wwPDB X-ray Structure Validation Summary Report (i)

Jun 16, 2024 – 10:39 PM EDT

PDB ID	:	2WRE
Title	:	structure of H2 japan hemagglutinin with human receptor
Authors	:	Liu, J.; Stevens, D.J.; Haire, L.F.; Walker, P.A.; Coombs, P.J.; Russell, R.J.; Gamblin, S.J.; Skehel, J.J.
Deposited on	:	2009-09-01
Resolution	:	3.00 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 (i) 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 (i)) were used in the production of this report:

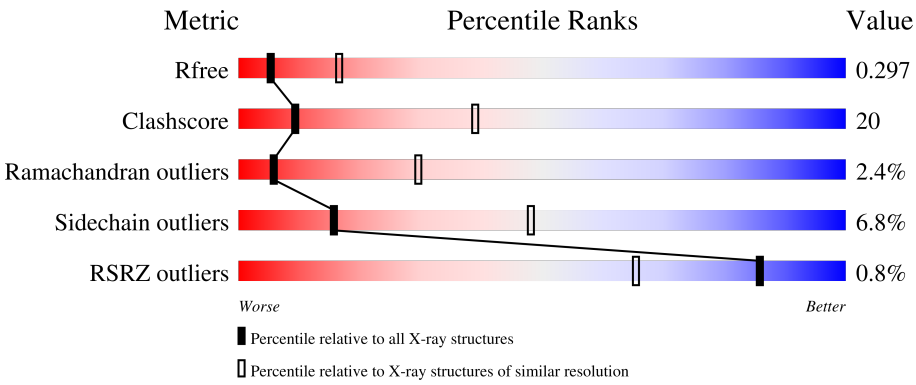
MolProbity	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	2.37.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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}	130704	2092 (3.00-3.00)
Clashscore	141614	2416 (3.00-3.00)
Ramachandran outliers	138981	2333 (3.00-3.00)
Sidechain outliers	138945	2336 (3.00-3.00)
RSRZ outliers	127900	1990 (3.00-3.00)

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 <=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	505	% 55% 35% • 7%
1	B	505	60% 33% • •
1	C	505	% 57% 34% • 5%
2	D	2	50% 50%
2	E	2	50% 50%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
2	F	2	50% 50%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 11443 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.

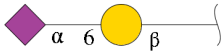
- Molecule 1 is a protein called HEMAGGLUTININ.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	471	3708	2335	633	716	24	0	0	0
1	B	486	3841	2417	658	742	24	0	0	0
1	C	481	3798	2392	652	730	24	0	0	0

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	107	HIS	TYR	conflict	UNP Q67085
A	136	GLN	ARG	conflict	UNP Q67085
A	159	ASN	ASP	conflict	UNP Q67085
A	185	ILE	ASN	conflict	UNP Q67085
A	188	LYS	THR	conflict	UNP Q67085
A	307	LYS	ARG	conflict	UNP Q67085
B	107	HIS	TYR	conflict	UNP Q67085
B	136	GLN	ARG	conflict	UNP Q67085
B	159	ASN	ASP	conflict	UNP Q67085
B	185	ILE	ASN	conflict	UNP Q67085
B	188	LYS	THR	conflict	UNP Q67085
B	307	LYS	ARG	conflict	UNP Q67085
C	107	HIS	TYR	conflict	UNP Q67085
C	136	GLN	ARG	conflict	UNP Q67085
C	159	ASN	ASP	conflict	UNP Q67085
C	185	ILE	ASN	conflict	UNP Q67085
C	188	LYS	THR	conflict	UNP Q67085
C	307	LYS	ARG	conflict	UNP Q67085

- Molecule 2 is an oligosaccharide called N-acetyl-alpha-neuraminic acid-(2-6)-beta-D-galacto pyranose.



