



# Full wwPDB X-ray Structure Validation Report ⓘ

Jan 18, 2018 – 08:26 AM EST

PDB ID : 5MDS  
Title : Crystal structure of outer membrane expressed Chitoporin VhChip from *Vibrio harveyi* in complex with chitotetraose  
Authors : Zahn, M.; van den Berg, B.  
Deposited on : 2016-11-13  
Resolution : 2.60 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-20030736  
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-20030736

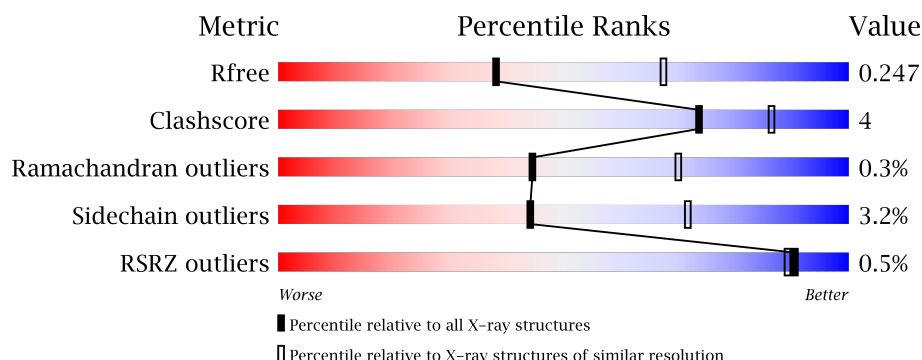
# 1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.60 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	2542 (2.60-2.60)
Clashscore	112137	2895 (2.60-2.60)
Ramachandran outliers	110173	2848 (2.60-2.60)
Sidechain outliers	110143	2848 (2.60-2.60)
RSRZ outliers	101464	2550 (2.60-2.60)

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	350	<div> <div>89%</div> <div>7%</div> <div>...</div> </div>
1	B	350	<div> <div>89%</div> <div>7%</div> <div>...</div> </div>
1	C	350	<div> <div>87%</div> <div>9%</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	NAG	A	403	-	-	-	X
2	NAG	B	402	-	-	-	X
2	NAG	B	403	-	-	-	X
2	NAG	C	402	-	-	-	X
2	NAG	C	403	-	-	-	X

## 2 Entry composition [i](#)

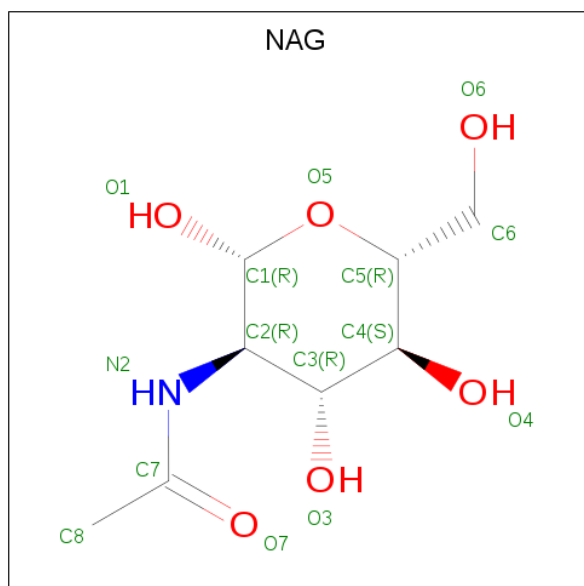
There are 2 unique types of molecules in this entry. The entry contains 8166 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Chitoporin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	341	Total	C	N	O	S	0	0	0
			2665	1680	438	538	9			
1	B	341	Total	C	N	O	S	0	0	0
			2665	1680	438	538	9			
1	C	341	Total	C	N	O	S	0	0	0
			2665	1680	438	538	9			

- Molecule 2 is N-ACETYL-D-GLUCOSAMINE (three-letter code: NAG) (formula:  $C_8H_{15}NO_6$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			15	8	1	6		
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	A	1	Total	C	N	O	0	0
			14	8	1	5		

