



# Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 09:22 PM GMT

PDB ID : 1ONA  
Title : CO-CRYSTALS OF CONCAVALIN A WITH METHYL-3,6-DI-O-(ALPHA-D-MANNOPYRANOSYL)-ALPHA-D-MANNOPYRANOSIDE  
Authors : Bouckaert, J.; Maes, D.; Poortmans, F.; Wyns, L.; Loris, R.  
Deposited on : 1996-07-07  
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](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 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
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) : trunk26865

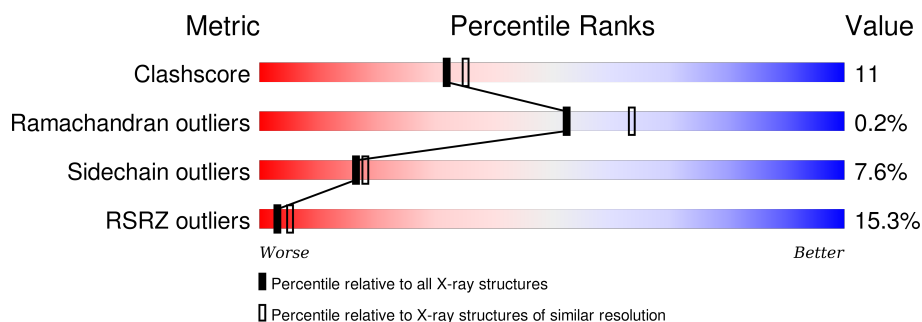
# 1 Overall quality at a glance

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))
Clashscore	102246	1456 (2.38-2.34)
Ramachandran outliers	100387	1435 (2.38-2.34)
Sidechain outliers	100360	1436 (2.38-2.34)
RSRZ outliers	91569	1358 (2.38-2.34)

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>16%</div> <div>74%</div> <div>19%</div> <div>.</div> <div>.</div> </div>
1	B	237	<div> <div>13%</div> <div>73%</div> <div>22%</div> <div>.</div> <div>.</div> </div>
1	C	237	<div> <div>14%</div> <div>75%</div> <div>19%</div> <div>.</div> <div>.</div> </div>
1	D	237	<div> <div>18%</div> <div>73%</div> <div>21%</div> <div>.</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	MAN	D	242	-	-	-	X

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 7368 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 CONCANAVALIN A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	231	Total	C	N	O	S	0	0	0
			1755	1111	291	351	2			
1	B	231	Total	C	N	O	S	0	0	0
			1755	1111	291	351	2			
1	C	231	Total	C	N	O	S	0	0	0
			1755	1111	291	351	2			
1	D	231	Total	C	N	O	S	0	0	0
			1755	1111	291	351	2			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	151	ASP	GLU	CONFLICT	UNP P02866
A	155	GLU	ARG	CONFLICT	UNP P02866
B	151	ASP	GLU	CONFLICT	UNP P02866
B	155	GLU	ARG	CONFLICT	UNP P02866
C	151	ASP	GLU	CONFLICT	UNP P02866
C	155	GLU	ARG	CONFLICT	UNP P02866
D	151	ASP	GLU	CONFLICT	UNP P02866
D	155	GLU	ARG	CONFLICT	UNP P02866

- Molecule 2 is a polymer of unknown type called SUGAR (3-MER).

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	3	Total	C	O	0	0
			35	19	16		
2	B	3	Total	C	O	0	0
			35	19	16		
2	C	3	Total	C	O	0	0
			35	19	16		
2	D	3	Total	C	O	0	0
			35	19	16		

- Molecule 3 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total	Mn	0	0
			1	1		
3	A	1	Total	Mn	0	0
			1	1		
3	D	1	Total	Mn	0	0
			1	1		
3	C	1	Total	Mn	0	0
			1	1		

- Molecule 4 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	1	Total	Ca	0	0
			1	1		
4	A	1	Total	Ca	0	0
			1	1		
4	D	1	Total	Ca	0	0
			1	1		
4	C	1	Total	Ca	0	0
			1	1		

