



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 29, 2016 – 02:19 PM EDT

PDB ID : 5DEZ
Title : Crystal structure of AcMNPV Chitinase A
Authors : Mou, T.-C.; Sprang, S.R.
Deposited on : 2015-08-26
Resolution : 2.30 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

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

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7.1 (RC1), CSD as537be (2016)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20027939
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) : rb-20027939

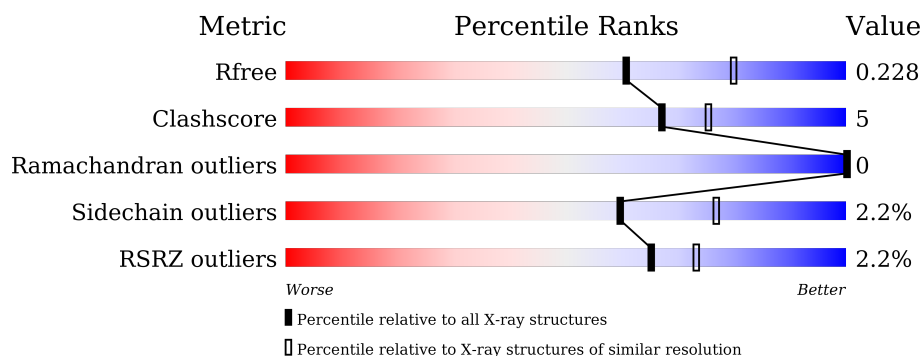
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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}	91344	3852 (2.30-2.30)
Clashscore	102246	4452 (2.30-2.30)
Ramachandran outliers	100387	4410 (2.30-2.30)
Sidechain outliers	100360	4409 (2.30-2.30)
RSRZ outliers	91569	3857 (2.30-2.30)

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 ≥ 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	551	<div> <div>2%</div> <div> <div></div> <div>82%</div> <div>13%</div> <div>..</div> </div> </div>
1	B	551	<div> <div>2%</div> <div> <div></div> <div>84%</div> <div>11%</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	NAG	A	601	-	-	-	X
2	NAG	A	602	-	-	-	X
2	NAG	A	603	-	-	-	X
2	NAG	A	604	-	-	-	X
2	NAG	A	605	-	-	-	X
2	NAG	B	601	-	-	-	X
2	NAG	B	602	-	-	-	X
2	NAG	B	603	-	-	-	X
2	NAG	B	604	-	-	-	X
2	NAG	B	605	-	-	-	X
2	NAG	B	606	-	-	-	X

2 Entry composition [i](#)

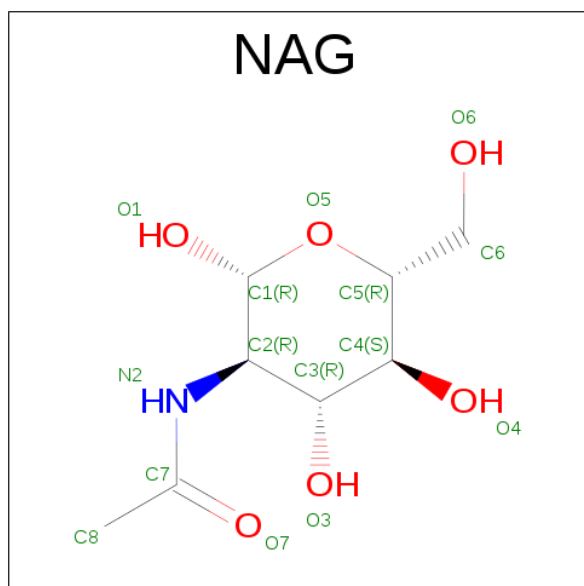
There are 5 unique types of molecules in this entry. The entry contains 9207 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Ac-ChiA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	528	Total	C	N	O	S	0	0	0
			4167	2672	685	800	10			
1	B	528	Total	C	N	O	S	0	1	0
			4172	2675	686	801	10			

- 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
			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
			15	8	1	6		