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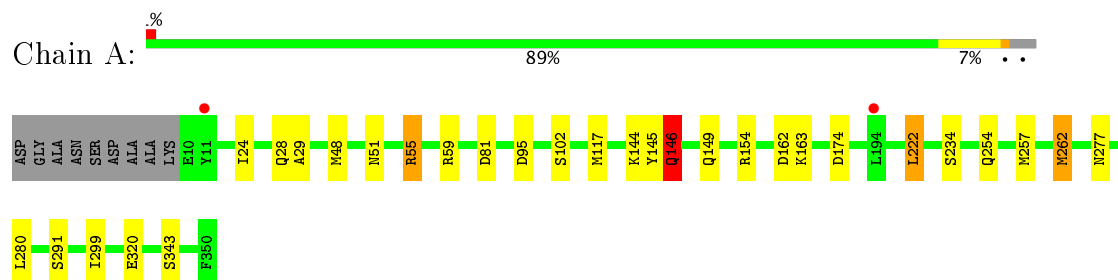
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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	B	1	Total	C	N	O	0	0
			15	8	1	6		
2	B	1	Total	C	N	O	0	0
			14	8	1	5		
2	B	1	Total	C	N	O	0	0
			14	8	1	5		
2	B	1	Total	C	N	O	0	0
			14	8	1	5		
2	C	1	Total	C	N	O	0	0
			15	8	1	6		
2	C	1	Total	C	N	O	0	0
			14	8	1	5		
2	C	1	Total	C	N	O	0	0
			14	8	1	5		
2	C	1	Total	C	N	O	0	0
			14	8	1	5		

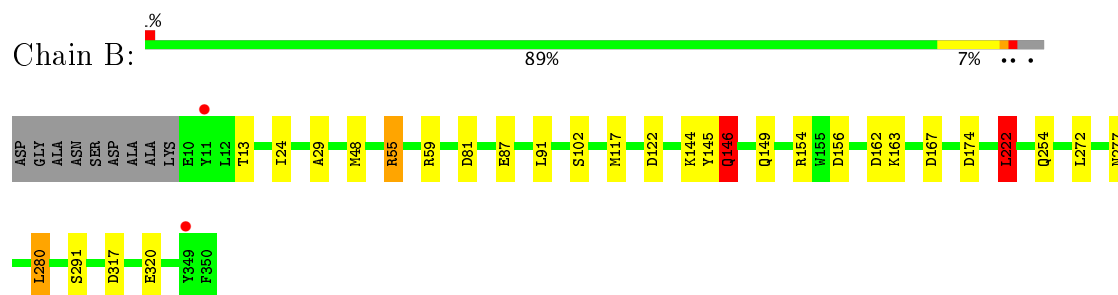
### 3 Residue-property plots [i](#)

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 ( $RSRZ > 2$ ). 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.