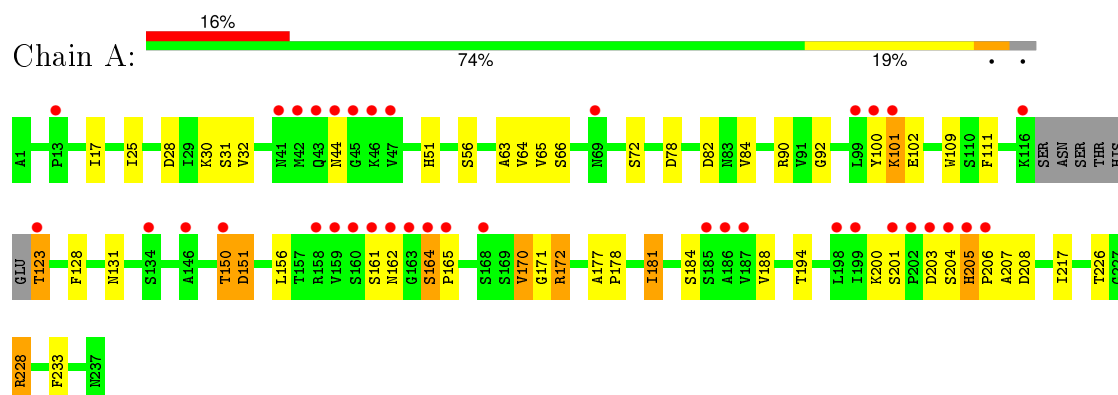
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	50	Total	O	0	0
			50	50		
5	B	47	Total	O	0	0
			47	47		
5	C	50	Total	O	0	0
			50	50		
5	D	53	Total	O	0	0
			53	53		

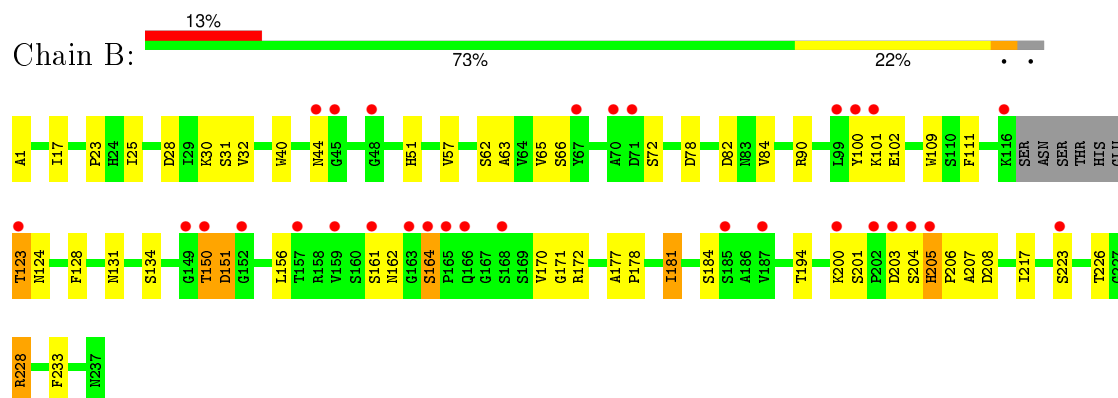
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