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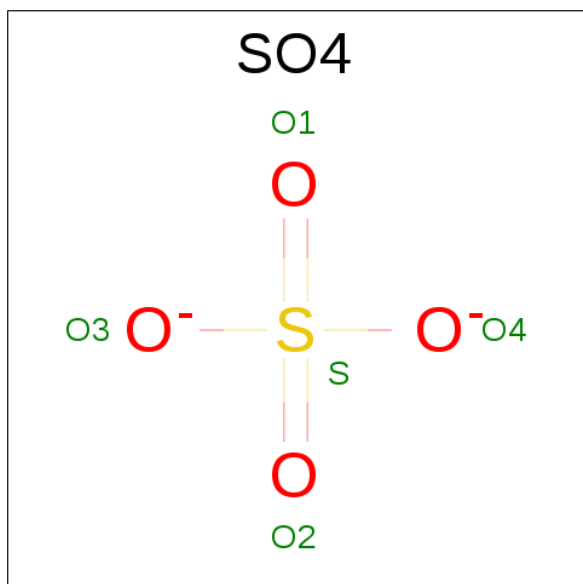
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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			15	8	1	6		
2	B	1	Total	C	N	O	0	0
			15	8	1	6		
2	B	1	Total	C	N	O	0	0
			15	8	1	6		
2	B	1	Total	C	N	O	0	0
			15	8	1	6		
2	B	1	Total	C	N	O	0	0
			14	8	1	5		
2	B	1	Total	C	N	O	0	0
	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

- Molecule 3 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total	Cl	0	0
			1	1		
3	A	2	Total	Cl	0	0
			2	2		

- Molecule 4 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	B	1	Total	O	S	0	0
			5	4	1		

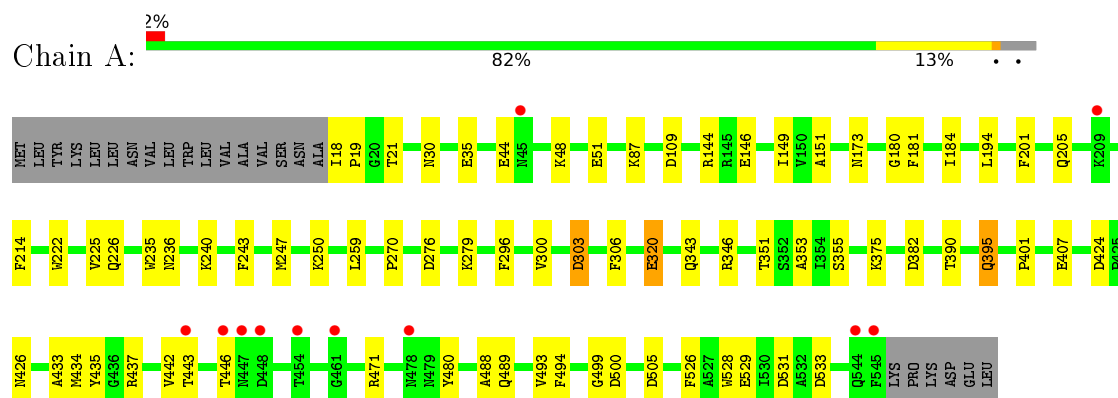
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	347	Total	O	0	0
			347	347		
5	B	351	Total	O	0	0
			351	351		