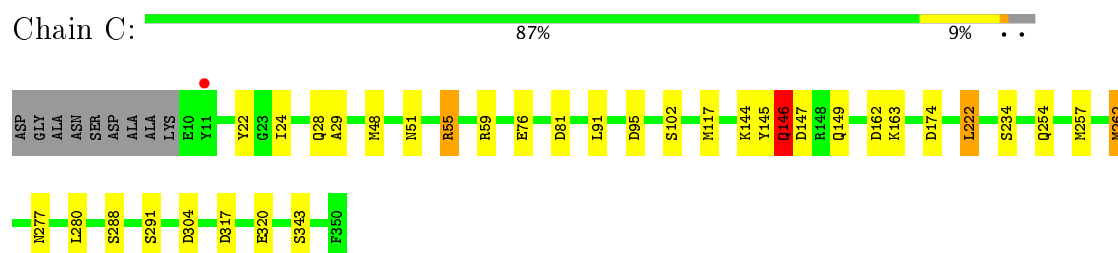
#### • Molecule 1: Chitoporin



#### • Molecule 1: Chitoporin



#### • Molecule 1: Chitoporin



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	250.01Å 145.05Å 55.16Å 90.00° 94.80° 90.00°	Depositor
Resolution (Å)	125.35 – 2.60 62.67 – 2.60	Depositor EDS
% Data completeness (in resolution range)	93.2 (125.35-2.60) 93.2 (62.67-2.60)	Depositor EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.55 (at 2.61Å)	Xtriage
Refinement program	REFMAC 5.8.0155	Depositor
R, $R_{free}$	0.221 , 0.247 0.225 , 0.247	Depositor DCC
$R_{free}$ test set	1653 reflections (3.04%)	DCC
Wilson B-factor (Å <sup>2</sup> )	49.1	Xtriage
Anisotropy	0.792	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 28.4	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	8166	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	63.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.93% of the height of the origin peak. No significant pseudotranslation is detected.*

<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 [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: NAG

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	0.96	6/2734 (0.2%)	1.00	8/3704 (0.2%)
1	B	0.94	4/2734 (0.1%)	1.03	14/3704 (0.4%)
1	C	0.95	6/2734 (0.2%)	1.00	8/3704 (0.2%)
All	All	0.95	16/8202 (0.2%)	1.01	30/11112 (0.3%)

All (16) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	146	GLN	CG-CD	10.37	1.75	1.51
1	C	146	GLN	CG-CD	10.20	1.74	1.51
1	A	320	GLU	CG-CD	8.64	1.65	1.51
1	A	146	GLN	CG-CD	8.26	1.70	1.51
1	C	320	GLU	CG-CD	7.90	1.63	1.51
1	A	320	GLU	CD-OE2	7.48	1.33	1.25
1	B	320	GLU	CG-CD	7.32	1.62	1.51
