0.85
1:C:103:VAL:HG12	1:C:158:LEU:HD11	1.57	0.85
1:A:57:VAL:HG13	1:A:122:VAL:HG21	1.58	0.84
1:A:68:ALA:O	1:A:71:VAL:HG12	1.78	0.83
1:C:23:GLN:O	1:C:24:LYS:HG3	1.79	0.81
1:B:70:VAL:HG21	3:B:201:PRL:HNF1	1.46	0.80
1:B:100:ARG:HG3	1:B:100:ARG:HH11	1.47	0.80
1:A:16:ALA:HB2	1:A:38:ALA:HB2	1.64	0.79
1:A:132:ALA:HA	1:A:135:ALA:HB3	1.66	0.77
1:A:9:ARG:NH1	1:A:40:VAL:HG22	1.99	0.77
1:B:19:ARG:NH1	1:B:37:GLU:OE1	2.18	0.76
1:C:127:ALA:O	1:C:130:VAL:HG22	1.86	0.76
1:C:99:ASP:HB3	4:C:317:HOH:O	1.84	0.75
1:C:137:ARG:HH11	1:C:137:ARG:HG3	1.52	0.75
1:B:16:ALA:O	1:B:20:VAL:HG23	1.88	0.74
1:B:149:VAL:HG21	1:B:176:LEU:HD21	1.70	0.73
1:C:110:TYR:HE1	4:C:325:HOH:O	1.71	0.73
1:C:71:VAL:HG13	1:C:77:LEU:HD23	1.69	0.73
1:A:29:LEU:HD23	1:A:56:MET:HE2	1.70	0.73
1:A:57:VAL:HG13	1:A:122:VAL:CG2	2.18	0.73
1:B:168:TYR:O	1:B:172:VAL:HG12	1.89	0.72
1:A:137:ARG:HH11	1:A:137:ARG:HB3	1.54	0.72
1:B:139:ASP:OD1	1:B:141:THR:HG22	1.88	0.72
1:C:117:PRO:HA	1:C:120:ARG:HG2	1.73	0.71
1:B:79:ASP:C	1:B:81:GLU:H	2.00	0.70
1:B:161:ASP:HB3	4:B:308:HOH:O	1.92	0.68
1:C:139:ASP:HB2	1:C:140:PRO:HD2	1.75	0.67
1:C:111:LEU:HD23	1:C:112:ALA:N	2.10	0.67
1:A:140:PRO:O	1:A:143:ALA:HB3	1.95	0.66
1:B:6:ASP:N	1:B:7:PRO:HD3	2.09	0.66
1:A:77:LEU:HD11	1:A:91:VAL:HG21	1.77	0.66
1:C:13:ILE:HD11	1:C:49:PHE:CD1	2.31	0.66
1:B:100:ARG:HG3	1:B:100:ARG:NH1	2.11	0.66
1:A:14:ILE:HD11	1:A:49:PHE:CZ	2.30	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:96:LEU:HD23	1:C:103:VAL:HG21	1.79	0.65
1:A:40:VAL:HG13	1:A:41:PRO:HD2	1.79	0.65
1:A:10:ARG:O	1:A:14:ILE:HG12	1.97	0.64
1:A:136:ALA:C	1:A:138:THR:H	2.05	0.64
1:C:87:GLU:OE1	1:C:90:ARG:NH2	2.24	0.64
1:A:12:ARG:HH21	1:A:40:VAL:HG22	1.60	0.64
1:B:102:GLY:O	1:B:106:GLU:HG3	1.98	0.64
1:C:65:GLU:HG2	4:C:323:HOH:O	1.97	0.63
1:C:69:ARG:HA	1:C:69:ARG:NE	2.13	0.63
1:C:133:LEU:C	1:C:133:LEU:HD23	2.23	0.63
1:B:124:ALA:O	1:B:128:GLU:HG3	1.99	0.63
1:C:160:THR:OG1	1:C:162:THR:HG23	2.00	0.62
1:C:66:GLY:O	1:C:67:PHE:HB2	1.98	0.61
1:C:42:LEU:H	1:C:42:LEU:CD1	2.04	0.61
1:A:173:LEU:O	1:A:177:ILE:HG12	2.01	0.60
1:C:9:ARG:O	1:C:13:ILE:HG23	2.02	0.60
1:C:84:LEU:O	1:C:88:LEU:HB2	2.02	0.59
1:A:30:SER:C	1:A:32:ARG:H	2.09	0.59
1:A:16:ALA:CB	1:A:38:ALA:HB2	2.33	0.59
1:C:120:ARG:N	1:C:121:PRO:HD2	2.17	0.59
1:C:107:TYR:OH	1:C:151:ASP:HA	2.02	0.59
1:C:165:ASP:O	1:C:168:TYR:HB3	2.02	0.59
