



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 18, 2026 – 03:54 AM UTC

PDB ID : 4OBZ / pdb_00004obz
Title : Structure of Cathepsin D with inhibitor 2-(3,4-dimethoxyphenyl)-N-[N-(4-methylbenzyl)carbamimidoyl]acetamide
Authors : Graedler, U.; Czodrowski, P.; Tsaklakis, C.; Klein, M.; Maskos, K.; Leuthner, B.
Deposited on : 2014-01-08
Resolution : 2.90 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
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
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

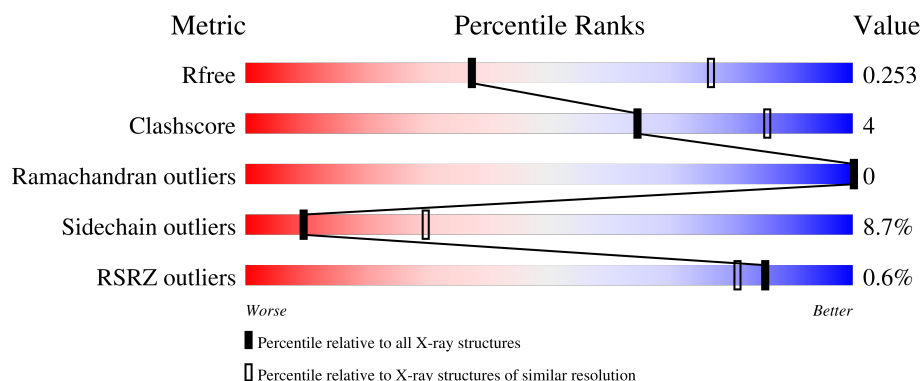
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

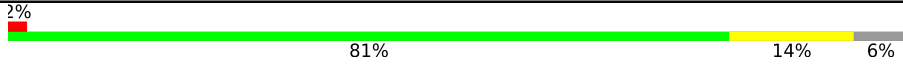
The reported resolution of this entry is 2.90 Å.

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.



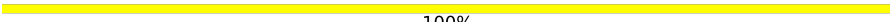
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	2481 (2.90-2.90)
Clashscore	190562	2690 (2.90-2.90)
Ramachandran outliers	187476	2623 (2.90-2.90)
Sidechain outliers	187428	2625 (2.90-2.90)
RSRZ outliers	180081	2481 (2.90-2.90)

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	103	
1	C	103	
2	B	243	
2	D	243	

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Mol	Chain	Length	Quality of chain
3	E	2	 100%

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 5307 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 Cathepsin D light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	97	Total	C	N	O	S	0	0	0
			753	481	120	147	5			
1	C	103	Total	C	N	O	S	0	0	0
			792	505	126	156	5			

- Molecule 2 is a protein called Cathepsin D heavy chain.

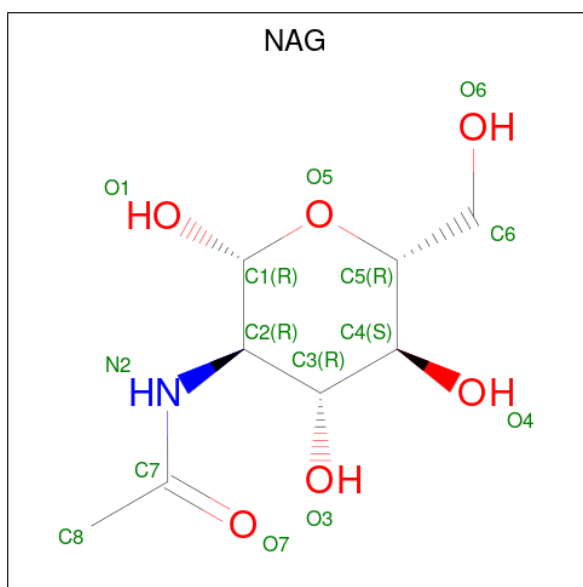
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	240	Total	C	N	O	S	0	0	0
			1840	1182	301	346	11			
2	D	237	Total	C	N	O	S	0	0	0
			1817	1168	296	342	11			

