



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 03:40 PM UTC

PDB ID : 2H6F / pdb_00002h6f
Title : Protein Farnesyltransferase Complexed with a Farnesylated DDPTASACVLS Peptide Product at 1.5Å Resolution
Authors : Terry, K.L.; Beese, L.S.
Deposited on : 2006-05-31
Resolution : 1.50 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

<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

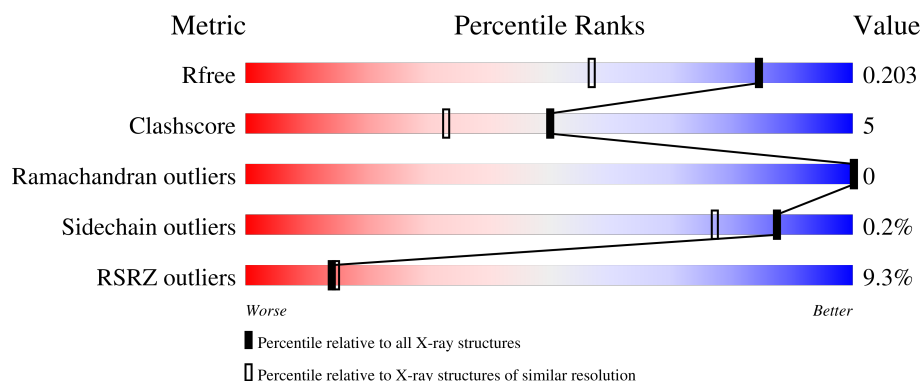
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.50 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	4037 (1.50-1.50)
Clashscore	190562	4235 (1.50-1.50)
Ramachandran outliers	187476	4153 (1.50-1.50)
Sidechain outliers	187428	4150 (1.50-1.50)
RSRZ outliers	180081	4039 (1.50-1.50)

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	382	10% 74% 9% 18%
2	B	437	7% 82% 11% 6%
3	P	11	18% 27% 9% 64%
4	C	2	100%

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
5	ACY	A	3001	-	-	X	-
5	ACY	A	3002	-	-	X	-
5	ACY	B	3003	-	-	X	-
7	FAR	P	2010	-	-	X	-

2 Entry composition [i](#)

There are 8 unique types of molecules in this entry. The entry contains 6717 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 Protein farnesyltransferase/geranylgeranyltransferase type I alpha subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	315	Total	C	N	O	S	0	0	0
			2683	1711	467	500	5			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	380	GLU	-	cloning artifact	UNP P49354
A	381	GLU	-	cloning artifact	UNP P49354
A	382	PHE	-	cloning artifact	UNP P49354

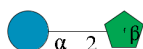
- Molecule 2 is a protein called Protein farnesyltransferase beta subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	410	Total	C	N	O	S	0	0	0
			3228	2065	552	589	22			

- Molecule 3 is a protein called farnesylated peptide.

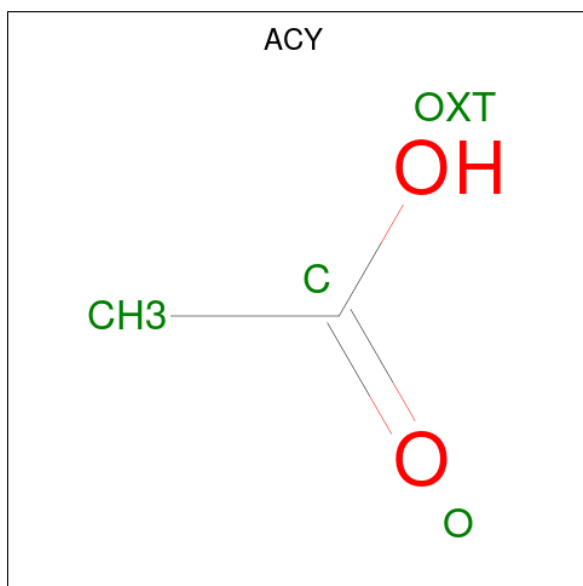
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	P	4	Total	C	N	O	S	0	0	0
			28	17	4	6	1			

- Molecule 4 is an oligosaccharide called beta-D-fructofuranose-(2-1)-alpha-D-glucopyranose.



