Full wwPDB X-ray Structure Validation Report (i)

Dec 20, 2023 – 07:06 AM EST

PDB ID	:	1VCL
Title	:	Crystal Structure of Hemolytic Lectin CEL-III
Authors	:	Uchida, T.; Yamasaki, T.; Eto, S.; Sugawara, H.; Kurisu, G.; Nakagawa, A.; Kusunoki, M.; Hatakeyama, T.
Deposited on	:	2004-03-09
Resolution	:	1.70 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 (i) 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 (i)) were used in the production of this report:

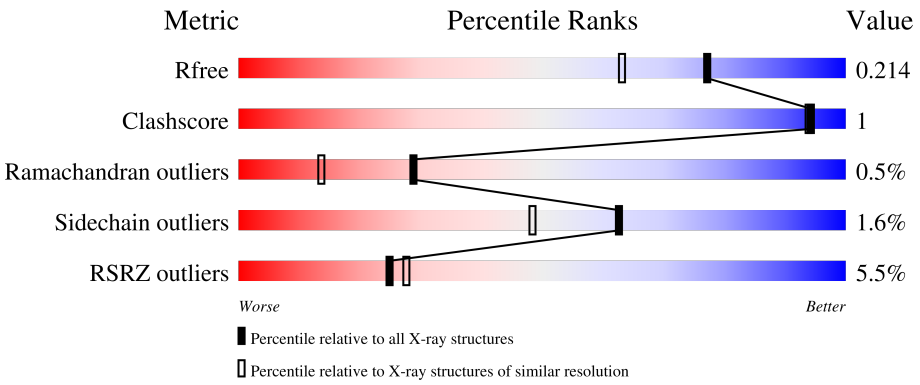
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 1.70 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}	130704	4298 (1.70-1.70)
Clashscore	141614	4695 (1.70-1.70)
Ramachandran outliers	138981	4610 (1.70-1.70)
Sidechain outliers	138945	4610 (1.70-1.70)
RSRZ outliers	127900	4222 (1.70-1.70)

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 <=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	432	6% 95% 5%
1	B	432	5% 94% 5% •

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
1	PCA	B	1	-	-	-	X

2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 7502 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 hemolytic lectin CEL-III.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	432	3313	2033	562	688	30	0	0	0
1	B	432	3313	2033	562	688	30	0	0	0

There are 26 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	15	SER	ASN	SEE REMARK 999	UNP Q868M7
A	16	PHE	TYR	SEE REMARK 999	UNP Q868M7
A	36	TYR	HIS	SEE REMARK 999	UNP Q868M7
A	48	ILE	MET	SEE REMARK 999	UNP Q868M7
A	92	GLN	LEU	SEE REMARK 999	UNP Q868M7
A	95	ARG	LYS	SEE REMARK 999	UNP Q868M7
A	97	THR	ALA	SEE REMARK 999	UNP Q868M7
A	122	ILE	VAL	SEE REMARK 999	UNP Q868M7
A	146	VAL	ILE	SEE REMARK 999	UNP Q868M7
A	173	ASP	GLU	SEE REMARK 999	UNP Q868M7
A	204	SER	GLN	SEE REMARK 999	UNP Q868M7
A	340	THR	SER	SEE REMARK 999	UNP Q868M7
A	404	VAL	ILE	SEE REMARK 999	UNP Q868M7
B	15	SER	ASN	SEE REMARK 999	UNP Q868M7
B	16	PHE	TYR	SEE REMARK 999	UNP Q868M7
B	36	TYR	HIS	SEE REMARK 999	UNP Q868M7
B	48	ILE	MET	SEE REMARK 999	UNP Q868M7
B	92	GLN	LEU	SEE REMARK 999	UNP Q868M7
B	95	ARG	LYS	SEE REMARK 999	UNP Q868M7
B	97	THR	ALA	SEE REMARK 999	UNP Q868M7
B	122	ILE	VAL	SEE REMARK 999	UNP Q868M7
B	146	VAL	ILE	SEE REMARK 999	UNP Q868M7
B	173	ASP	GLU	SEE REMARK 999	UNP Q868M7
B	204	SER	GLN	SEE REMARK 999	UNP Q868M7
B	340	THR	SER	SEE REMARK 999	UNP Q868M7