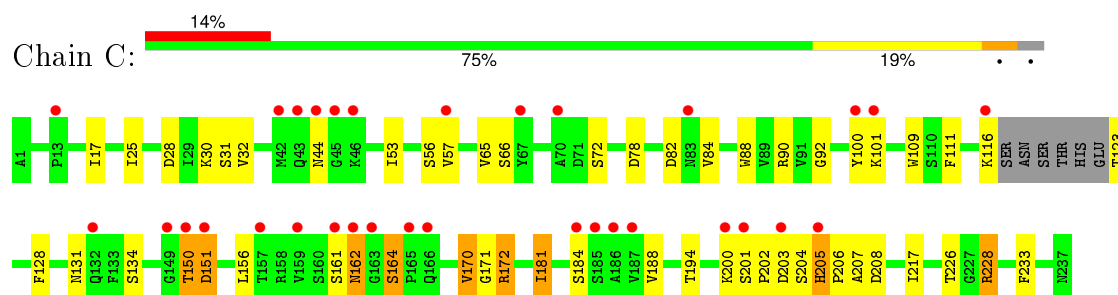
#### • Molecule 1: CONCANAVALIN A



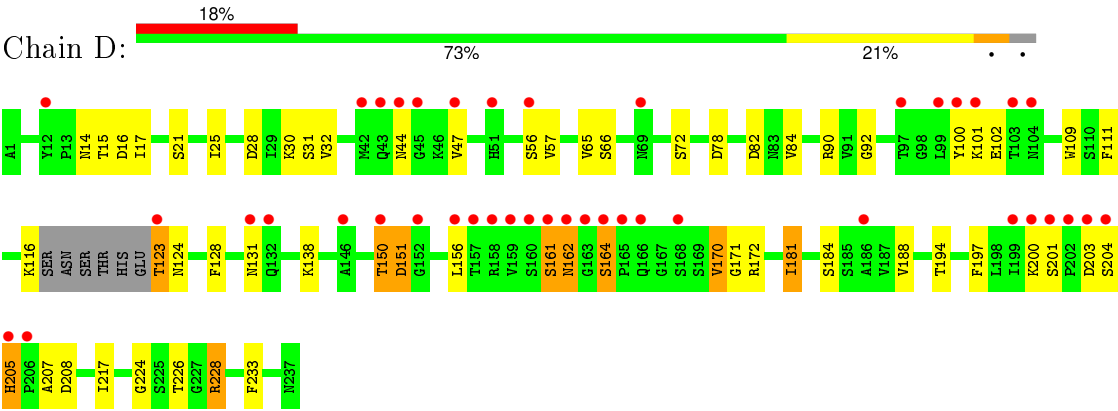
#### • Molecule 1: CONCANAVALIN A



#### • Molecule 1: CONCANAVALIN A



#### • Molecule 1: CONCANAVALIN A



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	59.83Å 64.84Å 125.92Å 90.00° 93.87° 90.00°	Depositor
Resolution (Å)	8.00 – 2.35 15.24 – 2.31	Depositor EDS
% Data completeness (in resolution range)	(Not available) (8.00-2.35) 69.7 (15.24-2.31)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	4.28 (at 2.32Å)	Xtriage
Refinement program	X-PLOR 3.1	Depositor
R, $R_{free}$	0.221 , 0.282 0.318 , (Not available)	Depositor DCC
$R_{free}$ test set	No test flags present.	DCC
Wilson B-factor (Å <sup>2</sup> )	24.7	Xtriage
Anisotropy	0.590	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 45.3	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.34$	Xtriage
Outliers	1 of 29481 reflections (0.003%)	Xtriage
$F_o, F_c$ correlation	0.84	EDS
Total number of atoms	7368	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	18.0	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 21.40 % 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 7.0631e-03. 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, 0.375 respectively for untwinned datasets, and 0.333, 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: CA, MN, MMA, MAN

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	0.61	1/1795 (0.1%)	0.82	1/2446 (0.0%)
1	B	0.59	0/1795	0.83	1/2446 (0.0%)
1	C	0.61	1/1795 (0.1%)	0.83	1/2446 (0.0%)
1	D	0.62	1/1795 (0.1%)	0.84	2/2446 (0.1%)
All	All	0.61	3/7180 (0.0%)	0.83	5/9784 (0.1%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	170	VAL	CB-CG2	-5.26	1.41	1.52
1	D	170	VAL	CB-CG2	-5.06	1.42	1.52
1	A	170	VAL	CB-CG2	-5.03	1.42	1.52

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	172	ARG	CB-CG-CD	-5.21	98.05	111.60
1	A	172	ARG	CB-CG-CD	-5.18	98.14	111.60
1	D	161	SER	CB-CA-C	-5.05	100.50	110.10
1	D	172	ARG	CB-CG-CD	-5.04	98.51	111.60
1	B	172	ARG	CB-CG-CD	-5.02	98.56	111.60

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	1755	0	1701	39	0
1	B	1755	0	1701	41	0
1	C	1755	0	1701	39	0
1	D	1755	0	1701	42	0
2	A	35	0	31	3	0
2	B	35	0	31	2	0
2	C	35	0	31	3	0
2	D	35	0	31	4	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
4	C	1	0	0	0	0
4	D	1	0	0	0	0
5	A	50	0	0	1	0
5	B	47	0	0	3	0
5	C	50	0	0	1	0
5	D	53	0	0	2	0
All	All	7368	0	6928	149	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 11.