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
4	C	2	Total	C	O	0	0	0
			23	12	11			

- Molecule 5 is ACETIC ACID (CCD ID: ACY) (formula: C₂H₄O₂).

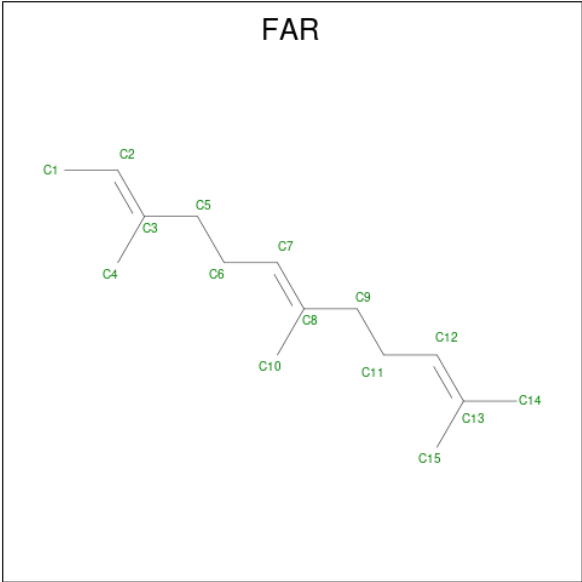


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			4	2	2		
5	A	1	Total	C	O	0	0
			4	2	2		
5	A	1	Total	C	O	0	0
			4	2	2		
5	B	1	Total	C	O	0	0
			4	2	2		
5	B	1	Total	C	O	0	0
			4	2	2		

- Molecule 6 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	B	1	Total	Zn	0	0
			1	1		

- Molecule 7 is FARNESYL (CCD ID: FAR) (formula: C₁₅H₂₆).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	P	1	Total	C	0	0
			15	15		

- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	330	Total	O	0	0
			330	330		
8	B	381	Total	O	0	0
			381	381		
8	P	8	Total	O	0	0
			8	8		

Chain C:

100%

GLU1
FRU2

4 Data and refinement statistics

Property	Value	Source
Space group	P 61	Depositor
Cell constants a, b, c, α , β , γ	178.57Å 178.57Å 64.66Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	38.66 – 1.50 38.66 – 1.50	Depositor EDS
% Data completeness (in resolution range)	98.7 (38.66-1.50) 98.9 (38.66-1.50)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.11 (at 1.50Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.190 , 0.203 0.190 , 0.203	Depositor DCC
R_{free} test set	9297 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å ²)	15.7	Xtriage
Anisotropy	0.006	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 36.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.019 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	6717	wwPDB-VP
Average B, all atoms (Å ²)	18.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.72% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ACY, FAR, ZN, GLC, FRU

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	0.31	0/2750	0.80	8/3735 (0.2%)
2	B	0.33	0/3317	0.84	10/4508 (0.2%)
3	P	0.57	0/27	1.57	1/34 (2.9%)
All	All	0.33	0/6094	0.83	19/8277 (0.2%)

There are no bond length outliers.

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	185	GLU	N-CA-C	8.72	120.47	110.97
3	P	2007	VAL	N-CA-CB	8.53	123.97	111.52
1	A	285	GLN	N-CA-C	7.39	119.33	111.28
2	B	920	VAL	N-CA-C	-7.04	102.05	108.95
2	B	875	HIS	N-CA-C	6.68	119.31	108.41
2	B	851	LEU	N-CA-C	5.90	116.88	108.74
2	B	801	SER	N-CA-C	-5.55	105.33	111.71
2	B	692	LEU	N-CA-C	-5.51	103.11	110.55
1	A	348	LYS	N-CA-C	5.46	119.66	112.89
2	B	795	LEU	N-CA-C	5.37	117.80	110.55
1	A	85	ASN	CA-C-N	5.33	125.27	119.78
1	A	85	ASN	C-N-CA	5.33	125.27	119.78
2	B	903	ILE	N-CA-C	-5.24	100.21	108.90
1	A	367	HIS	N-CA-C	5.18	119.35	112.30
2	B	664	GLY	N-CA-C	5.17	122.31	114.61
1	A	270	VAL	CA-C-N	5.14	125.43	119.47
1	A	270	VAL	C-N-CA	5.14	125.43	119.47
2	B	828	TRP	N-CA-C	-5.13	103.63	110.55
2	B	745	MET	N-CA-C	5.00	117.30	110.55