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Chain	Residue	Modelled	Actual	Comment	Reference
B	404	VAL	ILE	SEE REMARK 999	UNP Q868M7

- Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	5	Total Ca 5 5	0	0
2	B	5	Total Ca 5 5	0	0

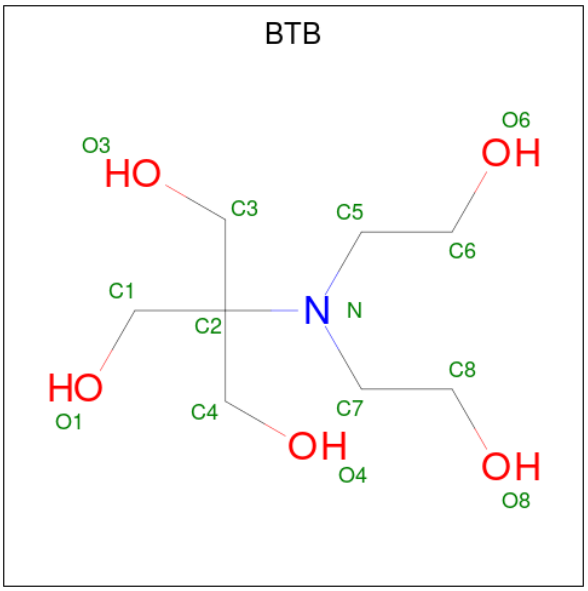
- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	2	Total Mg 2 2	0	0
3	B	2	Total Mg 2 2	0	0

- Molecule 4 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total Cl 1 1	0	0
4	B	1	Total Cl 1 1	0	0

- Molecule 5 is 2-[BIS-(2-HYDROXY-ETHYL)-AMINO]-2-HYDROXYMETHYL-PROPANE-1,3-DIOL (three-letter code: BTB) (formula: $C_8H_{19}NO_5$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
5	A	1	14	8	1	5	0	0

- Molecule 6 is water.

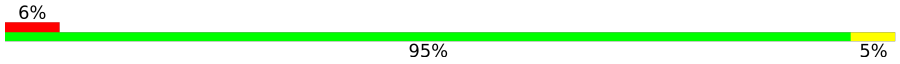
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
6	A	418	418	418	0	0
			Total	O		
6	B	428	428	428	0	0

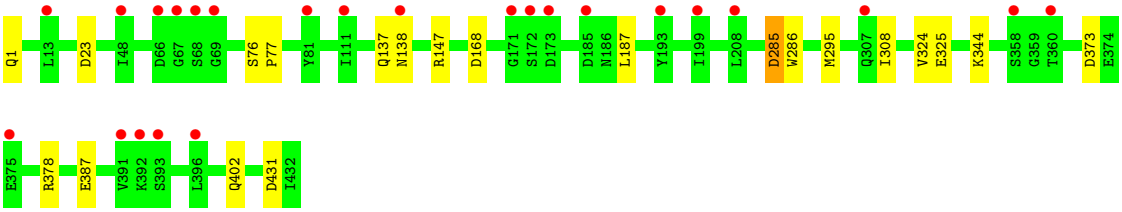
3 Residue-property plots (i)

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: hemolytic lectin CEL-III

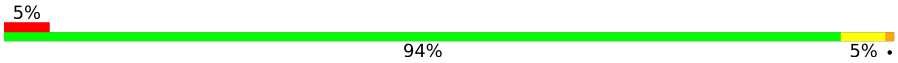
Chain A:

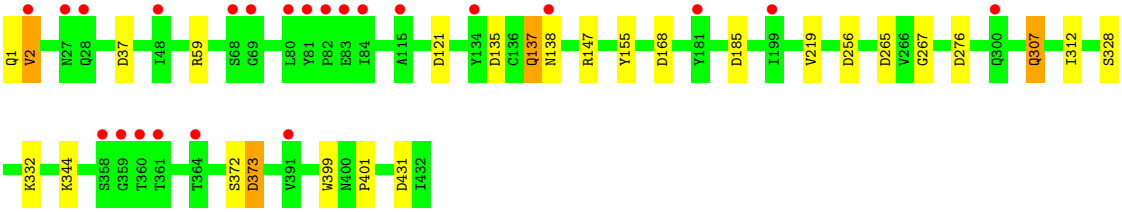




• Molecule 1: hemolytic lectin CEL-III

Chain B:





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	52.42Å 65.37Å 126.02Å 90.00° 98.18° 90.00°	Depositor
Resolution (Å)	26.17 – 1.70 26.19 – 1.70	Depositor EDS
% Data completeness (in resolution range)	99.9 (26.17-1.70) 100.0 (26.19-1.70)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.38 (at 1.70Å)	Xtriage
Refinement program	REFMAC 5.1.24	Depositor
R, R_{free}	0.165 , 0.201 0.179 , 0.214	Depositor DCC
R_{free} test set	4642 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å^2)	15.6	Xtriage
Anisotropy	0.368	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.36 , 49.6	EDS
L-test for twinning[2]	$< \|L\| > = 0.51$, $< L^2 > = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	7502	wwPDB-VP
Average B, all atoms (Å^2)	28.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 44.16 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.5890e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ 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)

Bond lengths and bond angles in the following residue types are not validated in this section: PCA, BTB, MG, CL, CA

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	0.52	0/3366	0.80	4/4566 (0.1%)
1	B	0.53	0/3366	0.83	9/4566 (0.2%)
All	All	0.53	0/6732	0.82	13/9132 (0.1%)

There are no bond length outliers.

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	431	ASP	CB-CG-OD2	7.51	125.06	118.30
1	B	168	ASP	CB-CG-OD2	6.58	124.22	118.30
1	B	256	ASP	CB-CG-OD2	6.39	124.05	118.30
1	B	121	ASP	CB-CG-OD2	5.79	123.51	118.30
1	A	168	ASP	CB-CG-OD2	5.78	123.50	118.30
1	A	431	ASP	CB-CG-OD2	5.65	123.39	118.30
1	A	23	ASP	CB-CG-OD2	5.61	123.35	118.30
1	B	265	ASP	CB-CG-OD1	5.50	123.25	118.30
1	B	185	ASP	CB-CG-OD2	5.48	123.23	118.30
1	B	276	ASP	CB-CG-OD2	5.35	123.11	118.30
1	B	135	ASP	CB-CG-OD2	5.32	123.08	118.30
1	B	37	ASP	CB-CG-OD2	5.20	122.98	118.30
1	A	285	ASP	CB-CG-OD2	5.09	122.89	118.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

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	3313	0	3082	8	0
1	B	3313	0	3082	8	0
2	A	5	0	0	0	0
2	B	5	0	0	0	0
3	A	2	0	0	0	0
3	B	2	0	0	0	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
5	A	14	0	19	0	0
6	A	418	0	0	3	0
6	B	428	0	0	4	0
All	All	7502	0	6183	16	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 1.

