



# Full wwPDB X-ray Structure Validation Report ⓘ

Oct 1, 2017 – 03:11 AM EDT

PDB ID : 2CYF  
Title : The Crystal Structure of Canavalia Maritima Lectin (ConM) in Complex with Trehalose and Maltose  
Authors : Delatorre, P.; Rocha, B.A.M.; Sousa, E.P.; Gadelha, C.A.A.; Azevedo Jr., W.F.; Cavada, B.S.  
Deposited on : unknown  
Resolution : 1.80 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](mailto:validation@mail.wwpdb.org)

A user guide is available at

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467  
Mogul : 1.7.2 (RC1), CSD as538be (2017)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20030345  
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : rb-20030345

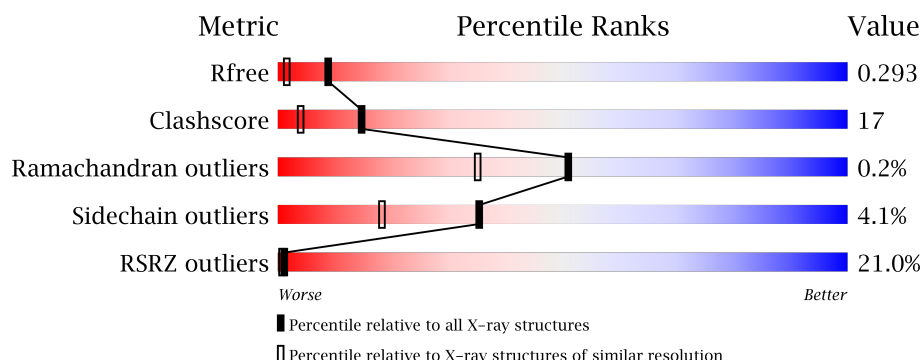
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.80 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))
$R_{free}$	100719	4827 (1.80-1.80)
Clashscore	112137	5742 (1.80-1.80)
Ramachandran outliers	110173	5676 (1.80-1.80)
Sidechain outliers	110143	5675 (1.80-1.80)
RSRZ outliers	101464	4906 (1.80-1.80)

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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	237	<div> <div>7%</div> <div>75%</div> <div>19%</div> <div>...</div> </div>
1	C	237	<div> <div>34%</div> <div>74%</div> <div>19%</div> <div>...</div> </div>

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
2	MAL	A	240	-	-	-	X
2	MAL	C	1240	-	-	-	X

## 2 Entry composition [i](#)

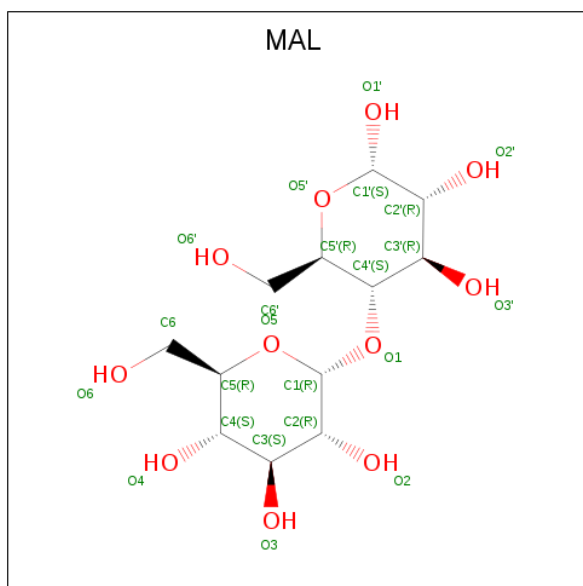
There are 5 unique types of molecules in this entry. The entry contains 3877 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Lectin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	230	Total	C	N	O	S	0	0	0
			1747	1104	292	350	1			
1	C	231	Total	C	N	O	S	0	0	0
			1755	1110	293	351	1			