1	A	343	SER	CB-OG	6.89	1.51	1.42
1	C	343	SER	CB-OG	6.73	1.51	1.42
1	A	320	GLU	CB-CG	5.88	1.63	1.52
1	C	320	GLU	CD-OE1	5.69	1.31	1.25
1	A	320	GLU	CD-OE1	5.62	1.31	1.25
1	C	320	GLU	CB-CG	5.53	1.62	1.52
1	B	320	GLU	CD-OE1	5.53	1.31	1.25
1	B	320	GLU	CB-CG	5.04	1.61	1.52
1	C	320	GLU	CD-OE2	5.04	1.31	1.25

All (30) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	146	GLN	CB-CA-C	8.66	127.72	110.40
1	B	146	GLN	CB-CA-C	8.42	127.24	110.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	146	GLN	CB-CA-C	8.26	126.92	110.40
1	A	81	ASP	CB-CG-OD2	-7.93	111.17	118.30
1	C	81	ASP	CB-CG-OD2	-7.80	111.28	118.30
1	A	257	MET	CG-SD-CE	7.49	112.19	100.20
1	B	59	ARG	NE-CZ-NH2	-7.41	116.59	120.30
1	A	59	ARG	NE-CZ-NH1	7.25	123.93	120.30
1	C	257	MET	CG-SD-CE	7.18	111.69	100.20
1	C	59	ARG	NE-CZ-NH2	-7.02	116.79	120.30
1	A	59	ARG	NE-CZ-NH2	-6.99	116.80	120.30
1	C	95	ASP	CB-CG-OD2	-6.94	112.05	118.30
1	A	95	ASP	CB-CG-OD2	-6.78	112.20	118.30
1	B	59	ARG	NE-CZ-NH1	6.60	123.60	120.30
1	B	87	GLU	OE1-CD-OE2	-6.21	115.85	123.30
1	C	59	ARG	NE-CZ-NH1	6.18	123.39	120.30
1	C	317	ASP	CB-CG-OD2	-6.10	112.81	118.30
1	B	122	ASP	CB-CG-OD2	-6.04	112.86	118.30
1	B	81	ASP	CB-CG-OD2	-5.92	112.98	118.30
1	A	154	ARG	NE-CZ-NH1	5.89	123.25	120.30
1	B	154	ARG	NE-CZ-NH1	5.88	123.24	120.30
1	B	222	LEU	CB-CG-CD2	5.76	120.80	111.00
1	C	304	ASP	CB-CG-OD1	5.53	123.27	118.30
1	B	222	LEU	CA-CB-CG	5.51	127.98	115.30
1	A	81	ASP	CB-CG-OD1	5.49	123.24	118.30
1	B	156	ASP	CB-CG-OD1	5.40	123.16	118.30
1	B	154	ARG	NE-CZ-NH2	-5.38	117.61	120.30
1	B	317	ASP	CB-CG-OD2	-5.09	113.72	118.30
1	B	167	ASP	CB-CG-OD1	5.08	122.87	118.30
1	B	81	ASP	CB-CG-OD1	5.01	122.81	118.30

There are no chirality outliers.

