



wwPDB X-ray Structure Validation Summary Report ⓘ

Jun 5, 2016 – 06:57 AM EDT

PDB ID : 5J67
Title : Structure of Astrotactin-2, a conserved vertebrate-specific and perforin-like membrane protein involved in neuronal development
Authors : Ni, T.; Harlos, K.; Gilbert, R.J.C.
Deposited on : 2016-04-04
Resolution : 3.16 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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.

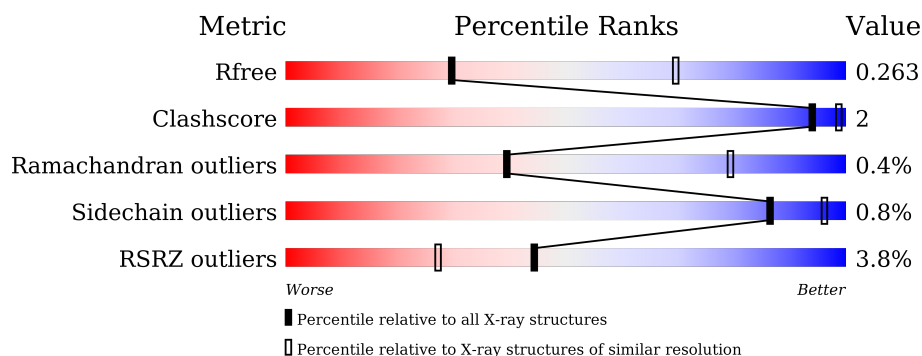
The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.7.1 (RC1), CSD as537be (2016)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20027674
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-20027674

i

X-RAY DIFFRACTION

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	1112 (3.20-3.12)
Clashscore	102246	1249 (3.20-3.12)
Ramachandran outliers	100387	1222 (3.20-3.12)
Sidechain outliers	100360	1221 (3.20-3.12)
RSRZ outliers	91569	1117 (3.20-3.12)

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	572	 <div>92%5%</div>
1	B	572	 <div>91%7%</div>
1	C	572	 <div>92%6%</div>
1	D	572	 <div>92%5%</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 crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	MAN	A	1307	X	-	-	-
4	MAN	B	1307	X	-	-	-
4	MAN	C	1307	X	-	-	-
4	MAN	D	1307	X	-	-	-
5	I3P	B	1311	-	-	-	X
5	I3P	D	1311	-	-	-	X

2 Entry composition [i](#)

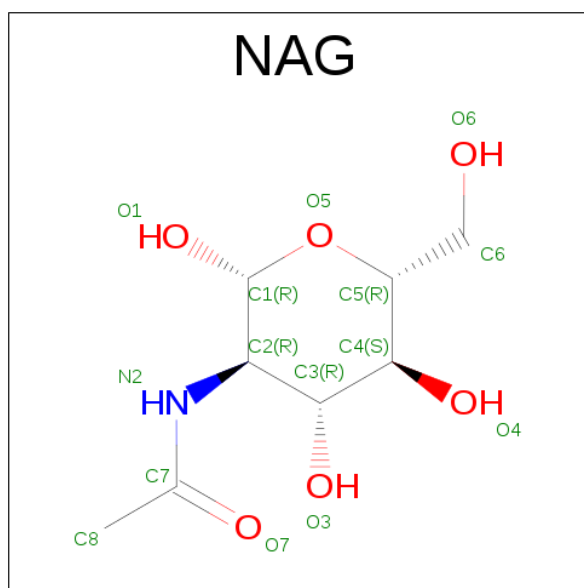
There are 5 unique types of molecules in this entry. The entry contains 18450 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Astrotactin-2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	559	Total	C	N	O	S	0	0	0
			4456	2823	758	846	29			
1	B	558	Total	C	N	O	S	0	0	0
			4445	2817	754	845	29			
1	C	563	Total	C	N	O	S	0	0	0
			4492	2845	762	856	29			
1	D	557	Total	C	N	O	S	0	0	0
			4441	2814	752	846	29			