All (149) 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:17:ILE:HD13	1:A:228:ARG:HD3	1.47	0.96
1:C:90:ARG:NH1	1:C:217:ILE:HG22	1.84	0.93
1:B:90:ARG:NH1	1:B:217:ILE:HG22	1.84	0.92
1:C:17:ILE:HD13	1:C:228:ARG:HD3	1.52	0.92
1:B:170:VAL:HG23	1:B:226:THR:HG22	1.52	0.92
1:A:170:VAL:HG23	1:A:226:THR:HG22	1.52	0.92
1:C:170:VAL:HG23	1:C:226:THR:HG22	1.51	0.91
1:A:90:ARG:NH1	1:A:217:ILE:HG22	1.87	0.90
1:D:90:ARG:NH1	1:D:217:ILE:HG22	1.86	0.90
1:B:17:ILE:HD13	1:B:228:ARG:HD3	1.54	0.89
1:D:170:VAL:HG23	1:D:226:THR:HG22	1.53	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:17:ILE:HD13	1:D:228:ARG:HD3	1.56	0.87
1:A:170:VAL:CG2	1:A:226:THR:HA	2.17	0.75
1:D:162:ASN:OD1	1:D:164:SER:HB2	1.87	0.75
1:C:131:ASN:HB2	1:D:123:THR:O	1.86	0.74
1:A:123:THR:HB	1:B:131:ASN:HD22	1.53	0.73
1:C:170:VAL:CG2	1:C:226:THR:HA	2.18	0.73
1:D:170:VAL:CG2	1:D:226:THR:HA	2.19	0.71
1:B:170:VAL:CG2	1:B:226:THR:HA	2.20	0.71
1:C:90:ARG:HH11	1:C:217:ILE:HG22	1.54	0.70
1:A:90:ARG:HH11	1:A:217:ILE:HG22	1.57	0.69
1:B:44:ASN:OD1	1:B:200:LYS:HA	1.94	0.68
1:A:100:TYR:CD2	2:A:240:MAN:H62	2.28	0.68
1:A:44:ASN:OD1	1:A:200:LYS:HA	1.94	0.67
1:A:100:TYR:HD2	2:A:240:MAN:H62	1.57	0.67
1:C:44:ASN:OD1	1:C:200:LYS:HA	1.93	0.67
1:B:90:ARG:HH11	1:B:217:ILE:HG22	1.55	0.67
1:D:44:ASN:OD1	1:D:200:LYS:HA	1.95	0.66
1:B:162:ASN:OD1	1:B:164:SER:HB2	1.96	0.66
1:D:90:ARG:HH11	1:D:217:ILE:HG22	1.59	0.66
1:B:1:ALA:HB1	5:B:245:HOH:O	1.96	0.66
1:A:162:ASN:OD1	1:A:164:SER:HB2	1.97	0.65
1:C:201:SER:HB3	1:C:206:PRO:HB3	1.79	0.64
1:A:123:THR:HB	1:B:131:ASN:ND2	2.13	0.62
1:C:162:ASN:OD1	1:C:164:SER:HB2	1.99	0.61
1:B:201:SER:HB3	1:B:206:PRO:HB3	1.82	0.61
1:D:16:ASP:N	2:D:242:MAN:O6	2.34	0.60
1:D:224:GLY:HA2	5:D:251:HOH:O	2.03	0.57
1:C:100:TYR:HB3	1:C:205:HIS:O	2.05	0.57
1:C:172:ARG:NH2	5:C:243:HOH:O	2.37	0.57
1:B:51:HIS:CD2	5:B:288:HOH:O	2.58	0.57
1:A:123:THR:CB	1:B:131:ASN:HD22	2.15	0.57
1:C:100:TYR:HD2	2:C:240:MAN:H62	1.70	0.56
1:D:17:ILE:CD1	1:D:228:ARG:HD3	2.30	0.56
1:B:100:TYR:HB3	1:B:205:HIS:O	2.06	0.56
1:D:170:VAL:CG2	1:D:226:THR:HG22	2.33	0.55
1:A:150:THR:O	1:A:151:ASP:HB2	2.07	0.54
1:B:28:ASP:HA	5:B:269:HOH:O	2.07	0.54
1:A:100:TYR:HD2	2:A:240:MAN:C6	2.21	0.54
1:D:150:THR:O	1:D:151:ASP:HB2	2.08	0.53
1:C:100:TYR:CD2	2:C:240:MAN:H62	2.44	0.53
1:A:100:TYR:HB3	1:A:205:HIS:O	2.07	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:150:THR:O	1:B:151:ASP:HB2	2.09	0.53
1:C:150:THR:O	1:C:151:ASP:HB2	2.09	0.52
1:B:62:SER:HB3	1:C:57:VAL:HG11	1.91	0.52
1:A:156:LEU:O	1:A:171:GLY:HA3	2.09	0.52
1:A:201:SER:HB3	1:A:206:PRO:HB3	1.90	0.52
1:B:28:ASP:HB3	1:B:31:SER:O	2.10	0.51
1:A:28:ASP:HB3	1:A:31:SER:O	2.10	0.51
1:A:17:ILE:CD1	1:A:228:ARG:HD3	2.29	0.51
1:D:156:LEU:O	1:D:171:GLY:HA3	2.11	0.51
1:C:207:ALA:HB1	1:C:208:ASP:CG	2.31	0.51
1:A:131:ASN:HB2	1:B:123:THR:O	2.11	0.50
1:B:123:THR:O	1:B:124:ASN:OD1	2.28	0.50
1:C:88:TRP:CG	1:D:138:LYS:HD2	2.48	0.49
1:A:25:ILE:HG21	1:A:65:VAL:HG21	1.94	0.49
1:B:17:ILE:CD1	1:B:228:ARG:HD3	2.37	0.49
1:D:100:TYR:HB3	1:D:205:HIS:O	2.12	0.49
1:C:156:LEU:O	1:C:171:GLY:HA3	2.13	0.48
1:B:181:ILE:HA	1:B:181:ILE:HD12	1.73	0.48
1:D:28:ASP:HB3	1:D:31:SER:O	2.13	0.48
1:B:156:LEU:O	1:B:171:GLY:HA3	2.12	0.48
1:D:207:ALA:HB1	1:D:208:ASP:CG	2.34	0.48
1:D:123:THR:O	1:D:124:ASN:OD1	2.31	0.47
1:B:170:VAL:CG2	1:B:226:THR:HG22	2.33	0.47
1:C:111:PHE:HB3	1:C:128:PHE:CZ	2.49	0.47
1:D:170:VAL:HG22	1:D:226:THR:HA	1.96	0.47