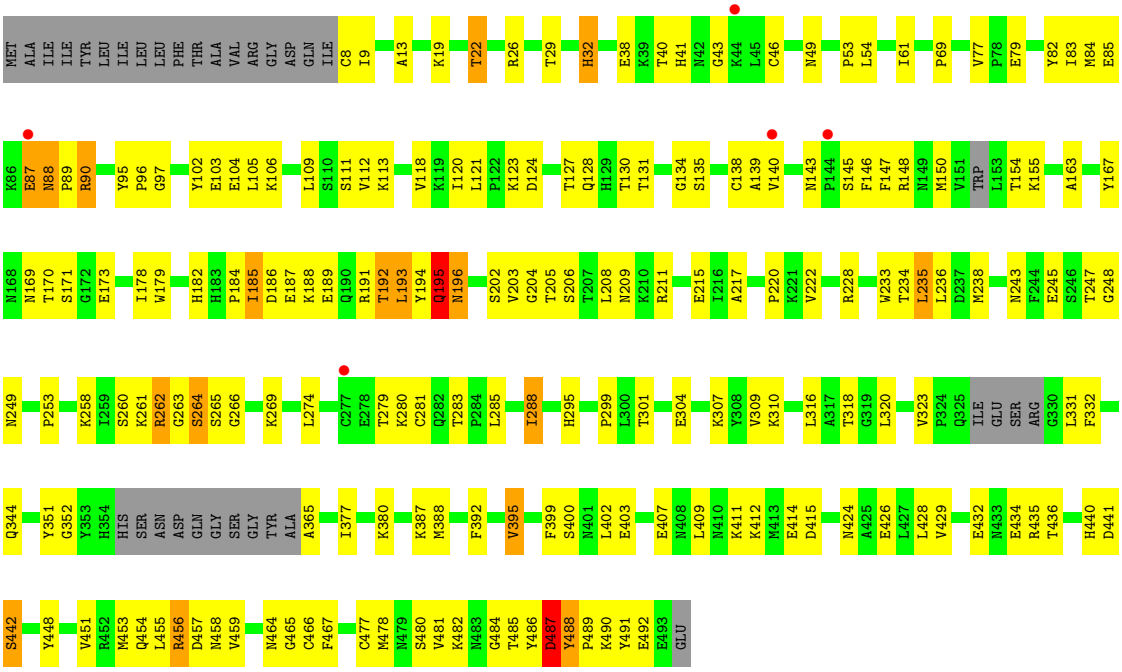
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
2	D	2	32	17	1	14	0	0	0
			Total	C	N	O			
2	E	2	32	17	1	14	0	0	0
			Total	C	N	O			
2	F	2	32	17	1	14	0	0	0

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.

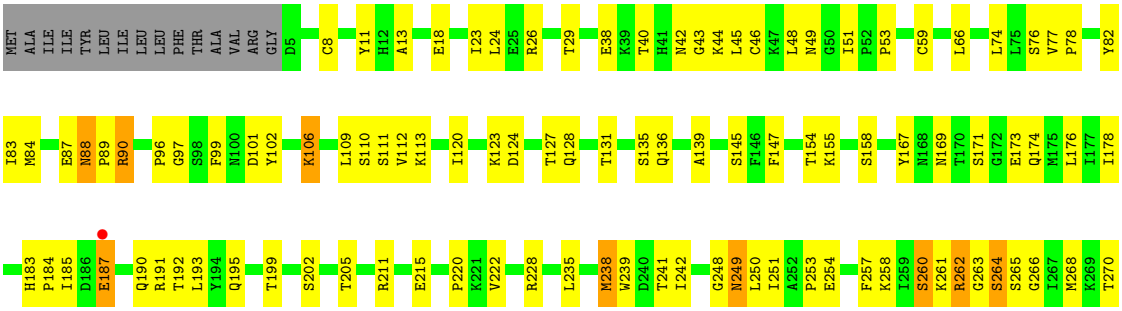
- Molecule 1: HEMAGGLUTININ

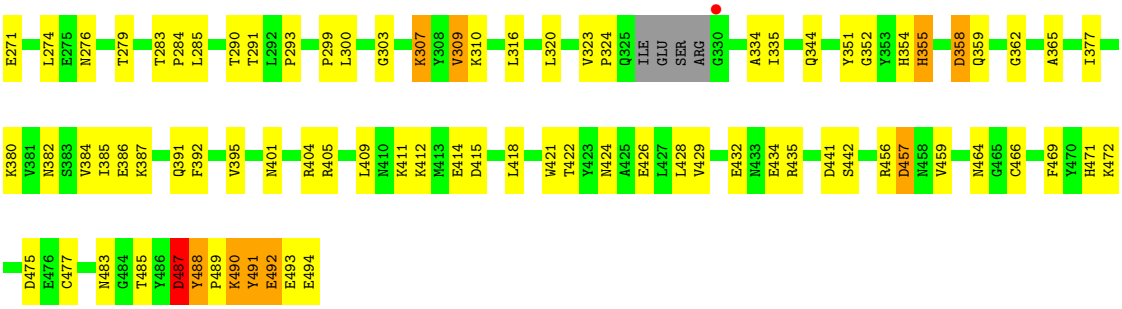
Chain A:



- Molecule 1: HEMAGGLUTININ

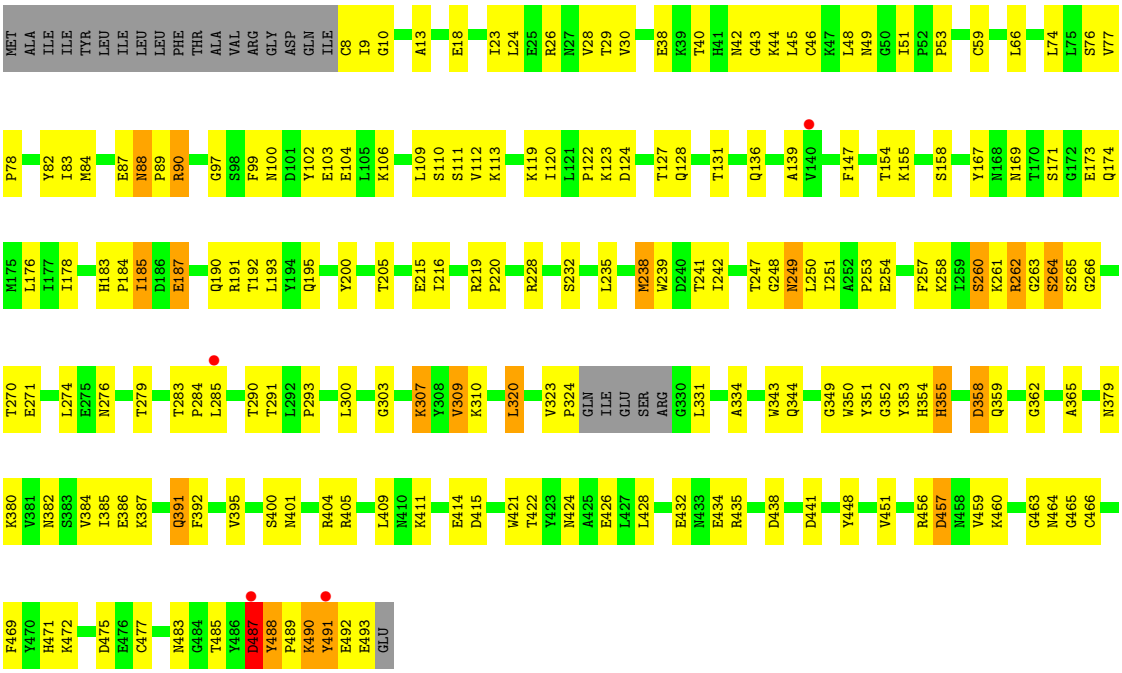
Chain B:





- Molecule 1: HEMAGGLUTININ

Chain C:



- Molecule 2: N-acetyl-alpha-neuraminic acid-(2-6)-beta-D-galactopyranose

Chain D:

- Molecule 2: N-acetyl-alpha-neuraminic acid-(2-6)-beta-D-galactopyranose

Chain E:

- Molecule 2: N-acetyl-alpha-neuraminic acid-(2-6)-beta-D-galactopyranose

Chain F:

GAL1
SIA2

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	75.97Å 117.46Å 225.37Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.98 – 3.00 46.27 – 3.00	Depositor EDS
% Data completeness (in resolution range)	96.8 (19.98-3.00) 96.8 (46.27-3.00)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.16 (at 3.01Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, R_{free}	0.239 , 0.295 0.239 , 0.297	Depositor DCC
R_{free} test set	2006 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å^2)	68.9	Xtriage
Anisotropy	0.014	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.33 , 42.6	EDS
L-test for twinning[2]	$< \|L\| > = 0.44$, $< L^2 > = 0.26$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.89	EDS
Total number of atoms	11443	wwPDB-VP
Average B, all atoms (Å^2)	68.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.70% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ 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: SIA, GAL

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	0/3788	0.62	0/5121
1	B	0.46	0/3928	0.60	0/5313
1	C	0.46	0/3885	0.60	0/5255
All	All	0.45	0/11601	0.61	0/15689

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	B	0	1
1	C	0	1
All	All	0	2

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	490	LYS	Peptide
1	C	490	LYS	Peptide

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	3708	0	3583	168	0
1	B	3841	0	3704	155	0
1	C	3798	0	3669	159	0
2	D	32	0	28	7	0
2	E	32	0	28	0	0
2	F	32	0	28	1	0
All	All	11443	0	11040	445	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 20.