- Molecule 3 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



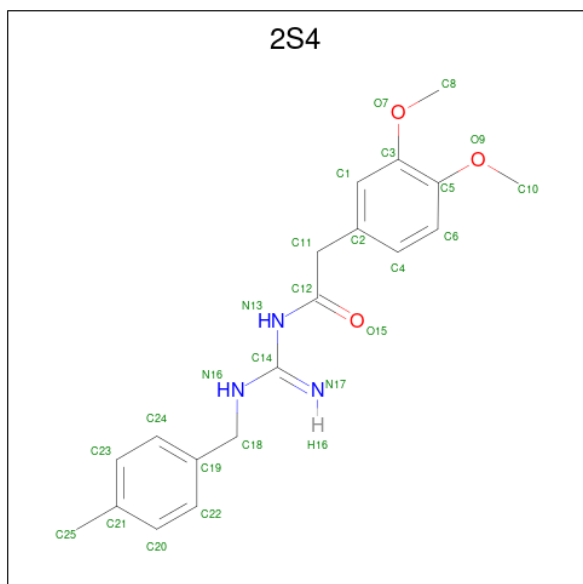
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	E	2	Total	C	N	O	0	0	0
			28	16	2	10			

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



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

- Molecule 5 is 2-(3,4-dimethoxyphenyl)-N-[N-(4-methylbenzyl)carbamimidoyl]acetamide (CCD ID: 2S4) (formula: $C_{19}H_{23}N_3O_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	B	1	Total	C	N	O	0	0
			25	19	3	3		

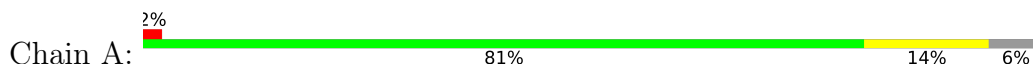
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	8	Total 8	O 8	0	0
6	B	6	Total 6	O 6	0	0
6	C	5	Total 5	O 5	0	0
6	D	19	Total 19	O 19	0	0

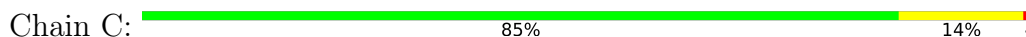
3 Residue-property plots [i](#)

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.

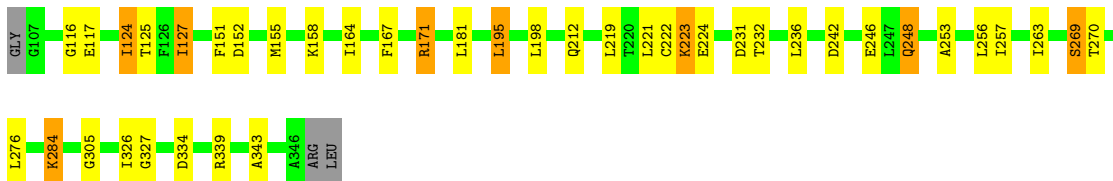
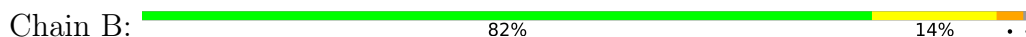
- Molecule 1: Cathepsin D light chain



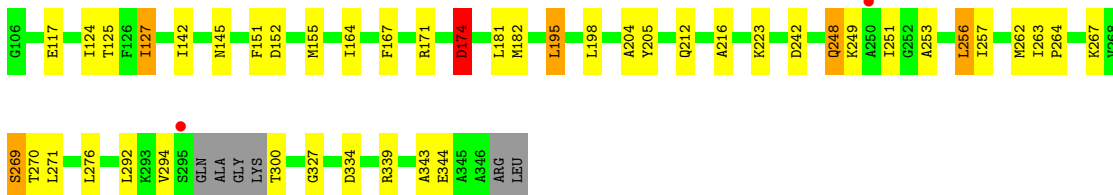
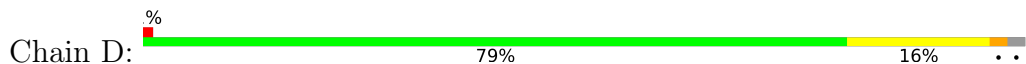
- Molecule 1: Cathepsin D light chain