1:A:67:PHE:O	1:A:70:VAL:HG22	2.03	0.59
1:A:71:VAL:HG11	1:A:133:LEU:HD21	1.84	0.59
1:B:119:LEU:O	1:B:122:VAL:HG13	2.03	0.59
1:B:65:GLU:CD	1:B:69:ARG:HH12	2.11	0.58
1:A:95:TRP:CH2	1:A:103:VAL:HG13	2.39	0.58
1:A:77:LEU:HD23	1:A:87:GLU:HB3	1.86	0.57
1:C:41:PRO:HB2	1:C:44:SER:HB2	1.86	0.57
1:B:18:ILE:HG23	1:B:105:LEU:HD11	1.87	0.57
1:A:149:VAL:HG22	1:B:149:VAL:HG22	1.86	0.57
1:A:132:ALA:C	1:A:134:LEU:H	2.13	0.56
1:A:16:ALA:O	1:A:20:VAL:HG23	2.06	0.56
1:A:117:PRO:HA	1:A:120:ARG:HG3	1.86	0.56
1:C:87:GLU:O	1:C:91:VAL:HG23	2.05	0.56
1:A:137:ARG:HB3	1:A:137:ARG:NH1	2.19	0.56
1:A:52:LEU:HG	1:A:56:MET:HE3	1.87	0.56
1:B:57:VAL:HG22	1:B:119:LEU:HD23	1.88	0.56
1:A:41:PRO:O	1:A:44:SER:HB3	2.06	0.55
1:B:56:MET:HE1	1:B:116:ARG:CZ	2.37	0.55
1:A:53:ASP:O	1:A:57:VAL:HG23	2.06	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:133:LEU:HD23	1:C:133:LEU:O	2.06	0.55
1:B:32:ARG:HG3	1:B:32:ARG:HH11	1.70	0.55
1:C:26:ILE:HD12	1:C:108:GLU:HG2	1.88	0.55
1:B:62:GLN:O	1:B:65:GLU:HB3	2.07	0.55
1:B:6:ASP:N	1:B:7:PRO:CD	2.70	0.55
1:B:149:VAL:CG2	1:B:176:LEU:HD21	2.37	0.54
1:A:78:SER:O	1:A:80:PRO:HD3	2.06	0.54
1:A:86:GLY:HA2	1:A:170:ARG:HG3	1.89	0.54
1:B:30:SER:OG	1:B:32:ARG:HG2	2.07	0.54
1:C:109:LEU:HD13	1:C:123:ALA:HA	1.90	0.54
1:B:70:VAL:HG21	3:B:201:PRL:N15	2.17	0.54
1:C:62:GLN:O	1:C:62:GLN:HG2	2.08	0.54
1:B:138:THR:HG22	1:B:139:ASP:H	1.73	0.53
1:B:138:THR:HG22	1:B:139:ASP:OD2	2.07	0.53
1:B:53:ASP:O	1:B:57:VAL:HG23	2.08	0.53
1:A:137:ARG:HH11	1:A:137:ARG:CB	2.21	0.53
1:C:16:ALA:O	1:C:20:VAL:HG23	2.09	0.53
1:A:84:LEU:HD22	1:A:88:LEU:HD12	1.91	0.53
1:C:9:ARG:HD3	1:C:44:SER:OG	2.09	0.53
1:B:149:VAL:HG21	1:B:176:LEU:CD2	2.39	0.53
1:C:66:GLY:O	1:C:95:TRP:CZ2	2.62	0.53
1:C:82:ALA:O	1:C:137:ARG:NH2	2.42	0.53
1:A:135:ALA:C	1:A:137:ARG:N	2.64	0.52
1:A:136:ALA:C	1:A:138:THR:N	2.66	0.52
1:B:95:TRP:CH2	1:B:103:VAL:HG13	2.45	0.52
1:C:56:MET:HE3	1:C:119:LEU:HD11	1.92	0.52
1:B:12:ARG:NH2	1:B:40:VAL:HG12	2.24	0.52
1:C:38:ALA:HB3	1:C:40:VAL:HG22	1.92	0.52
1:C:108:GLU:O	1:C:111:LEU:HB3	2.10	0.52
1:B:12:ARG:HD3	1:C:19:ARG:CZ	2.40	0.52
1:B:67:PHE:CE2	1:B:130:VAL:HG22	2.45	0.52
1:C:137:ARG:HG3	1:C:137:ARG:NH1	2.23	0.51
1:A:30:SER:O	1:A:32:ARG:N	2.41	0.51
1:C:79:ASP:OD1	1:C:79:ASP:C	2.53	0.51
1:A:18:ILE:CD1	1:A:59:ALA:HB1	2.41	0.51
1:B:126:TRP:O	1:B:130:VAL:HG23	2.11	0.51
1:A:86:GLY:HA2	1:A:170:ARG:CG	2.41	0.51
