wwPDB X-ray Structure Validation Summary Report (i)

Aug 10, 2020 – 07:31 AM BST

PDB ID	:	3WF2
Title	:	Crystal structure of human beta-galactosidase in complex with NBT-DGJ
Authors	:	Suzuki, H.; Ohto, U.; Shimizu, T.
Deposited on	:	2013-07-16
Resolution	:	2.30 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 following versions of software and data (see references (1)) were used in the production of this report:

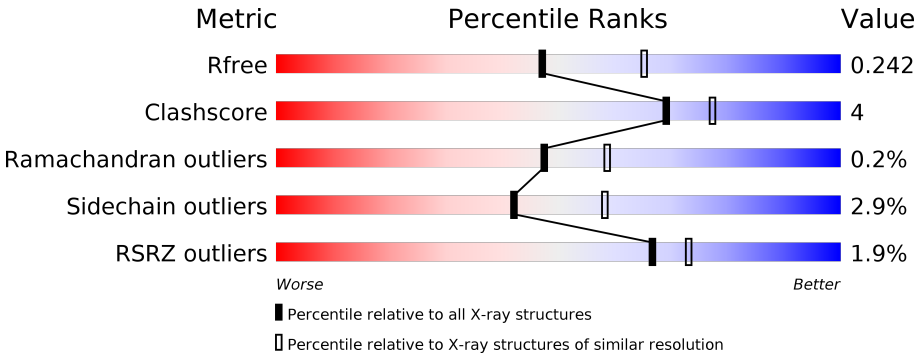
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.13.1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.13.1

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 2.30 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	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

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 on 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	678	% 81% 8% 11%
1	B	678	% 79% 9% 11%
1	C	678	% 79% 10% 11%
1	D	678	3% 78% 10% 11%

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 crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	NAG	C	701	-	-	-	X
6	EDO	A	710	-	-	X	-

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 20707 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 Beta-galactosidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	605	Total	C	N	O	S	0	2	0
			4820	3130	794	878	18			
1	B	605	Total	C	N	O	S	0	1	0
			4818	3129	794	878	17			
1	C	603	Total	C	N	O	S	0	4	0
			4805	3121	789	878	17			
1	D	603	Total	C	N	O	S	0	4	0
			4800	3115	789	879	17			

There are 96 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	GLU	-	expression tag	UNP P16278
A	1	ALA	-	expression tag	UNP P16278
A	2	GLU	-	expression tag	UNP P16278
A	3	ALA	-	expression tag	UNP P16278
A	4	TYR	-	expression tag	UNP P16278
A	5	VAL	-	expression tag	UNP P16278
A	6	GLU	-	expression tag	UNP P16278
A	7	PHE	-	expression tag	UNP P16278
A	8	HIS	-	expression tag	UNP P16278
A	9	HIS	-	expression tag	UNP P16278
A	10	HIS	-	expression tag	UNP P16278
A	11	HIS	-	expression tag	UNP P16278
A	12	HIS	-	expression tag	UNP P16278
A	13	HIS	-	expression tag	UNP P16278
A	14	ASP	-	expression tag	UNP P16278
A	15	TYR	-	expression tag	UNP P16278
A	16	LYS	-	expression tag	UNP P16278
A	17	ASP	-	expression tag	UNP P16278
A	18	ASP	-	expression tag	UNP P16278
A	19	ASP	-	expression tag	UNP P16278
A	20	ASP	-	expression tag	UNP P16278

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Chain	Residue	Modelled	Actual	Comment	Reference
A	21	LYS	-	expression tag	UNP P16278
A	22	THR	-	expression tag	UNP P16278
A	23	SER	-	expression tag	UNP P16278
B	0	GLU	-	expression tag	UNP P16278
B	1	ALA	-	expression tag	UNP P16278
B	2	GLU	-	expression tag	UNP P16278
B	3	ALA	-	expression tag	UNP P16278
B	4	TYR	-	expression tag	UNP P16278
B	5	VAL	-	expression tag	UNP P16278
B	6	GLU	-	expression tag	UNP P16278
B	7	PHE	-	expression tag	UNP P16278
B	8	HIS	-	expression tag	UNP P16278
B	9	HIS	-	expression tag	UNP P16278
B	10	HIS	-	expression tag	UNP P16278
B	11	HIS	-	expression tag	UNP P16278
B	12	HIS	-	expression tag	UNP P16278
B	13	HIS	-	expression tag	UNP P16278
B	14	ASP	-	expression tag	UNP P16278
B	15	TYR	-	expression tag	UNP P16278
B	16	LYS	-	expression tag	UNP P16278
B	17	ASP	-	expression tag	UNP P16278
B	18	ASP	-	expression tag	UNP P16278
B	19	ASP	-	expression tag	UNP P16278
B	20	ASP	-	expression tag	UNP P16278
B	21	LYS	-	expression tag	UNP P16278
B	22	THR	-	expression tag	UNP P16278
B	23	SER	-	expression tag	UNP P16278
C	0	GLU	-	expression tag	UNP P16278
C	1	ALA	-	expression tag	UNP P16278
C	2	GLU	-	expression tag	UNP P16278
C	3	ALA	-	expression tag	UNP P16278
C	4	TYR	-	expression tag	UNP P16278
C	5	VAL	-	expression tag	UNP P16278
C	6	GLU	-	expression tag	UNP P16278
C	7	PHE	-	expression tag	UNP P16278
C	8	HIS	-	expression tag	UNP P16278
C	9	HIS	-	expression tag	UNP P16278
C	10	HIS	-	expression tag	UNP P16278
C	11	HIS	-	expression tag	UNP P16278
C	12	HIS	-	expression tag	UNP P16278
C	13	HIS	-	expression tag	UNP P16278
C	14	ASP	-	expression tag	UNP P16278

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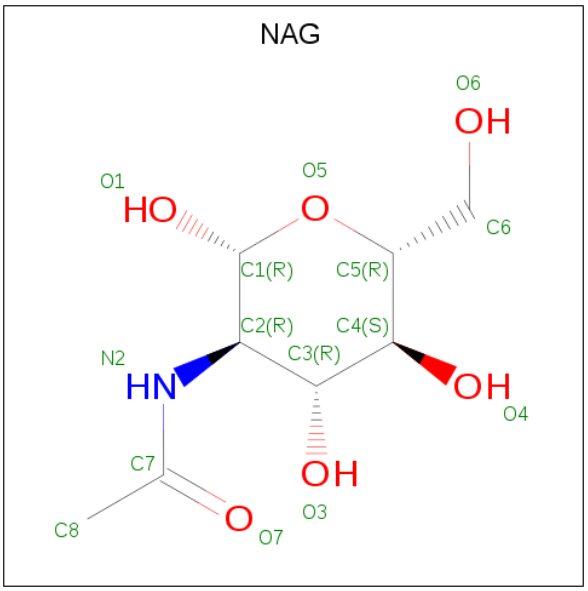
Chain	Residue	Modelled	Actual	Comment	Reference
C	15	TYR	-	expression tag	UNP P16278
C	16	LYS	-	expression tag	UNP P16278
C	17	ASP	-	expression tag	UNP P16278
C	18	ASP	-	expression tag	UNP P16278
C	19	ASP	-	expression tag	UNP P16278
C	20	ASP	-	expression tag	UNP P16278
C	21	LYS	-	expression tag	UNP P16278
C	22	THR	-	expression tag	UNP P16278
C	23	SER	-	expression tag	UNP P16278
D	0	GLU	-	expression tag	UNP P16278
D	1	ALA	-	expression tag	UNP P16278
D	2	GLU	-	expression tag	UNP P16278
D	3	ALA	-	expression tag	UNP P16278
D	4	TYR	-	expression tag	UNP P16278
D	5	VAL	-	expression tag	UNP P16278
D	6	GLU	-	expression tag	UNP P16278
D	7	PHE	-	expression tag	UNP P16278
D	8	HIS	-	expression tag	UNP P16278
D	9	HIS	-	expression tag	UNP P16278
D	10	HIS	-	expression tag	UNP P16278
D	11	HIS	-	expression tag	UNP P16278
D	12	HIS	-	expression tag	UNP P16278
D	13	HIS	-	expression tag	UNP P16278
D	14	ASP	-	expression tag	UNP P16278
D	15	TYR	-	expression tag	UNP P16278
D	16	LYS	-	expression tag	UNP P16278
D	17	ASP	-	expression tag	UNP P16278
D	18	ASP	-	expression tag	UNP P16278
D	19	ASP	-	expression tag	UNP P16278
D	20	ASP	-	expression tag	UNP P16278
D	21	LYS	-	expression tag	UNP P16278
D	22	THR	-	expression tag	UNP P16278
D	23	SER	-	expression tag	UNP P16278