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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	2683	0	2601	20	0
2	B	3228	0	3147	26	0
3	P	28	0	28	0	0
4	C	23	0	21	0	0
5	A	12	0	9	15	0
5	B	8	0	6	2	0
6	B	1	0	0	0	0
7	P	15	0	24	10	0
8	A	330	0	0	6	0
8	B	381	0	0	4	0
8	P	8	0	0	3	0
All	All	6717	0	5836	63	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 (63) 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)
5:A:3002:ACY:H2	8:P:1691:HOH:O	1.11	1.29
5:B:3003:ACY:H1	8:B:1551:HOH:O	1.10	1.27
5:B:3003:ACY:CH3	8:B:1551:HOH:O	1.75	0.93
5:A:3002:ACY:H3	7:P:2010:FAR:H102	1.50	0.91
2:B:627:CYS:HB3	2:B:671:ILE:HD11	1.52	0.88
5:A:3002:ACY:H3	7:P:2010:FAR:C10	2.04	0.87
5:A:3002:ACY:CH3	8:P:1691:HOH:O	1.88	0.80
2:B:845:CYS:HB2	2:B:851:LEU:HD21	1.66	0.76
5:A:3001:ACY:H3	7:P:2010:FAR:H42	1.69	0.74
1:A:316:VAL:O	1:A:320:GLU:HG3	1.89	0.72
1:A:221:GLN:HG3	8:A:1180:HOH:O	1.90	0.72
5:A:3002:ACY:CH3	7:P:2010:FAR:C10	2.69	0.71
2:B:766:ARG:HH21	2:B:818:GLN:HG2	1.55	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:881:MET:C	2:B:882:LEU:HD12	2.20	0.67
5:A:3002:ACY:CH3	7:P:2010:FAR:H103	2.26	0.66
5:A:3002:ACY:O	7:P:2010:FAR:C4	2.47	0.63
2:B:577:LYS:HD3	2:B:846:PRO:O	2.00	0.62
5:A:3002:ACY:O	7:P:2010:FAR:H41	1.99	0.61
5:A:3001:ACY:H3	7:P:2010:FAR:C4	2.30	0.61
1:A:298:GLN:O	1:A:302:LEU:HD23	2.03	0.59
1:A:303:GLN:N	1:A:304:PRO:HD2	2.20	0.56
1:A:342:GLU:CD	1:A:357:ARG:HH12	2.13	0.56
2:B:739:ILE:HB	2:B:752:THR:HA	1.87	0.56
2:B:801:SER:O	2:B:805:ALA:HB3	2.05	0.56
5:A:3001:ACY:H1	8:A:1438:HOH:O	2.06	0.55
1:A:304:PRO:HG2	8:A:1998:HOH:O	2.10	0.52
2:B:696:GLY:HA2	8:B:1901:HOH:O	2.10	0.51
2:B:763:LYS:HB2	2:B:763:LYS:NZ	2.26	0.51
1:A:335:ASN:O	1:A:339:GLU:HG3	2.12	0.50
1:A:58:LEU:HD11	1:A:126:LEU:HG	1.94	0.50
2:B:692:LEU:HD23	2:B:699:VAL:CG2	2.42	0.49
5:A:3002:ACY:CH3	7:P:2010:FAR:H102	2.30	0.48
1:A:84:PRO:C	1:A:86:PRO:HD3	2.39	0.48
2:B:806:GLY:HA2	2:B:872:ILE:HD13	1.96	0.48
2:B:526:LEU:HD13	2:B:563:LYS:HB2	1.95	0.47
2:B:635:SER:OG	2:B:637:GLU:HG2	2.15	0.47
1:A:354:GLU:HB2	8:A:1697:HOH:O	2.14	0.47
2:B:753:PHE:HA	2:B:807:LEU:HD21	1.97	0.47
5:A:3001:ACY:OXT	8:A:1360:HOH:O	2.19	0.47
2:B:624:THR:O	2:B:628:GLN:HG3	2.14	0.47
2:B:908:VAL:O	2:B:912:THR:HG23	2.14	0.46
2:B:627:CYS:CB	2:B:671:ILE:HD11	2.34	0.46
1:A:96:PHE:HA	1:A:126:LEU:HD13	1.99	0.45
2:B:687:PRO:HG2	8:B:1434:HOH:O	2.16	0.45
2:B:718:THR:HB	2:B:719:PRO:HD2	1.99	0.44
5:A:3002:ACY:C	8:P:1691:HOH:O	2.46	0.44
1:A:109:ARG:HG3	8:A:1256:HOH:O	2.16	0.44
2:B:651:ALA:HB3	2:B:652:PRO:CD	2.47	0.44
5:A:3002:ACY:O	7:P:2010:FAR:H42	2.15	0.44
1:A:109:ARG:HH11	1:A:109:ARG:CB	2.32	0.43
2:B:797:ASP:HB3	2:B:800:TYR:HD1	1.84	0.42
1:A:353:LYS:O	1:A:357:ARG:HG2	2.19	0.42
1:A:58:LEU:HD23	1:A:63:TYR:CZ	2.54	0.42
1:A:264:LEU:O	1:A:268:LYS:HG3	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:311:LEU:C	1:A:311:LEU:HD23	2.45	0.42
2:B:852:ASP:C	2:B:852:ASP:OD1	2.63	0.42
2:B:870:LEU:O	2:B:874:GLN:HG3	2.20	0.41
1:A:87:VAL:O	1:A:88:VAL:C	2.63	0.41
2:B:576:GLU:OE1	2:B:576:GLU:HA	2.20	0.41
1:A:58:LEU:HB2	1:A:125:GLU:OE1	2.21	0.41
1:A:189:ILE:HD11	1:A:205:HIS:HD2	1.86	0.40
2:B:850:LEU:HB2	2:B:863:THR:HA	2.02	0.40
2:B:806:GLY:O	2:B:809:PRO:HD2	2.21	0.40