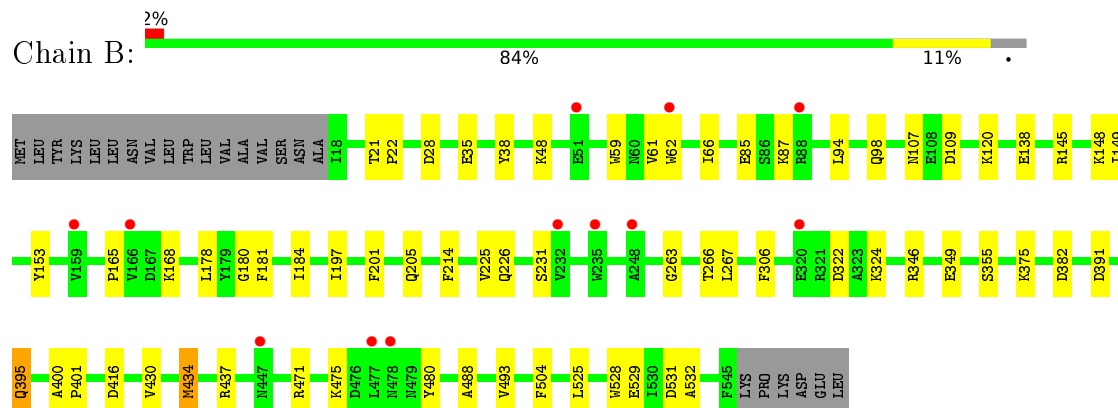
3 Residue-property plots

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: Ac-ChiA



• Molecule 1: Ac-ChiA



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	96.93Å 111.93Å 129.52Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	14.99 – 2.30 48.52 – 2.30	Depositor EDS
% Data completeness (in resolution range)	96.4 (14.99-2.30) 88.2 (48.52-2.30)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.12	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.18 (at 2.29Å)	Xtriage
Refinement program	PHENIX 1.8.2_1309	Depositor
R, R_{free}	0.172 , 0.229 0.168 , 0.228	Depositor DCC
R_{free} test set	1838 reflections (3.30%)	DCC
Wilson B-factor (Å ²)	31.9	Xtriage
Anisotropy	0.731	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 45.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	9207	wwPDB-VP
Average B, all atoms (Å ²)	22.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.63% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: CL, SO4, 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	0.43	1/4275 (0.0%)	0.55	1/5816 (0.0%)
1	B	0.37	0/4283	0.53	1/5827 (0.0%)
All	All	0.40	1/8558 (0.0%)	0.54	2/11643 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	320	GLU	CD-OE2	-5.29	1.19	1.25

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	303	ASP	CB-CG-OD1	8.67	126.10	118.30
1	B	322	ASP	CB-CG-OD1	5.04	122.83	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	4167	0	4004	45	0
1	B	4172	0	4009	35	0
2	A	74	0	72	7	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	88	0	85	3	0
3	A	2	0	0	0	0
3	B	1	0	0	0	0
4	B	5	0	0	0	0
5	A	347	0	0	7	0
5	B	351	0	0	1	0
All	All	9207	0	8170	80	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 5.