- Molecule 2 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



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

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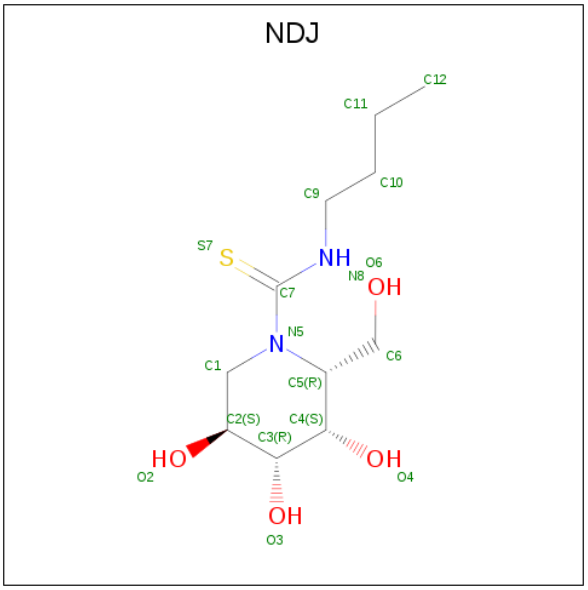
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	D	1	Total C N O 14 8 1 5	0	0
2	D	1	Total C N O 14 8 1 5	0	0

- Molecule 3 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	1	Total Cl 1 1	0	0
3	A	1	Total Cl 1 1	0	0
3	D	1	Total Cl 1 1	0	0
3	C	1	Total Cl 1 1	0	0

- Molecule 4 is (2R,3S,4R,5S)-N-butyl-3,4,5-trihydroxy-2-(hydroxymethyl)piperidine-1-carbothioamide (three-letter code: NDJ) (formula: $C_{11}H_{22}N_2O_4S$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C N O S 18 11 2 4 1	0	0
4	B	1	Total C N O S 18 11 2 4 1	0	0
4	C	1	Total C N O S 18 11 2 4 1	0	0

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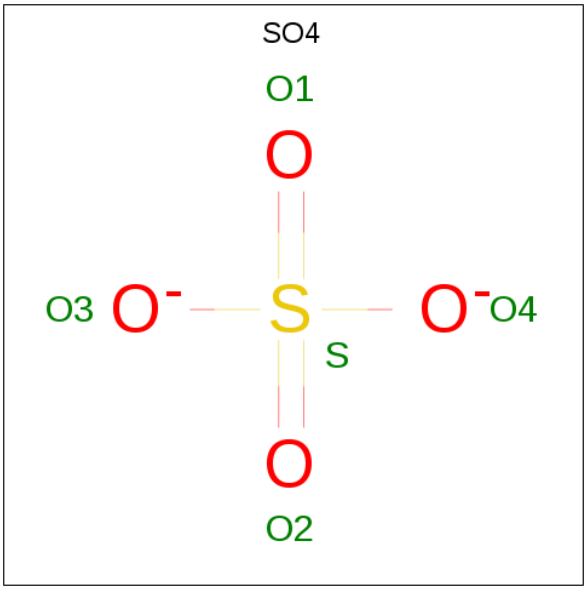
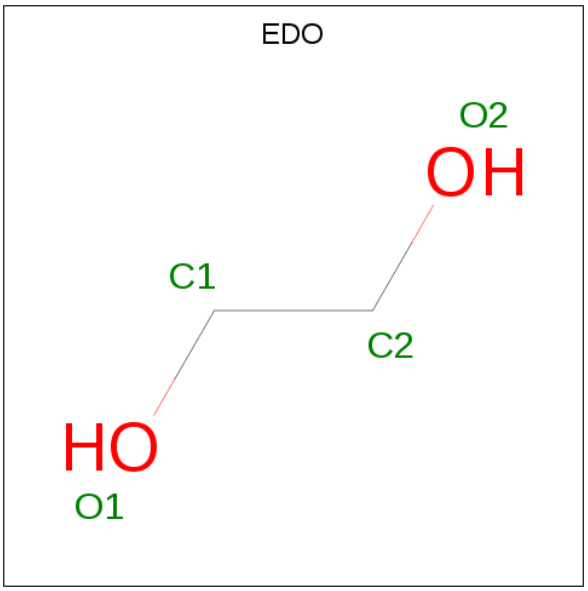
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	D	1	Total	C	N	O	S	0	0
			18	11	2	4	1		

- Molecule 5 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



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

- Molecule 6 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).



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

- Molecule 7 is water.

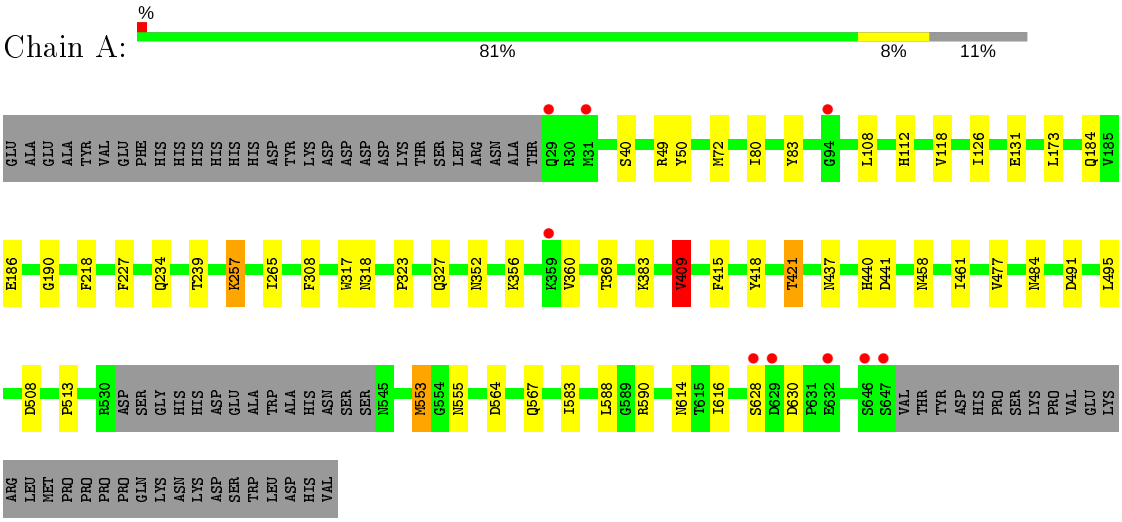
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	288	Total O 288 288	0	0
7	B	288	Total O 288 288	0	0
7	C	279	Total O 279 279	0	0
7	D	237	Total O 237 237	0	0

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.