- Molecule 2 is MALTOSE (three-letter code: MAL) (formula: C<sub>12</sub>H<sub>22</sub>O<sub>11</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			22	12	10		
2	C	1	Total	C	O	0	0
			22	12	10		

- Molecule 3 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total 1	Ca 1	0	0
3	C	1	Total 1	Ca 1	0	0

- Molecule 4 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total 1	Mn 1	0	0
4	C	1	Total 1	Mn 1	0	0

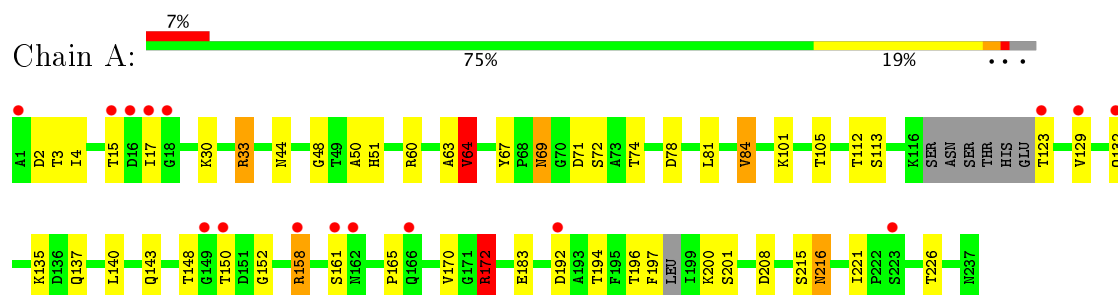
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	165	Total 165	O 165	0	0
5	C	162	Total 162	O 162	0	0

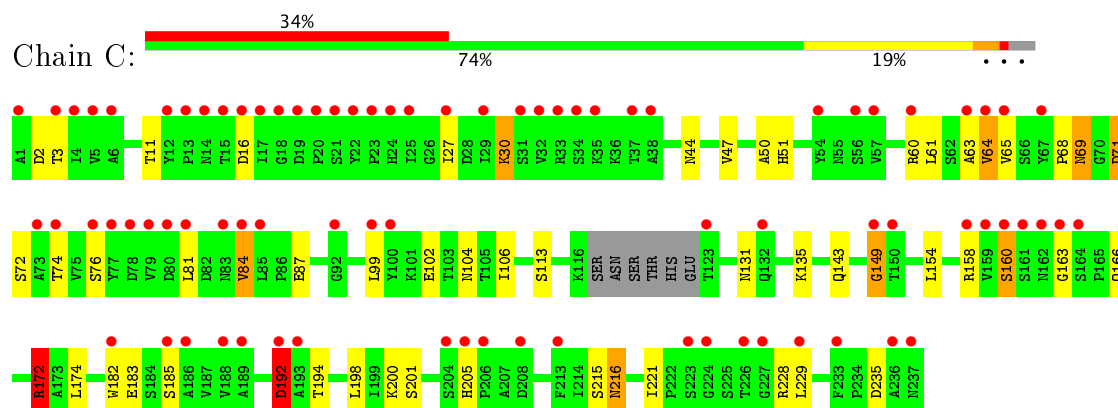
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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 ( $\text{RSRZ} > 2$ ). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

#### • Molecule 1: Lectin



#### • Molecule 1: Lectin



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 2 <sub>1</sub> 2 <sub>1</sub> 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	67.03Å 97.33Å 71.09Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	9.98 – 1.80 9.93 – 1.79	Depositor EDS
% Data completeness (in resolution range)	99.8 (9.98-1.80) 97.6 (9.93-1.79)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.34 (at 1.79Å)	Xtriage
Refinement program	REFMAC 5.2.0003	Depositor
R, $R_{free}$	0.186 , 0.238 0.266 , 0.293	Depositor DCC
$R_{free}$ test set	4341 reflections (11.15%)	DCC
Wilson B-factor (Å <sup>2</sup> )	17.8	Xtriage
Anisotropy	0.165	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.50 , 47.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.90	EDS
Total number of atoms	3877	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	19.0	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 55.53 % 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 3.1202e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<sup>1</sup> Intensities estimated from amplitudes.