There are no planarity outliers.

## 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	2665	0	2420	14	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	2665	0	2420	15	0
1	C	2665	0	2420	18	0
2	A	57	0	51	4	0
2	B	57	0	51	4	0
2	C	57	0	51	5	0
All	All	8166	0	7413	59	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 4.

All (59) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:146:GLN:CG	1:B:146:GLN:CD	1.74	1.56
1:C:146:GLN:CD	1:C:146:GLN:CG	1.74	1.55
2:C:401:NAG:O3	2:C:402:NAG:O5	2.05	0.73
1:C:146:GLN:NE2	1:C:149:GLN:OE1	2.24	0.71
1:B:146:GLN:NE2	1:B:149:GLN:OE1	2.25	0.69
1:C:146:GLN:OE1	1:C:174:ASP:OD2	2.10	0.69
1:A:146:GLN:OE1	1:A:174:ASP:OD2	2.11	0.68
1:A:146:GLN:NE2	1:A:149:GLN:OE1	2.27	0.68
1:B:146:GLN:OE1	1:B:174:ASP:OD2	2.13	0.65
1:B:146:GLN:OE1	1:B:174:ASP:OD1	2.15	0.64
1:C:146:GLN:OE1	1:C:174:ASP:OD1	2.16	0.64
2:A:401:NAG:O3	2:A:402:NAG:O5	2.15	0.63
1:A:146:GLN:OE1	1:A:174:ASP:OD1	2.16	0.62
2:A:401:NAG:HO3	2:A:402:NAG:C5	2.15	0.59
2:B:401:NAG:O3	2:B:401:NAG:C8	2.51	0.59
1:A:29:ALA:HB1	1:A:48:MET:CE	2.34	0.57
1:B:146:GLN:CD	1:B:149:GLN:OE1	2.43	0.57
1:C:146:GLN:OE1	1:C:174:ASP:CG	2.43	0.57
1:B:29:ALA:HB1	1:B:48:MET:CE	2.35	0.56
2:B:401:NAG:O3	2:B:402:NAG:O5	2.17	0.56
1:A:146:GLN:OE1	1:A:174:ASP:CG	2.44	0.56
1:B:146:GLN:OE1	1:B:174:ASP:CG	2.44	0.56
1:C:146:GLN:CD	1:C:149:GLN:OE1	2.43	0.56
1:A:146:GLN:CD	1:A:149:GLN:OE1	2.44	0.56
1:C:29:ALA:HB1	1:C:48:MET:CE	2.36	0.55
2:C:401:NAG:HO3	2:C:402:NAG:C1	2.16	0.55
1:A:29:ALA:HB1	1:A:48:MET:HE2	1.92	0.50
1:B:277:ASN:O	1:B:291:SER:HB2	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:147:ASP:OD2	2:C:404:NAG:H83	2.12	0.50
1:C:277:ASN:O	1:C:291:SER:HB2	2.12	0.50
1:B:29:ALA:HB1	1:B:48:MET:HE2	1.95	0.49
1:A:277:ASN:O	1:A:291:SER:HB2	2.14	0.47
1:A:222:LEU:C	1:A:222:LEU:HD12	2.35	0.47
1:C:222:LEU:C	1:C:222:LEU:HD12	2.35	0.46
1:C:234:SER:OG	1:C:262:MET:HG3	2.16	0.46
1:A:234:SER:OG	1:A:262:MET:HG3	2.15	0.46
2:B:404:NAG:O3	2:B:404:NAG:H82	2.16	0.45
2:A:403:NAG:O3	2:A:403:NAG:H82	2.15	0.45
1:C:29:ALA:HB1	1:C:48:MET:HE2	1.99	0.45
2:C:403:NAG:H82	2:C:403:NAG:O3	2.16	0.45
1:B:222:LEU:C	1:B:222:LEU:HD23	2.38	0.44
2:C:401:NAG:O3	2:C:401:NAG:C8	2.66	0.43
1:A:254:GLN:HB2	1:A:280:LEU:HD12	2.01	0.43
2:B:401:NAG:H82	2:B:401:NAG:O3	2.19	0.43
1:C:22:TYR:OH	1:C:76:GLU:OE1	2.31	0.43
1:C:254:GLN:HB2	1:C:280:LEU:HD12	2.01	0.43
1:B:24:ILE:HG21	1:B:55:ARG:CZ	2.50	0.42
1:B:254:GLN:HB2	1:B:280:LEU:HD12	2.02	0.42
2:A:401:NAG:HO3	2:A:402:NAG:C1	2.29	0.42
1:C:24:ILE:HG21	1:C:55:ARG:CZ	2.50	0.42
1:C:91:LEU:HA	1:C:91:LEU:HD23	1.85	0.42
1:A:24:ILE:HG21	1:A:55:ARG:CZ	2.50	0.41
1:C:28:GLN:HB3	1:C:51:ASN:HB3	2.02	0.41
1:B:91:LEU:HD23	1:B:91:LEU:HA	1.91	0.41
1:C:144:LYS:HD2	1:C:145:TYR:CZ	2.56	0.41
1:B:144:LYS:HD2	1:B:145:TYR:CZ	2.56	0.41
1:A:144:LYS:HD2	1:A:145:TYR:CZ	2.57	0.40
1:B:24:ILE:HG21	1:B:55:ARG:NH2	2.36	0.40
1:A:28:GLN:HB3	1:A:51:ASN:HB3	2.04	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	339/350 (97%)	325 (96%)	13 (4%)	1 (0%)	44	70
1	B	339/350 (97%)	325 (96%)	13 (4%)	1 (0%)	44	70
1	C	339/350 (97%)	325 (96%)	13 (4%)	1 (0%)	44	70
All	All	1017/1050 (97%)	975 (96%)	39 (4%)	3 (0%)	44	70

