W O R L D W I D E

wwPDB

P R O T E I N   D A T A   B A N K

wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 25, 2023 – 03:24 AM EDT

PDB ID	:	2Z65
Title	:	Crystal structure of the human TLR4 TV3 hybrid-MD-2-Eritoran complex
Authors	:	Lee, J.-O.; Kim, H.M.; Park, B.S.
Deposited on	:	2007-07-22
Resolution	:	2.70 Å(reported)

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

|		
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
buster-report	:	1.1.7 (2018)
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)	:	2.36

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 2.70 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	Percentile Ranks	Value
Rfree		0.282
Clashscore		12
Ramachandran outliers		1.0%
Sidechain outliers		8.0%
RSRZ outliers		2.2%

Worse — *Better*

▮ Percentile relative to all X-ray structures

▯ Percentile relative to X-ray structures of similar resolution
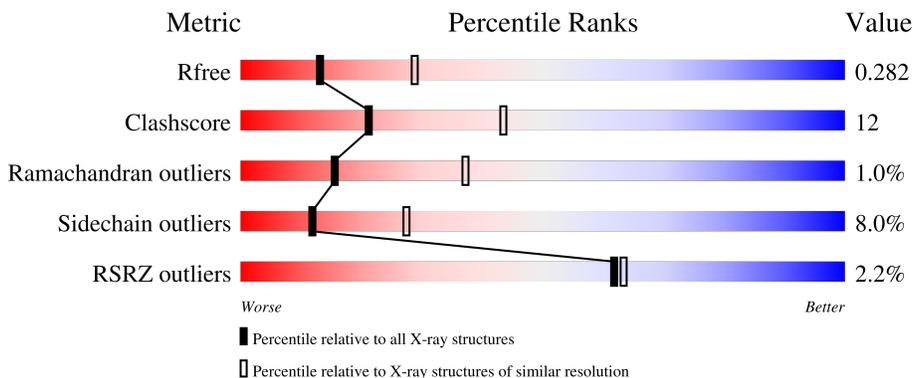
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	2808 (2.70-2.70)
Clashscore	141614	3122 (2.70-2.70)
Ramachandran outliers	138981	3069 (2.70-2.70)
Sidechain outliers	138945	3069 (2.70-2.70)
RSRZ outliers	127900	2737 (2.70-2.70)

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	276	72% / 25% / •
1	B	276	.% / 74% / 24% / •
2	C	140	4% / 64% / 29% / 7%
2	D	140	7% / 66% / 28% / 6%
3	E	3	100%

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PROTEIN DATA BANK

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
4	NAG	A	1201	X	-	-	-
4	NAG	B	1201	X	-	-	-
4	NAG	B	1301	X	-	-	-

2 Entry composition ⓘ

There are 6 unique types of molecules in this entry. The entry contains 7096 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 Toll-like receptor 4, Variable lymphocyte receptor B.

| Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	276	Total 2189	C 1400	N 366	O 412	S 11	0	0	0
1	B	276	Total 2189	C 1400	N 366	O 412	S 11	0	0	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	229	LYS	-	SEE REMARK 999	UNP O00206
A	230	GLU	-	SEE REMARK 999	UNP O00206
B	229	LYS	-	SEE REMARK 999	UNP O00206
B	230	GLU	-	SEE REMARK 999	UNP O00206

- Molecule 2 is a protein called Lymphocyte antigen 96.

| Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	140	Total 1134	C 730	N 186	O 208	S 10	0	0	0
2	D	140	Total 1134	C 730	N 186	O 208	S 10	0	0	0

- Molecule 3 is an oligosaccharide called beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.
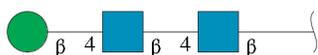
| Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	E	3	Total 39	C 22	N 2	O 15	0	0	0