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	313/382 (82%)	301 (96%)	12 (4%)	0	100	100
2	B	408/437 (93%)	402 (98%)	6 (2%)	0	100	100
3	P	2/11 (18%)	2 (100%)	0	0	100	100
All	All	723/830 (87%)	705 (98%)	18 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	294/344 (86%)	294 (100%)	0	100	100
2	B	346/370 (94%)	345 (100%)	1 (0%)	86	75
3	P	4/9 (44%)	4 (100%)	0	100	100
All	All	644/723 (89%)	643 (100%)	1 (0%)	87	77

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	851	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	81	ASN
1	A	135	HIS
1	A	218	ASN
1	A	221	GLN
1	A	234	ASN
1	A	278	ASN
1	A	297	ASN
1	A	364	GLN
2	B	910	GLN

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 ⓘ

2 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	$\# Z > 2$
4	GLC	C	1	4	11,11,12	2.97	3 (27%)	15,15,17	1.47	3 (20%)
4	FRU	C	2	4	11,12,12	1.41	1 (9%)	10,18,18	0.68	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	GLC	C	1	4	-	0/2/19/22	0/1/1/1
4	FRU	C	2	4	-	0/5/24/24	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	C	1	GLC	C2-C3	8.67	1.65	1.52
4	C	2	FRU	O2-C2	3.71	1.47	1.40
4	C	1	GLC	O5-C5	2.63	1.48	1.43
4	C	1	GLC	C4-C5	2.38	1.58	1.53

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	C	1	GLC	C1-O5-C5	3.93	117.45	112.19
4	C	1	GLC	C1-C2-C3	-2.40	106.15	109.64
4	C	1	GLC	O3-C3-C2	-2.14	105.68	110.05