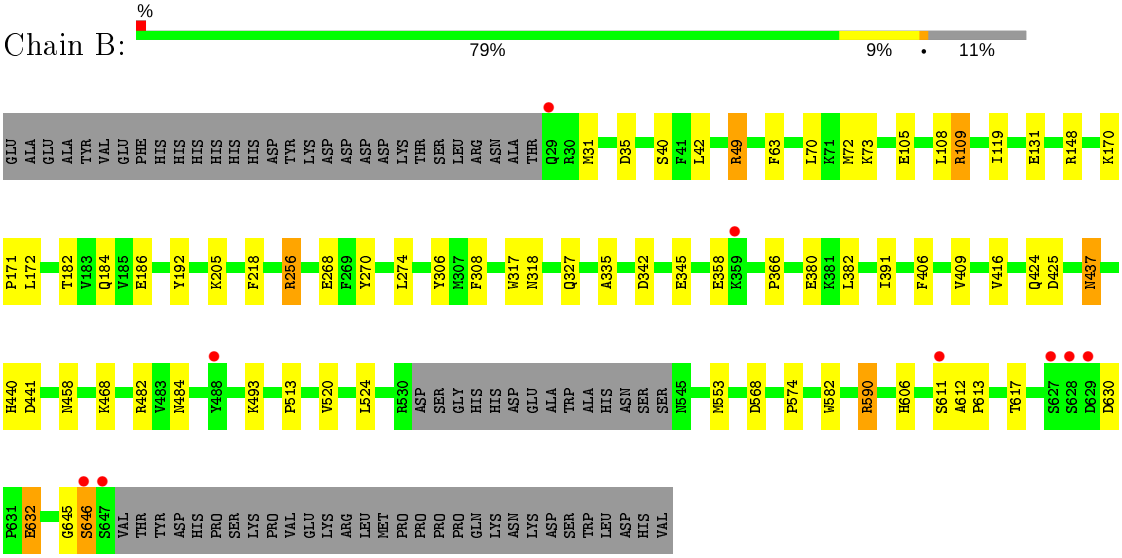
- Molecule 1: Beta-galactosidase

Chain A:



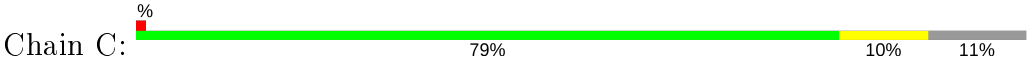
- Molecule 1: Beta-galactosidase

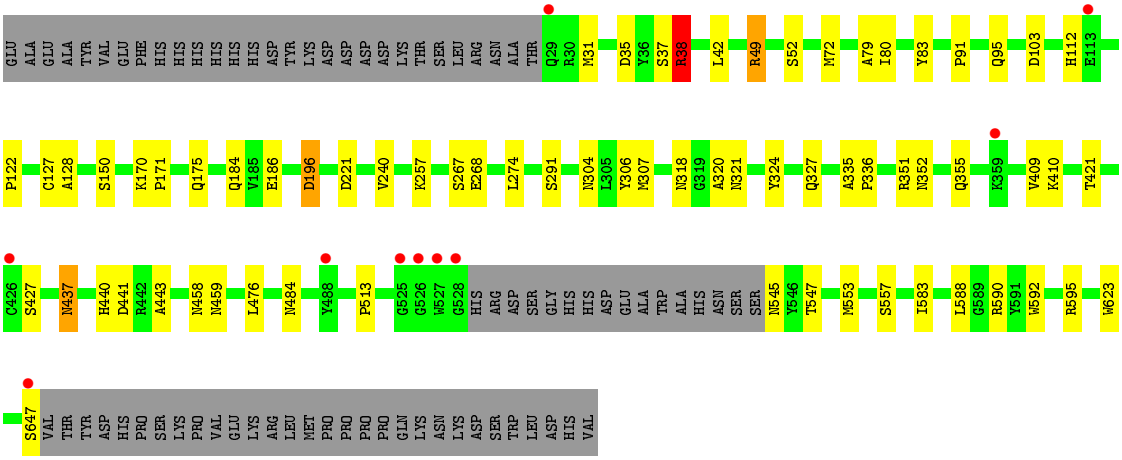
Chain B:



- Molecule 1: Beta-galactosidase

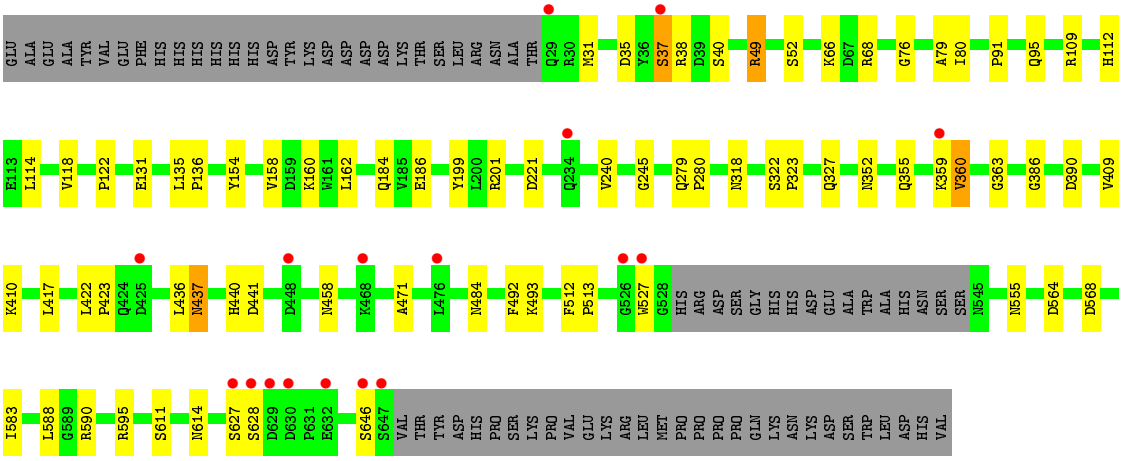
Chain C:





- Molecule 1: Beta-galactosidase

Chain D:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	95.12Å 116.26Å 141.77Å 90.00° 92.41° 90.00°	Depositor
Resolution (Å)	25.98 – 2.30 25.98 – 2.30	Depositor EDS
% Data completeness (in resolution range)	97.4 (25.98-2.30) 97.5 (25.98-2.30)	Depositor EDS
R_{merge}	0.17	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.79 (at 2.31Å)	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
R, R_{free}	0.175 , 0.240 0.182 , 0.242	Depositor DCC
R_{free} test set	6716 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å^2)	29.8	Xtriage
Anisotropy	0.102	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.33 , 35.1	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	0.044 for h,-k,-l	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	20707	wwPDB-VP
Average B, all atoms (Å^2)	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.73% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: SO4, NDJ, EDO, NAG, CL

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	0.80	0/4982	0.87	4/6796 (0.1%)
1	B	0.84	1/4974 (0.0%)	0.90	6/6786 (0.1%)
1	C	0.80	0/4977	0.86	5/6790 (0.1%)
1	D	0.78	0/4971	0.87	6/6782 (0.1%)
All	All	0.81	1/19904 (0.0%)	0.87	21/27154 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	317	TRP	CZ3-CH2	5.12	1.48	1.40

The worst 5 of 21 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	C	38	ARG	NE-CZ-NH1	7.51	124.05	120.30
1	B	342	ASP	CB-CG-OD1	7.22	124.80	118.30
1	A	491	ASP	CB-CG-OD1	6.82	124.44	118.30
1	D	109	ARG	NE-CZ-NH1	6.66	123.63	120.30
1	D	568	ASP	CB-CG-OD1	6.63	124.27	118.30

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	4820	0	4688	34	0
1	B	4818	0	4687	35	0
1	C	4805	0	4670	36	0
1	D	4800	0	4666	37	0
2	A	56	0	52	0	0
2	B	56	0	52	0	0
2	C	56	0	52	0	0
2	D	56	0	52	3	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
4	A	18	0	22	0	0
4	B	18	0	22	1	0
4	C	18	0	22	1	0
4	D	18	0	22	1	0
5	A	10	0	0	1	0
5	B	10	0	0	0	0
5	C	10	0	0	0	0
5	D	10	0	0	0	0
6	A	8	0	12	4	0
6	B	8	0	12	0	0
6	C	8	0	12	0	0
6	D	8	0	12	1	0
7	A	288	0	0	5	0
7	B	288	0	0	5	0
7	C	279	0	0	3	0
7	D	237	0	0	4	0
All	All	20707	0	19055	142	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.