- Molecule 4 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).
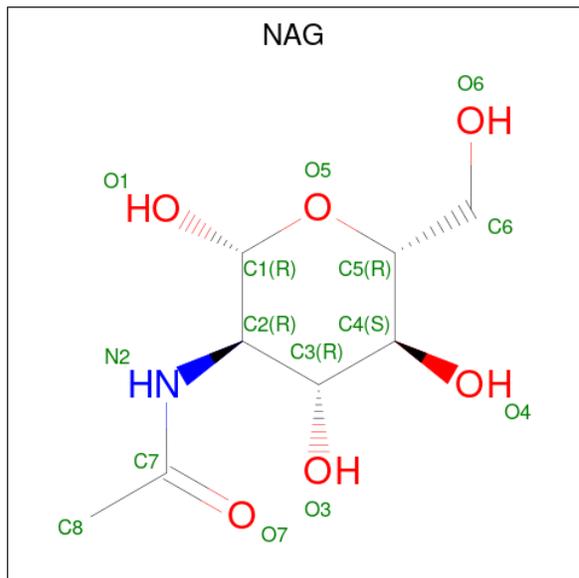
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total 14	C 8	N 1	O 5	0	0
4	A	1	Total 14	C 8	N 1	O 5	0	0
4	B	1	Total 14	C 8	N 1	O 5	0	0
4	B	1	Total 14	C 8	N 1	O 5	0	0
4	B	1	Total 14	C 8	N 1	O 5	0	0

- Molecule 5 is 3-O-DECYL-2-DEOXY-6-O-{2-DEOXY-3-O-[(3R)-3-METHOXYDECYL]-6-O-METHYL-2-[(11Z)-OCTADEC-11-ENOYLAMINO]-4-O-PHOSPHONO-BETA-D-GLUCOPYRANOSYL}-2-[(3-OXOTETRADECANOYL)AMINO]-1-O-PHOSPHONO-ALPHA-D-GLUCOPYRANOSE (three-letter code: E55) (formula: $C_{66}H_{126}N_2O_{19}P_2$).
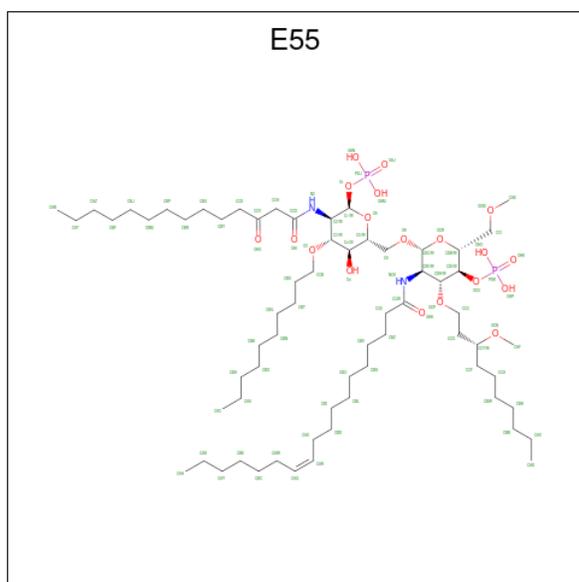
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E55

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	C	1	Total	C	N	O	P	0	0
			89	66	2	19	2		
5	D	1	Total	C	N	O	P	0	0
			89	66	2	19	2		

• Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	45	Total	O	0	0
			45	45		
6	B	54	Total	O	0	0
			54	54		
6	C	22	Total	O	0	0
			22	22		
6	D	42	Total	O	0	0
			42	42		

3 Residue-property plots ⓘ

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: Toll-like receptor 4, Variable lymphocyte receptor B

Chain A:
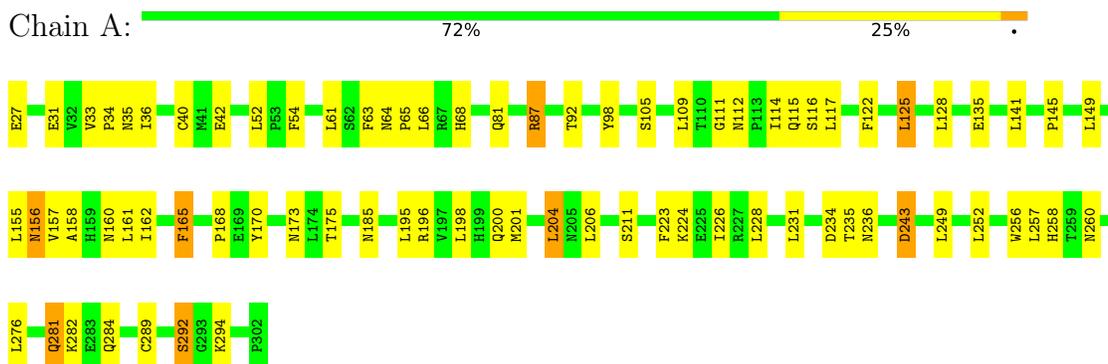
- Molecule 1: Toll-like receptor 4, Variable lymphocyte receptor B