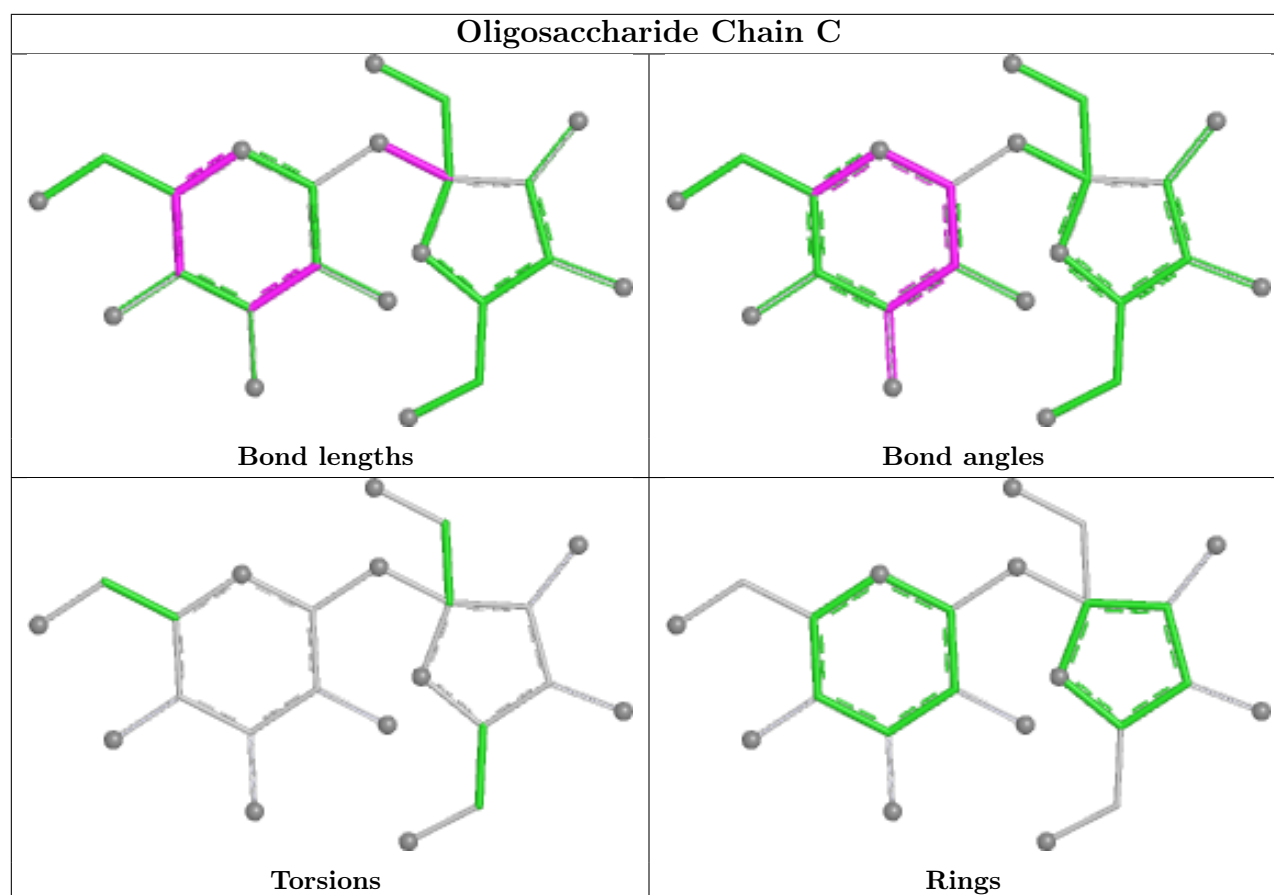
There are no chirality outliers.

There are no torsion outliers.

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.



5.6 Ligand geometry [i](#)

Of 7 ligands modelled in this entry, 1 is monoatomic - leaving 6 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	$\# Z > 2$
5	ACY	B	3003	-	3,3,3	1.26	0	3,3,3	1.61	1 (33%)
5	ACY	B	3005	-	3,3,3	1.28	1 (33%)	3,3,3	1.65	1 (33%)
5	ACY	A	3004	-	3,3,3	1.25	0	3,3,3	1.64	1 (33%)
7	FAR	P	2010	3	14,14,14	0.58	0	15,16,16	0.57	0
5	ACY	A	3002	-	3,3,3	1.26	0	3,3,3	1.60	1 (33%)
5	ACY	A	3001	-	3,3,3	1.27	0	3,3,3	1.61	1 (33%)

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
7	FAR	P	2010	3	-	1/14/14/14	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	3005	ACY	O-C	2.02	1.31	1.22

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	B	3005	ACY	O-C-CH3	-2.24	113.33	122.53
5	A	3004	ACY	O-C-CH3	-2.23	113.37	122.53
5	A	3001	ACY	O-C-CH3	-2.20	113.53	122.53
5	B	3003	ACY	O-C-CH3	-2.19	113.56	122.53
5	A	3002	ACY	O-C-CH3	-2.18	113.58	122.53

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	P	2010	FAR	C9-C11-C12-C13

There are no ring outliers.