All (16) 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:295:MET:HG2	6:A:1432:HOH:O	1.67	0.94
1:B:147:ARG:NH2	6:B:2370:HOH:O	2.30	0.64
1:A:308:ILE:HG22	1:A:402:GLN:HG2	1.84	0.60
1:A:295:MET:CG	6:A:1432:HOH:O	2.37	0.58
1:A:187:LEU:HD12	1:A:324:VAL:HG21	1.88	0.55
1:A:147:ARG:NH2	6:A:1315:HOH:O	2.41	0.54
1:A:286:TRP:NE1	1:A:325:GLU:HG2	2.25	0.51
1:B:137:GLN:NE2	6:B:2588:HOH:O	2.36	0.48
1:B:399:TRP:CZ2	1:B:401:PRO:HB3	2.51	0.46
1:A:76:SER:HB2	1:A:77:PRO:HD2	1.99	0.44
1:B:219:VAL:HG23	1:B:267:GLY:HA2	2.01	0.42
1:A:187:LEU:CD1	1:A:324:VAL:HG21	2.48	0.42
1:B:307:GLN:HG2	6:B:2625:HOH:O	2.19	0.42
1:B:155:TYR:CG	1:B:328:SER:HB3	2.55	0.41
1:B:312:ILE:HD11	6:B:2537:HOH:O	2.20	0.41
1:B:372:SER:O	1:B:373:ASP:CB	2.69	0.41

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	430/432 (100%)	423 (98%)	5 (1%)	2 (0%)	29	13
1	B	430/432 (100%)	422 (98%)	6 (1%)	2 (0%)	29	13
All	All	860/864 (100%)	845 (98%)	11 (1%)	4 (0%)	29	13

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	2	VAL
1	A	373	ASP
1	B	373	ASP
1	A	378	ARG

5.3.2 Protein sidechains (i)

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	370/370 (100%)	365 (99%)	5 (1%)	67	53
1	B	370/370 (100%)	363 (98%)	7 (2%)	57	41
All	All	740/740 (100%)	728 (98%)	12 (2%)	62	48

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	137	GLN
1	A	138	ASN

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Mol	Chain	Res	Type
1	A	285	ASP
1	A	344	LYS
1	A	387	GLU
1	B	2	VAL
1	B	59	ARG
1	B	137	GLN
1	B	138	ASN
1	B	307	GLN
1	B	332	LYS
1	B	344	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

2 non-standard protein/DNA/RNA residues are modelled in this entry.

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	$\#\|Z\| > 2$
1	PCA	B	1	1	7,8,9	2.39	2 (28%)	9,10,12	2.16	6 (66%)
1	PCA	A	1	1	7,8,9	2.01	2 (28%)	9,10,12	1.80	4 (44%)

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
1	PCA	B	1	1	-	0/0/11/13	0/1/1/1
1	PCA	A	1	1	-	0/0/11/13	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	1	PCA	CD-N	4.79	1.47	1.34
1	A	1	PCA	CD-N	4.56	1.46	1.34
1	B	1	PCA	CA-N	3.89	1.51	1.46
1	A	1	PCA	CA-N	2.41	1.49	1.46

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	1	PCA	OE-CD-CG	-3.01	121.51	126.76
1	B	1	PCA	CB-CA-C	-2.95	108.64	112.70
1	B	1	PCA	CA-N-CD	-2.77	104.11	113.58
1	A	1	PCA	CA-N-CD	-2.74	104.19	113.58
1	A	1	PCA	OE-CD-CG	-2.52	122.37	126.76
1	A	1	PCA	CG-CD-N	2.37	114.52	108.39
1	B	1	PCA	CB-CA-N	2.32	109.95	103.30
1	B	1	PCA	CG-CD-N	2.32	114.39	108.39
1	A	1	PCA	CB-CA-N	2.28	109.84	103.30
1	B	1	PCA	O-C-CA	-2.22	118.95	124.78

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 17 ligands modelled in this entry, 16 are monoatomic - leaving 1 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	$\#\|Z\| > 2$
5	BTB	A	1301	-	13,13,13	0.42	0	7,16,16	0.88	0