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



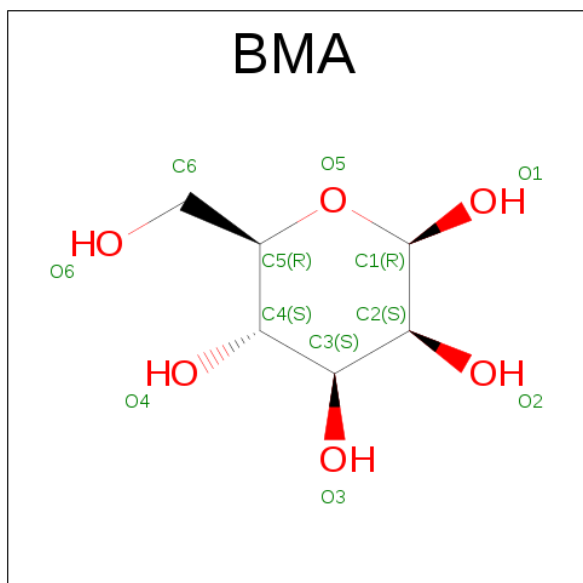
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	A	1	Total	C	N	O	0	0
			14	8	1	5		

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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
			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
			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		
2	D	1	Total	C	N	O	0	0
			14	8	1	5		
2	D	1	Total	C	N	O	0	0
			14	8	1	5		
2	D	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 3 is BETA-D-MANNOSE (three-letter code: BMA) (formula: $C_6H_{12}O_6$).



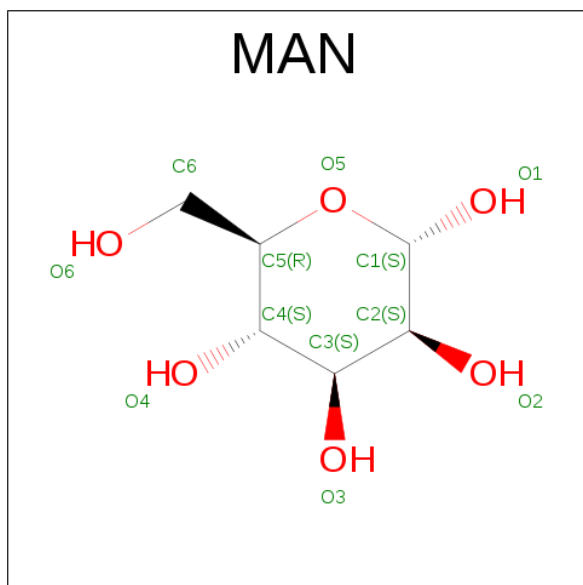
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			11	6	5		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	B	1	Total	C	O	0	0
			11	6	5		
3	C	1	Total	C	O	0	0
			11	6	5		
3	D	1	Total	C	O	0	0
			11	6	5		

- Molecule 4 is ALPHA-D-MANNOSE (three-letter code: MAN) (formula: C₆H₁₂O₆).



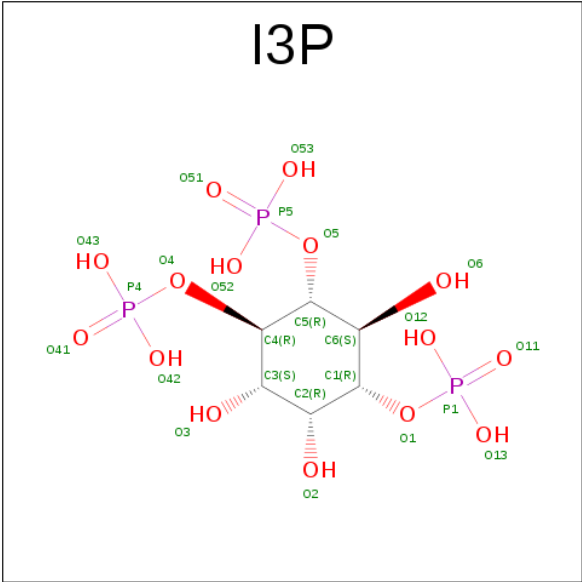
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			11	6	5		
4	A	1	Total	C	O	0	0
			11	6	5		
4	A	1	Total	C	O	0	0
			11	6	5		
4	A	1	Total	C	O	0	0
			11	6	5		
4	A	1	Total	C	O	0	0
			11	6	5		
4	A	1	Total	C	O	0	0
			11	6	5		
4	A	1	Total	C	O	0	0
			11	6	5		
4	B	1	Total	C	O	0	0
			11	6	5		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	B	1	Total	C	O	0	0
			11	6	5		
4	B	1	Total	C	O	0	0
			11	6	5		
4	B	1	Total	C	O	0	0
			11	6	5		
4	B	1	Total	C	O	0	0
			11	6	5		
4	B	1	Total	C	O	0	0
			11	6	5		
4	C	1	Total	C	O	0	0
			11	6	5		
4	C	1	Total	C	O	0	0
			11	6	5		
4	C	1	Total	C	O	0	0
			11	6	5		
4	C	1	Total	C	O	0	0
			11	6	5		
4	C	1	Total	C	O	0	0
			11	6	5		
4	C	1	Total	C	O	0	0
			11	6	5		
4	D	1	Total	C	O	0	0
			11	6	5		
4	D	1	Total	C	O	0	0
			11	6	5		
4	D	1	Total	C	O	0	0
			11	6	5		
4	D	1	Total	C	O	0	0
			11	6	5		
4	D	1	Total	C	O	0	0
			11	6	5		
4	D	1	Total	C	O	0	0
			11	6	5		