- Molecule 2: Cathepsin D heavy chain



- Molecule 2: Cathepsin D heavy chain



- Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain E:

100%

MAG1
MAG2

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	230.34Å 42.45Å 73.22Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	45.26 – 2.90 45.26 – 2.90	Depositor EDS
% Data completeness (in resolution range)	98.9 (45.26-2.90) 98.9 (45.26-2.90)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.62 (at 2.90Å)	Xtriage
Refinement program	BUSTER 2.11.4	Depositor
R, R_{free}	0.177 , 0.233 0.191 , 0.253	Depositor DCC
R_{free} test set	678 reflections (4.09%)	wwPDB-VP
Wilson B-factor (Å ²)	54.0	Xtriage
Anisotropy	0.466	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 69.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.26$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	5307	wwPDB-VP
Average B, all atoms (Å ²)	55.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.15% 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: 2S4, 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	0.79	0/776	1.23	6/1058 (0.6%)
1	C	0.90	0/816	1.37	8/1114 (0.7%)
2	B	0.83	0/1879	1.28	8/2546 (0.3%)
2	D	0.86	0/1855	1.32	11/2513 (0.4%)
All	All	0.85	0/5326	1.30	33/7231 (0.5%)

There are no bond length outliers.

All (33) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	70	ASN	OD1-CG-ND2	-11.17	111.43	122.60
1	C	70	ASN	CB-CG-ND2	10.64	132.36	116.40
2	D	174	ASP	CA-CB-CG	9.32	121.92	112.60
2	D	269	SER	CA-C-N	7.75	133.00	120.60
2	D	269	SER	C-N-CA	7.75	133.00	120.60
2	D	127	ILE	CA-C-N	6.53	129.36	120.54
2	D	127	ILE	C-N-CA	6.53	129.36	120.54
2	B	269	SER	CA-C-N	6.52	131.03	120.60
2	B	269	SER	C-N-CA	6.52	131.03	120.60
2	B	127	ILE	CA-C-N	6.23	128.95	120.54
2	B	127	ILE	C-N-CA	6.23	128.95	120.54
1	C	9	ASN	CA-CB-CG	6.20	118.80	112.60
1	C	70	ASN	N-CA-C	-6.03	105.00	112.72
1	C	33	ASP	CA-CB-CG	5.97	118.57	112.60
1	A	33	ASP	CA-CB-CG	5.95	118.55	112.60
1	C	52	ALA	CA-C-N	5.55	127.98	120.38
1	C	52	ALA	C-N-CA	5.55	127.98	120.38
2	D	216	ALA	CA-C-N	5.48	128.18	120.28
2	D	216	ALA	C-N-CA	5.48	128.18	120.28
1	A	9	ASN	CA-CB-CG	5.46	118.06	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	205	TYR	N-CA-C	-5.45	101.93	110.17
2	D	127	ILE	N-CA-C	-5.38	105.36	110.42
1	A	79	GLY	CA-C-N	5.37	127.42	120.44
1	A	79	GLY	C-N-CA	5.37	127.42	120.44
2	B	127	ILE	N-CA-C	-5.32	105.42	110.42
1	A	52	ALA	CA-C-N	5.29	127.64	120.38
1	A	52	ALA	C-N-CA	5.29	127.64	120.38
2	B	219	LEU	N-CA-C	5.17	117.18	109.59
1	C	81	GLY	N-CA-C	5.12	118.75	111.12
2	D	249	LYS	CA-C-N	5.02	127.50	120.28
2	D	249	LYS	C-N-CA	5.02	127.50	120.28
2	B	246	GLU	CA-C-N	5.00	127.30	120.54
2	B	246	GLU	C-N-CA	5.00	127.30	120.54

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	753	0	708	5	0
1	C	792	0	747	3	0
2	B	1840	0	1847	19	0
2	D	1817	0	1820	20	0
3	E	28	0	25	1	0
4	A	14	0	13	0	0
5	B	25	0	22	2	0
6	A	8	0	0	0	0
6	B	6	0	0	0	0
6	C	5	0	0	0	0
6	D	19	0	0	0	0
All	All	5307	0	5182	41	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 4.