1:A:30:SER:O	1:A:32:ARG:HG3	2.11	0.50
1:C:164:TYR:CE2	1:C:166:GLU:HA	2.47	0.50
1:A:95:TRP:CZ2	1:A:103:VAL:HA	2.46	0.50
1:B:79:ASP:C	1:B:81:GLU:N	2.68	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:137:ARG:O	1:A:138:THR:HG22	2.12	0.49
1:B:78:SER:O	1:B:80:PRO:HD3	2.12	0.49
1:B:34:VAL:HG21	1:B:55:LEU:HD21	1.94	0.49
1:C:41:PRO:O	1:C:43:GLY:N	2.46	0.49
1:C:41:PRO:C	1:C:43:GLY:H	2.21	0.49
1:C:57:VAL:HG22	1:C:119:LEU:HD23	1.95	0.49
1:C:111:LEU:CD2	1:C:112:ALA:N	2.76	0.49
1:B:115:ARG:O	1:B:117:PRO:HD3	2.12	0.49
1:A:120:ARG:HD2	1:B:161:ASP:HB2	1.95	0.48
1:A:145:ALA:O	1:A:149:VAL:HG23	2.13	0.48
1:A:132:ALA:C	1:A:134:LEU:N	2.70	0.48
1:A:146:LEU:HD21	1:A:177:ILE:CD1	2.44	0.48
1:C:151:ASP:O	1:C:155:LEU:HD22	2.14	0.48
1:C:13:ILE:HD11	1:C:49:PHE:CE1	2.48	0.48
1:C:117:PRO:HA	1:C:120:ARG:CG	2.42	0.48
1:A:30:SER:HB3	1:A:33:THR:OG1	2.13	0.48
1:A:135:ALA:HB1	1:A:143:ALA:HB2	1.95	0.48
1:B:6:ASP:H	1:B:7:PRO:HD3	1.78	0.48
1:A:100:ARG:HH21	1:A:100:ARG:HG3	1.79	0.48
1:C:64:ASN:O	1:C:69:ARG:HG3	2.14	0.48
1:B:142:THR:HG21	1:B:177:ILE:HA	1.95	0.48
1:C:107:TYR:HE2	1:C:155:LEU:HD22	1.79	0.48
1:A:105:LEU:C	1:A:105:LEU:HD12	2.39	0.48
1:B:79:ASP:O	1:B:81:GLU:N	2.47	0.47
1:B:146:LEU:HD11	1:B:177:ILE:HG12	1.96	0.47
1:C:16:ALA:CB	1:C:38:ALA:HB2	2.44	0.47
1:C:137:ARG:NH1	1:C:137:ARG:CG	2.76	0.47
1:A:77:LEU:CD2	1:A:87:GLU:HB3	2.45	0.47
1:A:131:GLY:C	1:A:135:ALA:HB2	2.39	0.47
1:A:161:ASP:HB2	1:B:120:ARG:HD3	1.97	0.47
1:B:67:PHE:HB2	1:B:126:TRP:HZ3	1.78	0.47
1:B:155:LEU:O	1:B:159:LEU:HB2	2.14	0.47
1:C:143:ALA:O	1:C:147:VAL:HG23	2.14	0.47
1:A:120:ARG:N	1:A:121:PRO:HD2	2.30	0.47
1:A:120:ARG:HD3	1:B:159:LEU:O	2.15	0.47
1:C:66:GLY:O	1:C:67:PHE:CB	2.62	0.47
1:C:78:SER:O	1:C:79:ASP:C	2.58	0.47
1:B:60:LEU:HD23	1:B:122:VAL:HG22	1.97	0.46
1:B:6:ASP:HB3	1:B:48:HIS:CE1	2.49	0.46
1:A:12:ARG:HH21	1:A:40:VAL:CG2	2.25	0.46
1:B:65:GLU:HG2	1:B:69:ARG:NH1	2.30	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:132:ALA:O	1:A:134:LEU:N	2.49	0.46
1:C:42:LEU:HD12	1:C:42:LEU:N	2.12	0.46
1:C:92:LEU:O	1:C:95:TRP:HB3	2.16	0.46
1:A:34:VAL:HG21	1:A:55:LEU:HD11	1.97	0.46
1:A:30:SER:C	1:A:32:ARG:N	2.74	0.46
1:A:29:LEU:HD23	1:A:56:MET:CE	2.41	0.45
1:A:168:TYR:CZ	1:B:144:ARG:HG2	2.52	0.45
1:A:135:ALA:C	1:A:137:ARG:H	2.23	0.45
1:A:165:ASP:HB3	1:A:168:TYR:HB3	1.98	0.45
1:B:65:GLU:HG2	1:B:69:ARG:HH12	1.81	0.45