All (80) 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:343:GLN:NE2	5:A:703:HOH:O	2.21	0.73
1:B:471:ARG:NH2	1:B:531:ASP:O	2.23	0.72
1:B:391:ASP:OD2	2:B:605:NAG:O6	2.12	0.68
1:A:184:ILE:HB	1:A:270:PRO:HG2	1.79	0.65
1:B:346:ARG:HG2	2:B:601:NAG:H5	1.79	0.64
1:A:30:ASN:ND2	2:A:602:NAG:O7	2.28	0.63
1:B:66:ILE:HD12	1:B:85:GLU:HA	1.80	0.63
1:A:296:PHE:HA	2:A:601:NAG:H81	1.81	0.62
1:A:346:ARG:HG2	2:A:601:NAG:H61	1.81	0.62
1:A:222:TRP:HA	1:A:226:GLN:HB2	1.83	0.60
1:B:98:GLN:HG2	1:B:120:LYS:HG2	1.83	0.60
1:A:382:ASP:OD1	1:A:437:ARG:NH1	2.35	0.58
1:B:395:GLN:HG3	1:B:437:ARG:HD2	1.86	0.57
2:A:604:NAG:O1	5:A:701:HOH:O	2.18	0.57
1:A:235:TRP:CH2	2:A:602:NAG:H83	2.40	0.56
1:A:437:ARG:NH2	5:A:710:HOH:O	2.37	0.56
1:A:149:ILE:HG13	1:A:375:LYS:HD3	1.87	0.55
1:A:303:ASP:OD1	1:A:353:ALA:HB3	2.06	0.55
1:A:18:ILE:HD12	1:A:109:ASP:HB3	1.89	0.54
1:A:201:PHE:O	1:A:205:GLN:HG2	2.08	0.54
1:B:349:GLU:OE1	1:B:375:LYS:NZ	2.38	0.54
1:B:480:TYR:HB3	1:B:493:VAL:HB	1.91	0.52
1:A:87:LYS:NZ	5:A:708:HOH:O	2.34	0.52
1:A:407:GLU:OE2	2:A:605:NAG:O4	2.28	0.51
1:A:480:TYR:HB3	1:A:493:VAL:HB	1.92	0.51
1:B:35:GLU:HB2	1:B:48:LYS:HB3	1.93	0.51
1:A:435:TYR:HE1	1:A:528:TRP:HD1	1.58	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:61:VAL:HG21	1:B:66:ILE:HA	1.95	0.49
1:A:401:PRO:HA	1:A:488:ALA:HB2	1.94	0.48
1:B:306:PHE:CE1	1:B:355:SER:HB2	2.49	0.48
1:A:214:PHE:CZ	1:A:279:LYS:HD3	2.49	0.47
1:A:471:ARG:NH2	1:A:531:ASP:O	2.42	0.47
1:A:51:GLU:H	1:A:51:GLU:CD	2.18	0.47
1:B:430:VAL:HB	1:B:525:LEU:HD23	1.97	0.47
1:B:382:ASP:OD2	2:B:603:NAG:H62	2.15	0.46
1:A:194:LEU:HB3	1:A:201:PHE:HB2	1.96	0.46
1:A:489:GLN:NE2	5:A:714:HOH:O	2.39	0.46
1:B:21:THR:HA	1:B:22:PRO:HD3	1.84	0.46
1:A:35:GLU:HB2	1:A:48:LYS:HB3	1.96	0.46
1:A:433:ALA:O	1:A:505:ASP:HB2	2.16	0.46
1:B:138:GLU:OE2	1:B:471:ARG:NH1	2.48	0.46
1:B:38:TYR:HE1	1:B:226:GLN:HA	1.80	0.46
1:B:401:PRO:HA	1:B:488:ALA:HB2	1.98	0.46
1:A:144:ARG:HB2	1:A:173:ASN:HA	1.98	0.45
1:A:236:ASN:HD22	2:A:602:NAG:C7	2.30	0.45
1:A:320:GLU:OE2	5:A:702:HOH:O	2.21	0.44
1:A:146:GLU:H	1:B:62:TRP:HZ3	1.65	0.44
1:B:59:TRP:CE2	1:B:87:LYS:HA	2.52	0.44
1:B:201:PHE:O	1:B:205:GLN:HG2	2.17	0.44
1:B:107[A]:ASN:HB2	5:B:766:HOH:O	2.18	0.44
1:B:153:TYR:CE1	1:B:178:LEU:HD12	2.53	0.44
1:B:263:GLY:O	1:B:267:LEU:HB2	2.18	0.43
1:B:475:LYS:HE3	1:B:475:LYS:HB2	1.74	0.43
1:A:434:MET:SD	1:A:533:ASP:HB2	2.58	0.43
1:B:145:ARG:HG2	1:B:148:LYS:HB2	2.00	0.43
1:A:528:TRP:HA	1:A:529:GLU:HA	1.80	0.43
1:A:151:ALA:O	1:A:526:PHE:HA	2.18	0.43
1:B:434:MET:HB2	1:B:532:ALA:HB3	2.00	0.43
1:A:306:PHE:CE1	1:A:355:SER:HB2	2.54	0.43
1:A:435:TYR:CE1	1:A:528:TRP:HD1	2.36	0.43
1:A:18:ILE:HA	1:A:19:PRO:HD3	1.94	0.42
1:B:197:ILE:HD11	1:B:266:THR:HG21	2.00	0.42
1:A:180:GLY:HA2	1:A:181:PHE:HA	1.72	0.42
1:B:149:ILE:HG13	1:B:375:LYS:HD3	2.00	0.42
1:A:276:ASP:OD2	1:A:279:LYS:NZ	2.53	0.42
1:A:351:THR:HG22	1:A:375:LYS:HB2	2.02	0.42
1:A:250:LYS:HG2	5:A:843:HOH:O	2.19	0.41
1:A:494:PHE:HA	1:A:500:ASP:O	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:225:VAL:O	1:A:240:LYS:HB2	2.20	0.41
1:A:194:LEU:HA	1:A:194:LEU:HD12	1.79	0.41
1:A:442:VAL:HG12	1:A:499:GLY:O	2.19	0.41
1:B:165:PRO:HD2	1:B:168:LYS:HD2	2.01	0.41
1:B:528:TRP:HA	1:B:529:GLU:HA	1.72	0.41
1:B:180:GLY:HA2	1:B:181:PHE:HA	1.67	0.41
1:B:184:ILE:HG22	1:B:214:PHE:HA	2.03	0.41
1:B:98:GLN:OE1	1:B:120:LYS:HE2	2.22	0.41
1:B:400:ALA:HA	1:B:401:PRO:HD3	1.97	0.40
1:A:395:GLN:HG3	1:A:437:ARG:CG	2.51	0.40
1:A:243:PHE:O	1:A:247:MET:HG3	2.21	0.40
1:B:493:VAL:HG13	1:B:504:PHE:CE1	2.56	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	526/551 (96%)	510 (97%)	16 (3%)	0	100	100
1	B	527/551 (96%)	512 (97%)	15 (3%)	0	100	100
All	All	1053/1102 (96%)	1022 (97%)	31 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	441/462 (96%)	431 (98%)	10 (2%)	58	75
1	B	442/462 (96%)	433 (98%)	9 (2%)	63	79
All	All	883/924 (96%)	864 (98%)	19 (2%)	60	77