All (41) 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:A:77:HIS:CE1	2:D:174:ASP:HB2	2.29	0.67
1:C:43:SER:HB2	2:D:117:GLU:HB3	1.79	0.63
2:D:195:LEU:HD13	2:D:343:ALA:HB2	1.81	0.61
2:D:248:GLN:HG2	2:D:253:ALA:HB3	1.83	0.59
2:B:284:LYS:HD3	2:B:284:LYS:H	1.68	0.58
2:B:248:GLN:HG2	2:B:253:ALA:HB3	1.85	0.57
1:A:77:HIS:HE1	2:D:174:ASP:HB2	1.73	0.54
2:B:195:LEU:HD13	2:B:343:ALA:HB2	1.90	0.53
2:D:171:ARG:HD3	2:D:327:GLY:HA3	1.89	0.53
2:D:256:LEU:HD12	2:D:257:ILE:H	1.74	0.53
2:B:152:ASP:HA	2:B:155:MET:HE3	1.91	0.51
2:D:124:ILE:HA	2:D:127:ILE:HD12	1.91	0.51
2:B:124:ILE:HA	2:B:127:ILE:HD12	1.93	0.51
2:D:152:ASP:HA	2:D:155:MET:HE3	1.93	0.50
2:B:171:ARG:HD2	2:B:327:GLY:HA3	1.93	0.50
2:B:231:ASP:OD2	5:B:401:2S4:N17	2.44	0.50
1:A:43:SER:HB2	2:B:117:GLU:HB3	1.94	0.49
1:C:70:ASN:OD1	1:C:87:LEU:HB2	2.12	0.48
2:D:256:LEU:HD21	2:D:262:MET:HE3	1.95	0.48
2:B:164:ILE:HG22	2:B:334:ASP:HA	1.96	0.47
2:D:256:LEU:CD1	2:D:257:ILE:H	2.28	0.46
2:B:236:LEU:HD22	2:B:305:GLY:HA2	1.99	0.45
2:B:253:ALA:HB2	2:B:263:ILE:HG12	1.99	0.45
2:B:167:PHE:CZ	2:B:181:LEU:HD13	2.52	0.44
1:A:11:MET:HE2	1:A:11:MET:HA	2.00	0.44
2:D:164:ILE:HG22	2:D:334:ASP:HA	2.00	0.44
2:D:253:ALA:HB2	2:D:263:ILE:HG12	1.99	0.44
2:D:264:PRO:HG2	2:D:267:LYS:HE2	1.99	0.44
2:B:248:GLN:HE21	2:B:248:GLN:HB2	1.66	0.43
1:C:2:PRO:HB2	2:D:182:MET:SD	2.59	0.43
2:B:222:CYS:SG	2:B:222:CYS:O	2.76	0.43
2:D:142:ILE:HG23	2:D:204:ALA:HB1	2.01	0.42
2:B:223:LYS:H	2:B:223:LYS:HG2	1.60	0.42
2:B:151:PHE:HD2	2:B:155:MET:HE2	1.85	0.42
2:B:231:ASP:OD2	5:B:401:2S4:H18	2.20	0.42
2:D:151:PHE:HD2	2:D:155:MET:HE2	1.85	0.42
2:D:145:ASN:O	3:E:2:NAG:H83	2.19	0.42
2:D:167:PHE:CZ	2:D:181:LEU:HD13	2.55	0.42
2:D:251:ILE:HB	2:D:271:LEU:HD22	2.02	0.42
2:B:232:THR:HG22	2:B:326:ILE:HD13	2.03	0.41
1:A:40:TRP:HA	2:B:116:GLY:O	2.21	0.40

There are no symmetry-related clashes.