1:C:52:LEU:O	1:C:56:MET:HG3	2.17	0.45
1:C:13:ILE:HD11	1:C:49:PHE:HD1	1.79	0.45
1:C:13:ILE:HG13	1:C:14:ILE:N	2.30	0.45
1:C:151:ASP:O	1:C:155:LEU:CD2	2.64	0.45
1:A:18:ILE:HD13	1:A:59:ALA:HB1	1.99	0.44
1:B:32:ARG:CD	1:B:32:ARG:H	2.30	0.44
1:A:135:ALA:HB1	1:A:143:ALA:CB	2.47	0.44
1:C:111:LEU:HD23	1:C:111:LEU:C	2.42	0.44
1:C:113:ALA:O	1:C:120:ARG:NE	2.50	0.44
1:C:9:ARG:HA	1:C:12:ARG:HG2	1.99	0.44
1:B:16:ALA:HB1	1:B:37:GLU:HB3	1.99	0.44
1:C:57:VAL:HG13	1:C:122:VAL:HG21	2.00	0.44
1:A:135:ALA:O	1:A:137:ARG:N	2.50	0.44
1:B:65:GLU:CG	1:B:69:ARG:HH12	2.31	0.43
1:A:28:GLY:O	1:A:33:THR:HG21	2.18	0.43
1:C:110:TYR:CE1	4:C:325:HOH:O	2.57	0.43
1:C:23:GLN:O	1:C:24:LYS:CG	2.60	0.43
1:B:73:ALA:O	1:B:75:PRO:HD3	2.19	0.43
1:B:6:ASP:HB3	1:B:48:HIS:HE1	1.83	0.43
1:B:21:VAL:O	1:B:25:GLY:N	2.52	0.43
1:B:155:LEU:HD12	1:B:155:LEU:HA	1.77	0.43
1:A:10:ARG:HG3	1:A:49:PHE:CZ	2.54	0.42
1:C:130:VAL:O	1:C:134:LEU:HG	2.19	0.42
1:C:66:GLY:O	1:C:106:GLU:OE1	2.37	0.42
1:C:149:VAL:HG13	1:C:150:LEU:N	2.35	0.42
1:A:113:ALA:O	1:A:114:LEU:C	2.62	0.42
1:C:65:GLU:HB2	1:C:66:GLY:H	1.59	0.42
1:C:162:THR:HB	1:C:163:PRO:CD	2.50	0.42
1:A:118:ALA:O	1:A:121:PRO:HD2	2.20	0.42
1:C:47:TYR:CD1	1:C:47:TYR:C	2.98	0.42
1:B:26:ILE:HG13	1:B:108:GLU:CD	2.45	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:16:ALA:HB3	1:C:38:ALA:HB2	2.02	0.41
1:A:131:GLY:O	1:A:135:ALA:N	2.53	0.41
1:B:100:ARG:NH1	1:B:100:ARG:CG	2.80	0.41
1:A:55:LEU:HD23	1:A:55:LEU:HA	1.90	0.41
1:C:68:ALA:HA	1:C:130:VAL:HG13	2.02	0.41
1:A:95:TRP:CE2	1:A:103:VAL:HG22	2.55	0.41
1:C:142:THR:O	1:C:146:LEU:HG	2.21	0.41
1:C:159:LEU:C	1:C:161:ASP:H	2.28	0.41
1:A:131:GLY:O	1:A:135:ALA:HB2	2.21	0.41
1:C:120:ARG:HH11	1:C:120:ARG:HG3	1.85	0.41
1:C:41:PRO:C	1:C:43:GLY:N	2.78	0.41
1:B:32:ARG:H	1:B:32:ARG:HD3	1.86	0.41
1:A:100:ARG:HG3	1:A:100:ARG:NH2	2.35	0.41
1:B:155:LEU:HG	1:B:159:LEU:HD22	2.03	0.41
1:C:120:ARG:N	1:C:121:PRO:CD	2.83	0.41
1:A:9:ARG:O	1:A:13:ILE:HG13	2.21	0.40
1:B:42:LEU:O	1:B:42:LEU:HD23	2.21	0.40
1:C:133:LEU:C	1:C:133:LEU:CD2	2.91	0.40
1:C:51:THR:O	1:C:54:ASP:HB2	2.22	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	169/217 (78%)	144 (85%)	17 (10%)	8 (5%)	2	3
1	B	171/217 (79%)	159 (93%)	9 (5%)	3 (2%)	6	18
1	C	168/217 (77%)	140 (83%)	21 (12%)	7 (4%)	2	4
All	All	508/651 (78%)	443 (87%)	47 (9%)	18 (4%)	3	6