<sup>2</sup> Theoretical 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: CA, MN, MAL

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	1/1785 (0.1%)	1.03	6/2428 (0.2%)
1	C	0.93	0/1794	1.05	9/2442 (0.4%)
All	All	0.92	1/3579 (0.0%)	1.04	15/4870 (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	A	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	129	VAL	CB-CG1	-5.57	1.41	1.52

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	172	ARG	NE-CZ-NH2	-13.76	113.42	120.30
1	C	172	ARG	NE-CZ-NH2	-10.80	114.90	120.30
1	C	192	ASP	CB-CG-OD2	8.36	125.82	118.30
1	A	64	VAL	CB-CA-C	-8.12	95.97	111.40
1	C	64	VAL	CB-CA-C	-7.92	96.35	111.40
1	A	172	ARG	NE-CZ-NH1	7.65	124.13	120.30
1	C	172	ARG	NE-CZ-NH1	6.55	123.58	120.30
1	C	71	ASP	CB-CG-OD2	6.31	123.98	118.30
1	C	30	LYS	CD-CE-NZ	6.12	125.78	111.70
1	C	16	ASP	CB-CG-OD2	6.10	123.79	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	64	VAL	CG1-CB-CG2	5.92	120.37	110.90
1	A	78	ASP	CB-CG-OD2	5.35	123.12	118.30
1	C	235	ASP	CB-CG-OD2	5.22	123.00	118.30
1	A	158	ARG	NE-CZ-NH1	5.22	122.91	120.30
1	A	33	ARG	NE-CZ-NH2	-5.01	117.79	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	148	THR	Peptide

## 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	1747	0	1699	60	0
1	C	1755	0	1711	61	0
2	A	22	0	20	0	0
2	C	22	0	20	4	0
3	A	1	0	0	0	0
3	C	1	0	0	0	0
4	A	1	0	0	0	0
4	C	1	0	0	0	0
5	A	165	0	0	22	0
5	C	162	0	0	19	0
All	All	3877	0	3450	120	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 17.

All (120) 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:113:SER:HB2	5:A:497:HOH:O	1.19	1.29