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	95/103 (92%)	93 (98%)	2 (2%)	0	100	100
1	C	101/103 (98%)	100 (99%)	1 (1%)	0	100	100
2	B	238/243 (98%)	228 (96%)	10 (4%)	0	100	100
2	D	233/243 (96%)	223 (96%)	10 (4%)	0	100	100
All	All	667/692 (96%)	644 (97%)	23 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	87/91 (96%)	81 (93%)	6 (7%)	14	41
1	C	91/91 (100%)	83 (91%)	8 (9%)	9	29
2	B	199/201 (99%)	180 (90%)	19 (10%)	8	26
2	D	197/201 (98%)	180 (91%)	17 (9%)	10	30
All	All	574/584 (98%)	524 (91%)	50 (9%)	9	30

All (50) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	47	LYS
1	A	53	CYS
1	A	75	ASP
1	A	82	SER
1	A	83	LEU
1	A	93	SER
2	B	124	ILE
2	B	125	THR
2	B	158	LYS
2	B	171	ARG
2	B	195	LEU
2	B	198	LEU
2	B	212	GLN
2	B	221	LEU
2	B	223	LYS
2	B	224	GLU
2	B	242	ASP
2	B	248	GLN
2	B	256	LEU
2	B	257	ILE
2	B	269	SER
2	B	270	THR
2	B	276	LEU
2	B	284	LYS
2	B	339	ARG
1	C	11	MET
1	C	48	LEU
1	C	69	LYS
1	C	70	ASN
1	C	76	ILE
1	C	83	LEU
1	C	84	SER
1	C	93	SER
2	D	125	THR
2	D	174	ASP
2	D	195	LEU
2	D	198	LEU
2	D	212	GLN
2	D	223	LYS
2	D	242	ASP
2	D	248	GLN
2	D	256	LEU
2	D	269	SER

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Mol	Chain	Res	Type
2	D	270	THR
2	D	276	LEU
2	D	292	LEU
2	D	294	VAL
2	D	300	THR
2	D	339	ARG
2	D	344	GLU

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	45	HIS
2	B	162	GLN
2	B	163	ASN
2	B	338	ASN
1	C	45	HIS
2	D	163	ASN
2	D	176	GLN
2	D	337	ASN
2	D	338	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](#)

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
3	NAG	E	1	3,1	14,14,15	0.49	0	17,19,21	1.46	1 (5%)
3	NAG	E	2	3	14,14,15	0.38	0	17,19,21	0.89	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
3	NAG	E	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	E	2	3	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
3	E	1	NAG	C1-O5-C5	-5.02	105.45	112.19

There are no chirality outliers.

All (2) torsion outliers are listed below:

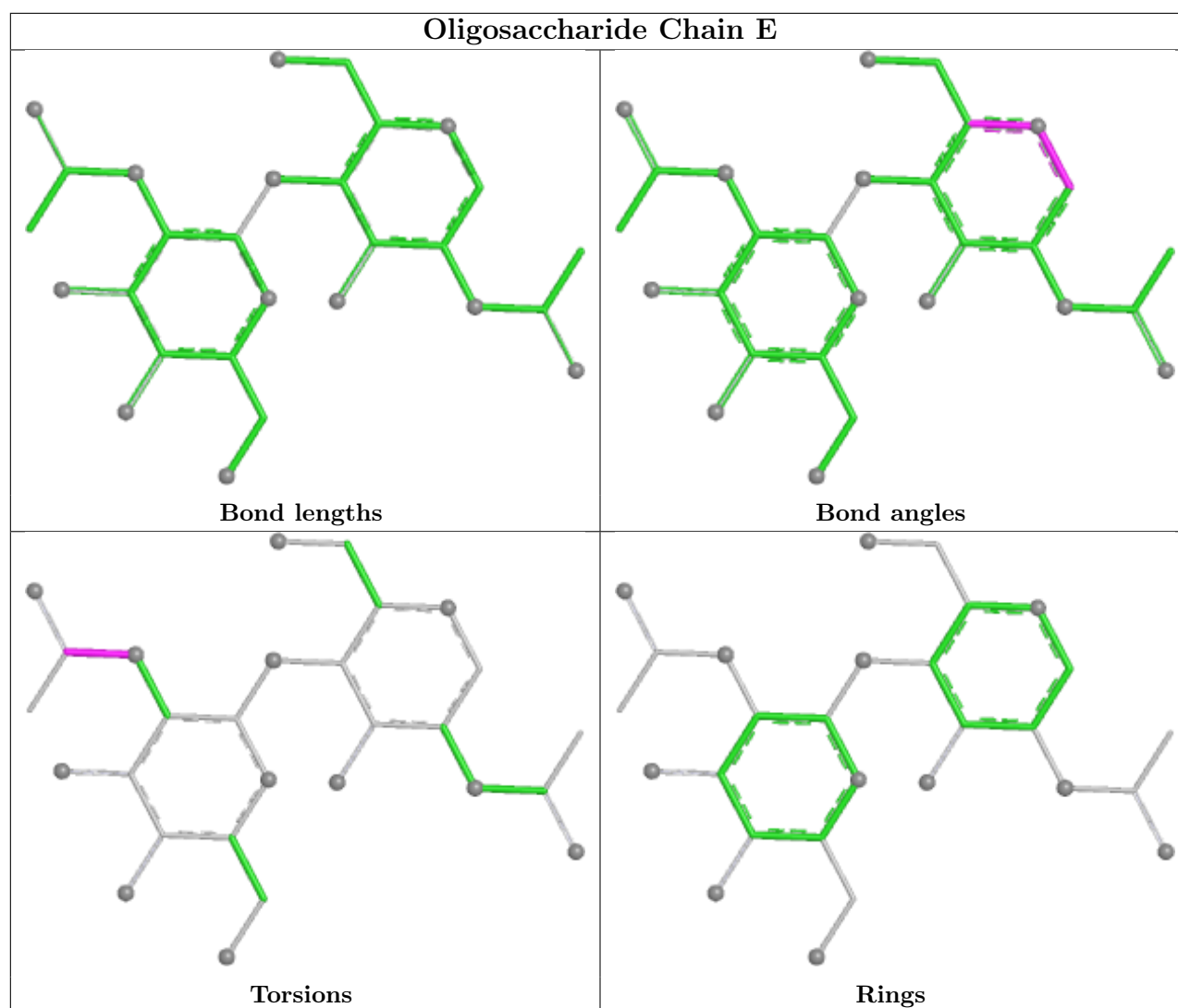
Mol	Chain	Res	Type	Atoms
3	E	2	NAG	C8-C7-N2-C2
3	E	2	NAG	O7-C7-N2-C2

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	E	2	NAG	1	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.



5.6 Ligand geometry [i](#)

2 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	$\# Z > 2$
5	2S4	B	401	-	24,26,26	0.67	0	33,34,34	2.32	12 (36%)
4	NAG	A	400	1	14,14,15	0.35	0	17,19,21	0.85	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
5	2S4	B	401	-	-	2/17/17/17	0/2/2/2
4	NAG	A	400	1	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	B	401	2S4	C10-O9-C5	5.85	126.10	117.51
5	B	401	2S4	O9-C5-C3	5.38	122.70	115.40
5	B	401	2S4	O7-C3-C5	3.80	120.56	115.40
5	B	401	2S4	O7-C3-C1	-3.47	118.10	124.08
5	B	401	2S4	O9-C5-C6	-3.30	118.73	124.30
5	B	401	2S4	N13-C14-N16	3.22	126.35	118.08
5	B	401	2S4	C8-O7-C3	3.13	122.11	117.51
5	B	401	2S4	C19-C18-N16	2.83	119.04	113.07
4	A	400	NAG	C1-O5-C5	2.69	115.79	112.19
5	B	401	2S4	C11-C2-C4	-2.44	117.30	120.89
5	B	401	2S4	C18-C19-C22	-2.24	116.37	120.94
5	B	401	2S4	C24-C23-C21	-2.17	118.87	121.37
5	B	401	2S4	C11-C12-N13	2.11	116.98	114.40

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	B	401	2S4	C1-C3-O7-C8
5	B	401	2S4	C5-C3-O7-C8