The worst 5 of 445 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:487:ASP:HA	1:B:488:TYR:HB2	1.43	0.99
1:C:487:ASP:HA	1:C:488:TYR:HB2	1.46	0.95
1:C:488:TYR:CD2	1:C:488:TYR:O	2.23	0.91
1:A:140:VAL:HG21	1:A:148:ARG:HH22	1.34	0.91
1:C:492:GLU:HA	1:C:493:GLU:C	1.91	0.91

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	463/505 (92%)	389 (84%)	63 (14%)	11 (2%)	6 29
1	B	482/505 (95%)	433 (90%)	37 (8%)	12 (2%)	5 28
1	C	477/505 (94%)	429 (90%)	37 (8%)	11 (2%)	6 30
All	All	1422/1515 (94%)	1251 (88%)	137 (10%)	34 (2%)	6 29

5 of 34 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	262	ARG
1	B	262	ARG
1	B	487	ASP
1	B	488	TYR
1	C	262	ARG

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	409/442 (92%)	376 (92%)	33 (8%)	11	40
1	B	423/442 (96%)	396 (94%)	27 (6%)	17	51
1	C	418/442 (95%)	393 (94%)	25 (6%)	19	53
All	All	1250/1326 (94%)	1165 (93%)	85 (7%)	16	48

5 of 85 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	457	ASP
1	C	264	SER
1	B	487	ASP
1	C	109	LEU
1	C	309	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 23 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	359	GLN
1	C	129	HIS
1	B	454	GLN
1	C	190	GLN
1	A	249	ASN

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)

6 monosaccharides 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	GAL	D	1	2	12,12,12	0.37	0	17,17,17	0.90	0
2	SIA	D	2	2	20,20,21	0.78	0	21,28,31	1.16	2 (9%)
2	GAL	E	1	2	12,12,12	0.67	0	17,17,17	0.48	0
2	SIA	E	2	2	20,20,21	1.18	2 (10%)	21,28,31	1.51	4 (19%)
2	GAL	F	1	2	12,12,12	0.53	0	17,17,17	0.97	1 (5%)
2	SIA	F	2	2	20,20,21	0.92	1 (5%)	21,28,31	1.43	3 (14%)

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	GAL	D	1	2	-	1/2/22/22	0/1/1/1
2	SIA	D	2	2	-	1/18/34/38	0/1/1/1
2	GAL	E	1	2	-	2/2/22/22	0/1/1/1
2	SIA	E	2	2	-	1/18/34/38	0/1/1/1
2	GAL	F	1	2	-	0/2/22/22	0/1/1/1
2	SIA	F	2	2	-	2/18/34/38	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	2	SIA	C4-C5	-2.83	1.50	1.53
2	F	2	SIA	C2-C1	2.24	1.55	1.52
2	E	2	SIA	C2-C1	2.15	1.54	1.52

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	F	2	SIA	O9-C9-C8	-3.60	103.59	111.16
2	E	2	SIA	C4-C5-N5	-3.37	103.80	110.44
2	E	2	SIA	C8-C7-C6	-2.92	107.57	113.05
2	E	2	SIA	O1B-C1-C2	2.85	120.12	112.71
2	D	2	SIA	C8-C7-C6	-2.44	108.48	113.05

There are no chirality outliers.

5 of 7 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	F	2	SIA	C7-C8-C9-O9
2	F	2	SIA	O8-C8-C9-O9
2	E	1	GAL	O5-C5-C6-O6
2	D	2	SIA	O8-C8-C9-O9
2	E	1	GAL	C4-C5-C6-O6

