



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2026 – 01:40 PM UTC

PDB ID : 5DO2 / pdb_00005do2
Title : Complex structure of MERS-RBD bound with 4C2 antibody
Authors : Li, Y.; Wan, Y.; Liu, P.; Zhao, J.; Lu, G.; Qi, J.; Wang, Q.; Lu, X.; Wu, Y.;
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Deposited on : 2015-09-10
Resolution : 2.41 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

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

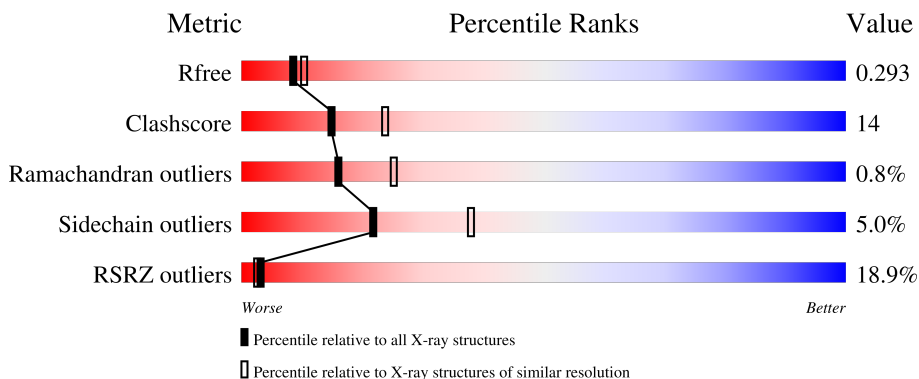
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.41 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}	180053	4912 (2.40-2.40)
Clashscore	190562	5391 (2.40-2.40)
Ramachandran outliers	187476	5320 (2.40-2.40)
Sidechain outliers	187428	5321 (2.40-2.40)
RSRZ outliers	180081	4916 (2.40-2.40)

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 of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. 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	251	 4% 62% 18% 17%
1	B	251	 56% 55% 25% 17%
2	C	219	 20% 72% 23% 17%
2	H	219	 2% 79% 17% 17%
3	D	214	 18% 80% 20%

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Mol	Chain	Length	Quality of chain
3	L	214	 <p>A horizontal bar chart representing the quality of the chain. The bar is divided into two segments: a green segment on the left labeled '83%' and a yellow segment on the right labeled '15%'. A small red square is at the beginning of the bar, and a small black dot is at the end. A '%' symbol is positioned above the start of the bar.</p>

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 9937 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 S protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	208	1608	1026	256	315	11	0	0	0
1	B	208	1608	1026	256	315	11	0	0	0

There are 22 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	362	ALA	-	expression tag	UNP W5ZZM0
A	363	ASP	-	expression tag	UNP W5ZZM0
A	364	GLY	-	expression tag	UNP W5ZZM0
A	365	ILE	-	expression tag	UNP W5ZZM0
A	366	GLN	-	expression tag	UNP W5ZZM0
A	607	HIS	-	expression tag	UNP W5ZZM0
A	608	HIS	-	expression tag	UNP W5ZZM0
A	609	HIS	-	expression tag	UNP W5ZZM0
A	610	HIS	-	expression tag	UNP W5ZZM0
A	611	HIS	-	expression tag	UNP W5ZZM0
A	612	HIS	-	expression tag	UNP W5ZZM0
B	362	ALA	-	expression tag	UNP W5ZZM0
B	363	ASP	-	expression tag	UNP W5ZZM0
B	364	GLY	-	expression tag	UNP W5ZZM0
B	365	ILE	-	expression tag	UNP W5ZZM0
B	366	GLN	-	expression tag	UNP W5ZZM0
B	607	HIS	-	expression tag	UNP W5ZZM0
B	608	HIS	-	expression tag	UNP W5ZZM0
B	609	HIS	-	expression tag	UNP W5ZZM0
B	610	HIS	-	expression tag	UNP W5ZZM0
B	611	HIS	-	expression tag	UNP W5ZZM0
B	612	HIS	-	expression tag	UNP W5ZZM0