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	21	THR
1	A	44	GLU
1	A	259	LEU
1	A	300	VAL
1	A	390	THR
1	A	395	GLN
1	A	424	ASP
1	A	426	ASN
1	A	443	THR
1	A	446	THR
1	B	28	ASP
1	B	94	LEU
1	B	109	ASP
1	B	225	VAL
1	B	231	SER
1	B	324	LYS
1	B	395	GLN
1	B	416	ASP
1	B	434	MET

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

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 [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 15 ligands modelled in this entry, 3 are monoatomic - leaving 12 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	NAG	A	601	-	15,15,15	1.72	6 (40%)	17,21,21	0.93	0
2	NAG	A	602	-	15,15,15	1.64	4 (26%)	17,21,21	1.75	5 (29%)
2	NAG	A	603	2	14,14,15	1.17	2 (14%)	15,19,21	1.25	2 (13%)
2	NAG	A	604	2	15,15,15	0.67	0	17,21,21	1.13	1 (5%)
2	NAG	A	605	-	15,15,15	1.49	3 (20%)	17,21,21	1.24	1 (5%)
2	NAG	B	601	-	15,15,15	1.75	4 (26%)	17,21,21	2.22	6 (35%)
2	NAG	B	602	-	15,15,15	1.62	6 (40%)	17,21,21	1.13	1 (5%)
2	NAG	B	603	2	15,15,15	2.14	5 (33%)	17,21,21	1.51	1 (5%)
2	NAG	B	604	2	14,14,15	1.80	5 (35%)	14,19,21	1.20	2 (14%)
2	NAG	B	605	-	15,15,15	1.57	4 (26%)	17,21,21	1.39	3 (17%)
2	NAG	B	606	1	14,14,15	1.71	4 (28%)	15,19,21	1.21	1 (6%)
4	SO4	B	607	-	4,4,4	0.14	0	6,6,6	0.20	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	NAG	A	601	-	-	0/6/26/26	0/1/1/1
2	NAG	A	602	-	-	0/6/26/26	0/1/1/1
2	NAG	A	603	2	-	0/6/23/26	0/1/1/1
2	NAG	A	604	2	-	0/6/26/26	0/1/1/1
2	NAG	A	605	-	-	0/6/26/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	B	601	-	-	0/6/26/26	0/1/1/1
2	NAG	B	602	-	-	0/6/26/26	0/1/1/1
2	NAG	B	603	2	-	0/6/26/26	0/1/1/1
2	NAG	B	604	2	-	0/6/22/26	0/1/1/1
2	NAG	B	605	-	-	0/6/26/26	0/1/1/1
2	NAG	B	606	1	-	0/6/23/26	0/1/1/1
4	SO4	B	607	-	-	0/0/0/0	0/0/0/0