- Molecule 5 is D-MYO-INOSITOL-1,4,5-TRIPHOSPHATE (three-letter code: I3P) (formula: $C_6H_{15}O_{15}P_3$).

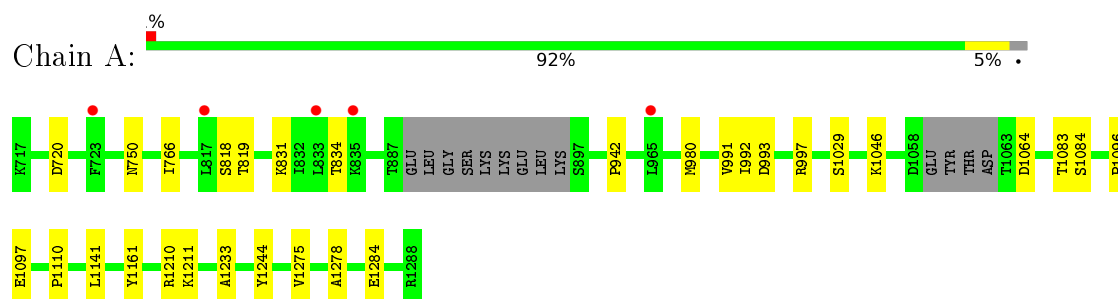


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	O	P	0	0
			24	6	15	3		
5	B	1	Total	C	O	P	0	0
			24	6	15	3		
5	C	1	Total	C	O	P	0	0
			24	6	15	3		
5	D	1	Total	C	O	P	0	0
			24	6	15	3		

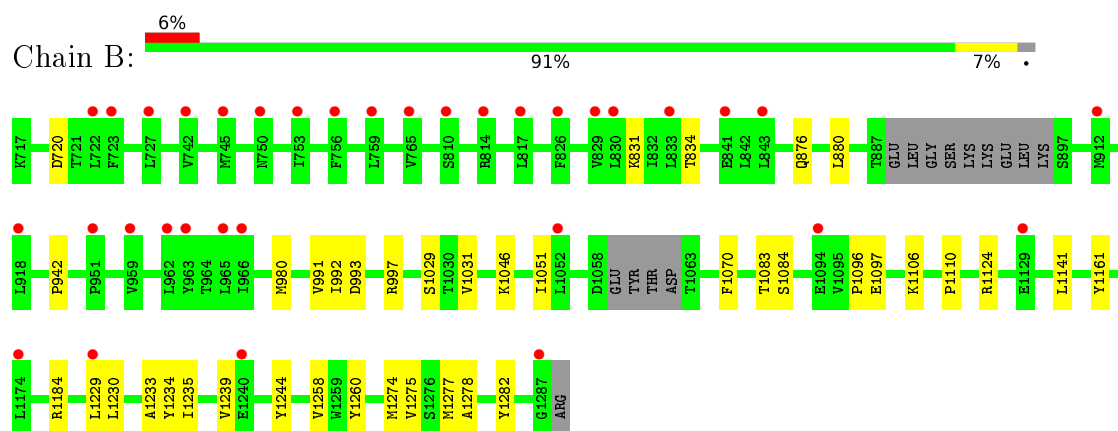
3 Residue-property plots [i](#)

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.