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
5	BTB	A	1301	-	-	4/21/21/21	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	1301	BTB	C1-C2-N-C7
5	A	1301	BTB	C4-C2-N-C7
5	A	1301	BTB	C8-C7-N-C2
5	A	1301	BTB	C3-C2-N-C7

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

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	431/432 (99%)	0.33	24 (5%)	24	27	15, 27, 47, 61	0
1	B	431/432 (99%)	0.34	23 (5%)	26	29	14, 25, 45, 65	0
All	All	862/864 (99%)	0.33	47 (5%)	25	27	14, 26, 46, 65	0

All (47) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	81	TYR	12.0
1	B	358	SER	9.1
1	B	82	PRO	8.5
1	B	80	LEU	6.1
1	A	81	TYR	5.8
1	A	172	SER	5.2
1	B	2	VAL	4.9
1	A	69	GLY	4.6
1	B	69	GLY	4.6
1	A	171	GLY	4.4
1	A	360	THR	3.7
1	B	138	ASN	3.7
1	B	68	SER	3.6
1	A	66	ASP	3.6
1	A	391	VAL	3.5
1	B	28	GLN	3.3
1	B	84	ILE	3.2
1	B	361	THR	3.2
1	A	68	SER	3.1
1	B	83	GLU	3.1
1	B	360	THR	2.9
1	B	115	ALA	2.8
1	B	300	GLN	2.8
1	B	391	VAL	2.8

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Mol	Chain	Res	Type	RSRZ
1	B	48	ILE	2.7
1	A	138	ASN	2.7
1	B	27	ASN	2.7
1	A	13	LEU	2.6
1	A	396	LEU	2.6
1	A	173	ASP	2.5
1	A	392	LYS	2.4
1	A	185	ASP	2.4
1	B	199	ILE	2.4
1	A	199	ILE	2.3
1	A	375	GLU	2.3
1	A	48	ILE	2.2
1	B	359	GLY	2.2
1	A	358	SER	2.2
1	A	208	LEU	2.2
1	B	181	TYR	2.2
1	A	67	GLY	2.2
1	A	307	GLN	2.1
1	A	393	SER	2.1
1	B	364	THR	2.1
1	A	193	TYR	2.1
1	A	111	ILE	2.0
1	B	134	TYR	2.0

6.2 Non-standard residues in protein, DNA, RNA chains (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
1	PCA	B	1	8/9	0.72	0.55	46,48,49,50	0
1	PCA	A	1	8/9	0.79	0.22	37,38,39,39	0

6.3 Carbohydrates (i)

There are no monosaccharides 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
5	BTB	A	1301	14/14	0.84	0.15	25,28,28,30	0
4	CL	A	1201	1/1	0.93	0.06	45,45,45,45	0
2	CA	A	1003	1/1	0.93	0.17	57,57,57,57	0
2	CA	B	1001	1/1	0.95	0.14	43,43,43,43	0
2	CA	B	1003	1/1	0.96	0.23	44,44,44,44	0
3	MG	B	1101	1/1	0.96	0.05	41,41,41,41	0
2	CA	B	1004	1/1	0.98	0.11	28,28,28,28	0
4	CL	B	2201	1/1	0.98	0.09	44,44,44,44	0
2	CA	A	1004	1/1	0.98	0.10	31,31,31,31	0
3	MG	A	1101	1/1	0.99	0.09	38,38,38,38	0
3	MG	A	1102	1/1	0.99	0.05	25,25,25,25	0
2	CA	A	1001	1/1	0.99	0.07	33,33,33,33	0
2	CA	B	1002	1/1	0.99	0.05	45,45,45,45	0
2	CA	A	1002	1/1	0.99	0.08	44,44,44,44	0
2	CA	A	1005	1/1	0.99	0.04	27,27,27,27	0
3	MG	B	1102	1/1	1.00	0.06	21,21,21,21	0
2	CA	B	1005	1/1	1.00	0.04	26,26,26,26	0

6.5 Other polymers (i)

There are no such residues in this entry.