The worst 5 of 142 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:409:VAL:HG13	1:A:513:PRO:HG3	1.62	0.81
1:B:437:ASN:HD21	1:B:458:ASN:H	1.29	0.80
1:D:555:ASN:HB2	2:D:704:NAG:O5	1.83	0.78
1:D:35:ASP:HB3	7:D:1006:HOH:O	1.82	0.78
1:C:318:ASN:HD21	1:C:590:ARG:HH21	1.31	0.77

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	603/678 (89%)	570 (94%)	32 (5%)	1 (0%)	47	58
1	B	602/678 (89%)	575 (96%)	26 (4%)	1 (0%)	47	58
1	C	603/678 (89%)	576 (96%)	26 (4%)	1 (0%)	47	58
1	D	603/678 (89%)	569 (94%)	32 (5%)	2 (0%)	41	50
All	All	2411/2712 (89%)	2290 (95%)	116 (5%)	5 (0%)	47	58

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	646	SER
1	A	508	ASP
1	C	127	CYS
1	D	423	PRO
1	D	386	GLY

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	520/585 (89%)	510 (98%)	10 (2%)	57	73
1	B	519/585 (89%)	502 (97%)	17 (3%)	38	53
1	C	520/585 (89%)	502 (96%)	18 (4%)	36	50

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	D	520/585 (89%)	503 (97%)	17 (3%)	38 53
All	All	2079/2340 (89%)	2017 (97%)	62 (3%)	42 57

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

Mol	Chain	Res	Type
1	C	37	SER
1	C	257	LYS
1	D	611[A]	SER
1	C	175[A]	GLN
1	C	291	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 26 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	437	ASN
1	C	279	GLN
1	D	437	ASN
1	B	484	ASN
1	C	102	HIS

5.3.3 RNA (i)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains (i)

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

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 40 ligands modelled in this entry, 4 are monoatomic - leaving 36 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	$\#\|Z\| > 2$
2	NAG	D	703	1	14,14,15	0.66	0	17,19,21	1.70	5 (29%)
2	NAG	B	703	1	14,14,15	0.85	1 (7%)	17,19,21	2.34	4 (23%)
5	SO4	C	706	-	4,4,4	0.38	0	6,6,6	0.23	0
2	NAG	D	705	1	14,14,15	0.93	0	17,19,21	1.60	4 (23%)
2	NAG	C	704	1	14,14,15	0.70	0	17,19,21	1.81	6 (35%)
2	NAG	A	703	1	14,14,15	1.51	3 (21%)	17,19,21	3.15	8 (47%)
2	NAG	A	704	1	14,14,15	0.83	0	17,19,21	1.50	3 (17%)
6	EDO	B	710	-	3,3,3	0.50	0	2,2,2	0.31	0
2	NAG	D	704	1	14,14,15	0.65	0	17,19,21	2.70	5 (29%)
6	EDO	D	707	-	3,3,3	0.57	0	2,2,2	0.18	0
2	NAG	C	701	1	14,14,15	0.68	0	17,19,21	1.94	3 (17%)
5	SO4	B	707	-	4,4,4	0.42	0	6,6,6	0.28	0
2	NAG	A	701	1	14,14,15	1.00	2 (14%)	17,19,21	1.90	3 (17%)
2	NAG	B	701	1	14,14,15	0.61	0	17,19,21	1.41	1 (5%)
2	NAG	C	702	1	14,14,15	0.70	1 (7%)	17,19,21	1.82	2 (11%)
5	SO4	C	707	-	4,4,4	0.48	0	6,6,6	0.80	0
6	EDO	C	710	-	3,3,3	0.60	0	2,2,2	0.28	0
4	NDJ	D	708	-	18,18,18	1.71	3 (16%)	20,24,24	1.75	4 (20%)
2	NAG	C	703	1	14,14,15	0.78	0	17,19,21	1.69	5 (29%)
2	NAG	D	701	1	14,14,15	0.30	0	17,19,21	0.62	0
4	NDJ	B	706	-	18,18,18	2.06	5 (27%)	20,24,24	1.89	5 (25%)
5	SO4	D	709	-	4,4,4	0.29	0	6,6,6	0.52	0
6	EDO	C	709	-	3,3,3	0.75	0	2,2,2	0.29	0
6	EDO	A	709	-	3,3,3	0.43	0	2,2,2	0.73	0
6	EDO	B	709	-	3,3,3	0.43	0	2,2,2	0.59	0
6	EDO	A	710	-	3,3,3	0.37	0	2,2,2	0.26	0
2	NAG	B	702	1	14,14,15	0.82	0	17,19,21	1.57	3 (17%)
6	EDO	D	706	-	3,3,3	0.30	0	2,2,2	1.72	1 (50%)
5	SO4	B	708	-	4,4,4	0.51	0	6,6,6	1.04	0
2	NAG	A	702	1	14,14,15	0.51	0	17,19,21	2.45	5 (29%)
2	NAG	B	704	1	14,14,15	0.49	0	17,19,21	0.80	0
5	SO4	A	708	-	4,4,4	0.64	0	6,6,6	0.82	0
5	SO4	A	707	-	4,4,4	0.44	0	6,6,6	0.28	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
4	NDJ	A	706	-	18,18,18	1.80	5 (27%)	20,24,24	1.78	5 (25%)
5	SO4	D	710	-	4,4,4	0.57	0	6,6,6	1.08	0
4	NDJ	C	705	-	18,18,18	1.87	3 (16%)	20,24,24	1.94	4 (20%)

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	NAG	D	703	1	-	2/6/23/26	0/1/1/1
2	NAG	B	703	1	-	0/6/23/26	0/1/1/1
2	NAG	D	705	1	-	0/6/23/26	0/1/1/1
2	NAG	C	704	1	-	1/6/23/26	0/1/1/1
2	NAG	A	703	1	-	1/6/23/26	0/1/1/1
6	EDO	B	710	-	-	1/1/1/1	-
2	NAG	D	704	1	-	2/6/23/26	0/1/1/1
6	EDO	D	707	-	-	1/1/1/1	-
2	NAG	C	701	1	-	0/6/23/26	0/1/1/1
2	NAG	D	701	1	-	2/6/23/26	0/1/1/1
2	NAG	A	701	1	-	2/6/23/26	0/1/1/1
2	NAG	B	701	1	-	1/6/23/26	0/1/1/1
2	NAG	C	702	1	-	0/6/23/26	0/1/1/1
4	NDJ	C	705	-	-	5/11/31/31	0/1/1/1
6	EDO	C	710	-	-	1/1/1/1	-
4	NDJ	D	708	-	-	8/11/31/31	0/1/1/1
2	NAG	C	703	1	-	1/6/23/26	0/1/1/1
4	NDJ	B	706	-	-	6/11/31/31	0/1/1/1
6	EDO	C	709	-	-	1/1/1/1	-
6	EDO	A	709	-	-	0/1/1/1	-
6	EDO	B	709	-	-	1/1/1/1	-
6	EDO	A	710	-	-	1/1/1/1	-
2	NAG	B	702	1	-	0/6/23/26	0/1/1/1
6	EDO	D	706	-	-	0/1/1/1	-
2	NAG	A	702	1	-	2/6/23/26	0/1/1/1
2	NAG	B	704	1	-	2/6/23/26	0/1/1/1
2	NAG	A	704	1	-	2/6/23/26	0/1/1/1
4	NDJ	A	706	-	-	5/11/31/31	0/1/1/1

The worst 5 of 23 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	C	705	NDJ	C7-N5	5.84	1.42	1.34
4	D	708	NDJ	C7-N5	4.79	1.40	1.34
4	A	706	NDJ	C7-N5	4.71	1.40	1.34
4	B	706	NDJ	C7-N5	4.50	1.40	1.34
4	D	708	NDJ	C7-S7	-4.39	1.60	1.67

The worst 5 of 76 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	D	704	NAG	C1-O5-C5	8.08	123.14	112.19
2	A	702	NAG	C1-O5-C5	7.90	122.89	112.19
2	B	703	NAG	C1-O5-C5	7.40	122.22	112.19
2	A	703	NAG	C1-O5-C5	6.48	120.98	112.19
2	A	701	NAG	C1-C2-N2	-5.49	101.12	110.49

There are no chirality outliers.