Chain B:

- Molecule 2: Lymphocyte antigen 96

Chain C:

- Molecule 2: Lymphocyte antigen 96

Chain D:
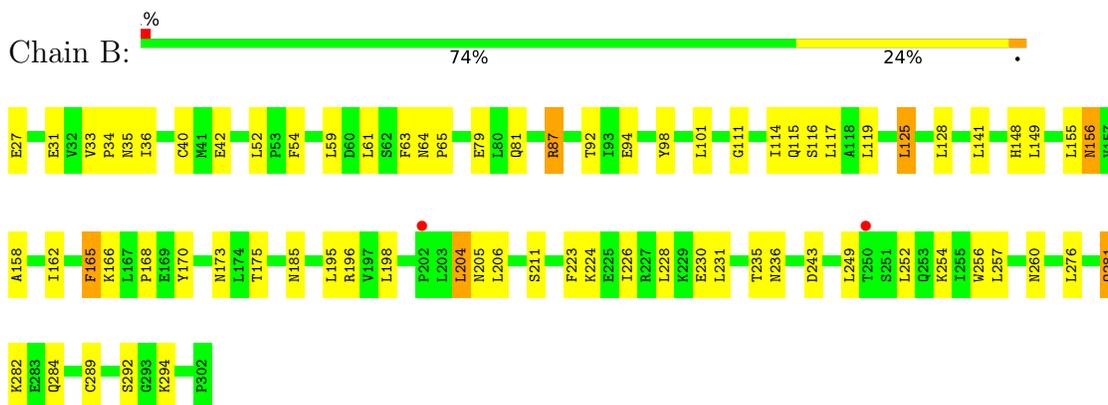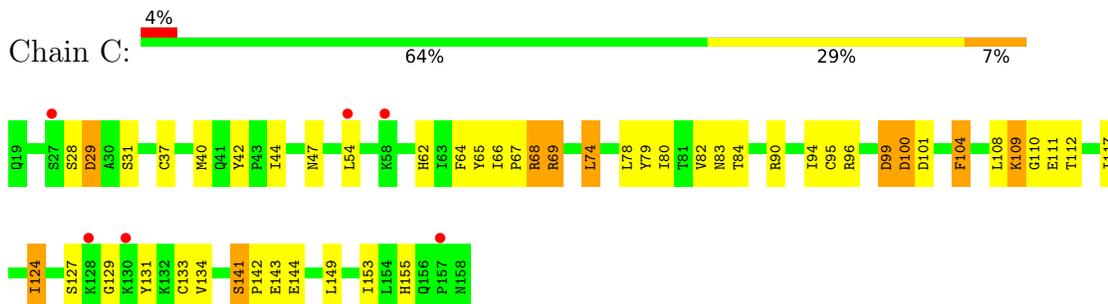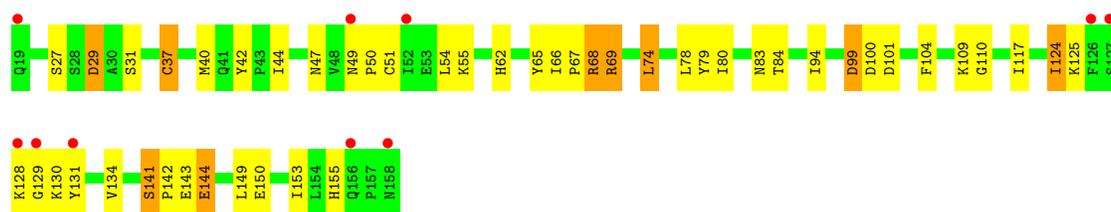
● Molecule 3: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-ac etamido-2-deoxy-beta-D-glucopyranose

Chain E:

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	67.19Å 80.99Å 107.76Å 90.00° 93.01° 90.00°	Depositor
Resolution (Å)	20.00 – 2.70 40.94 – 2.60	Depositor EDS
% Data completeness (in resolution range)	92.3 (20.00-2.70) 86.9 (40.94-2.60)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.09	Depositor
$< I/\sigma(I) >$ [1]	2.29 (at 2.61Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.238 , 0.289 0.231 , 0.282	Depositor DCC
R_{free} test set	1558 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å^2)	57.4	Xtriage
Anisotropy	0.253	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.32 , 44.7	EDS
L-test for twinning[2]	$< |L| > = 0.42, < L^2 > = 0.24$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.92	EDS
Total number of atoms	7096	wwPDB-VP
Average B, all atoms (Å^2)	50.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 10.29% of the height of the origin peak. No significant pseudotranslation is detected.*