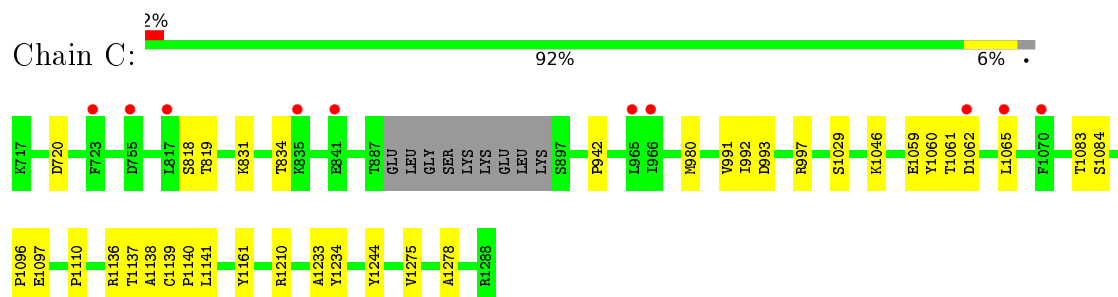
• Molecule 1: Astrotactin-2



• Molecule 1: Astrotactin-2

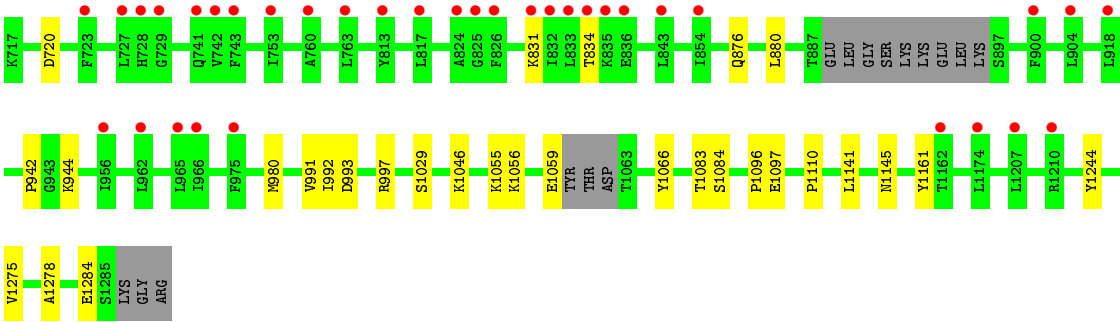


• Molecule 1: Astrotactin-2



• Molecule 1: Astrotactin-2





4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	101.24Å 108.19Å 111.36Å 87.18° 84.50° 65.67°	Depositor
Resolution (Å)	98.58 – 3.16 98.58 – 3.16	Depositor EDS
% Data completeness (in resolution range)	99.9 (98.58-3.16) 99.6 (98.58-3.16)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.32 (at 3.13Å)	Xtriage
Refinement program	REFMAC 5.8.0135	Depositor
R, R_{free}	0.233 , 0.259 0.235 , 0.263	Depositor DCC
R_{free} test set	3722 reflections (5.34%)	DCC
Wilson B-factor (Å ²)	109.3	Xtriage
Anisotropy	0.149	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 77.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	18450	wwPDB-VP
Average B, all atoms (Å ²)	136.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.94% 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, 0.375 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: MAN, I3P, BMA, 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	0.39	0/4552	0.65	0/6166
1	B	0.39	0/4540	0.65	0/6149
1	C	0.40	0/4588	0.69	5/6214 (0.1%)
1	D	0.38	0/4537	0.65	0/6148
All	All	0.39	0/18217	0.66	5/24677 (0.0%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	1210	ARG	NE-CZ-NH2	9.94	125.27	120.30
1	C	1210	ARG	NE-CZ-NH1	-6.12	117.24	120.30
1	C	1136	ARG	NE-CZ-NH1	-5.58	117.51	120.30
1	C	1062	ASP	CB-CG-OD2	5.21	122.99	118.30
1	C	1136	ARG	NE-CZ-NH2	5.02	122.81	120.30

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	4456	0	4386	14	1
1	B	4445	0	4372	29	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	4492	0	4411	19	0
1	D	4441	0	4363	11	1
2	A	42	0	37	0	0
2	B	42	0	37	0	0
2	C	42	0	37	0	0
2	D	42	0	37	0	0
3	A	11	0	8	0	0
3	B	11	0	8	0	0
3	C	11	0	8	0	0
3	D	11	0	8	0	0
4	A	77	0	65	0	0
4	B	77	0	65	0	0
4	C	77	0	65	0	0
4	D	77	0	65	0	0
5	A	24	0	9	0	0
5	B	24	0	9	0	0
5	C	24	0	9	0	0
5	D	24	0	9	0	0
All	All	18450	0	18008	66	1

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 2.