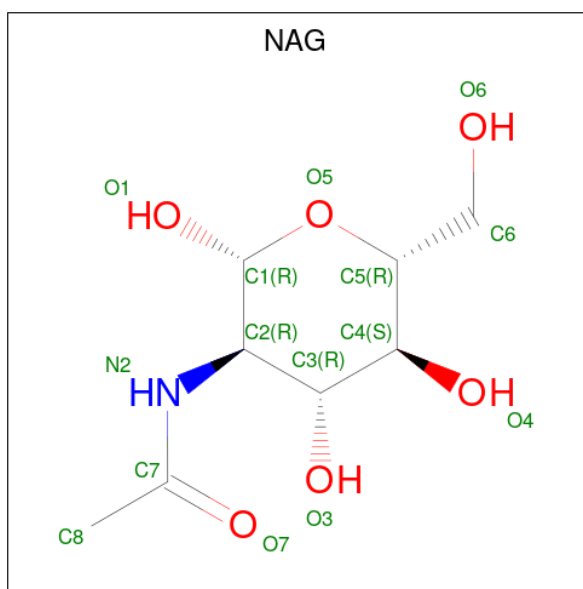
- Molecule 2 is a protein called 4C2 heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	H	215	Total 1621	C 1021	N 264	O 327	S 9	0	0	0
2	C	215	Total 1621	C 1021	N 264	O 327	S 9	0	0	0

- Molecule 3 is a protein called 4C2 light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	L	214	Total 1663	C 1026	N 284	O 346	S 7	0	0	0
3	D	214	Total 1663	C 1026	N 284	O 346	S 7	0	0	0

- Molecule 4 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).



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

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
5	A	24	Total 24	O 24	0	0
5	H	31	Total 31	O 31	0	0

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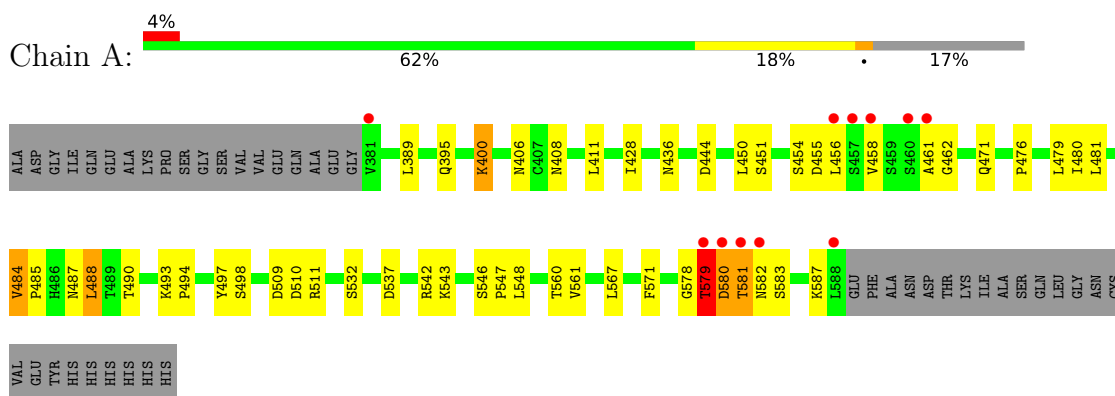
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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	L	29	Total O 29 29	0	0
5	B	23	Total O 23 23	0	0
5	C	11	Total O 11 11	0	0
5	D	21	Total O 21 21	0	0

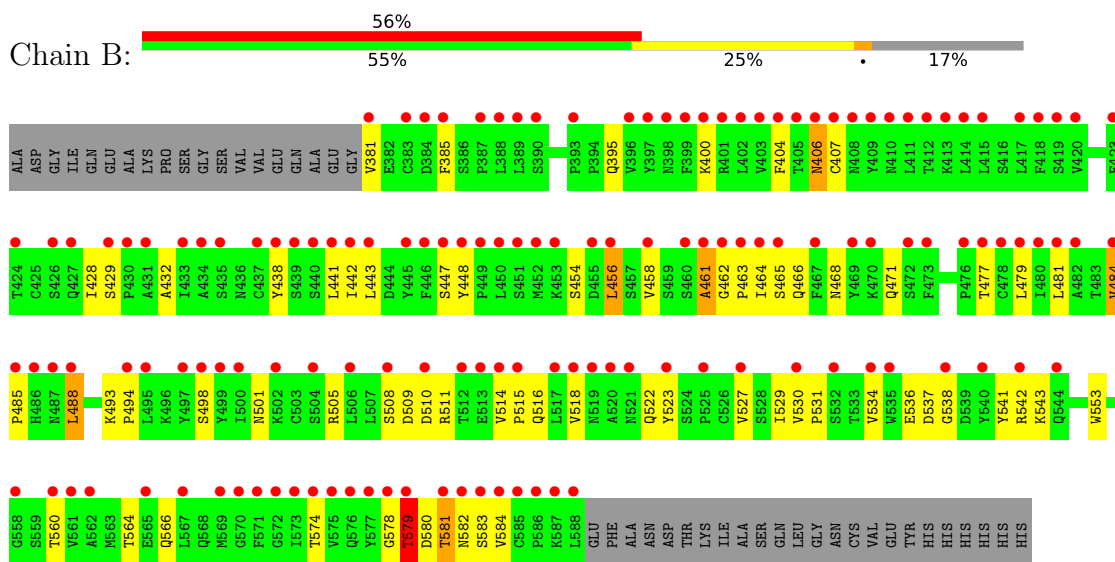
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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.