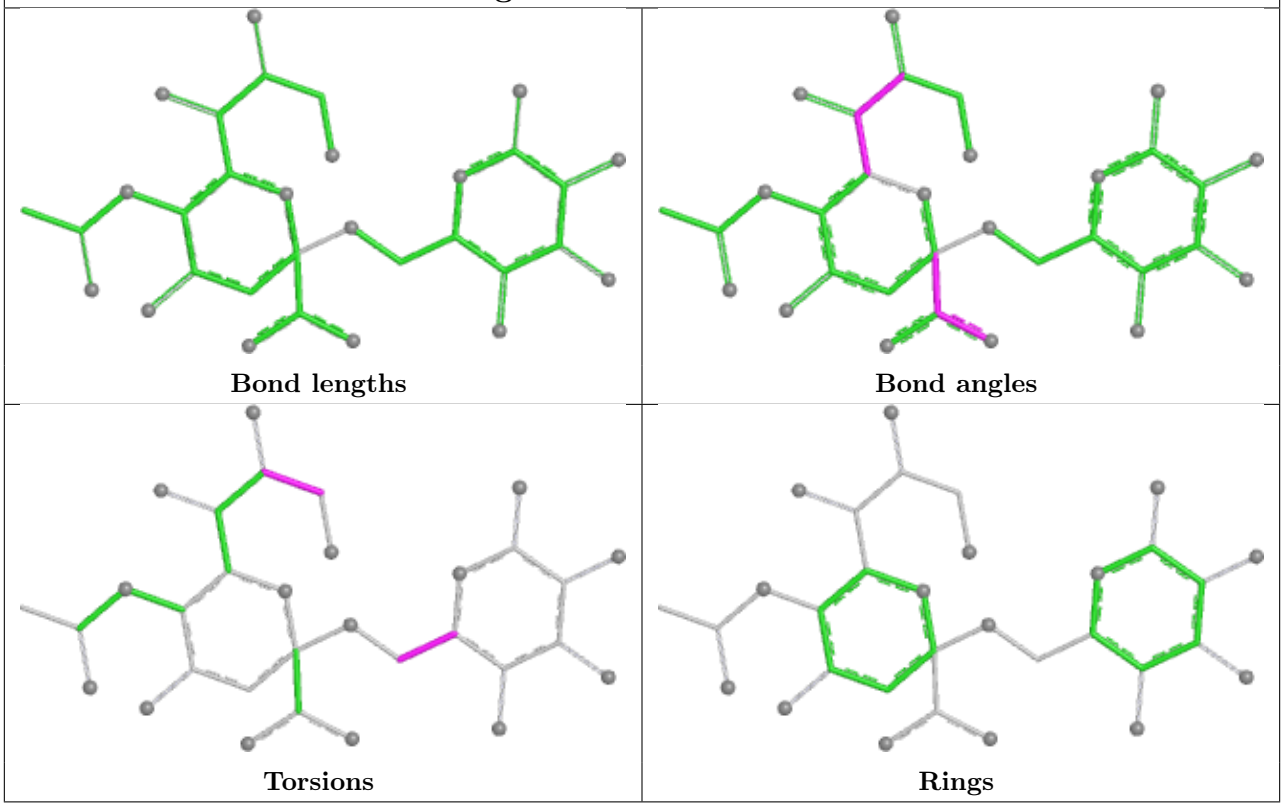
There are no ring outliers.

2 monomers are involved in 8 short contacts:

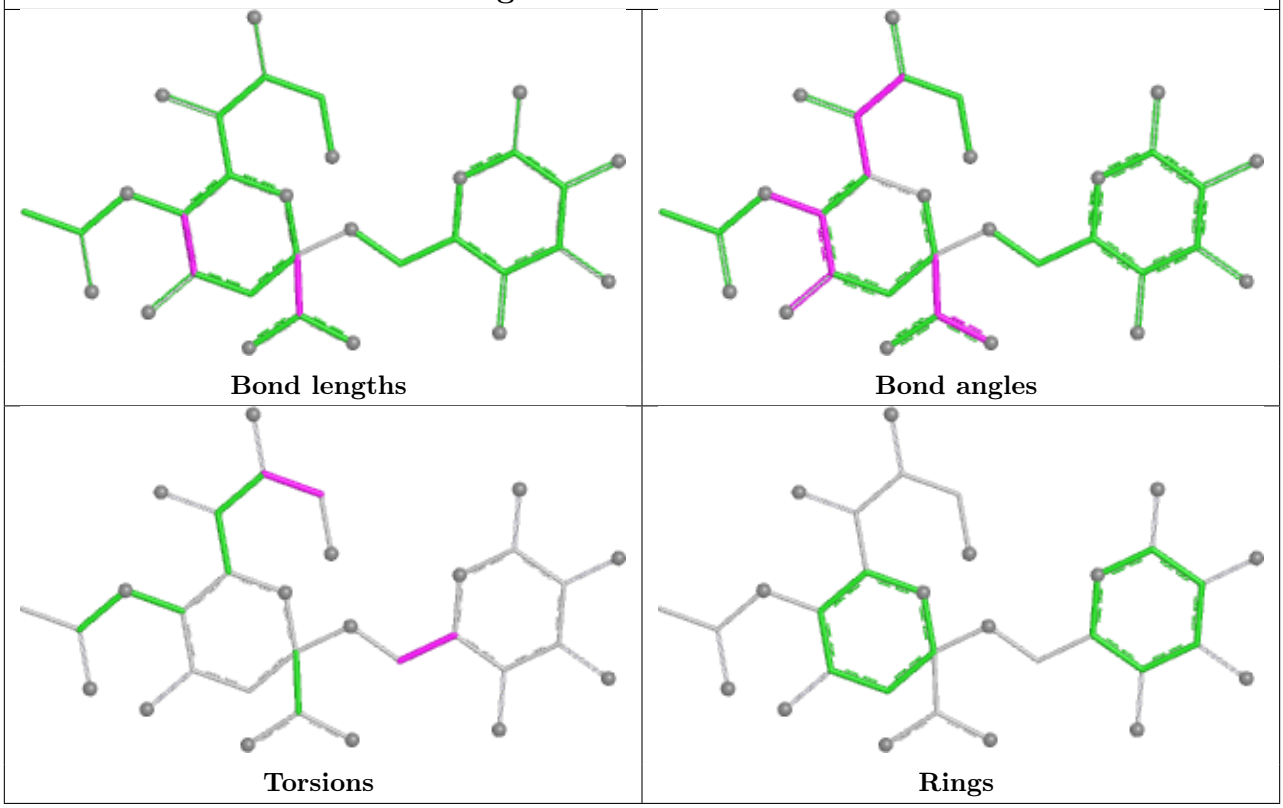
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	F	2	SIA	1	0
2	D	2	SIA	7	0

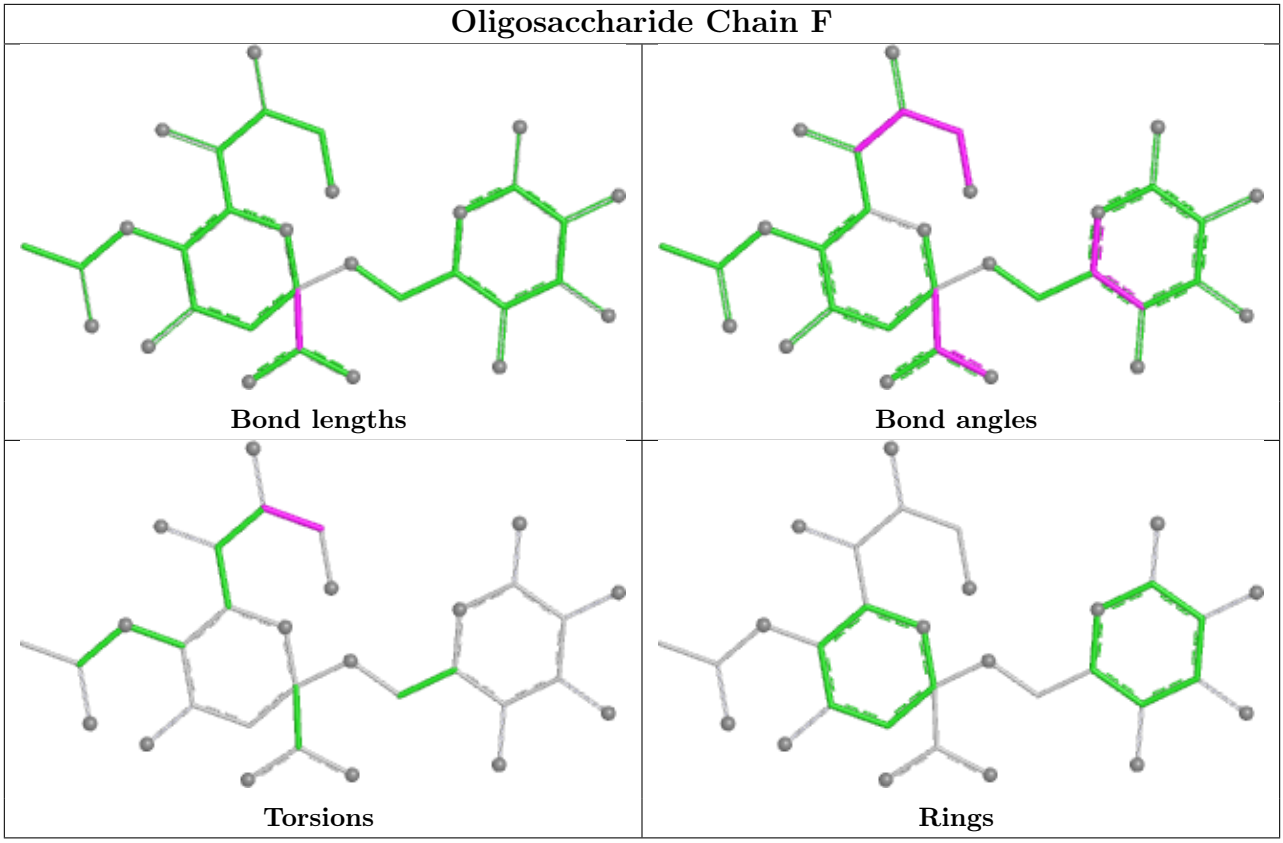
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