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	162	ASP
1	B	162	ASP
1	C	162	ASP

### 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	262/267 (98%)	254 (97%)	8 (3%)	45	73
1	B	262/267 (98%)	253 (97%)	9 (3%)	42	69
1	C	262/267 (98%)	254 (97%)	8 (3%)	45	73
All	All	786/801 (98%)	761 (97%)	25 (3%)	44	72

All (25) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	55	ARG
1	A	102	SER
1	A	117	MET
1	A	146	GLN
1	A	163	LYS
1	A	222	LEU
1	A	262	MET

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Mol	Chain	Res	Type
1	A	299	ILE
1	B	13	THR
1	B	55	ARG
1	B	102	SER
1	B	117	MET
1	B	146	GLN
1	B	163	LYS
1	B	222	LEU
1	B	272	LEU
1	B	280	LEU
1	C	55	ARG
1	C	102	SER
1	C	117	MET
1	C	146	GLN
1	C	163	LYS
1	C	222	LEU
1	C	262	MET
1	C	288	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	146	GLN
1	A	226	GLN
1	B	226	GLN
1	C	63	GLN
1	C	226	GLN
1	C	269	GLN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

### 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry

12 ligands 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	NAG	A	401	2	15,15,15	0.84	0	21,21,21	3.01	11 (52%)
2	NAG	A	402	2	14,14,15	1.32	2 (14%)	15,19,21	2.76	8 (53%)
2	NAG	A	403	2	14,14,15	1.40	2 (14%)	15,19,21	2.63	5 (33%)
2	NAG	A	404	2	14,14,15	1.24	1 (7%)	15,19,21	3.24	6 (40%)
2	NAG	B	401	2	15,15,15	1.67	2 (13%)	21,21,21	3.48	13 (61%)
2	NAG	B	402	2	14,14,15	1.16	2 (14%)	15,19,21	2.21	8 (53%)
2	NAG	B	403	2	14,14,15	1.23	2 (14%)	15,19,21	2.68	6 (40%)
2	NAG	B	404	2	14,14,15	1.09	1 (7%)	15,19,21	3.10	7 (46%)
2	NAG	C	401	2	15,15,15	1.40	1 (6%)	21,21,21	4.00	13 (61%)
2	NAG	C	402	2	14,14,15	1.08	1 (7%)	15,19,21	2.11	6 (40%)
2	NAG	C	403	2	14,14,15	0.97	0	15,19,21	2.60	5 (33%)
2	NAG	C	404	2	14,14,15	1.01	1 (7%)	15,19,21	3.09	5 (33%)

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	NAG	A	401	2	-	0/6/26/26	0/1/1/1
2	NAG	A	402	2	-	0/6/23/26	0/1/1/1
2	NAG	A	403	2	-	0/6/23/26	0/1/1/1
2	NAG	A	404	2	-	0/6/23/26	0/1/1/1
2	NAG	B	401	2	-	0/6/26/26	0/1/1/1
2	NAG	B	402	2	-	0/6/23/26	0/1/1/1
2	NAG	B	403	2	-	0/6/23/26	0/1/1/1
2	NAG	B	404	2	-	0/6/23/26	0/1/1/1
2	NAG	C	401	2	-	0/6/26/26	0/1/1/1
2	NAG	C	402	2	-	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	C	403	2	-	0/6/23/26	0/1/1/1
2	NAG	C	404	2	-	0/6/23/26	0/1/1/1

All (15) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	404	NAG	C1-C2	2.01	1.55	1.52
2	B	402	NAG	C4-C5	2.02	1.57	1.53
2	A	402	NAG	C4-C3	2.03	1.57	1.52
2	B	402	NAG	O4-C4	2.11	1.47	1.43
2	C	402	NAG	C4-C3	2.16	1.57	1.52
2	A	403	NAG	C3-C2	2.19	1.57	1.52
2	B	403	NAG	C1-C2	2.33	1.55	1.52
2	A	402	NAG	C2-N2	2.45	1.50	1.46
2	B	403	NAG	C3-C2	2.51	1.58	1.52
2	B	401	NAG	C2-N2	2.52	1.50	1.45
2	B	404	NAG	C1-C2	2.92	1.56	1.52
2	A	403	NAG	C1-C2	3.31	1.57	1.52
2	A	404	NAG	C1-C2	3.42	1.57	1.52
2	C	401	NAG	C1-C2	3.67	1.57	1.52
2	B	401	NAG	C1-C2	4.49	1.58	1.52

All (93) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	401	NAG	C4-C3-C2	-5.66	101.92	110.33
2	C	401	NAG	O7-C7-N2	-4.95	112.40	121.92
2	C	404	NAG	C4-C3-C2	-4.69	104.14	111.02
2	A	401	NAG	C3-C2-N2	-4.42	102.15	110.61
2	A	403	NAG	O7-C7-C8	-4.36	114.13	122.06
2	A	402	NAG	O7-C7-C8	-4.09	114.61	122.06
2	B	401	NAG	O7-C7-N2	-4.05	114.12	121.92
2	A	401	NAG	C8-C7-N2	-3.97	108.93	116.11
2	A	401	NAG	C1-C2-C3	-3.84	105.31	110.54
2	B	401	NAG	C4-C3-C2	-3.66	104.90	110.33
2	C	403	NAG	O7-C7-C8	-3.48	115.73	122.06
2	A	404	NAG	C4-C3-C2	-3.40	106.04	111.02
2	C	402	NAG	C1-C2-N2	-3.36	104.76	110.49
2	B	404	NAG	C4-C3-C2	-3.14	106.41	111.02
2	B	403	NAG	O7-C7-C8	-3.13	116.36	122.06
2	C	404	NAG	O7-C7-C8	-3.10	116.42	122.06
2	B	402	NAG	C3-C4-C5	-3.01	104.91	110.22