All (18) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	138	THR
1	C	24	LYS
1	C	67	PHE
1	C	163	PRO
1	A	99	ASP
1	C	42	LEU
1	C	98	GLY
1	A	83	ASP
1	A	134	LEU
1	C	64	ASN
1	A	133	LEU
1	A	136	ALA
1	A	139	ASP
1	C	128	GLU
1	B	6	ASP
1	B	7	PRO
1	A	117	PRO
1	B	80	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	129/165 (78%)	114 (88%)	15 (12%)	5	13
1	B	131/165 (79%)	116 (88%)	15 (12%)	5	14
1	C	127/165 (77%)	117 (92%)	10 (8%)	11	28
All	All	387/495 (78%)	347 (90%)	40 (10%)	7	18

All (40) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	31	HIS
1	A	32	ARG
1	A	33	THR
1	A	55	LEU
1	A	64	ASN

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Mol	Chain	Res	Type
1	A	84	LEU
1	A	90	ARG
1	A	101	THR
1	A	107	TYR
1	A	117	PRO
1	A	146	LEU
1	A	150	LEU
1	A	170	ARG
1	A	171	GLU
1	A	176	LEU
1	B	7	PRO
1	B	23	GLN
1	B	32	ARG
1	B	84	LEU
1	B	105	LEU
1	B	107	TYR
1	B	122	VAL
1	B	125	GLU
1	B	138	THR
1	B	144	ARG
1	B	147	VAL
1	B	155	LEU
1	B	159	LEU
1	B	170	ARG
1	B	172	VAL
1	C	13	ILE
1	C	42	LEU
1	C	55	LEU
1	C	64	ASN
1	C	77	LEU
1	C	88	LEU
1	C	92	LEU
1	C	109	LEU
1	C	137	ARG
1	C	155	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	31	HIS
1	A	48	HIS
1	A	64	ASN