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:172:ARG:HG2	5:A:515:HOH:O	1.34	1.26
1:A:170:VAL:HB	5:A:558:HOH:O	1.09	1.23
1:A:72:SER:HB3	5:A:505:HOH:O	1.19	1.23
1:A:113:SER:CB	5:A:497:HOH:O	1.77	1.15
1:C:192:ASP:HB3	5:C:531:HOH:O	1.48	1.11
1:A:72:SER:CB	5:A:505:HOH:O	1.72	1.10
1:C:143:GLN:OE1	1:C:172:ARG:HD2	1.57	1.04
1:C:113:SER:HB2	5:C:487:HOH:O	0.87	1.04
1:C:99:LEU:HD22	2:C:1240:MAL:H4'	1.41	1.02
1:C:143:GLN:OE1	1:C:172:ARG:CD	2.06	1.02
1:A:69:ASN:ND2	5:A:539:HOH:O	1.93	0.99
1:A:170:VAL:CG2	1:A:226:THR:HA	1.97	0.94
1:C:44:ASN:HD21	1:C:201:SER:H	1.15	0.89
1:A:215:SER:HB2	5:A:506:HOH:O	1.70	0.89
1:A:170:VAL:HG23	1:A:226:THR:HG22	1.57	0.85
1:A:44:ASN:HD21	1:A:201:SER:H	1.23	0.85
1:C:143:GLN:OE1	1:C:172:ARG:HD3	1.79	0.83
1:C:87:GLU:OE2	5:C:546:HOH:O	1.96	0.83
1:A:143:GLN:OE1	1:A:172:ARG:CD	2.28	0.81
1:C:99:LEU:HD13	2:C:1240:MAL:H1	1.62	0.80
1:C:172:ARG:CG	5:C:474:HOH:O	2.27	0.79
1:C:192:ASP:CB	5:C:531:HOH:O	2.15	0.79
1:C:30:LYS:HE3	1:C:84:VAL:HG23	1.63	0.78
1:C:3:THR:H	1:C:216:ASN:ND2	1.82	0.77
1:A:143:GLN:OE1	1:A:172:ARG:HD2	1.86	0.76
1:C:205:HIS:HB2	5:C:502:HOH:O	1.85	0.76
1:C:172:ARG:HG2	5:C:474:HOH:O	1.83	0.74
1:A:67:TYR:HB3	5:A:539:HOH:O	1.91	0.71
1:A:143:GLN:OE1	1:A:172:ARG:HD3	1.91	0.70
1:C:192:ASP:CG	5:C:531:HOH:O	2.30	0.69
1:A:170:VAL:HG21	1:A:226:THR:HA	1.73	0.69
1:C:172:ARG:NE	5:C:474:HOH:O	1.67	0.68
1:A:172:ARG:NE	5:A:515:HOH:O	1.80	0.67
1:C:87:GLU:CD	5:C:546:HOH:O	2.33	0.67
1:A:64:VAL:HG13	1:A:74:THR:OG1	1.95	0.66
1:C:135:LYS:HA	1:C:149:GLY:HA3	1.76	0.66
1:C:3:THR:HG23	1:C:30:LYS:HE2	1.79	0.64
1:A:60:ARG:CZ	5:A:559:HOH:O	2.46	0.64
1:A:172:ARG:CG	5:A:515:HOH:O	2.06	0.64
1:C:44:ASN:HD21	1:C:201:SER:N	1.93	0.63
1:C:102:GLU:OE2	1:C:104:ASN:ND2	2.27	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:160:SER:CB	5:C:554:HOH:O	2.50	0.60
1:C:81:LEU:HA	1:C:84:VAL:HG13	1.84	0.60
1:A:123:THR:N	1:C:131:ASN:HD22	2.00	0.59
1:C:143:GLN:HB2	1:C:172:ARG:HG3	1.85	0.58
1:A:135:LYS:HB2	1:A:150:THR:HG22	1.86	0.58
1:A:170:VAL:HG22	1:A:226:THR:HA	1.83	0.58
1:C:228:ARG:HG2	2:C:1240:MAL:O3	2.04	0.58
1:C:163:GLY:N	5:C:554:HOH:O	2.35	0.58
1:A:3:THR:HG23	1:A:30:LYS:CE	2.36	0.56
1:A:60:ARG:NE	5:A:559:HOH:O	2.38	0.56
1:A:170:VAL:CG2	1:A:226:THR:CA	2.80	0.56
1:C:216:ASN:HD22	1:C:216:ASN:H	1.53	0.55
1:A:216:ASN:HD22	1:A:216:ASN:H	1.54	0.55
1:A:60:ARG:NH2	5:A:559:HOH:O	2.38	0.55
1:C:182:TRP:CZ3	5:C:546:HOH:O	2.61	0.54
1:C:158:ARG:HG2	1:C:166:GLN:HG3	1.89	0.53
1:C:135:LYS:CA	1:C:149:GLY:HA3	2.40	0.52
1:A:74:THR:HG22	5:A:532:HOH:O	2.09	0.52
1:C:160:SER:C	5:C:554:HOH:O	2.46	0.52
1:A:3:THR:H	1:A:216:ASN:ND2	2.08	0.52