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	404	NAG	O7-C7-C8	-3.01	116.58	122.06
2	C	401	NAG	O4-C4-C5	-2.92	101.93	109.28
2	B	404	NAG	O7-C7-C8	-2.86	116.85	122.06
2	B	401	NAG	O7-C7-C8	-2.54	117.44	122.06
2	B	401	NAG	O1-C1-O5	-2.22	103.64	110.20
2	B	403	NAG	O5-C1-C2	-2.19	108.43	111.47
2	B	401	NAG	O5-C5-C4	-2.17	105.66	109.66
2	B	402	NAG	O7-C7-C8	-2.15	118.14	122.06
2	C	401	NAG	O1-C1-O5	-2.10	103.98	110.20
2	C	401	NAG	O7-C7-C8	-2.07	118.29	122.06
2	A	401	NAG	O4-C4-C5	-2.05	104.13	109.28
2	A	401	NAG	O3-C3-C2	-2.04	105.47	109.61
2	A	401	NAG	C2-N2-C7	2.01	128.28	123.19
2	C	402	NAG	O4-C4-C3	2.01	114.73	110.36
2	C	402	NAG	O5-C1-C2	2.08	114.37	111.47
2	C	401	NAG	O4-C4-C3	2.11	114.94	110.36
2	B	402	NAG	O3-C3-C4	2.12	114.97	110.36
2	B	402	NAG	O7-C7-N2	2.20	126.15	121.92
2	C	402	NAG	O3-C3-C4	2.20	115.15	110.36
2	A	404	NAG	O5-C1-C2	2.38	114.79	111.47
2	B	402	NAG	O4-C4-C3	2.39	115.55	110.36
2	A	402	NAG	C6-C5-C4	2.40	118.62	113.00
2	A	401	NAG	O7-C7-N2	2.41	126.56	121.92
2	A	401	NAG	C1-O5-C5	2.52	117.93	113.39
2	B	401	NAG	O5-C5-C6	2.54	112.50	106.41
2	A	401	NAG	O4-C4-C3	2.60	116.02	110.36
2	C	402	NAG	C1-O5-C5	2.61	115.76	112.17
2	C	401	NAG	O3-C3-C4	2.68	116.19	110.36
2	B	401	NAG	C1-O5-C5	2.82	118.48	113.39
2	B	402	NAG	C2-N2-C7	2.89	127.16	122.94
2	C	404	NAG	C1-C2-N2	2.92	115.47	110.49
2	B	401	NAG	O4-C4-C3	2.98	116.84	110.36
2	A	402	NAG	C1-C2-N2	3.02	115.64	110.49
2	A	402	NAG	C1-O5-C5	3.05	116.37	112.17
2	A	404	NAG	O3-C3-C2	3.15	116.14	109.39
2	B	401	NAG	C3-C2-N2	3.17	116.68	110.61
2	B	404	NAG	O3-C3-C2	3.17	116.19	109.39
2	A	403	NAG	O4-C4-C3	3.18	117.27	110.36
2	A	402	NAG	C4-C3-C2	3.21	115.72	111.02
2	C	401	NAG	O5-C5-C6	3.27	114.25	106.41
2	A	402	NAG	O4-C4-C3	3.28	117.50	110.36
2	B	404	NAG	C2-N2-C7	3.37	127.86	122.94