5 of 48 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	D	708	NDJ	N8-C7-N5-C1
4	D	708	NDJ	N8-C7-N5-C5
4	D	708	NDJ	S7-C7-N5-C5
4	B	706	NDJ	N8-C7-N5-C1
4	B	706	NDJ	S7-C7-N5-C1

There are no ring outliers.

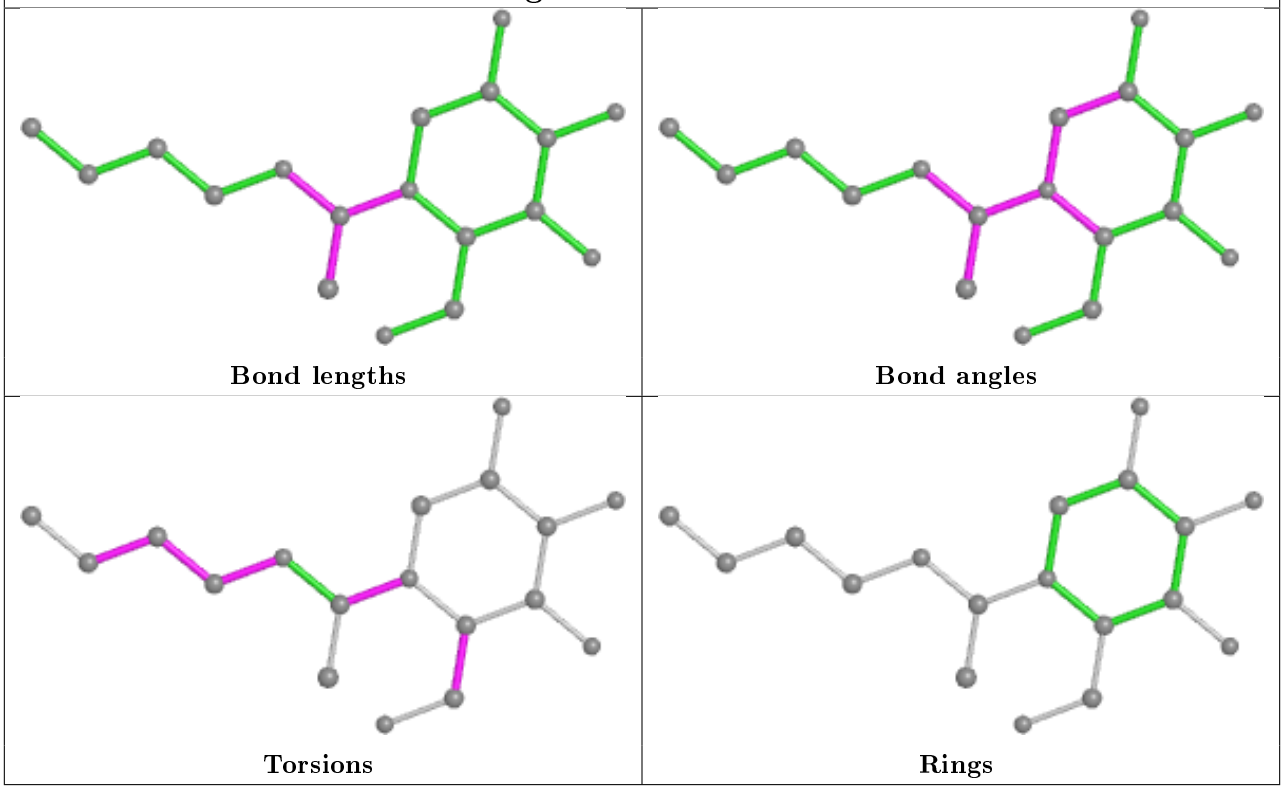
7 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	704	NAG	3	0
4	D	708	NDJ	1	0
4	B	706	NDJ	1	0
6	A	710	EDO	4	0
6	D	706	EDO	1	0
5	A	708	SO4	1	0
4	C	705	NDJ	1	0

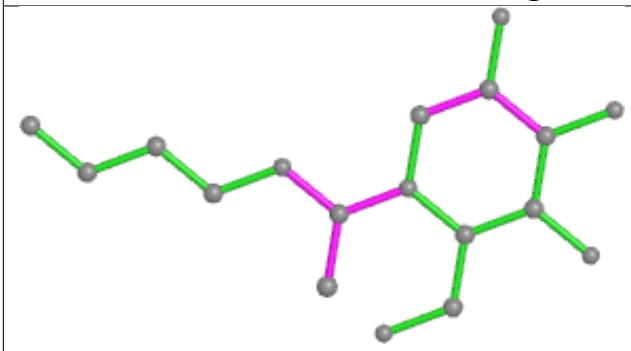
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.