The worst 5 of 66 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:C:1138:ALA:C	1:C:1139:CYS:N	2.21	0.94
1:B:880:LEU:HD22	1:C:1065:LEU:HD23	1.56	0.88
1:B:880:LEU:HD22	1:C:1065:LEU:CD2	2.07	0.85
1:B:1051:ILE:HG23	1:B:1070:PHE:HE1	1.46	0.80
1:B:1051:ILE:HG23	1:B:1070:PHE:CE1	2.19	0.78

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1210:ARG:NH1	1:D:1145:ASN:OD1[1_554]	2.03	0.17

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	553/572 (97%)	521 (94%)	29 (5%)	3 (0%)	34	76
1	B	550/572 (96%)	520 (94%)	28 (5%)	2 (0%)	39	79
1	C	555/572 (97%)	524 (94%)	29 (5%)	2 (0%)	39	79
1	D	551/572 (96%)	521 (95%)	28 (5%)	2 (0%)	39	79
All	All	2209/2288 (96%)	2086 (94%)	114 (5%)	9 (0%)	39	79

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1064	ASP
1	A	1161	TYR
1	B	1161	TYR
1	C	942	PRO
1	C	1161	TYR

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	501/513 (98%)	498 (99%)	3 (1%)	90	97
1	B	500/513 (98%)	497 (99%)	3 (1%)	90	97
1	C	505/513 (98%)	501 (99%)	4 (1%)	86	96
1	D	500/513 (98%)	494 (99%)	6 (1%)	78	93
All	All	2006/2052 (98%)	1990 (99%)	16 (1%)	86	96

5 of 16 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	993	ASP
1	C	1046	LYS
1	D	1046	LYS
1	C	720	ASP
1	D	1056	LYS

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

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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](#)