Oligosaccharide Chain D



Oligosaccharide Chain E





5.6 Ligand geometry (i)

There are no ligands in this entry.

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	471/505 (93%)	-0.11	5 (1%)	80	56	34, 72, 122, 234	0
1	B	486/505 (96%)	-0.16	2 (0%)	92	79	34, 62, 103, 186	0
1	C	481/505 (95%)	-0.12	4 (0%)	86	65	35, 59, 106, 206	0
All	All	1438/1515 (94%)	-0.13	11 (0%)	86	65	34, 64, 112, 234	0

The worst 5 of 11 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	330	GLY	3.0
1	A	140	VAL	3.0
1	C	487	ASP	2.9
1	B	187	GLU	2.8
1	A	44	LYS	2.7

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)

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
2	GAL	E	1	12/12	0.72	0.31	86,86,86,86	0
2	GAL	D	1	12/12	0.86	0.28	110,110,110,110	0
2	SIA	D	2	20/21	0.90	0.30	110,110,110,110	0

Continued on next page...

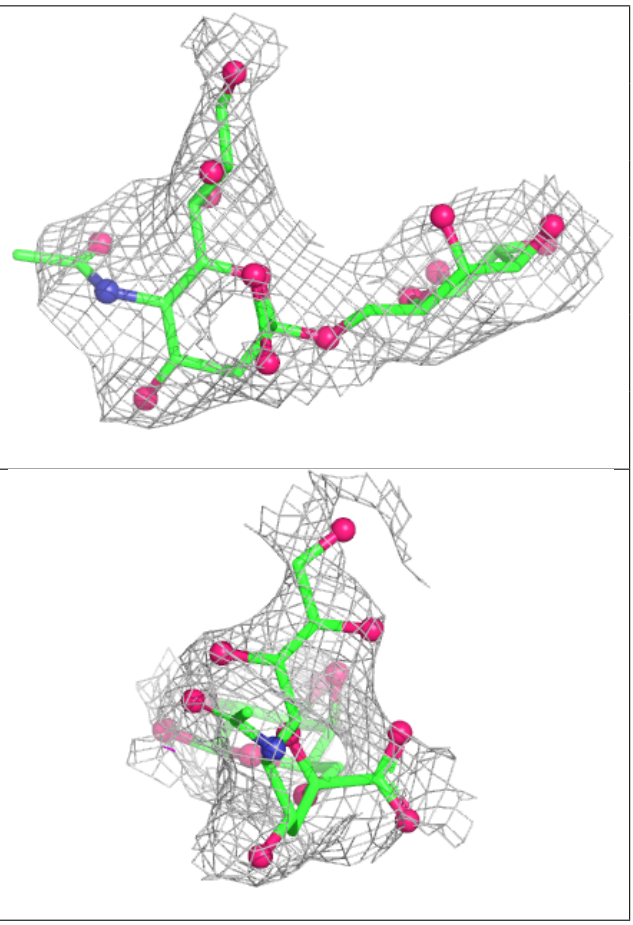
Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	GAL	F	1	12/12	0.90	0.19	78,78,78,78	0
2	SIA	F	2	20/21	0.91	0.24	78,78,78,78	0
2	SIA	E	2	20/21	0.93	0.19	86,86,86,86	0

The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.