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[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 ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: E55, 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	0.46	0/2238	0.62	1/3039 (0.0%)
1	B	0.45	0/2238	0.62	1/3039 (0.0%)
2	C	0.55	0/1160	0.67	0/1562
2	D	0.55	0/1160	0.69	0/1562
All	All	0.49	0/6796	0.64	2/9202 (0.0%)

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
2	C	0	1
2	D	0	1
All	All	0	2

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	155	LEU	CA-CB-CG	6.38	129.96	115.30
1	A	155	LEU	CA-CB-CG	6.12	129.37	115.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	C	141	SER	Peptide
2	D	141	SER	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	2189	0	2193	47	0
1	B	2189	0	2194	43	0
2	C	1134	0	1132	38	0
2	D	1134	0	1132	38	0
3	E	39	0	34	0	0
4	A	28	0	26	0	0
4	B	42	0	39	2	0
5	C	89	0	122	3	0
5	D	89	0	122	3	0
6	A	45	0	0	3	0
6	B	54	0	0	6	0
6	C	22	0	0	0	0
6	D	42	0	0	5	0
All	All	7096	0	6994	166	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 12.

The worst 5 of 166 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)
2:C:127:SER:HB2	2:C:131:TYR:OH	1.56	1.04
2:D:83:ASN:HB2	2:D:129:GLY:HA3	1.51	0.90
2:C:127:SER:CB	2:C:131:TYR:OH	2.21	0.87
2:C:29:ASP:O	2:C:155:HIS:CD2	2.32	0.82
2:D:49:ASN:HB2	6:D:163:HOH:O	1.76	0.82

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	274/276 (99%)	240 (88%)	33 (12%)	1 (0%)	34	60
1	B	274/276 (99%)	240 (88%)	32 (12%)	2 (1%)	22	46
2	C	138/140 (99%)	123 (89%)	13 (9%)	2 (1%)	11	28
2	D	138/140 (99%)	121 (88%)	14 (10%)	3 (2%)	6	17
All	All	824/832 (99%)	724 (88%)	92 (11%)	8 (1%)	15	37

5 of 8 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	C	109	LYS
2	D	109	LYS
2	D	128	LYS
1	A	65	PRO
1	B	65	PRO

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	256/256 (100%)	237 (93%)	19 (7%)	13	32
1	B	256/256 (100%)	238 (93%)	18 (7%)	15	35
2	C	130/130 (100%)	117 (90%)	13 (10%)	7	18
2	D	130/130 (100%)	118 (91%)	12 (9%)	9	21
All	All	772/772 (100%)	710 (92%)	62 (8%)	12	27

5 of 62 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	165	PHE
2	D	69	ARG

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Mol	Chain	Res	Type
1	B	243	ASP
2	D	68	ARG
2	D	100	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 16 such sidechains are listed below:

Mol	Chain	Res	Type
2	D	62	HIS
2	C	155	HIS
1	B	185	ASN
2	C	62	HIS
1	B	156	ASN

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 ⓘ

3 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	$\#|Z| > 2$
3	NAG	E	1	1,3	14,14,15	0.61	0	17,19,21	1.69	2 (11%)
3	NAG	E	2	3	14,14,15	0.79	0	17,19,21	1.30	2 (11%)
3	BMA	E	3	3	11,11,12	0.62	0	15,15,17	2.16	2 (13%)

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
3	NAG	E	1	1,3	-	0/6/23/26	0/1/1/1
3	NAG	E	2	3	-	3/6/23/26	0/1/1/1
3	BMA	E	3	3	-	1/2/19/22	0/1/1/1

There are no bond length outliers.