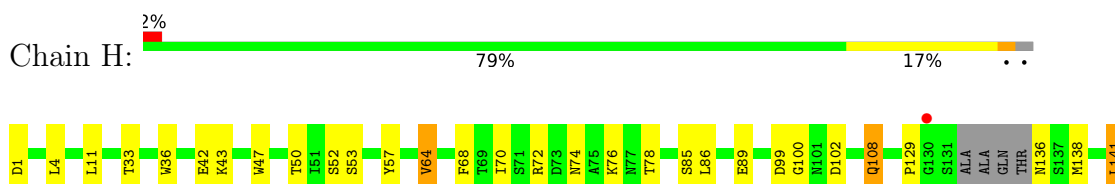
- Molecule 1: S protein

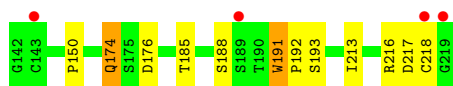


- Molecule 1: S protein

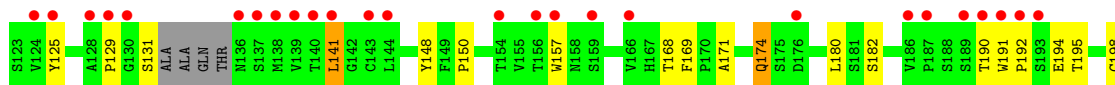
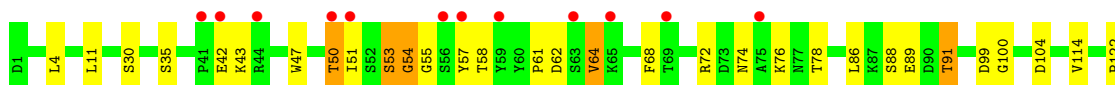


- Molecule 2: 4C2 heavy chain

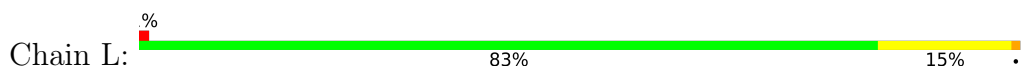




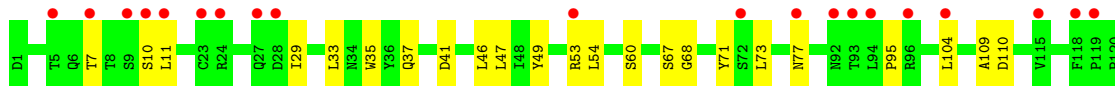
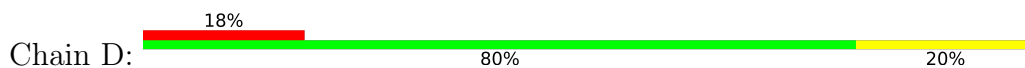
- Molecule 2: 4C2 heavy chain



- Molecule 3: 4C2 light chain



- Molecule 3: 4C2 light chain



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	74.08Å 110.40Å 172.98Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.53 – 2.41 46.53 – 2.41	Depositor EDS
% Data completeness (in resolution range)	98.8 (46.53-2.41) 93.6 (46.53-2.41)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	0.10	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.19 (at 2.42Å)	Xtrriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.245 , 0.289 0.251 , 0.293	Depositor DCC
R_{free} test set	2789 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	42.6	Xtrriage
Anisotropy	0.323	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 39.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	9937	wwPDB-VP
Average B, all atoms (Å ²)	73.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.37% 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:
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	0.33	0/1647	0.79	2/2249 (0.1%)
1	B	0.31	0/1647	0.78	1/2249 (0.0%)
2	C	0.34	0/1662	0.79	2/2266 (0.1%)
2	H	0.41	1/1662 (0.1%)	0.79	0/2266
3	D	0.31	0/1696	0.73	0/2299
3	L	0.31	0/1696	0.74	0/2299
All	All	0.34	1/10010 (0.0%)	0.77	5/13628 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	H	191	TRP	CA-C	-5.27	1.48	1.52