1:C:28:ASP:HB3	1:C:31:SER:O	2.15	0.47
1:C:228:ARG:HG2	2:C:240:MAN:O3	2.14	0.47
1:C:25:ILE:HG21	1:C:65:VAL:HG21	1.97	0.46
1:B:170:VAL:HG22	1:B:226:THR:HA	1.98	0.46
1:D:102:GLU:HA	1:D:201:SER:HB2	1.98	0.46
1:C:116:LYS:HB3	1:C:123:THR:HG23	1.99	0.45
1:B:66:SER:HB3	1:B:72:SER:HB3	1.98	0.45
1:B:57:VAL:HB	1:C:53:ILE:HD11	1.99	0.45
1:A:170:VAL:CG2	1:A:226:THR:HG22	2.35	0.45
1:C:92:GLY:HA2	1:C:109:TRP:CH2	2.52	0.45
1:C:170:VAL:HG22	1:C:226:THR:HA	1.96	0.45
1:B:102:GLU:HA	1:B:201:SER:HB2	1.97	0.45
1:C:88:TRP:CE3	1:D:138:LYS:HB2	2.51	0.45
1:B:207:ALA:HB1	1:B:208:ASP:CG	2.37	0.44
1:D:25:ILE:HG21	1:D:65:VAL:HG21	2.00	0.44
1:D:14:ASN:HB3	5:D:288:HOH:O	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:23:PRO:HB2	1:B:40:TRP:O	2.17	0.44
1:C:88:TRP:CD2	1:D:138:LYS:HB2	2.53	0.44
1:A:172:ARG:NH2	5:A:278:HOH:O	2.50	0.44
1:C:181:ILE:HD12	1:C:181:ILE:HA	1.76	0.44
1:D:207:ALA:HA	1:D:208:ASP:HA	1.76	0.44
1:B:207:ALA:HA	1:B:208:ASP:HA	1.81	0.43
1:C:201:SER:CB	1:C:206:PRO:HB3	2.47	0.43
1:B:111:PHE:HB3	1:B:128:PHE:CZ	2.53	0.43
1:B:25:ILE:HG21	1:B:65:VAL:HG21	2.01	0.43
1:D:116:LYS:HB3	1:D:123:THR:HG23	2.00	0.43
1:A:170:VAL:HG22	1:A:226:THR:HA	1.96	0.43
1:D:16:ASP:H	2:D:242:MAN:HO6	1.66	0.43
1:B:30:LYS:HD2	1:B:84:VAL:HG13	2.01	0.43
1:C:17:ILE:CD1	1:C:228:ARG:HD3	2.34	0.43
1:A:181:ILE:HD12	1:A:181:ILE:HA	1.71	0.43
1:C:123:THR:O	1:D:131:ASN:HB2	2.19	0.43
1:C:56:SER:OG	1:C:188:VAL:HA	2.19	0.42
1:A:66:SER:HB3	1:A:72:SER:HB3	2.01	0.42
1:A:111:PHE:HB3	1:A:128:PHE:CZ	2.54	0.42
1:D:56:SER:OG	1:D:188:VAL:HA	2.19	0.42
1:C:32:VAL:HB	1:C:233:PHE:CD2	2.53	0.42
1:C:201:SER:HA	1:C:202:PRO:HD2	1.85	0.42
1:A:109:TRP:HA	1:A:194:THR:O	2.20	0.42
1:A:56:SER:OG	1:A:188:VAL:HA	2.18	0.42
1:A:101:LYS:HD2	1:A:165:PRO:O	2.20	0.42
1:C:170:VAL:CG2	1:C:226:THR:HG22	2.34	0.42
1:D:15:THR:HB	2:D:242:MAN:O6	2.19	0.42
1:D:217:ILE:HG21	1:D:217:ILE:HD13	1.83	0.42
1:D:111:PHE:HB3	1:D:128:PHE:CZ	2.55	0.42
1:B:177:ALA:HA	1:B:178:PRO:HD3	1.91	0.42
1:C:66:SER:HB3	1:C:72:SER:HB3	2.01	0.41
1:A:64:VAL:HG21	1:D:57:VAL:HG22	2.02	0.41
1:A:92:GLY:HA2	1:A:109:TRP:CH2	2.55	0.41
1:D:181:ILE:HD12	1:D:181:ILE:HA	1.72	0.41
1:B:100:TYR:HD2	2:B:240:MAN:H62	1.84	0.41
1:B:109:TRP:HA	1:B:194:THR:O	2.20	0.41
1:D:32:VAL:HB	1:D:233:PHE:CD2	2.56	0.41
1:B:32:VAL:HB	1:B:233:PHE:CD2	2.55	0.41
1:D:228:ARG:HG2	2:D:240:MAN:O3	2.21	0.41
1:D:92:GLY:HA2	1:D:109:TRP:CH2	2.55	0.41
1:C:30:LYS:HD2	1:C:84:VAL:HG13	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:228:ARG:HG2	2:B:240:MAN:O3	2.21	0.41
1:A:207:ALA:HA	1:A:208:ASP:HA	1.79	0.41
1:A:30:LYS:HD2	1:A:84:VAL:HG13	2.03	0.41
1:D:30:LYS:HD2	1:D:84:VAL:HG13	2.02	0.41
1:D:66:SER:HB3	1:D:72:SER:HB3	2.03	0.41
1:B:90:ARG:NH1	1:B:217:ILE:CG2	2.71	0.41
1:A:90:ARG:HG3	1:A:217:ILE:HG23	2.02	0.41
1:D:109:TRP:HA	1:D:194:THR:O	2.21	0.41
1:A:32:VAL:HB	1:A:233:PHE:CD2	2.56	0.40
1:A:51:HIS:O	1:A:63:ALA:HA	2.20	0.40
1:C:109:TRP:HA	1:C:194:THR:O	2.20	0.40
1:D:47:VAL:HA	1:D:197:PHE:O	2.20	0.40
1:B:51:HIS:O	1:B:63:ALA:HA	2.21	0.40
1:A:177:ALA:HA	1:A:178:PRO:HD3	1.89	0.40
1:A:102:GLU:HA	1:A:201:SER:HB2	2.04	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	227/237 (96%)	215 (95%)	12 (5%)	0	100	100
1	B	227/237 (96%)	212 (93%)	15 (7%)	0	100	100
1	C	227/237 (96%)	212 (93%)	14 (6%)	1 (0%)	39	46
1	D	227/237 (96%)	213 (94%)	13 (6%)	1 (0%)	39	46
All	All	908/948 (96%)	852 (94%)	54 (6%)	2 (0%)	52	63