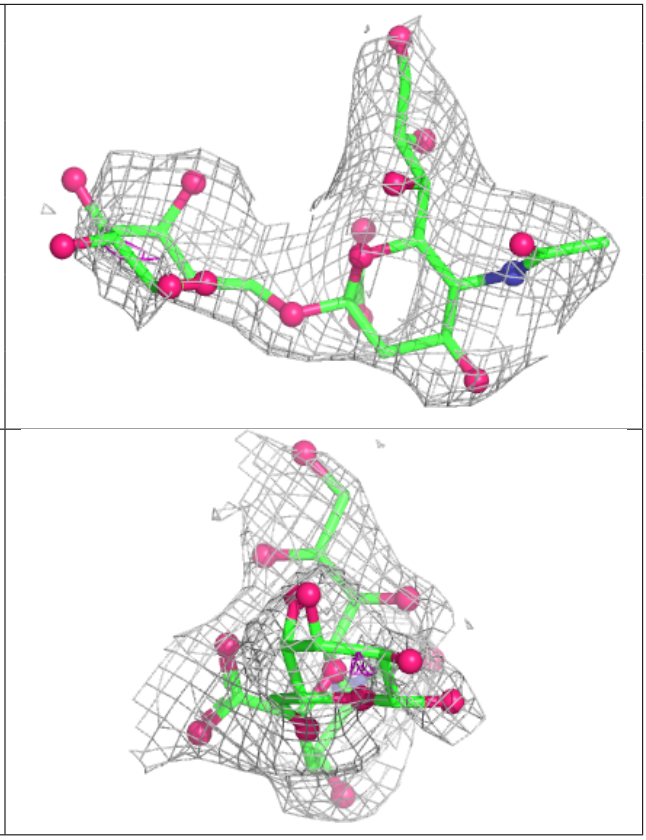
Electron density around Chain D:

2mF$_o$-DF$_c$ (at 0.7 rmsd) in gray
mF$_o$-DF$_c$ (at 3 rmsd) in purple (negative) and green (positive)



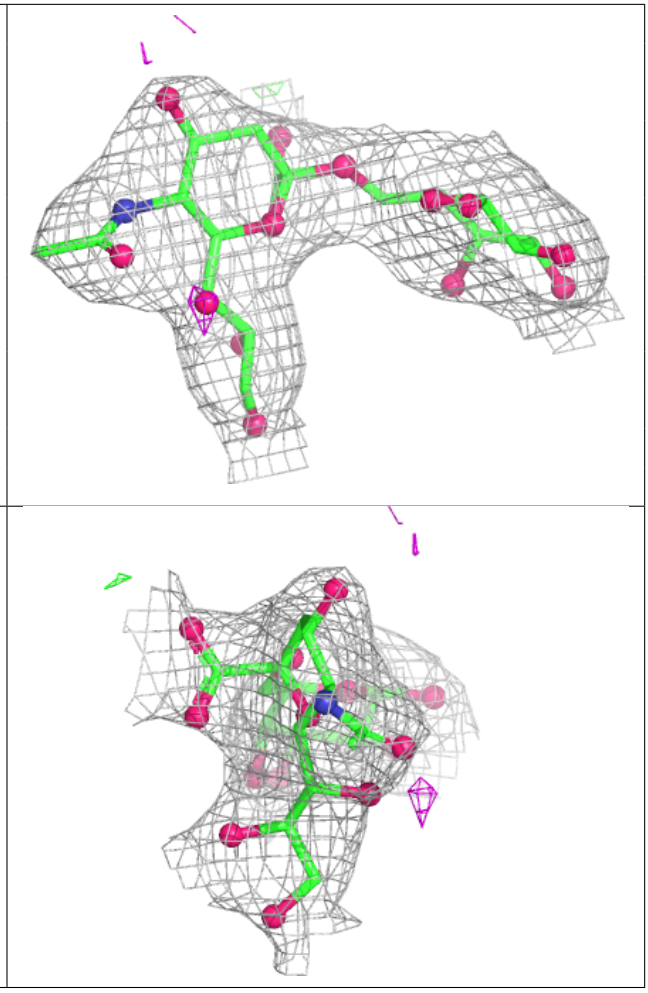
Electron density around Chain E:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around Chain F:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.4 Ligands (i)

There are no ligands in this entry.

6.5 Other polymers (i)

There are no such residues in this entry.