48 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	1300	1,2	14,14,15	0.56	0	15,19,21	2.60	5 (33%)
2	NAG	A	1301	3,2	14,14,15	0.29	0	15,19,21	0.83	0
3	BMA	A	1302	2,4	11,11,12	0.19	0	15,15,17	0.81	0
4	MAN	A	1303	3,4	11,11,12	0.43	0	15,15,17	1.20	1 (6%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	MAN	A	1304	4	11,11,12	0.46	0	15,15,17	1.06	1 (6%)
4	MAN	A	1305	4	11,11,12	0.29	0	15,15,17	0.98	1 (6%)
4	MAN	A	1306	4	11,11,12	0.62	0	15,15,17	1.19	2 (13%)
4	MAN	A	1307	4	11,11,12	0.58	0	15,15,17	2.03	2 (13%)
4	MAN	A	1308	3,4	11,11,12	0.29	0	15,15,17	0.63	0
4	MAN	A	1309	4	11,11,12	0.37	0	15,15,17	0.88	1 (6%)
2	NAG	A	1310	1	14,14,15	0.28	0	15,19,21	0.96	1 (6%)
5	I3P	A	1311	-	21,24,24	0.57	0	39,39,39	1.10	2 (5%)
2	NAG	B	1300	1,2	14,14,15	0.44	0	15,19,21	2.59	5 (33%)
2	NAG	B	1301	3,2	14,14,15	0.37	0	15,19,21	0.73	0
3	BMA	B	1302	2,4	11,11,12	0.30	0	15,15,17	0.69	0
4	MAN	B	1303	3,4	11,11,12	0.46	0	15,15,17	0.97	2 (13%)
4	MAN	B	1304	4	11,11,12	0.41	0	15,15,17	1.30	1 (6%)
4	MAN	B	1305	4	11,11,12	0.28	0	15,15,17	0.81	1 (6%)
4	MAN	B	1306	4	11,11,12	0.44	0	15,15,17	1.48	4 (26%)
4	MAN	B	1307	4	11,11,12	0.44	0	15,15,17	1.75	1 (6%)
4	MAN	B	1308	3,4	11,11,12	0.32	0	15,15,17	1.05	1 (6%)
4	MAN	B	1309	4	11,11,12	0.44	0	15,15,17	0.78	0
2	NAG	B	1310	1	14,14,15	0.37	0	15,19,21	0.76	0
5	I3P	B	1311	-	21,24,24	0.58	0	39,39,39	1.14	1 (2%)
2	NAG	C	1300	1,2	14,14,15	0.43	0	15,19,21	2.24	4 (26%)
2	NAG	C	1301	3,2	14,14,15	0.42	0	15,19,21	0.70	0
3	BMA	C	1302	2,4	11,11,12	0.29	0	15,15,17	0.71	0
4	MAN	C	1303	3,4	11,11,12	0.28	0	15,15,17	0.72	0
4	MAN	C	1304	4	11,11,12	0.29	0	15,15,17	0.78	0
4	MAN	C	1305	4	11,11,12	0.36	0	15,15,17	0.95	1 (6%)
4	MAN	C	1306	4	11,11,12	0.45	0	15,15,17	1.11	1 (6%)
4	MAN	C	1307	4	11,11,12	0.42	0	15,15,17	1.62	3 (20%)
4	MAN	C	1308	3,4	11,11,12	0.24	0	15,15,17	0.60	0
4	MAN	C	1309	4	11,11,12	0.33	0	15,15,17	0.80	0
2	NAG	C	1310	1	14,14,15	0.35	0	15,19,21	1.48	2 (13%)
5	I3P	C	1311	-	21,24,24	0.64	0	39,39,39	1.46	5 (12%)
2	NAG	D	1300	1,2	14,14,15	0.41	0	15,19,21	2.61	5 (33%)
2	NAG	D	1301	3,2	14,14,15	0.33	0	15,19,21	0.78	0
3	BMA	D	1302	2,4	11,11,12	0.29	0	15,15,17	1.00	0
4	MAN	D	1303	3,4	11,11,12	0.40	0	15,15,17	0.58	0
4	MAN	D	1304	4	11,11,12	0.40	0	15,15,17	1.03	1 (6%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	MAN	D	1305	4	11,11,12	0.36	0	15,15,17	0.82	1 (6%)
4	MAN	D	1306	4	11,11,12	0.33	0	15,15,17	0.78	1 (6%)
4	MAN	D	1307	4	11,11,12	0.36	0	15,15,17	1.49	2 (13%)
4	MAN	D	1308	3,4	11,11,12	0.34	0	15,15,17	0.95	1 (6%)
4	MAN	D	1309	4	11,11,12	0.44	0	15,15,17	0.90	1 (6%)
2	NAG	D	1310	1	14,14,15	0.35	0	15,19,21	0.77	0
5	I3P	D	1311	-	21,24,24	0.61	0	39,39,39	1.33	4 (10%)