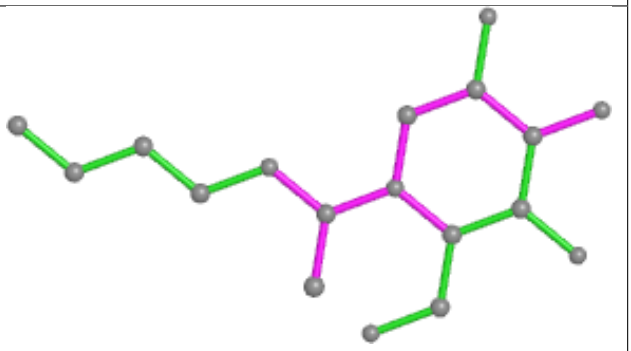
Ligand NDJ D 708



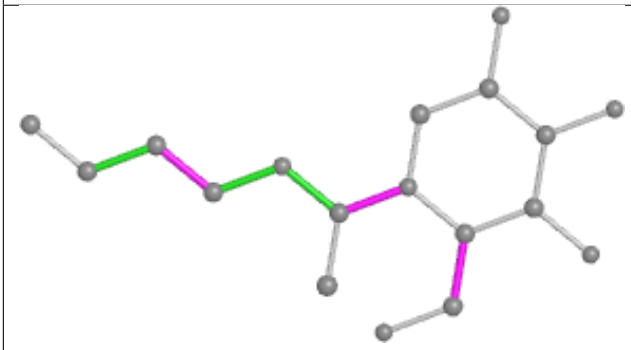
Ligand NDJ B 706



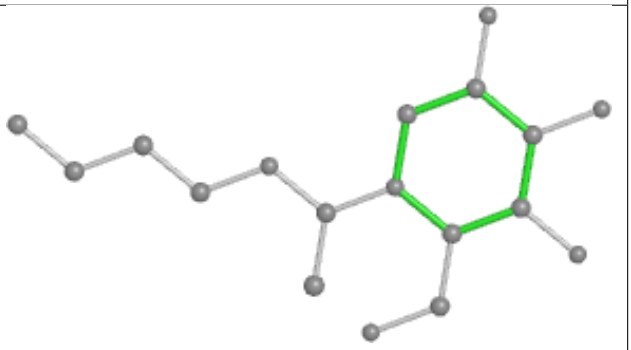
Bond lengths



Bond angles

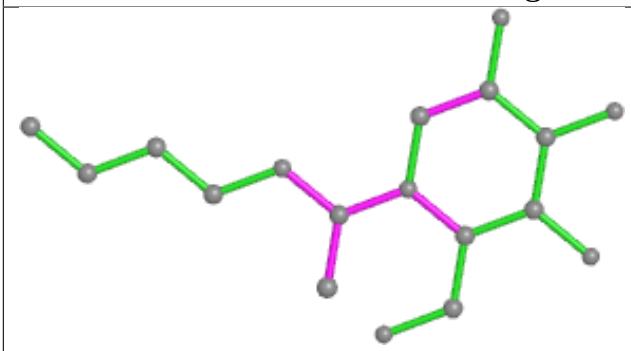


Torsions

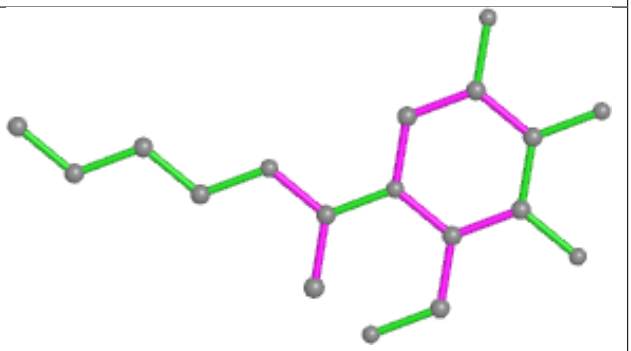


Rings

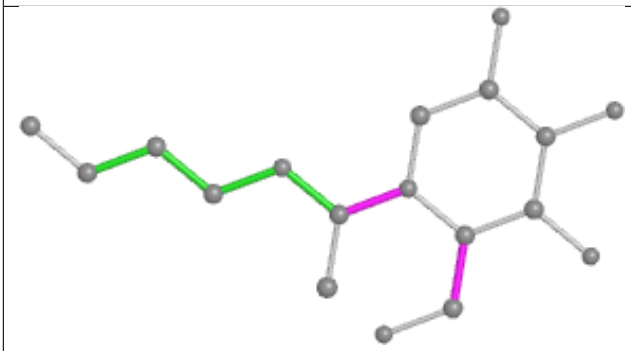
Ligand NDJ A 706



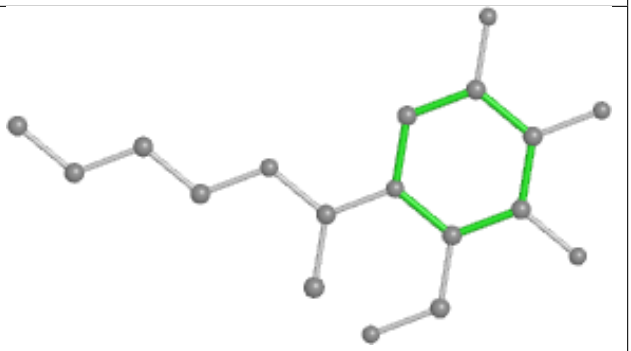
Bond lengths



Bond angles

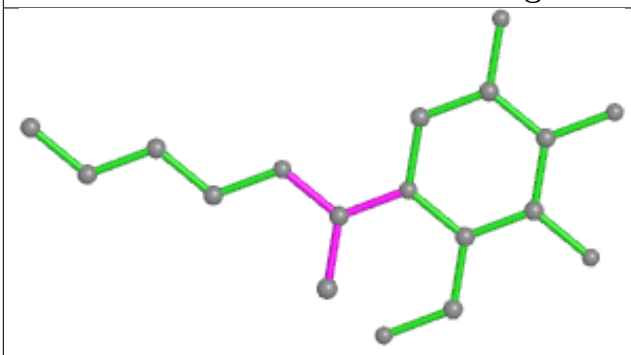


Torsions

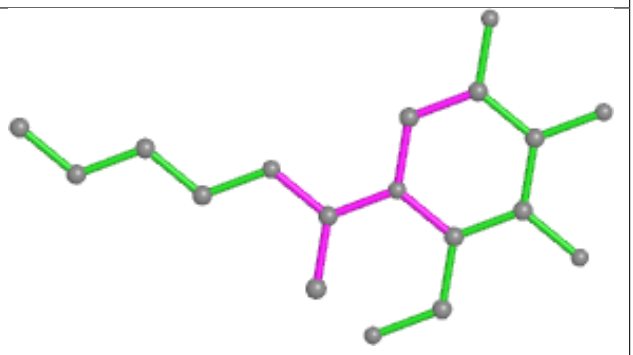


Rings

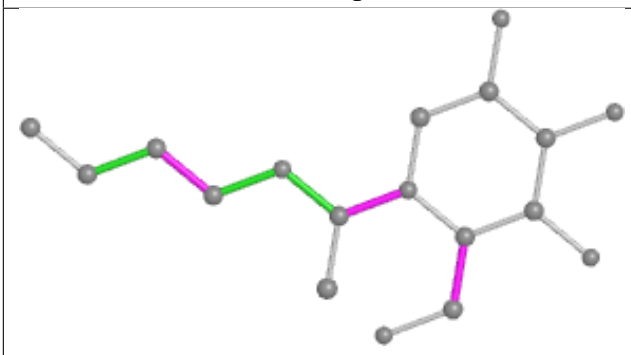
Ligand NDJ C 705



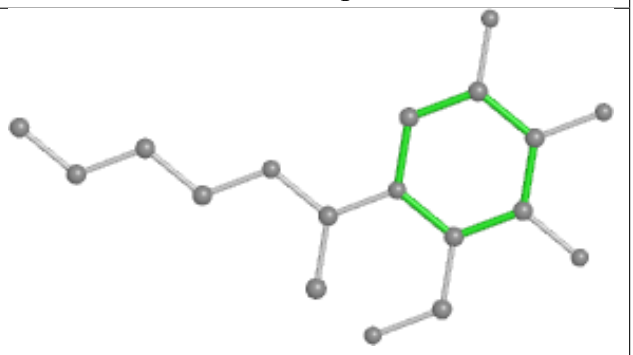
Bond lengths



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, 95^{th} 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	605/678 (89%)	-0.24	9 (1%)	73	79	18, 29, 48, 104	0
1	B	605/678 (89%)	-0.29	9 (1%)	73	79	16, 27, 46, 93	0
1	C	603/678 (88%)	-0.17	10 (1%)	70	76	17, 29, 56, 87	0
1	D	603/678 (88%)	-0.14	17 (2%)	53	60	17, 30, 58, 97	0
All	All	2416/2712 (89%)	-0.21	45 (1%)	66	73	16, 29, 54, 104	0

The worst 5 of 45 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	647	SER	6.2
1	C	527	TRP	6.1
1	A	29	GLN	5.4
1	A	647	SER	5.4
1	D	629	ASP	4.9

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

There are no monosaccharides in this entry.

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, 95^{th} 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.