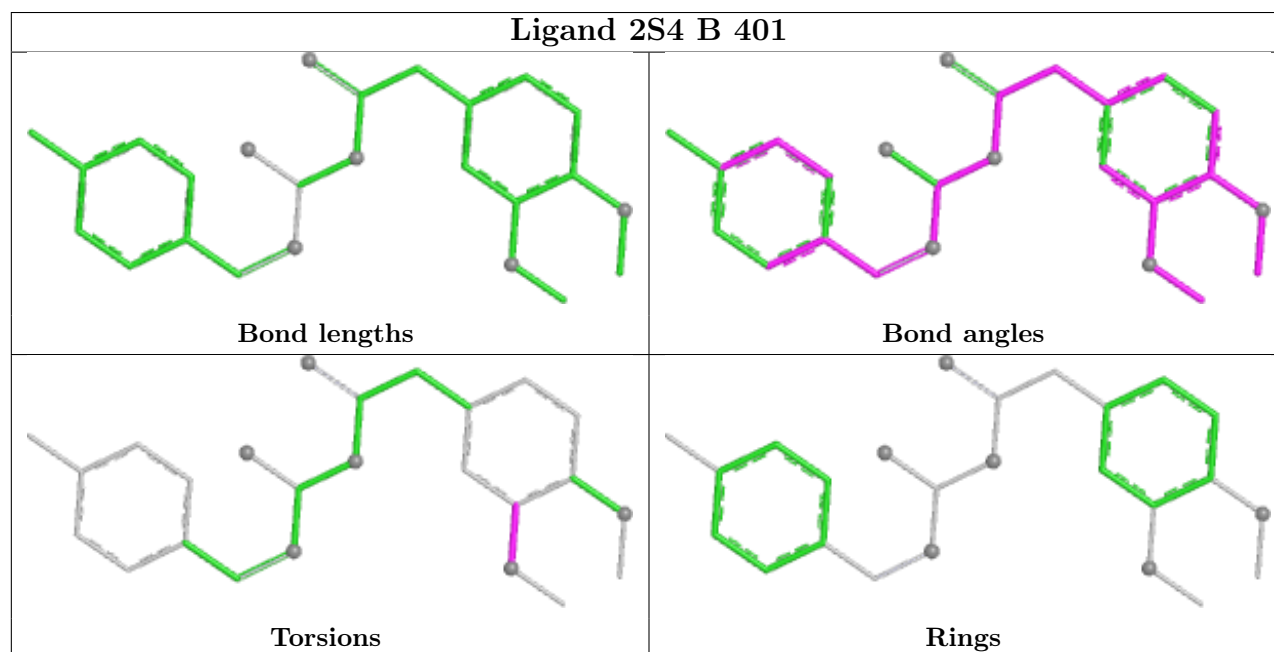
There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	401	2S4	2	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 than 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.



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	97/103 (94%)	-0.28	2 (2%) 63 54	31, 51, 79, 93	0
1	C	103/103 (100%)	-0.30	0 100 100	30, 51, 71, 78	0
2	B	240/243 (98%)	-0.16	0 100 100	30, 61, 85, 105	0
2	D	237/243 (97%)	-0.27	2 (0%) 82 77	23, 49, 72, 96	0
All	All	677/692 (97%)	-0.24	4 (0%) 85 81	23, 54, 79, 105	0

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	80	SER	2.6
2	D	295	SER	2.3
1	A	98	SER	2.2
2	D	250	ALA	2.1