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	162	ASN
1	D	162	ASN

### 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	195/203 (96%)	181 (93%)	14 (7%)	18	19
1	B	195/203 (96%)	179 (92%)	16 (8%)	14	15
1	C	195/203 (96%)	181 (93%)	14 (7%)	18	19
1	D	195/203 (96%)	180 (92%)	15 (8%)	16	17
All	All	780/812 (96%)	721 (92%)	59 (8%)	16	18

All (59) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	78	ASP
1	A	82	ASP
1	A	101	LYS
1	A	123	THR
1	A	150	THR
1	A	151	ASP
1	A	161	SER
1	A	164	SER
1	A	181	ILE
1	A	184	SER
1	A	203	ASP
1	A	204	SER
1	A	205	HIS
1	A	228	ARG
1	B	78	ASP
1	B	82	ASP
1	B	101	LYS
1	B	123	THR
1	B	134	SER
1	B	150	THR

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Mol	Chain	Res	Type
1	B	151	ASP
1	B	161	SER
1	B	164	SER
1	B	181	ILE
1	B	184	SER
1	B	203	ASP
1	B	204	SER
1	B	205	HIS
1	B	223	SER
1	B	228	ARG
1	C	78	ASP
1	C	82	ASP
1	C	101	LYS
1	C	134	SER
1	C	150	THR
1	C	151	ASP
1	C	161	SER
1	C	164	SER
1	C	181	ILE
1	C	184	SER
1	C	203	ASP
1	C	204	SER
1	C	205	HIS
1	C	228	ARG
1	D	21	SER
1	D	78	ASP
1	D	82	ASP
1	D	101	LYS
1	D	123	THR
1	D	150	THR
1	D	151	ASP
1	D	161	SER
1	D	164	SER
1	D	181	ILE
1	D	184	SER
1	D	203	ASP
1	D	204	SER
1	D	205	HIS
1	D	228	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:



Mol	Chain	Res	Type
1	A	41	ASN
1	A	237	ASN
1	B	41	ASN
1	B	51	HIS
1	B	131	ASN
1	B	237	ASN
1	C	41	ASN
1	C	237	ASN
1	D	41	ASN
1	D	237	ASN