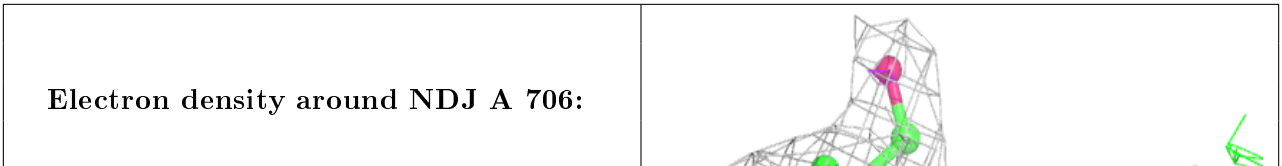
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	NAG	D	704	14/15	0.59	0.33	72,93,100,101	0
2	NAG	C	701	14/15	0.70	0.40	75,92,97,100	0
6	EDO	B	709	4/4	0.77	0.21	47,51,53,55	0
2	NAG	D	701	14/15	0.80	0.37	78,83,85,86	0
2	NAG	A	704	14/15	0.80	0.36	59,71,84,84	0
2	NAG	A	703	14/15	0.83	0.18	43,50,55,55	0
4	NDJ	A	706	18/18	0.85	0.20	25,29,59,66	0
4	NDJ	D	708	18/18	0.86	0.18	27,35,58,77	0
2	NAG	B	704	14/15	0.87	0.26	59,67,70,71	0
5	SO4	A	707	5/5	0.87	0.26	65,69,76,83	0
2	NAG	D	703	14/15	0.87	0.22	42,53,62,63	0
2	NAG	C	702	14/15	0.87	0.22	53,58,61,63	0
2	NAG	A	702	14/15	0.88	0.19	25,36,42,45	0
2	NAG	C	703	14/15	0.88	0.23	40,52,55,58	0
4	NDJ	B	706	18/18	0.88	0.19	22,29,81,83	0
6	EDO	A	709	4/4	0.88	0.17	42,47,53,58	0
5	SO4	D	710	5/5	0.88	0.20	54,59,70,70	0
6	EDO	C	710	4/4	0.88	0.22	37,46,54,55	0
4	NDJ	C	705	18/18	0.89	0.16	19,31,63,77	0
6	EDO	B	710	4/4	0.90	0.19	43,43,47,48	0
2	NAG	B	703	14/15	0.90	0.18	46,52,61,61	0
5	SO4	D	709	5/5	0.91	0.35	68,76,78,87	0
5	SO4	C	707	5/5	0.93	0.19	58,58,62,62	0
6	EDO	C	709	4/4	0.93	0.20	30,34,35,35	0
2	NAG	B	702	14/15	0.93	0.14	31,35,38,39	0
6	EDO	D	706	4/4	0.93	0.15	35,38,39,40	0
5	SO4	B	708	5/5	0.93	0.20	57,58,61,66	0
5	SO4	C	706	5/5	0.93	0.42	70,73,82,83	0
2	NAG	C	704	14/15	0.94	0.10	27,31,34,34	0
5	SO4	A	708	5/5	0.94	0.19	47,48,59,62	0
2	NAG	D	705	14/15	0.94	0.14	32,36,39,44	0
2	NAG	A	701	14/15	0.95	0.10	26,30,34,38	0
6	EDO	D	707	4/4	0.95	0.16	35,44,47,49	0
6	EDO	A	710	4/4	0.96	0.19	34,45,46,47	0
5	SO4	B	707	5/5	0.96	0.28	73,74,81,82	0
2	NAG	B	701	14/15	0.96	0.10	35,40,49,49	0
3	CL	B	705	1/1	0.99	0.09	21,21,21,21	0
3	CL	A	705	1/1	0.99	0.05	21,21,21,21	0
3	CL	D	702	1/1	0.99	0.12	22,22,22,22	0
3	CL	C	708	1/1	1.00	0.10	19,19,19,19	0

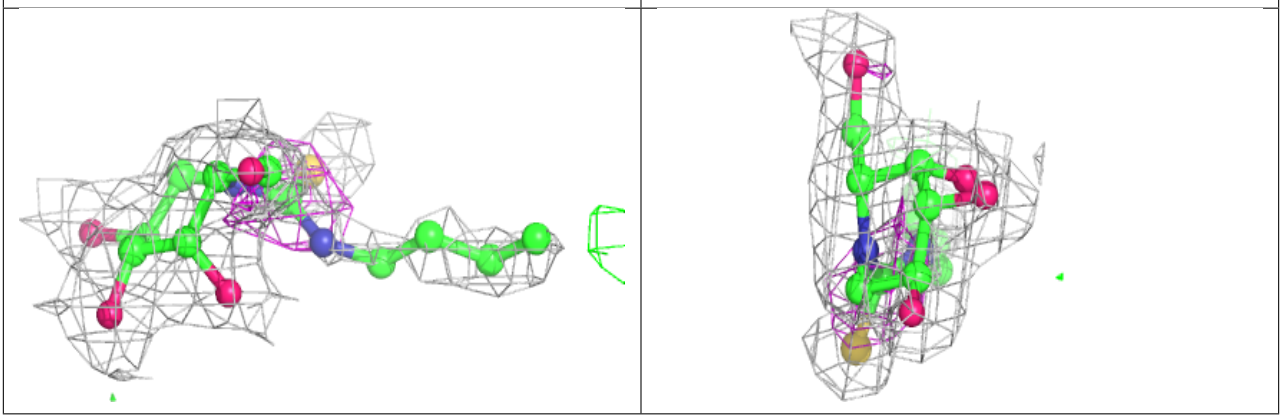
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different

orientation to approximate a three-dimensional view.

Electron density around NDJ A 706:

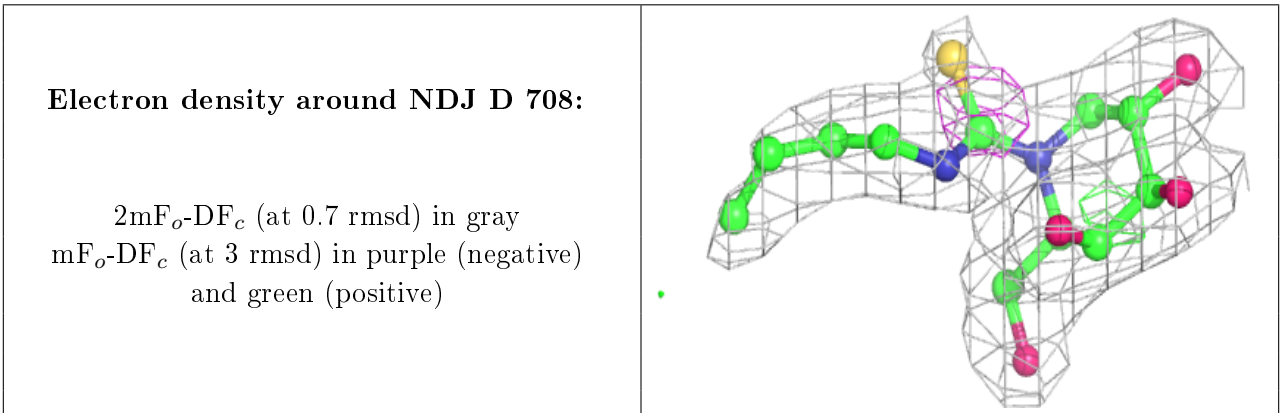
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

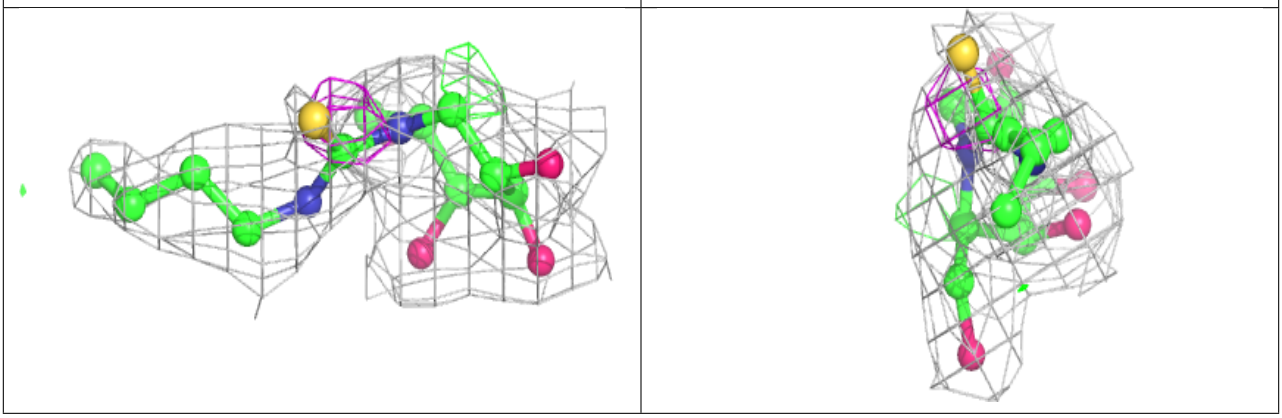




Electron density around NDJ D 708:

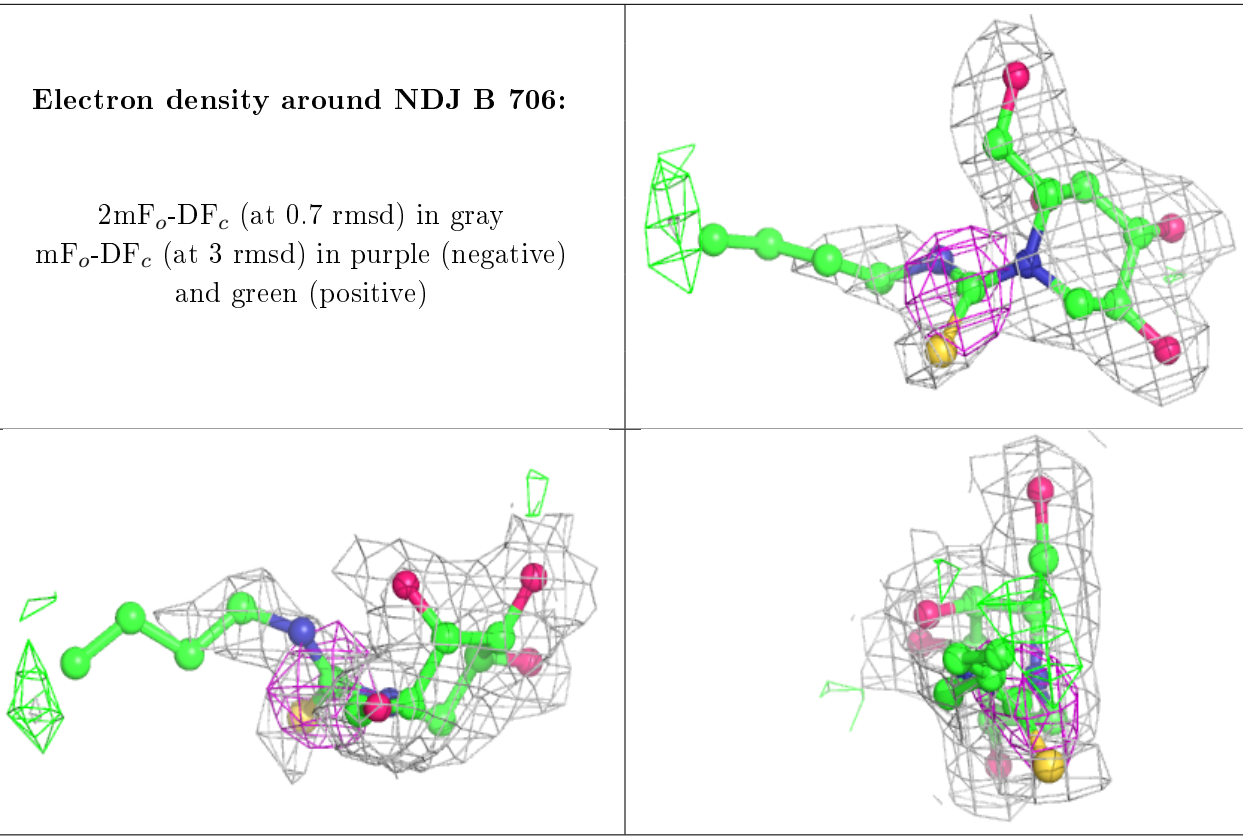
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)





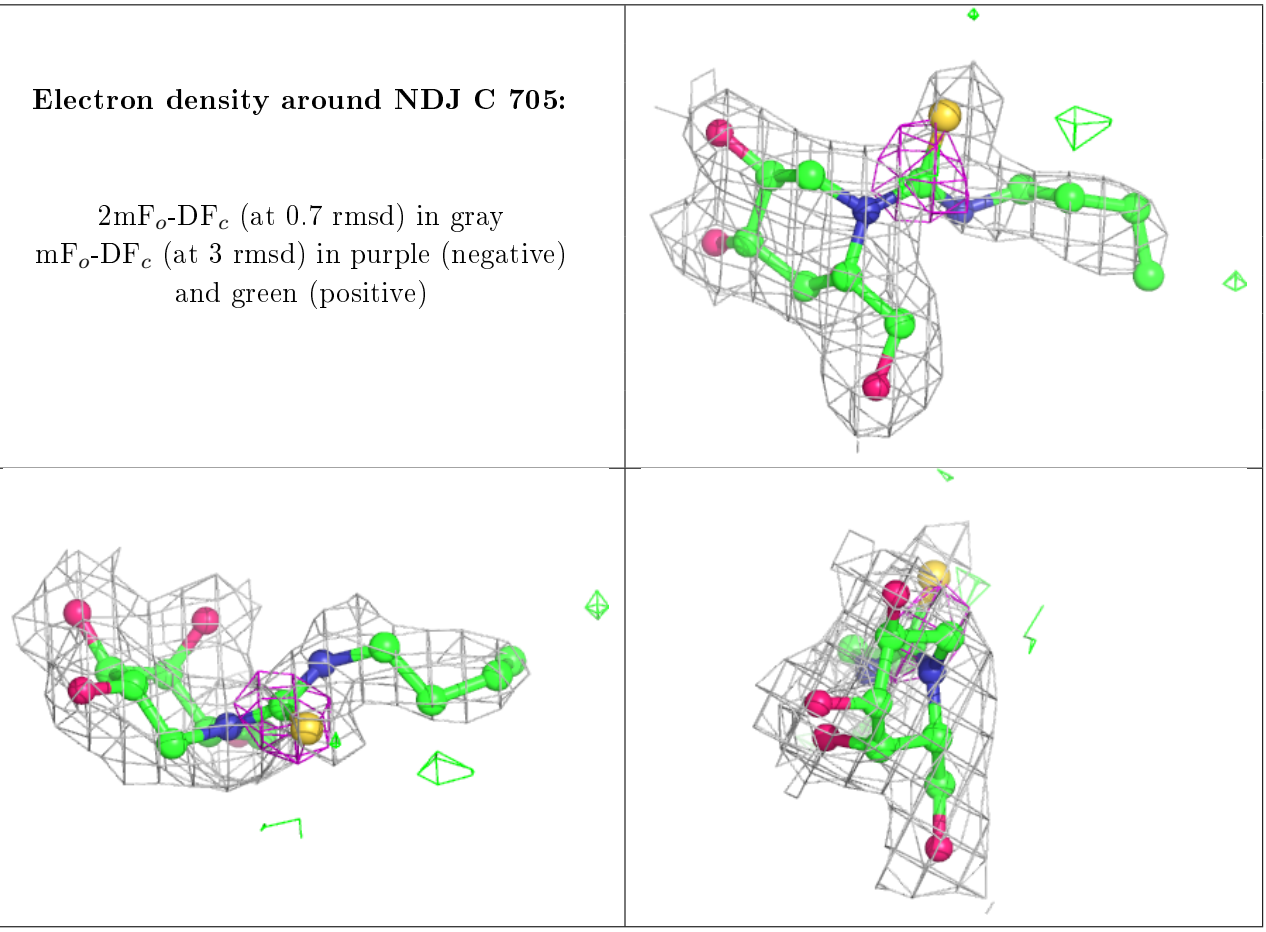
Electron density around NDJ B 706:

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



Electron density around NDJ C 705:

$2mF_o$-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 (i)

There are no such residues in this entry.