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	1300	1,2	-	0/6/23/26	0/1/1/1
2	NAG	A	1301	3,2	-	0/6/23/26	0/1/1/1
3	BMA	A	1302	2,4	-	0/2/19/22	0/1/1/1
4	MAN	A	1303	3,4	-	0/2/19/22	0/1/1/1
4	MAN	A	1304	4	-	0/2/19/22	0/1/1/1
4	MAN	A	1305	4	-	0/2/19/22	0/1/1/1
4	MAN	A	1306	4	-	0/2/19/22	0/1/1/1
4	MAN	A	1307	4	1/1/4/5	0/2/19/22	0/1/1/1
4	MAN	A	1308	3,4	-	0/2/19/22	0/1/1/1
4	MAN	A	1309	4	-	0/2/19/22	0/1/1/1
2	NAG	A	1310	1	-	0/6/23/26	0/1/1/1
5	I3P	A	1311	-	-	0/15/39/39	0/1/1/1
2	NAG	B	1300	1,2	-	0/6/23/26	0/1/1/1
2	NAG	B	1301	3,2	-	0/6/23/26	0/1/1/1
3	BMA	B	1302	2,4	-	0/2/19/22	0/1/1/1
4	MAN	B	1303	3,4	-	0/2/19/22	0/1/1/1
4	MAN	B	1304	4	-	0/2/19/22	0/1/1/1
4	MAN	B	1305	4	-	0/2/19/22	0/1/1/1
4	MAN	B	1306	4	-	0/2/19/22	0/1/1/1
4	MAN	B	1307	4	1/1/4/5	0/2/19/22	0/1/1/1
4	MAN	B	1308	3,4	-	0/2/19/22	0/1/1/1
4	MAN	B	1309	4	-	0/2/19/22	0/1/1/1
2	NAG	B	1310	1	-	0/6/23/26	0/1/1/1
5	I3P	B	1311	-	-	0/15/39/39	0/1/1/1
2	NAG	C	1300	1,2	-	0/6/23/26	0/1/1/1
2	NAG	C	1301	3,2	-	0/6/23/26	0/1/1/1
3	BMA	C	1302	2,4	-	0/2/19/22	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	MAN	C	1303	3,4	-	0/2/19/22	0/1/1/1
4	MAN	C	1304	4	-	0/2/19/22	0/1/1/1
4	MAN	C	1305	4	-	0/2/19/22	0/1/1/1
4	MAN	C	1306	4	-	0/2/19/22	0/1/1/1
4	MAN	C	1307	4	1/1/4/5	0/2/19/22	0/1/1/1
4	MAN	C	1308	3,4	-	0/2/19/22	0/1/1/1
4	MAN	C	1309	4	-	0/2/19/22	0/1/1/1
2	NAG	C	1310	1	-	0/6/23/26	0/1/1/1
5	I3P	C	1311	-	-	0/15/39/39	0/1/1/1
2	NAG	D	1300	1,2	-	0/6/23/26	0/1/1/1
2	NAG	D	1301	3,2	-	0/6/23/26	0/1/1/1
3	BMA	D	1302	2,4	-	0/2/19/22	0/1/1/1
4	MAN	D	1303	3,4	-	0/2/19/22	0/1/1/1
4	MAN	D	1304	4	-	0/2/19/22	0/1/1/1
4	MAN	D	1305	4	-	0/2/19/22	0/1/1/1
4	MAN	D	1306	4	-	0/2/19/22	0/1/1/1
4	MAN	D	1307	4	1/1/4/5	0/2/19/22	0/1/1/1
4	MAN	D	1308	3,4	-	0/2/19/22	0/1/1/1
4	MAN	D	1309	4	-	0/2/19/22	0/1/1/1
2	NAG	D	1310	1	-	0/6/23/26	0/1/1/1
5	I3P	D	1311	-	-	0/15/39/39	0/1/1/1

There are no bond length outliers.

The worst 5 of 64 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	1300	NAG	C4-C3-C2	-2.40	107.61	111.34
4	B	1306	MAN	O5-C1-C2	-2.39	107.08	110.89
2	A	1300	NAG	C4-C3-C2	-2.31	107.76	111.34
2	B	1300	NAG	C4-C3-C2	-2.25	107.84	111.34
5	D	1311	I3P	C6-C5-C4	-2.19	106.77	111.39

All (4) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
4	A	1307	MAN	C1
4	D	1307	MAN	C1
4	B	1307	MAN	C1
4	C	1307	MAN	C1

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	C	2
1	B	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B	1233:ALA	C	1234:TYR	N	3.09
1	C	1233:ALA	C	1234:TYR	N	3.08
1	C	1138:ALA	C	1139:CYS	N	2.21

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	559/572 (97%)	0.22	5 (0%) 85 77	74, 109, 161, 198	0
1	B	558/572 (97%)	0.38	34 (6%) 25 12	92, 151, 226, 251	0
1	C	563/572 (98%)	0.28	10 (1%) 71 56	72, 113, 169, 215	0
1	D	557/572 (97%)	0.48	35 (6%) 23 12	99, 153, 222, 243	0
All	All	2237/2288 (97%)	0.34	84 (3%) 44 27	72, 126, 211, 251	0

The worst 5 of 84 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	833	LEU	9.3
1	D	965	LEU	8.7
1	D	826	PHE	6.2
1	D	1174	LEU	5.7
1	D	966	ILE	5.7