1:C:2:ASP:HB3	1:C:216:ASN:HD21	1.76	0.51
1:C:216:ASN:H	1:C:216:ASN:ND2	2.09	0.51
1:A:170:VAL:HG21	1:A:226:THR:CA	2.40	0.51
1:A:44:ASN:HD21	1:A:201:SER:N	2.01	0.51
1:C:172:ARG:HD2	1:C:221:ILE:HG13	1.92	0.50
1:A:3:THR:HG23	1:A:30:LYS:HE3	1.93	0.50
1:A:183:GLU:HB3	5:A:477:HOH:O	2.12	0.50
1:C:11:THR:O	1:C:205:HIS:HE1	1.96	0.49
1:A:216:ASN:HB3	5:A:504:HOH:O	2.12	0.49
1:A:69:ASN:ND2	1:A:71:ASP:H	2.09	0.49
1:A:81:LEU:HA	1:A:84:VAL:HG13	1.94	0.49
1:C:3:THR:HG23	1:C:30:LYS:CE	2.41	0.49
1:A:172:ARG:HD2	1:A:221:ILE:HG13	1.94	0.49
1:C:27:ILE:HG23	1:C:61:LEU:HD23	1.95	0.48
1:A:4:ILE:HD13	5:A:506:HOH:O	2.12	0.48
1:A:170:VAL:HG23	1:A:226:THR:CG2	2.37	0.48
1:A:170:VAL:CG2	1:A:226:THR:HG22	2.37	0.47
1:A:216:ASN:ND2	1:A:216:ASN:H	2.11	0.47
1:C:3:THR:H	1:C:216:ASN:HD22	1.59	0.47
1:A:3:THR:HG23	1:A:30:LYS:HE2	1.97	0.47
1:A:2:ASP:CB	1:A:216:ASN:HD21	2.26	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:105:THR:O	1:A:197:PHE:HA	2.14	0.47
1:C:182:TRP:CH2	5:C:546:HOH:O	2.55	0.47
1:A:112:THR:HB	1:A:192:ASP:OD1	2.15	0.47
1:A:69:ASN:CG	5:A:539:HOH:O	2.44	0.47
1:A:101:LYS:HD3	1:A:165:PRO:O	2.16	0.46
1:C:158:ARG:HD3	5:C:555:HOH:O	2.17	0.45
1:A:67:TYR:CB	5:A:539:HOH:O	2.54	0.45
1:C:172:ARG:HD3	1:C:174:LEU:HD11	1.97	0.45
1:C:2:ASP:CB	1:C:216:ASN:HD21	2.29	0.45
1:C:183:GLU:OE2	1:C:185:SER:HB2	2.16	0.45
1:A:215:SER:CB	5:A:506:HOH:O	2.45	0.44
1:A:3:THR:O	5:A:506:HOH:O	2.21	0.44
1:C:113:SER:CB	5:C:487:HOH:O	1.75	0.44
1:C:64:VAL:HG13	1:C:74:THR:OG1	2.18	0.44
1:C:30:LYS:HA	5:C:492:HOH:O	2.18	0.43
1:C:60:ARG:HD3	1:C:76:SER:HB3	2.00	0.43
1:A:30:LYS:HE3	1:A:84:VAL:HG23	1.99	0.43
1:C:44:ASN:ND2	1:C:200:LYS:HA	2.33	0.43
1:C:99:LEU:HB2	2:C:1240:MAL:O5	2.17	0.43
1:C:3:THR:O	1:C:215:SER:HA	2.19	0.43
1:A:17:ILE:O	1:A:33:ARG:HG2	2.19	0.43
1:A:51:HIS:O	1:A:63:ALA:HA	2.19	0.42
1:A:2:ASP:HB3	1:A:216:ASN:HD21	1.84	0.42
1:A:132:GLN:HG3	1:A:152:GLY:HA2	2.00	0.42
1:A:48:GLY:O	1:A:196:THR:HA	2.20	0.42
1:C:106:ILE:HB	1:C:154:LEU:HB3	2.02	0.42
1:C:50:ALA:O	1:C:194:THR:HA	2.19	0.42
1:C:69:ASN:ND2	1:C:71:ASP:H	2.16	0.42
1:A:44:ASN:ND2	1:A:200:LYS:HA	2.34	0.41
1:C:47:VAL:O	1:C:68:PRO:HD3	2.20	0.41
1:C:51:HIS:O	1:C:63:ALA:HA	2.19	0.41
1:C:228:ARG:HG3	1:C:229:LEU:HG	2.03	0.41
1:C:65:VAL:O	1:C:72:SER:HA	2.21	0.41
1:A:50:ALA:O	1:A:194:THR:HA	2.21	0.41
1:A:137:GLN:HG2	1:A:140:LEU:HD12	2.02	0.40
1:C:172:ARG:HB3	5:C:474:HOH:O	2.20	0.40
1:C:87:GLU:HG3	1:C:182:TRP:O	2.20	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	224/237 (94%)	218 (97%)	6 (3%)	0	100	100
1	C	227/237 (96%)	217 (96%)	9 (4%)	1 (0%)	38	23
All	All	451/474 (95%)	435 (96%)	15 (3%)	1 (0%)	51	35