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	403	NAG	O4-C4-C3	3.55	118.08	110.36
2	B	404	NAG	C1-C2-N2	3.58	116.60	110.49
2	C	404	NAG	O3-C3-C2	3.59	117.09	109.39
2	B	401	NAG	O3-C3-C4	3.67	118.33	110.36
2	B	402	NAG	C1-O5-C5	3.68	117.24	112.17
2	C	403	NAG	O4-C4-C3	3.69	118.39	110.36
2	B	402	NAG	C6-C5-C4	3.91	122.15	113.00
2	B	403	NAG	C8-C7-N2	4.02	123.36	116.11
2	A	403	NAG	C1-O5-C5	4.14	117.88	112.17
2	C	403	NAG	C2-N2-C7	4.21	129.09	122.94
2	A	402	NAG	O7-C7-N2	4.37	130.33	121.92
2	B	404	NAG	C8-C7-N2	4.61	124.43	116.11
2	B	403	NAG	C2-N2-C7	4.75	129.87	122.94
2	A	403	NAG	C8-C7-N2	4.85	124.87	116.11
2	C	401	NAG	C3-C2-N2	4.93	120.06	110.61
2	C	402	NAG	C2-N2-C7	4.95	130.16	122.94
2	C	403	NAG	C1-O5-C5	4.99	119.05	112.17
2	C	403	NAG	C8-C7-N2	5.00	125.13	116.11
2	A	403	NAG	C2-N2-C7	5.03	130.28	122.94
2	C	401	NAG	C1-O5-C5	5.16	122.69	113.39
2	A	402	NAG	C2-N2-C7	5.19	130.51	122.94
2	A	401	NAG	O3-C3-C4	5.19	121.66	110.36
2	B	403	NAG	C1-O5-C5	5.44	119.67	112.17
2	B	401	NAG	C2-N2-C7	5.46	137.03	123.19
2	A	404	NAG	C1-C2-N2	5.56	119.99	110.49
2	C	401	NAG	C2-N2-C7	5.91	138.15	123.19
2	B	401	NAG	C8-C7-N2	6.82	128.43	116.11
2	C	401	NAG	C8-C7-N2	7.29	129.27	116.11
2	B	404	NAG	C1-O5-C5	7.95	123.13	112.17
2	A	401	NAG	C1-C2-N2	8.39	120.45	110.73
2	B	401	NAG	O5-C1-C2	8.81	118.36	109.52
2	C	404	NAG	C1-O5-C5	9.05	124.65	112.17
2	A	404	NAG	C1-O5-C5	9.21	124.86	112.17
2	C	401	NAG	O5-C1-C2	9.85	119.42	109.52

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

10 monomers are involved in 13 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	401	NAG	3	0
2	A	402	NAG	3	0
2	A	403	NAG	1	0
2	B	401	NAG	3	0
2	B	402	NAG	1	0
2	B	404	NAG	1	0
2	C	401	NAG	3	0
2	C	402	NAG	2	0
2	C	403	NAG	1	0
2	C	404	NAG	1	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, 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	341/350 (97%)	-0.26	2 (0%) 89 88	46, 62, 82, 123	0
1	B	341/350 (97%)	-0.28	2 (0%) 89 88	44, 59, 80, 119	0
1	C	341/350 (97%)	-0.27	1 (0%) 93 93	43, 59, 79, 114	0
All	All	1023/1050 (97%)	-0.27	5 (0%) 90 89	43, 60, 81, 123	0

All (5) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	11	TYR	4.3
1	C	11	TYR	3.2
1	B	349	TYR	2.2
1	A	194	LEU	2.2
1	A	11	TYR	2.1

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

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

### 6.3 Carbohydrates [i](#)

There are no 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( $\text{\AA}^2$ )	Q<0.9
2	NAG	B	403	14/15	0.80	0.25	7.12	82,98,104,113	0
2	NAG	C	403	14/15	0.78	0.22	4.71	88,107,112,115	0
2	NAG	B	402	14/15	0.85	0.24	3.86	73,91,100,103	0
2	NAG	C	402	14/15	0.80	0.23	3.85	69,88,98,105	0
2	NAG	A	403	14/15	0.72	0.21	3.81	78,101,110,116	0
2	NAG	A	402	14/15	0.89	0.19	1.99	71,97,110,112	0
2	NAG	A	401	15/15	0.82	0.21	1.17	66,80,95,114	0
2	NAG	B	401	15/15	0.79	0.20	0.72	54,69,84,86	0
2	NAG	C	401	15/15	0.84	0.16	0.10	49,69,78,82	0
2	NAG	C	404	14/15	0.75	0.39	-	95,108,117,126	0
2	NAG	B	404	14/15	0.79	0.24	-	83,95,105,112	0
2	NAG	A	404	14/15	0.71	0.33	-	97,106,109,110	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.