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	580	ASP	N-CA-C	-6.60	99.71	109.81
2	C	54	GLY	N-CA-C	5.67	119.35	112.49
2	C	57	TYR	N-CA-C	5.63	115.55	108.45
1	A	582	ASN	N-CA-C	-5.53	106.32	112.57
1	B	582	ASN	N-CA-C	-5.16	107.50	112.97

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	1608	0	1573	38	0
1	B	1608	0	1574	87	0
2	C	1621	0	1572	46	0
2	H	1621	0	1572	30	0
3	D	1663	0	1587	53	0
3	L	1663	0	1587	22	0
4	A	14	0	13	1	0
5	A	24	0	0	12	0
5	B	23	0	0	56	0
5	C	11	0	0	19	0
5	D	21	0	0	40	0
5	H	31	0	0	12	0
5	L	29	0	0	7	0
All	All	9937	0	9478	266	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 14.

The worst 5 of 266 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:514:VAL:HG12	5:B:704:HOH:O	1.22	1.26
1:B:432:ALA:HB3	5:B:705:HOH:O	1.07	1.22
5:H:328:HOH:O	3:L:214:CYS:SG	2.01	1.17
1:B:447:SER:C	5:B:701:HOH:O	1.86	1.16
3:D:186:TYR:HB3	5:D:304:HOH:O	1.47	1.14

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	206/251 (82%)	192 (93%)	10 (5%)	4 (2%)	6	8
1	B	206/251 (82%)	189 (92%)	13 (6%)	4 (2%)	6	8
2	C	211/219 (96%)	204 (97%)	6 (3%)	1 (0%)	24	37
2	H	211/219 (96%)	205 (97%)	5 (2%)	1 (0%)	24	37
3	D	212/214 (99%)	203 (96%)	9 (4%)	0	100	100
3	L	212/214 (99%)	204 (96%)	8 (4%)	0	100	100
All	All	1258/1368 (92%)	1197 (95%)	51 (4%)	10 (1%)	16	25

5 of 10 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	H	217	ASP
1	B	510	ASP
1	B	579	THR
1	A	462	GLY
1	A	510	ASP

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	190/224 (85%)	180 (95%)	10 (5%)	20	36
1	B	190/224 (85%)	181 (95%)	9 (5%)	23	41
2	C	187/189 (99%)	176 (94%)	11 (6%)	18	31
2	H	187/189 (99%)	177 (95%)	10 (5%)	20	36
3	D	192/192 (100%)	184 (96%)	8 (4%)	26	45
3	L	192/192 (100%)	183 (95%)	9 (5%)	23	41
All	All	1138/1210 (94%)	1081 (95%)	57 (5%)	22	38

5 of 57 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	L	214	CYS

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Mol	Chain	Res	Type
3	D	203	SER
1	B	508	SER
3	D	181	LEU
3	D	7	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
3	D	31	ASN
2	C	82	GLN
1	B	410	ASN
3	L	38	GLN
1	B	471	GLN

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

1 ligand is 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
4	NAG	A	701	1	14,14,15	0.43	0	17,19,21	0.34	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
4	NAG	A	701	1	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	701	NAG	O5-C5-C6-O6
4	A	701	NAG	C4-C5-C6-O6

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	701	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, 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	208/251 (82%)	0.49	11 (5%) 32 28	36, 55, 103, 127	0
1	B	208/251 (82%)	2.58	141 (67%) 0 0	44, 131, 190, 230	0
2	C	215/219 (98%)	1.20	44 (20%) 2 2	42, 78, 147, 206	0
2	H	215/219 (98%)	0.08	5 (2%) 61 57	26, 40, 65, 179	0
3	D	214/214 (100%)	1.18	38 (17%) 4 3	38, 76, 130, 220	0
3	L	214/214 (100%)	0.10	2 (0%) 81 78	28, 42, 62, 168	0
All	All	1274/1368 (93%)	0.93	241 (18%) 3 2	26, 60, 154, 230	0

The worst 5 of 241 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	571	PHE	6.8
1	B	441	LEU	6.3
1	A	579	THR	6.2
1	B	573	ILE	5.9
1	B	414	LEU	5.6

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 oligosaccharides 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. 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	B-factors(Å ²)	Q<0.9
4	NAG	A	701	14/15	0.61	0.16	81,81,81,81	0

6.5 Other polymers [i](#)

There are no such residues in this entry.