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	149	GLY

### 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	195/202 (96%)	186 (95%)	9 (5%)	31	15
1	C	196/202 (97%)	189 (96%)	7 (4%)	40	23
All	All	391/404 (97%)	375 (96%)	16 (4%)	35	18

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	15	THR
1	A	64	VAL
1	A	69	ASN
1	A	84	VAL
1	A	158	ARG

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Mol	Chain	Res	Type
1	A	161	SER
1	A	172	ARG
1	A	208	ASP
1	A	216	ASN
1	C	69	ASN
1	C	84	VAL
1	C	160	SER
1	C	172	ARG
1	C	192	ASP
1	C	198	LEU
1	C	216	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	43	GLN
1	A	44	ASN
1	A	69	ASN
1	A	216	ASN
1	A	237	ASN
1	C	43	GLN
1	C	44	ASN
1	C	69	ASN
1	C	132	GLN
1	C	216	ASN
1	C	237	ASN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry

Of 6 ligands modelled in this entry, 4 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
2	MAL	A	240	-	23,23,24	0.40	0	32,33,35	1.18	3 (9%)
2	MAL	C	1240	-	23,23,24	0.83	0	32,33,35	2.07	7 (21%)

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
2	MAL	A	240	-	-	0/8/45/48	0/2/2/2
2	MAL	C	1240	-	-	0/8/45/48	0/2/2/2

There are no bond length outliers.

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	1240	MAL	C4-C3-C2	-5.02	101.99	110.84
2	C	1240	MAL	C1-C2-C3	-3.21	104.01	109.98
2	C	1240	MAL	O4-C4-C5	-3.15	101.34	109.28
2	C	1240	MAL	O5-C1-C2	-2.73	105.03	110.30
2	A	240	MAL	O5'-C1'-C2'	-2.33	107.14	110.79
2	A	240	MAL	C1'-O5'-C5'	2.32	115.36	112.17
2	C	1240	MAL	O2-C2-C1	2.58	115.43	110.03
2	A	240	MAL	O5'-C5'-C4'	2.83	115.13	109.98
2	C	1240	MAL	O4-C4-C3	3.15	117.22	110.36
2	C	1240	MAL	O3-C3-C4	6.93	125.45	110.36

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	1240	MAL	4	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

### 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	230/237 (97%)	0.78	16 (6%) 17 14	11, 18, 31, 40	0
1	C	231/237 (97%)	1.75	81 (35%) 0 0	11, 18, 28, 38	0
All	All	461/474 (97%)	1.27	97 (21%) 1 1	11, 18, 30, 40	0