All (43) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	601	NAG	C1-C2	-3.96	1.48	1.53
2	B	606	NAG	O5-C1	-3.52	1.38	1.43
2	B	604	NAG	O5-C5	-3.13	1.38	1.44
2	A	601	NAG	C1-C2	-2.92	1.49	1.53
2	B	604	NAG	C1-C2	-2.91	1.49	1.53
2	B	604	NAG	C3-C2	-2.77	1.50	1.53
2	B	602	NAG	C1-C2	-2.76	1.49	1.53
2	B	601	NAG	O5-C1	-2.75	1.37	1.43
2	A	601	NAG	O5-C1	-2.65	1.38	1.43
2	A	602	NAG	C1-C2	-2.55	1.50	1.53
2	B	605	NAG	O5-C5	-2.53	1.38	1.44
2	A	603	NAG	C1-C2	-2.47	1.49	1.52
2	B	604	NAG	O5-C1	-2.45	1.38	1.43
2	A	603	NAG	C2-N2	-2.43	1.42	1.46
2	A	601	NAG	O5-C5	-2.43	1.38	1.44
2	A	602	NAG	O3-C3	-2.40	1.37	1.43
2	A	605	NAG	C1-C2	-2.37	1.50	1.53
2	B	605	NAG	O5-C1	-2.37	1.38	1.43
2	B	606	NAG	O5-C5	-2.35	1.38	1.43
2	B	603	NAG	O5-C1	-2.35	1.38	1.43
2	B	603	NAG	C1-C2	-2.34	1.50	1.53
2	A	601	NAG	O3-C3	-2.27	1.37	1.43
2	B	602	NAG	O5-C1	-2.25	1.38	1.43
2	B	602	NAG	C3-C2	-2.16	1.48	1.53
2	B	606	NAG	O4-C4	-2.14	1.37	1.43
2	B	603	NAG	O5-C5	-2.13	1.39	1.44
2	A	602	NAG	O5-C1	-2.09	1.39	1.43
2	A	605	NAG	O4-C4	-2.09	1.38	1.43
2	B	602	NAG	O4-C4	-2.08	1.38	1.43
2	B	602	NAG	O5-C5	-2.08	1.39	1.44
2	B	601	NAG	O4-C4	-2.05	1.38	1.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	605	NAG	O4-C4	-2.04	1.38	1.43
2	A	601	NAG	O4-C4	-2.04	1.38	1.43
2	B	602	NAG	C7-N2	2.25	1.43	1.34
2	A	601	NAG	C7-N2	2.27	1.43	1.34
2	B	606	NAG	C7-N2	2.32	1.43	1.34
2	B	601	NAG	C7-N2	2.46	1.43	1.34
2	A	605	NAG	C7-N2	2.60	1.44	1.34
2	B	603	NAG	C7-N2	2.64	1.44	1.34
2	B	604	NAG	C7-N2	2.67	1.44	1.34
2	A	602	NAG	C7-N2	2.68	1.44	1.34
2	B	605	NAG	C7-N2	2.92	1.45	1.34
2	B	603	NAG	O1-C1	5.85	1.60	1.39