4 monomers are involved in 17 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	3003	ACY	2	0
7	P	2010	FAR	10	0
5	A	3002	ACY	11	0
5	A	3001	ACY	4	0

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	315/382 (82%)	0.79	37 (11%) 9 9	11, 19, 33, 48	0
2	B	410/437 (93%)	0.18	29 (7%) 22 24	9, 14, 24, 34	0
3	P	4/11 (36%)	1.93	2 (50%) 0 0	13, 16, 22, 25	0
All	All	729/830 (87%)	0.45	68 (9%) 14 15	9, 16, 28, 48	0

All (68) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	55	PHE	10.0
1	A	369	THR	7.9
1	A	56	VAL	5.5
1	A	368	SER	5.1
2	B	515	SER	5.1
1	A	307	SER	4.8
1	A	303	GLN	4.7
1	A	58	LEU	4.6
3	P	2006	CYS	4.6
1	A	300	LEU	4.4
2	B	924	GLU	4.4
1	A	328	ASP	4.3
2	B	880	ALA	4.2
1	A	301	ASP	4.1
2	B	879	GLY	4.0
1	A	302	LEU	4.0
1	A	304	PRO	3.9
1	A	59	ASP	3.8
2	B	819	GLY	3.7
2	B	618	ILE	3.5
1	A	326	GLN	3.5
2	B	620	GLN	3.4
2	B	923	PHE	3.3

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Mol	Chain	Res	Type	RSRZ
1	A	306	HIS	3.3
1	A	57	SER	3.2
1	A	109	ARG	3.2
1	A	305	SER	3.2
2	B	881	MET	3.2
2	B	516	SER	3.1
2	B	588	GLN	3.1
2	B	917	GLN	3.0
1	A	329	ASN	2.9
2	B	532	ARG	2.9
2	B	766	ARG	2.8
1	A	299	LEU	2.8
3	P	2007	VAL	2.7
2	B	576	GLU	2.7
1	A	81	ASN	2.7
1	A	327	CYS	2.7
1	A	330	LYS	2.6
1	A	346	LYS	2.6
1	A	150	GLU	2.6
1	A	145	GLN	2.6
2	B	825	MET	2.6
2	B	818	GLN	2.5
2	B	846	PRO	2.5
2	B	877	GLY	2.5
1	A	342	GLU	2.4
2	B	817	ALA	2.4
1	A	75	ILE	2.4
2	B	671	ILE	2.4
2	B	617	PRO	2.3
2	B	813	ARG	2.3
1	A	268	LYS	2.3
2	B	719	PRO	2.3
1	A	73	ALA	2.2
1	A	367	HIS	2.2
1	A	164	LYS	2.2
1	A	325	ASN	2.2
2	B	527	ARG	2.1
2	B	878	SER	2.1
1	A	225	GLN	2.1
2	B	851	LEU	2.1
1	A	262	TYR	2.1
1	A	286	ASP	2.1

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Mol	Chain	Res	Type	RSRZ
2	B	592	ALA	2.0
2	B	553	GLU	2.0
1	A	297	ASN	2.0