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Mol	Chain	Res	Type
1	A	156	GLN
1	B	48	HIS
1	B	156	GLN
1	C	11	GLN
1	C	62	GLN
1	C	64	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 5 ligands modelled in this entry, 3 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	PRL	B	201	-	18,18,18	2.30	2 (11%)	26,26,26	1.14	2 (7%)
3	PRL	A	201	-	18,18,18	2.43	3 (16%)	26,26,26	1.15	2 (7%)

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	PRL	B	201	-	-	-	0/3/3/3
3	PRL	A	201	-	-	-	0/3/3/3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	201	PRL	C13-C11	6.59	1.52	1.42
3	A	201	PRL	C12-C14	6.26	1.51	1.42
3	B	201	PRL	C12-C14	6.18	1.51	1.42
3	B	201	PRL	C13-C11	5.88	1.51	1.42
3	A	201	PRL	C2-C3	2.06	1.44	1.40

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	201	PRL	C14-N10-C11	3.03	122.04	117.74
3	A	201	PRL	C14-N10-C11	2.89	121.85	117.74
3	A	201	PRL	C13-C9-C12	-2.59	118.19	121.93
3	B	201	PRL	C13-C9-C12	-2.36	118.51	121.93

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	201	PRL	2	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [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	171/217 (78%)	0.22	4 (2%) 61 58	50, 78, 102, 114	0
1	B	173/217 (79%)	0.01	6 (3%) 47 43	28, 67, 95, 114	0
1	C	170/217 (78%)	0.30	6 (3%) 47 43	51, 76, 96, 112	0
All	All	514/651 (78%)	0.17	16 (3%) 51 48	28, 73, 97, 114	0

All (16) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	8	GLU	4.7
1	C	66	GLY	3.7
1	B	177	ILE	3.0
1	A	7	PRO	3.0
1	C	42	LEU	2.8
1	B	136	ALA	2.5
1	C	103	VAL	2.5
1	B	133	LEU	2.5
1	C	111	LEU	2.4
1	C	67	PHE	2.2
1	C	40	VAL	2.2
1	A	64	ASN	2.2
1	A	136	ALA	2.1
1	B	5	HIS	2.1
1	B	7	PRO	2.1
1	A	34	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](#)

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
2	NI	A	199	1/1	0.91	0.15	88,88,88,88	1
3	PRL	A	201	16/16	0.93	0.11	63,64,67,67	0
3	PRL	B	201	16/16	0.93	0.15	99,101,103,103	0
2	NI	A	200	1/1	0.99	0.03	73,73,73,73	0
2	NI	C	200	1/1	1.00	0.02	63,63,63,63	1

6.5 Other polymers [i](#)

There are no such residues in this entry.