All (97) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	16	ASP	7.0
1	A	15	THR	6.1
1	C	15	THR	6.1
1	A	16	ASP	5.1
1	A	149	GLY	4.9
1	C	149	GLY	4.9
1	C	18	GLY	4.5
1	C	237	ASN	4.4
1	A	150	THR	4.4
1	A	162	ASN	3.9
1	C	158	ARG	3.9
1	C	17	ILE	3.9
1	C	21	SER	3.8
1	C	236	ALA	3.7
1	C	22	TYR	3.6
1	A	161	SER	3.5
1	C	34	SER	3.5
1	C	1	ALA	3.5
1	C	205	HIS	3.5
1	C	233	PHE	3.3
1	C	84	VAL	3.3
1	C	182	TRP	3.2
1	C	150	THR	3.2
1	C	99	LEU	3.2

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Mol	Chain	Res	Type	RSRZ
1	C	100	TYR	3.1
1	C	162	ASN	3.1
1	C	54	TYR	3.0
1	C	161	SER	3.0
1	C	164	SER	3.0
1	C	20	PRO	2.9
1	C	83	ASN	2.9
1	C	204	SER	2.8
1	C	185	SER	2.8
1	C	12	TYR	2.7
1	A	1	ALA	2.7
1	A	123	THR	2.7
1	C	65	VAL	2.7
1	A	132	GLN	2.7
1	C	60	ARG	2.7
1	C	3	THR	2.7
1	C	193	ALA	2.7
1	C	74	THR	2.7
1	C	31	SER	2.6
1	C	23	PRO	2.6
1	C	19	ASP	2.6
1	C	192	ASP	2.5
1	C	77	TYR	2.5
1	C	24	HIS	2.5
1	C	78	ASP	2.5
1	C	186	ALA	2.5
1	C	56	SER	2.5
1	C	38	ALA	2.5
1	C	37	THR	2.5
1	C	123	THR	2.5
1	C	189	ALA	2.4
1	C	5	VAL	2.4
1	C	57	VAL	2.4
1	A	166	GLN	2.4
1	C	224	GLY	2.4
1	C	229	LEU	2.4
1	C	132	GLN	2.4
1	C	4	ILE	2.4
1	C	25	ILE	2.4
1	C	188	VAL	2.4
1	A	158	ARG	2.4
1	A	17	ILE	2.4

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Mol	Chain	Res	Type	RSRZ
1	C	27	ILE	2.3
1	C	6	ALA	2.3
1	C	35	LYS	2.3
1	C	64	VAL	2.3
1	C	223	SER	2.3
1	A	129	VAL	2.3
1	C	63	ALA	2.3
1	A	192	ASP	2.3
1	C	227	GLY	2.2
1	C	159	VAL	2.2
1	C	76	SER	2.2
1	C	32	VAL	2.2
1	C	163	GLY	2.2
1	C	29	ILE	2.2
1	C	13	PRO	2.2
1	C	206	PRO	2.2
1	C	81	LEU	2.2
1	C	92	GLY	2.2
1	C	33	ARG	2.1
1	A	18	GLY	2.1
1	C	73	ALA	2.1
1	C	67	TYR	2.1
1	C	213	PHE	2.1
1	C	79	VAL	2.1
1	C	226	THR	2.1
1	C	208	ASP	2.1
1	A	223	SER	2.0
1	C	160	SER	2.0
1	C	80	ASP	2.0
1	C	14	ASN	2.0
1	C	85	LEU	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 carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> 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	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
2	MAL	A	240	22/23	0.74	0.26	6.35	16,26,33,36	0
2	MAL	C	1240	22/23	0.48	0.45	6.17	18,37,51,53	0
3	CA	C	238	1/1	0.70	0.21	-1.33	17,17,17,17	0
4	MN	C	239	1/1	0.71	0.16	-2.76	18,18,18,18	0
3	CA	A	238	1/1	0.99	0.06	-5.30	17,17,17,17	0
4	MN	A	239	1/1	0.97	0.05	-6.20	18,18,18,18	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.