### 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 ⓘ

12 carbohydrates 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	$\# Z  > 2$
2	MAN	A	240	2	12,12,12	0.39	0	17,17,17	0.75	0
2	MMA	A	241	2	10,11,13	0.43	0	11,15,18	0.94	0
2	MAN	A	242	2	12,12,12	0.49	0	17,17,17	0.90	0
2	MAN	B	240	2	12,12,12	0.66	0	17,17,17	0.88	0
2	MMA	B	241	2	10,11,13	0.43	0	11,15,18	1.00	1 (9%)
2	MAN	B	242	2	12,12,12	0.29	0	17,17,17	1.03	0
2	MAN	C	240	2	12,12,12	0.51	0	17,17,17	0.60	0
2	MMA	C	241	2	10,11,13	0.45	0	11,15,18	0.90	0
2	MAN	C	242	2	12,12,12	0.42	0	17,17,17	0.92	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	MAN	D	240	2	12,12,12	0.28	0	17,17,17	0.90	1 (5%)
2	MMA	D	241	2	10,11,13	0.59	0	11,15,18	0.79	0
2	MAN	D	242	2	12,12,12	0.46	0	17,17,17	0.91	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
2	MAN	A	240	2	-	0/2/22/22	0/1/1/1
2	MMA	A	241	2	-	0/2/18/24	0/1/1/1
2	MAN	A	242	2	-	0/2/22/22	0/1/1/1
2	MAN	B	240	2	-	0/2/22/22	0/1/1/1
2	MMA	B	241	2	-	0/2/18/24	0/1/1/1
2	MAN	B	242	2	-	0/2/22/22	0/1/1/1
2	MAN	C	240	2	-	0/2/22/22	0/1/1/1
2	MMA	C	241	2	-	0/2/18/24	0/1/1/1
2	MAN	C	242	2	-	0/2/22/22	0/1/1/1
2	MAN	D	240	2	-	0/2/22/22	0/1/1/1
2	MMA	D	241	2	-	0/2/18/24	0/1/1/1
2	MAN	D	242	2	-	0/2/22/22	0/1/1/1

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	240	MAN	C4-C3-C2	-2.89	105.40	110.79
2	B	241	MMA	C6-C5-C4	-2.08	109.01	112.83
2	C	242	MAN	C6-C5-C4	-2.08	107.89	113.02

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	240	MAN	3	0
2	B	240	MAN	2	0
2	C	240	MAN	3	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	240	MAN	1	0
2	D	242	MAN	3	0

## 5.6 Ligand geometry [i](#)

Of 8 ligands modelled in this entry, 8 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

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

### 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	231/237 (97%)	0.90	37 (16%) <b>3</b> <b>4</b>	2, 14, 51, 65	0
1	B	231/237 (97%)	0.80	30 (12%) <b>5</b> <b>9</b>	3, 14, 46, 67	0
1	C	231/237 (97%)	0.80	32 (13%) <b>4</b> <b>7</b>	2, 13, 48, 64	0
1	D	231/237 (97%)	0.99	42 (18%) <b>2</b> <b>3</b>	3, 15, 49, 70	0
All	All	924/948 (97%)	0.87	141 (15%) <b>3</b> <b>5</b>	2, 14, 49, 70	0

All (141) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	203	ASP	8.8
1	C	150	THR	7.3
1	C	205	HIS	6.3
1	C	185	SER	6.0
1	A	186	ALA	5.8
1	A	205	HIS	5.7
1	C	161	SER	5.7
1	B	150	THR	5.6
1	D	100	TYR	5.5
1	B	185	SER	5.5
1	C	163	GLY	5.2
1	D	205	HIS	5.2
1	A	206	PRO	5.2
1	B	163	GLY	5.2
1	A	165	PRO	5.1
1	D	186	ALA	5.0
1	A	100	TYR	4.9
1	B	203	ASP	4.9
1	A	123	THR	4.6
1	A	47	VAL	4.6
1	D	202	PRO	4.4

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Mol	Chain	Res	Type	RSRZ
1	D	204	SER	4.3
1	D	163	GLY	4.3
1	A	198	LEU	4.3
1	B	205	HIS	4.2
1	A	187	VAL	4.2
1	A	45	GLY	4.1
1	D	206	PRO	4.0
1	C	201	SER	4.0
1	D	45	GLY	3.9
1	A	160	SER	3.9
1	C	187	VAL	3.8
1	C	70	ALA	3.8
1	B	71	ASP	3.8
1	A	150	THR	3.7
1	C	100	TYR	3.7
1	D	123	THR	3.7
1	A	42	MET	3.7
1	D	161	SER	3.7
1	A	162	ASN	3.6
1	B	70	ALA	3.6
1	B	100	TYR	3.6
1	A	69	ASN	3.6
1	C	42	MET	3.6
1	A	203	ASP	3.5
1	B	161	SER	3.5
1	D	97	THR	3.5
1	A	161	SER	3.5
1	D	150	THR	3.5
1	C	45	GLY	3.5
1	A	43	GLN	3.4
1	D	199	ILE	3.4
1	B	204	SER	3.4
1	D	162	ASN	3.4
1	A	134	SER	3.4
1	C	165	PRO	3.3
1	B	159	VAL	3.3
1	B	165	PRO	3.3
1	D	159	VAL	3.3
1	C	159	VAL	3.3
1	D	43	GLN	3.3
1	D	165	PRO	3.1
1	B	101	LYS	3.1