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

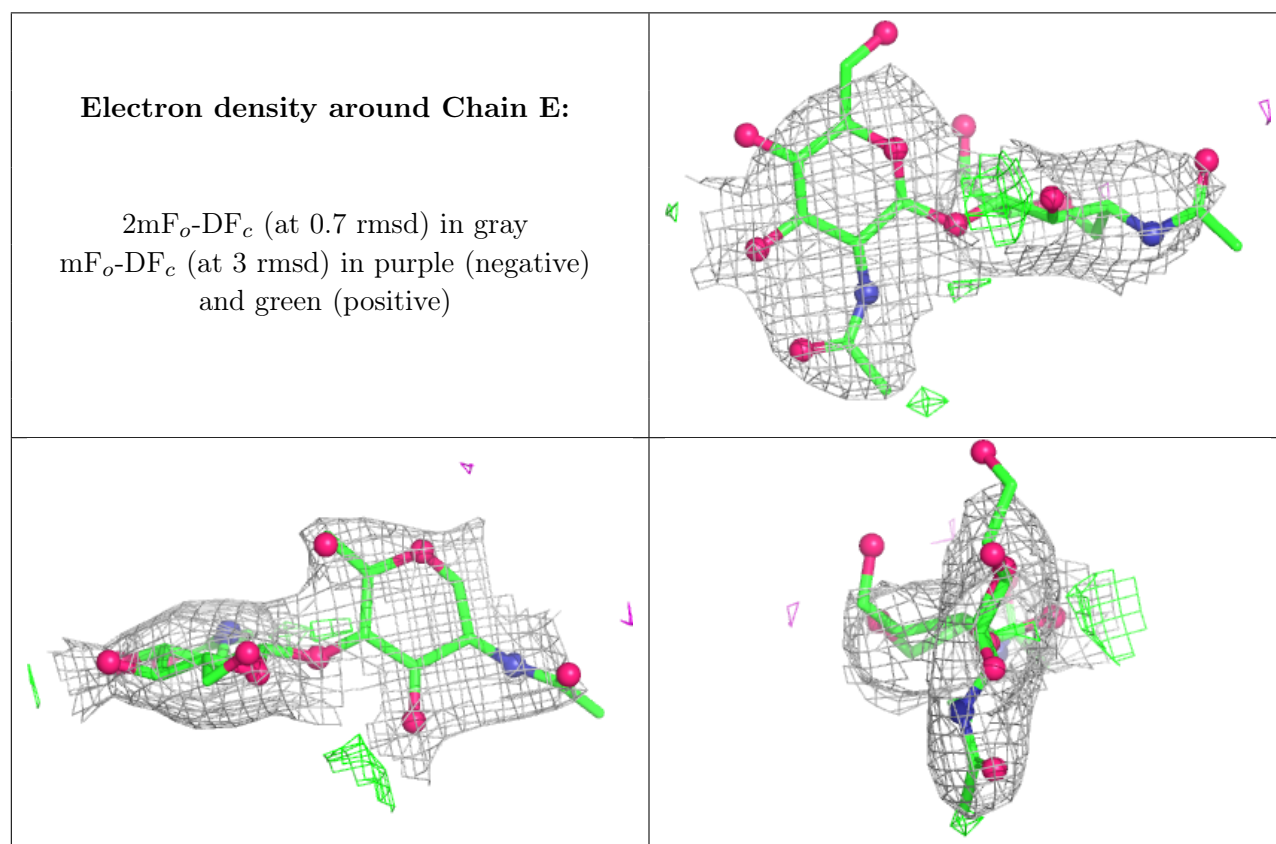
There are no non-standard protein/DNA/RNA residues in this entry.

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
3	NAG	E	1	14/15	0.74	0.15	82,90,91,92	0
3	NAG	E	2	14/15	0.80	0.10	85,95,98,101	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 [i](#)

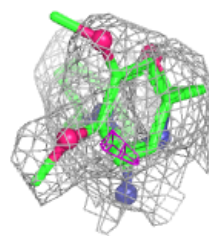
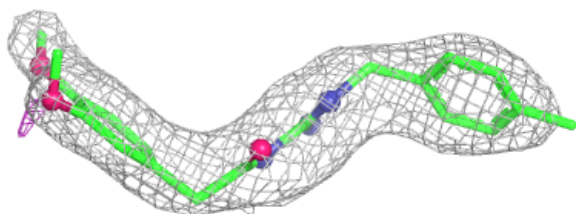
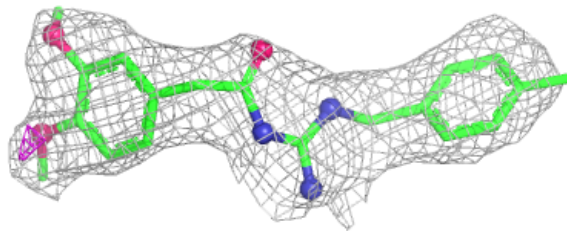
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q<0.9' lists 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	400	14/15	0.77	0.14	73,82,84,84	0
5	2S4	B	401	25/25	0.91	0.10	39,45,68,71	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 2S4 B 401:

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



6.5 Other polymers ⓘ

There are no such residues in this entry.