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	E	3	BMA	C1-O5-C5	6.86	121.49	112.19
3	E	1	NAG	O5-C5-C6	4.38	114.06	107.20
3	E	1	NAG	C4-C3-C2	3.73	116.48	111.02
3	E	2	NAG	C2-N2-C7	3.26	127.54	122.90
3	E	3	BMA	C1-C2-C3	2.72	113.02	109.67

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	E	2	NAG	C3-C2-N2-C7
3	E	2	NAG	C8-C7-N2-C2
3	E	2	NAG	O7-C7-N2-C2
3	E	3	BMA	C4-C5-C6-O6

There are no ring outliers.

No monomer is involved in short contacts.

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 E

Bond lengths

Bond angles

Torsions

Rings
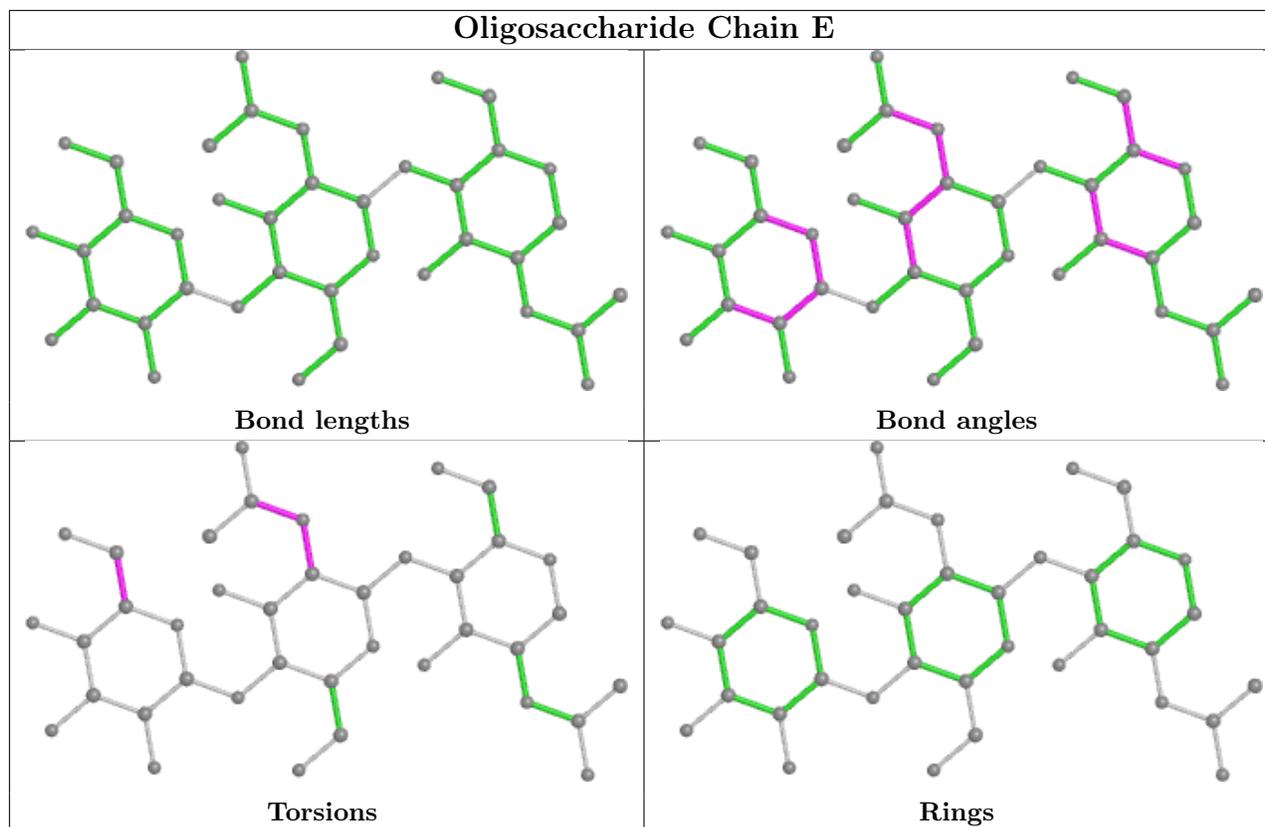
5.6   Ligand geometry ⓘ

7 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	$\#|Z| > 2$
4	NAG	B	1401	-	14,14,15	0.60	0	17,19,21	1.13	1 (5%)
4	NAG	B	1301	1	14,14,15	0.58	0	17,19,21	1.25	1 (5%)
4	NAG	B	1201	1	14,14,15	0.56	0	17,19,21	0.80	0
5	E55	C	1	-	89,90,90	0.83	1 (1%)	106,111,111	1.21	8 (7%)
5	E55	D	1	-	89,90,90	0.84	1 (1%)	106,111,111	1.10	6 (5%)
4	NAG	A	1201	1	14,14,15	0.65	0	17,19,21	1.06	2 (11%)
4	NAG	A	1401	-	14,14,15	0.67	0	17,19,21	1.26	1 (5%)