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Mol	Chain	Res	Type	RSRZ
1	C	186	ALA	3.1
1	A	163	GLY	3.1
1	C	101	LYS	3.0
1	D	200	LYS	3.0
1	D	164	SER	3.0
1	D	201	SER	3.0
1	A	168	SER	3.0
1	D	158	ARG	3.0
1	B	149	GLY	3.0
1	B	187	VAL	2.9
1	B	202	PRO	2.9
1	A	185	SER	2.9
1	A	202	PRO	2.8
1	D	132	GLN	2.8
1	C	162	ASN	2.8
1	D	69	ASN	2.7
1	D	152	GLY	2.7
1	C	67	TYR	2.7
1	A	158	ARG	2.7
1	A	101	LYS	2.6
1	B	200	LYS	2.6
1	B	67	TYR	2.6
1	D	168	SER	2.6
1	C	166	GLN	2.6
1	A	13	PRO	2.5
1	C	203	ASP	2.5
1	A	46	LYS	2.5
1	D	131	ASN	2.5
1	D	156	LEU	2.5
1	A	146	ALA	2.5
1	B	45	GLY	2.5
1	D	104	ASN	2.5
1	C	149	GLY	2.5
1	D	44	ASN	2.5
1	B	116	LYS	2.5
1	D	47	VAL	2.5
1	D	160	SER	2.4
1	B	152	GLY	2.4
1	D	99	LEU	2.4
1	C	57	VAL	2.4
1	C	184	SER	2.4
1	A	159	VAL	2.3

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Mol	Chain	Res	Type	RSRZ
1	C	200	LYS	2.3
1	A	199	ILE	2.3
1	B	166	GLN	2.3
1	C	116	LYS	2.3
1	C	151	ASP	2.3
1	D	103	THR	2.3
1	A	99	LEU	2.3
1	B	168	SER	2.2
1	C	13	PRO	2.2
1	C	46	LYS	2.2
1	D	12	TYR	2.2
1	C	157	THR	2.2
1	B	164	SER	2.2
1	B	48	GLY	2.2
1	D	56	SER	2.2
1	C	83	ASN	2.2
1	D	166	GLN	2.2
1	D	42	MET	2.2
1	D	146	ALA	2.2
1	A	164	SER	2.2
1	B	44	ASN	2.2
1	B	99	LEU	2.1
1	D	157	THR	2.1
1	C	132	GLN	2.1
1	A	204	SER	2.1
1	B	157	THR	2.1
1	A	41	ASN	2.1
1	D	51	HIS	2.1
1	A	116	LYS	2.1
1	A	201	SER	2.1
1	C	44	ASN	2.1
1	B	123	THR	2.0
1	D	101	LYS	2.0
1	A	44	ASN	2.0
1	C	43	GLN	2.0
1	B	223	SER	2.0

## 6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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

### 6.3 Carbohydrates ⓘ

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	MAN	D	242	12/12	0.59	0.33	4.97	45,51,59,64	0
2	MMA	A	241	11/13	0.67	0.31	0.93	24,30,33,34	0
2	MAN	A	240	12/12	0.84	0.20	-0.29	16,25,29,37	0
2	MAN	C	240	12/12	0.88	0.18	-0.37	2,6,11,16	0
2	MAN	D	240	12/12	0.82	0.19	-0.56	8,18,26,27	0
2	MAN	B	240	12/12	0.83	0.18	-0.84	2,17,19,20	0
2	MAN	B	242	12/12	0.64	0.29	-	20,28,37,38	0
2	MMA	C	241	11/13	0.81	0.20	-	4,15,24,26	0
2	MAN	A	242	12/12	0.73	0.24	-	30,33,39,41	0
2	MMA	B	241	11/13	0.77	0.20	-	20,24,27,29	0
2	MAN	C	242	12/12	0.65	0.30	-	15,24,35,47	0
2	MMA	D	241	11/13	0.69	0.22	-	28,43,55,58	0

### 6.4 Ligands ⓘ

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
4	CA	A	239	1/1	0.89	0.11	-2.31	10,10,10,10	0
3	MN	A	238	1/1	0.75	0.11	-3.12	20,20,20,20	0
3	MN	B	238	1/1	0.96	0.06	-3.26	14,14,14,14	0
3	MN	C	238	1/1	0.95	0.05	-3.39	21,21,21,21	0
4	CA	B	239	1/1	0.94	0.08	-3.52	12,12,12,12	0
4	CA	C	239	1/1	0.99	0.05	-3.74	18,18,18,18	0
3	MN	D	238	1/1	0.96	0.05	-4.23	15,15,15,15	0
4	CA	D	239	1/1	0.89	0.07	-4.66	14,14,14,14	0



## 6.5 Other polymers [i](#)

There are no such residues in this entry.