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

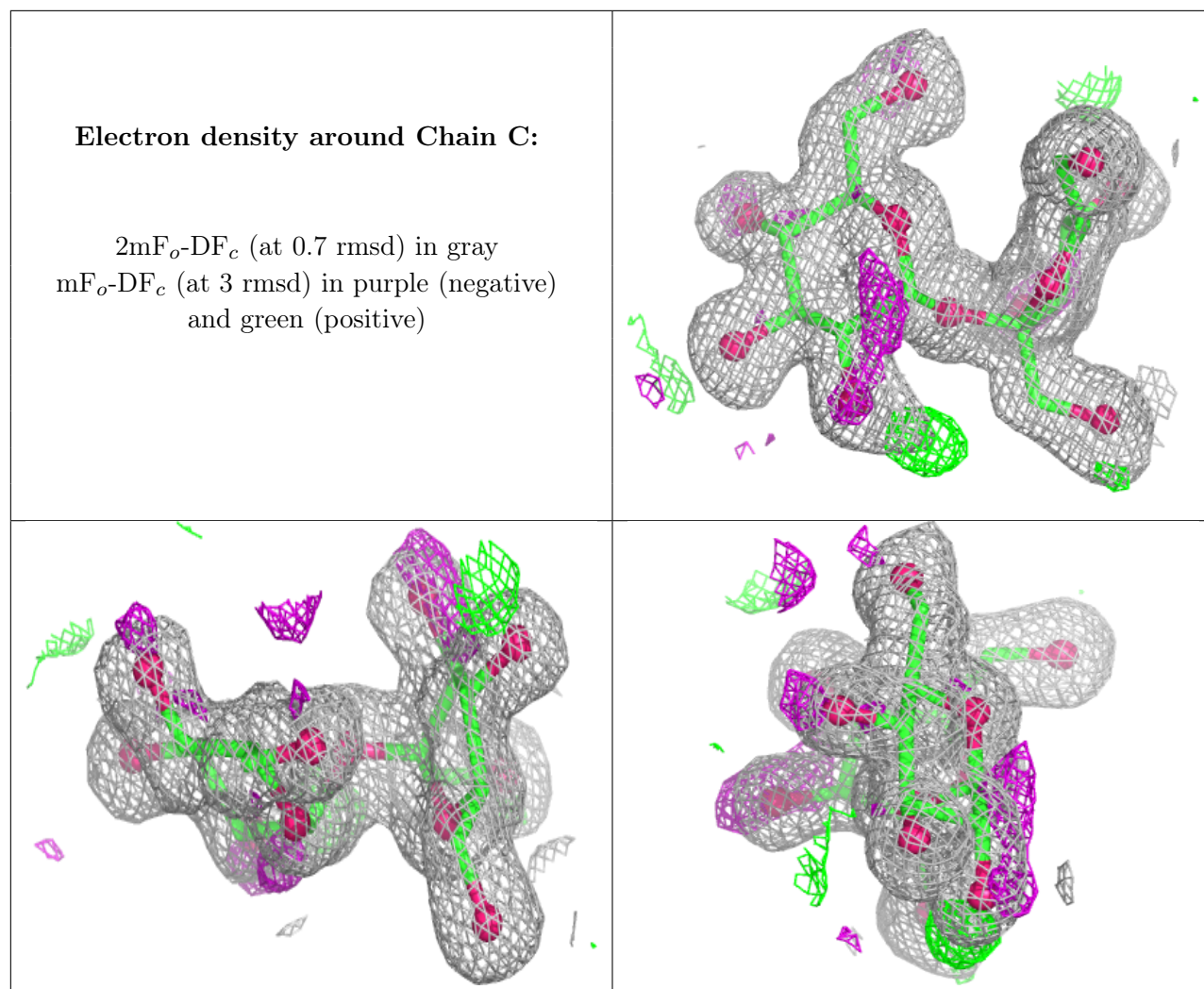
There are no non-standard protein/DNA/RNA residues in this entry.

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($\text{\AA}^2$)	Q<0.9
4	GLC	C	1	11/12	-	-	20,20,21,21	0
4	FRU	C	2	12/12	-	-	17,19,20,20	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.



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($\text{\AA}^2$)	Q<0.9
5	ACY	A	3001	4/4	0.77	0.23	40,41,41,41	0
5	ACY	B	3003	4/4	0.77	0.21	40,41,41,41	0
5	ACY	A	3002	4/4	0.78	0.17	40,41,41,41	0
5	ACY	B	3005	4/4	0.78	0.25	37,37,38,38	0
7	FAR	P	2010	15/15	0.90	0.12	16,19,24,24	0
5	ACY	A	3004	4/4	0.98	0.07	15,15,15,15	0
6	ZN	B	1001	1/1	1.00	0.03	13,13,13,13	0

6.5 Other polymers [i](#)

There are no such residues in this entry.