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	B	1401	-	-	4/6/23/26	0/1/1/1
4	NAG	B	1301	1	1/1/5/7	4/6/23/26	0/1/1/1
4	NAG	B	1201	1	1/1/5/7	4/6/23/26	0/1/1/1
5	E55	C	1	-	-	25/83/124/124	0/2/2/2
5	E55	D	1	-	-	22/83/124/124	0/2/2/2
4	NAG	A	1201	1	1/1/5/7	2/6/23/26	0/1/1/1
4	NAG	A	1401	-	-	4/6/23/26	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	C	1	E55	O6-CDC	2.95	1.45	1.40
5	D	1	E55	PDK-OCU	2.48	1.64	1.59

The worst 5 of 19 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	C	1	E55	O5-C1-O1	-4.74	105.17	111.36
5	C	1	E55	O3-C3-C4	-4.71	99.98	109.83
4	A	1401	NAG	O5-C5-C6	3.85	113.24	107.20
5	D	1	E55	O3-C3-C4	-3.80	101.89	109.83
4	B	1301	NAG	C4-C3-C2	3.46	116.08	111.02

All (3) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
4	A	1201	NAG	C1
4	B	1301	NAG	C1
4	B	1201	NAG	C1

5 of 65 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	1401	NAG	C8-C7-N2-C2
4	A	1401	NAG	O7-C7-N2-C2
4	A	1201	NAG	C8-C7-N2-C2

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Mol	Chain	Res	Type	Atoms
4	A	1201	NAG	O7-C7-N2-C2
4	B	1401	NAG	O7-C7-N2-C2

There are no ring outliers.

4 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	1401	NAG	1	0
4	B	1301	NAG	1	0
5	C	1	E55	3	0
5	D	1	E55	3	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