All (23) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	601	NAG	C4-C3-C2	-3.17	105.55	110.37
2	A	602	NAG	O7-C7-C8	-2.70	117.11	122.07
2	B	606	NAG	C2-N2-C7	-2.68	119.62	123.11
2	B	602	NAG	C4-C3-C2	-2.68	106.31	110.37
2	B	605	NAG	O7-C7-C8	-2.41	117.64	122.07
2	B	605	NAG	C6-C5-C4	-2.39	107.00	112.99
2	B	601	NAG	O7-C7-N2	-2.37	117.02	121.84
2	A	602	NAG	O3-C3-C4	-2.36	105.04	110.36
2	A	602	NAG	C6-C5-C4	-2.34	107.13	112.99
2	A	603	NAG	C3-C4-C5	-2.29	106.14	110.23
2	B	601	NAG	O7-C7-C8	-2.13	118.14	122.07
2	B	604	NAG	O5-C5-C6	2.02	109.14	106.67
2	B	604	NAG	C8-C7-N2	2.53	120.95	116.10
2	A	602	NAG	C2-N2-C7	2.60	130.05	123.21
2	A	602	NAG	C3-C2-N2	2.73	116.34	110.67
2	A	603	NAG	O4-C4-C5	2.83	116.69	109.23
2	A	604	NAG	O5-C5-C6	2.89	113.87	106.38
2	B	605	NAG	C4-C3-C2	2.96	114.86	110.37
2	A	605	NAG	C1-O5-C5	3.36	119.97	113.54
2	B	601	NAG	C2-N2-C7	3.61	132.70	123.21
2	B	601	NAG	C8-C7-N2	4.56	124.83	116.10
2	B	601	NAG	C3-C2-N2	4.70	120.44	110.67
2	B	603	NAG	O1-C1-O5	5.29	125.06	110.33

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

7 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	601	NAG	2	0
2	A	602	NAG	3	0
2	A	604	NAG	1	0
2	A	605	NAG	1	0
2	B	601	NAG	1	0
2	B	603	NAG	1	0
2	B	605	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 ⓘ

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, 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	528/551 (95%)	-0.02	11 (2%)	67 74	8, 19, 41, 73	0
1	B	528/551 (95%)	0.16	12 (2%)	64 72	9, 20, 37, 49	0
All	All	1056/1102 (95%)	0.07	23 (2%)	65 73	8, 20, 39, 73	0

All (23) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	446	THR	5.7
1	B	62	TRP	4.4
1	A	447	ASN	4.2
1	B	447	ASN	3.8
1	A	443	THR	3.4
1	A	545	PHE	2.9
1	B	478	ASN	2.7
1	A	544	GLN	2.6
1	B	159	VAL	2.4
1	A	478	ASN	2.4
1	A	45	ASN	2.3
1	A	448	ASP	2.3
1	B	51	GLU	2.3
1	B	320	GLU	2.3
1	A	454	THR	2.3
1	B	232	VAL	2.2
1	B	88	ARG	2.2
1	B	235	TRP	2.2
1	A	461	GLY	2.2
1	B	477	LEU	2.1
1	A	209	LYS	2.1
1	B	248	ALA	2.1
1	B	166	VAL	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, 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	LLDF	B-factors(Å ²)	Q<0.9
2	NAG	B	604	14/15	0.77	0.34	9.46	37,46,53,53	14
2	NAG	B	605	15/15	0.79	0.32	8.19	37,46,59,64	0
2	NAG	A	602	15/15	0.86	0.24	5.98	32,40,43,45	0
2	NAG	B	603	15/15	0.82	0.26	4.72	38,52,61,63	1
2	NAG	A	604	15/15	0.78	0.24	4.49	31,36,42,46	15
2	NAG	A	605	15/15	0.85	0.19	3.98	39,48,63,69	0
2	NAG	A	601	15/15	0.89	0.23	3.82	28,47,55,67	0
2	NAG	B	606	14/15	0.90	0.18	3.25	24,34,36,36	0
2	NAG	B	601	15/15	0.80	0.28	3.04	28,41,67,68	0
2	NAG	A	603	14/15	0.76	0.26	2.55	24,33,44,46	14
2	NAG	B	602	15/15	0.83	0.21	2.06	28,39,57,60	0
4	SO4	B	607	5/5	0.99	0.12	-0.26	17,21,24,29	0
3	CL	A	606	1/1	0.96	0.08	-2.74	46,46,46,46	0
3	CL	B	608	1/1	0.96	0.11	-	39,39,39,39	0
3	CL	A	607	1/1	0.97	0.06	-	27,27,27,27	0

6.5 Other polymers [i](#)

There are no such residues in this entry.