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
5	I3P	B	1311	24/24	0.70	0.41	3.33	204,209,217,218	0
5	I3P	D	1311	24/24	0.62	0.46	1.42	190,201,218,219	0
5	I3P	C	1311	24/24	0.69	0.35	0.68	166,178,188,190	0
2	NAG	A	1310	14/15	0.90	0.21	-0.30	115,121,126,130	0
5	I3P	A	1311	24/24	0.72	0.21	-1.10	185,204,218,219	0
2	NAG	D	1301	14/15	0.91	0.18	-1.66	108,117,123,127	0
2	NAG	A	1301	14/15	0.91	0.20	-1.83	92,95,101,102	0
2	NAG	C	1310	14/15	0.92	0.10	-2.16	96,104,107,108	0
2	NAG	C	1301	14/15	0.95	0.17	-3.74	75,77,80,82	0
4	MAN	A	1308	11/12	0.95	0.14	-	120,127,130,134	0
2	NAG	D	1300	14/15	0.86	0.21	-	111,113,119,121	0
4	MAN	A	1305	11/12	0.83	0.20	-	149,154,160,162	0
4	MAN	D	1307	11/12	0.87	0.19	-	132,138,140,141	0
2	NAG	B	1310	14/15	0.83	0.40	-	82,86,86,87	0
2	NAG	B	1301	14/15	0.89	0.22	-	122,122,123,124	0
4	MAN	A	1309	11/12	0.87	0.17	-	138,146,150,150	0
4	MAN	D	1306	11/12	0.83	0.18	-	141,143,144,146	0
4	MAN	C	1304	11/12	0.93	0.11	-	133,137,141,142	0
4	MAN	B	1305	11/12	0.72	0.41	-	148,149,152,153	0
4	MAN	B	1309	11/12	0.85	0.17	-	120,125,127,129	0
2	NAG	C	1300	14/15	0.94	0.19	-	78,83,89,94	0
4	MAN	B	1306	11/12	0.90	0.18	-	136,140,146,152	0
4	MAN	A	1303	11/12	0.91	0.10	-	119,122,130,136	0
4	MAN	B	1307	11/12	0.58	0.23	-	145,156,159,159	0
4	MAN	D	1303	11/12	0.90	0.08	-	126,129,134,138	0
4	MAN	A	1307	11/12	0.67	0.26	-	152,156,159,159	0
4	MAN	A	1304	11/12	0.81	0.15	-	147,150,152,153	0
4	MAN	B	1308	11/12	0.93	0.15	-	124,126,128,128	0
4	MAN	D	1304	11/12	0.88	0.16	-	124,135,139,144	0
4	MAN	C	1305	11/12	0.80	0.16	-	138,145,149,150	0
3	BMA	C	1302	11/12	0.96	0.16	-	86,89,99,100	0
3	BMA	B	1302	11/12	0.90	0.15	-	118,122,125,128	0
4	MAN	B	1304	11/12	0.83	0.19	-	138,140,143,146	0
3	BMA	A	1302	11/12	0.96	0.16	-	103,105,113,115	0
4	MAN	D	1309	11/12	0.89	0.12	-	133,136,138,138	0
4	MAN	C	1303	11/12	0.94	0.13	-	106,110,120,123	0
4	MAN	B	1303	11/12	0.86	0.19	-	131,134,140,140	0
4	MAN	C	1307	11/12	0.85	0.18	-	135,143,146,150	0
4	MAN	C	1309	11/12	0.79	0.26	-	127,133,140,143	0
2	NAG	D	1310	14/15	0.69	0.44	-	100,104,106,106	0
4	MAN	A	1306	11/12	0.86	0.16	-	131,134,143,151	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
4	MAN	C	1308	11/12	0.97	0.12	-	107,110,114,123	0
3	BMA	D	1302	11/12	0.92	0.09	-	113,118,120,122	0
4	MAN	D	1305	11/12	0.82	0.26	-	142,147,150,150	0
2	NAG	B	1300	14/15	0.90	0.12	-	109,115,121,122	0
2	NAG	A	1300	14/15	0.94	0.20	-	94,96,99,99	0
4	MAN	D	1308	11/12	0.93	0.12	-	121,123,125,131	0
4	MAN	C	1306	11/12	0.88	0.12	-	126,129,131,135	0

6.5 Other polymers [i](#)

There are no such residues in this entry.