Ligand E55 C 1

Bond lengths

Bond angles

Torsions

Rings

Ligand E55 D 1

Bond lengths

Bond angles

Torsions

Rings
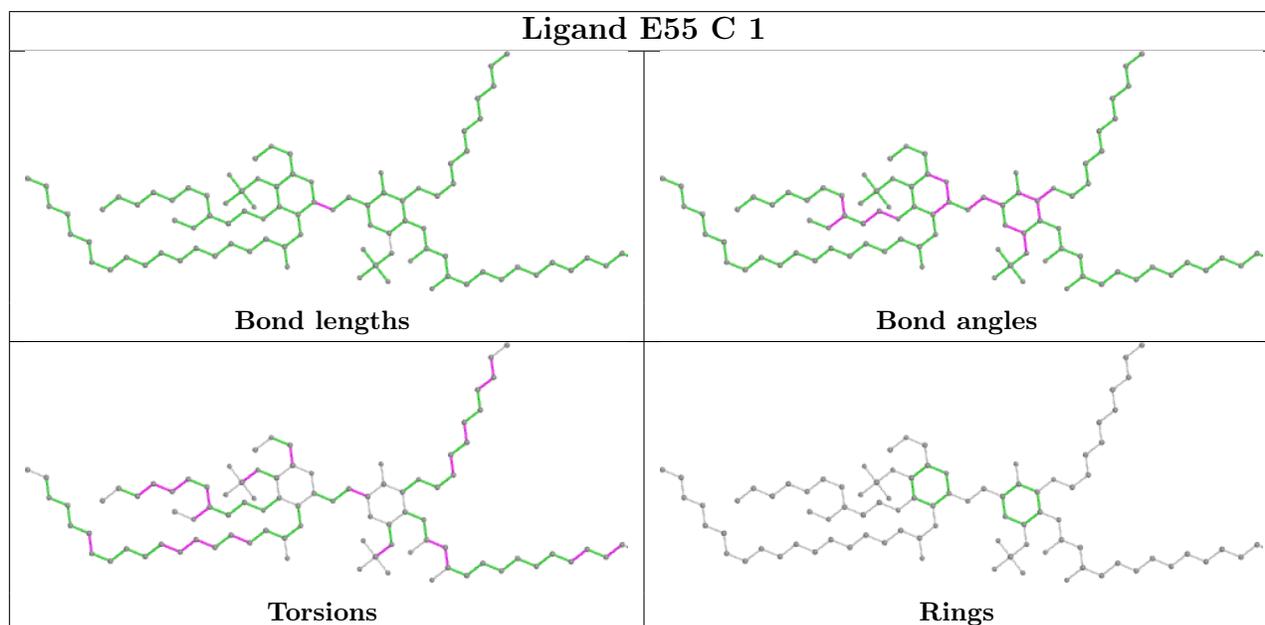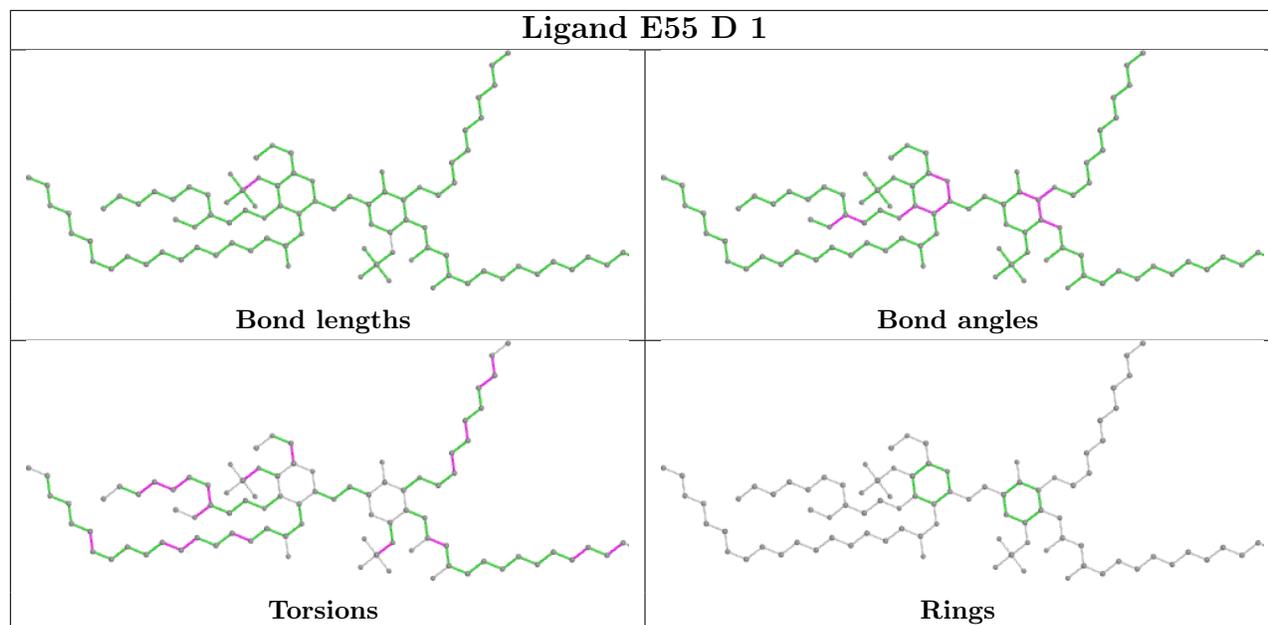
5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

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	276/276 (100%)	-0.14	0	100	100	33, 49, 64, 74	0
1	B	276/276 (100%)	-0.13	2 (0%)	87	89	33, 49, 64, 74	0
2	C	140/140 (100%)	0.25	6 (4%)	35	33	34, 49, 63, 69	0
2	D	140/140 (100%)	0.27	10 (7%)	16	14	32, 49, 66, 68	0
All	All	832/832 (100%)	-0.00	18 (2%)	62	63	32, 49, 64, 74	0

The worst 5 of 18 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	128	LYS	4.4
2	D	129	GLY	4.0
2	D	158	ASN	3.3
2	D	52	ILE	3.2
2	D	156	GLN	3.2

6.2   Non-standard residues in protein, DNA, RNA chains ⓘ

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

6.3   Carbohydrates ⓘ

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
3	BMA	E	3	11/12	0.66	0.20	64,88,106,112	0
3	NAG	E	1	14/15	0.78	0.33	97,108,113,114	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	NAG	E	2	14/15	0.79	0.21	98,111,114,115	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.
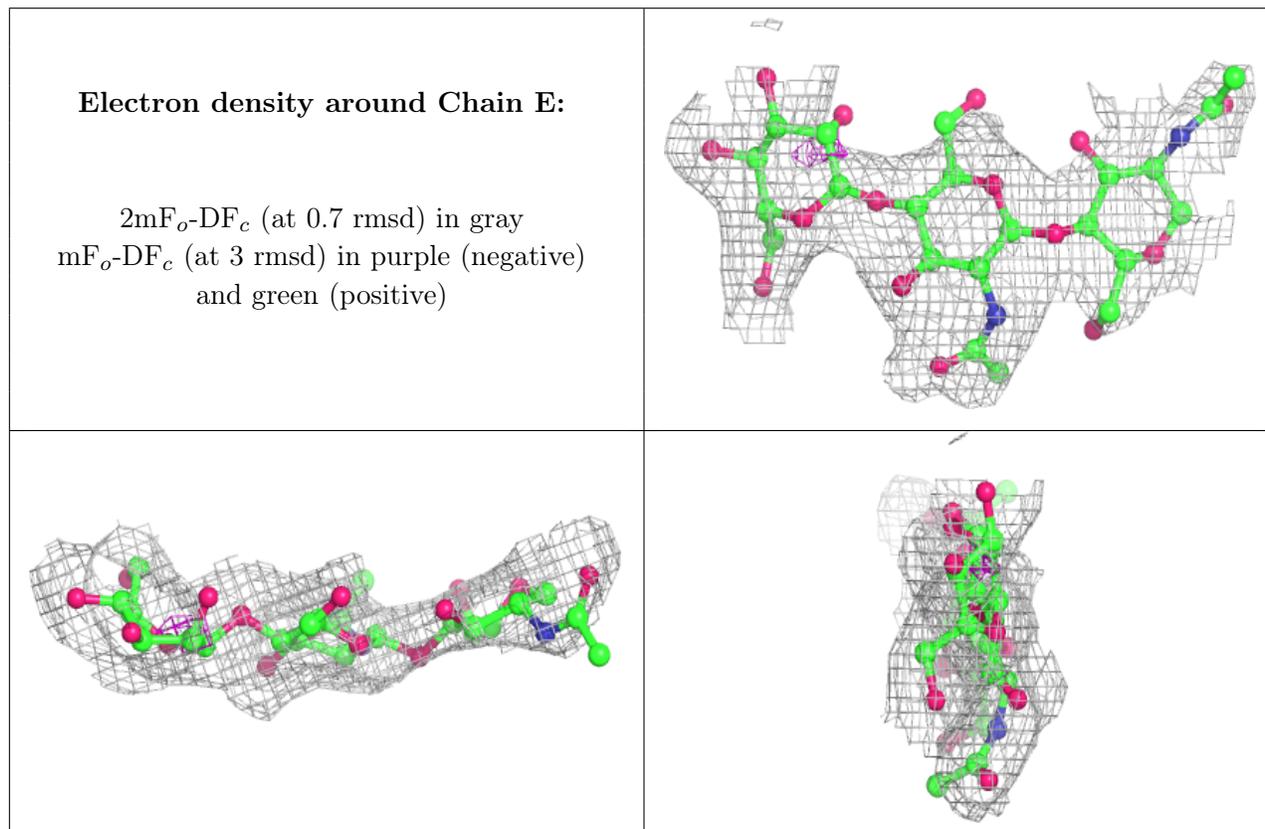

Electron density around Chain E:

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

6.4 Ligands ⓘ

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	B	1201	14/15	0.70	0.21	97,108,116,117	0
4	NAG	B	1301	14/15	0.71	0.24	116,128,138,139	0
4	NAG	A	1201	14/15	0.79	0.19	100,108,114,115	0
4	NAG	B	1401	14/15	0.84	0.14	108,114,120,123	0
4	NAG	A	1401	14/15	0.86	0.13	52,73,89,91	0
5	E55	C	1	89/89	0.95	0.19	23,49,66,73	0
5	E55	D	1	89/89	0.95	0.20	27,49,65,69	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around E55 C 1:

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

Electron density around E55 D 1:

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

6.5 Other polymers ⓘ

There are no such residues in this entry.