



# wwPDB X-ray Structure Validation Summary Report ⓘ

Jun 24, 2024 – 07:49 PM EDT

PDB ID : 6TBK  
Title : Structure of a beta galactosidase with inhibitor  
Authors : Offen, W.; Davies, G.  
Deposited on : 2019-11-01  
Resolution : 1.60 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](mailto: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>.

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

MolProbity	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	2.37.1
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)	:	2.37.1

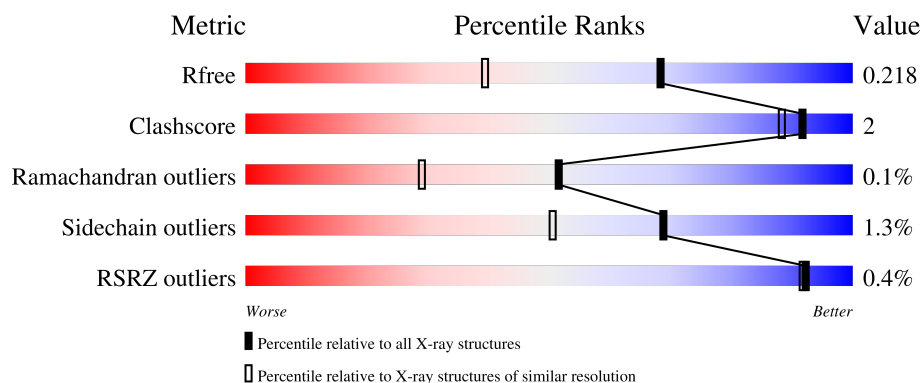
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.60 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	3398 (1.60-1.60)
Clashscore	141614	3665 (1.60-1.60)
Ramachandran outliers	138981	3564 (1.60-1.60)
Sidechain outliers	138945	3563 (1.60-1.60)
RSRZ outliers	127900	3321 (1.60-1.60)

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  $\geq 3$ , 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	550	<div> <div>%</div> <div> <div></div> <div>88%</div> <div>7%</div> <div>.</div> </div> </div>
1	B	550	<div> <div></div> <div>92%</div> <div>5%</div> <div>.</div> </div>
1	C	550	<div> <div>%</div> <div> <div></div> <div>92%</div> <div>5%</div> <div>.</div> </div> </div>
1	D	550	<div> <div></div> <div>93%</div> <div>.</div> <div>.</div> </div>
1	E	550	<div> <div></div> <div>93%</div> <div>5%</div> <div>.</div> </div>

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Mol	Chain	Length	Quality of chain
1	F	550	<div><div></div><div>92%</div><div>5%</div><div></div></div>
1	G	550	<div><div></div><div>90%</div><div>6%</div><div></div></div>
1	H	550	<div><div></div><div>91%</div><div>6%</div><div></div></div>

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 36143 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, putative, bgl35A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	527	Total	C	N	O	S	0	0	0
			4138	2655	699	769	15			
1	B	533	Total	C	N	O	S	0	1	0
			4182	2683	708	776	15			
1	C	533	Total	C	N	O	S	0	0	0
			4153	2664	702	772	15			
1	D	537	Total	C	N	O	S	0	3	0
			4227	2708	718	785	16			
1	E	537	Total	C	N	O	S	0	2	0
			4207	2698	710	784	15			
1	F	535	Total	C	N	O	S	0	5	0
			4245	2718	721	791	15			
1	G	526	Total	C	N	O	S	0	4	0
			4162	2673	706	767	16			
1	H	532	Total	C	N	O	S	0	2	0
			4170	2673	708	774	15			

There are 80 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	26	MET	-	initiating methionine	UNP B3PBE0
A	27	GLY	-	expression tag	UNP B3PBE0
A	28	SER	-	expression tag	UNP B3PBE0
A	29	SER	-	expression tag	UNP B3PBE0
A	30	HIS	-	expression tag	UNP B3PBE0
A	31	HIS	-	expression tag	UNP B3PBE0
A	32	HIS	-	expression tag	UNP B3PBE0
A	33	HIS	-	expression tag	UNP B3PBE0
A	34	HIS	-	expression tag	UNP B3PBE0
A	35	HIS	-	expression tag	UNP B3PBE0
B	26	MET	-	initiating methionine	UNP B3PBE0
B	27	GLY	-	expression tag	UNP B3PBE0
B	28	SER	-	expression tag	UNP B3PBE0

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Chain	Residue	Modelled	Actual	Comment	Reference
B	29	SER	-	expression tag	UNP B3PBE0
B	30	HIS	-	expression tag	UNP B3PBE0
B	31	HIS	-	expression tag	UNP B3PBE0
B	32	HIS	-	expression tag	UNP B3PBE0
B	33	HIS	-	expression tag	UNP B3PBE0
B	34	HIS	-	expression tag	UNP B3PBE0
B	35	HIS	-	expression tag	UNP B3PBE0
C	26	MET	-	initiating methionine	UNP B3PBE0
C	27	GLY	-	expression tag	UNP B3PBE0
C	28	SER	-	expression tag	UNP B3PBE0
C	29	SER	-	expression tag	UNP B3PBE0
C	30	HIS	-	expression tag	UNP B3PBE0
C	31	HIS	-	expression tag	UNP B3PBE0
C	32	HIS	-	expression tag	UNP B3PBE0
C	33	HIS	-	expression tag	UNP B3PBE0
C	34	HIS	-	expression tag	UNP B3PBE0
C	35	HIS	-	expression tag	UNP B3PBE0
D	26	MET	-	initiating methionine	UNP B3PBE0
D	27	GLY	-	expression tag	UNP B3PBE0
D	28	SER	-	expression tag	UNP B3PBE0
D	29	SER	-	expression tag	UNP B3PBE0
D	30	HIS	-	expression tag	UNP B3PBE0
D	31	HIS	-	expression tag	UNP B3PBE0
D	32	HIS	-	expression tag	UNP B3PBE0
D	33	HIS	-	expression tag	UNP B3PBE0
D	34	HIS	-	expression tag	UNP B3PBE0
D	35	HIS	-	expression tag	UNP B3PBE0
E	26	MET	-	initiating methionine	UNP B3PBE0
E	27	GLY	-	expression tag	UNP B3PBE0
E	28	SER	-	expression tag	UNP B3PBE0
E	29	SER	-	expression tag	UNP B3PBE0
E	30	HIS	-	expression tag	UNP B3PBE0
E	31	HIS	-	expression tag	UNP B3PBE0
E	32	HIS	-	expression tag	UNP B3PBE0
E	33	HIS	-	expression tag	UNP B3PBE0
E	34	HIS	-	expression tag	UNP B3PBE0
E	35	HIS	-	expression tag	UNP B3PBE0
F	26	MET	-	initiating methionine	UNP B3PBE0
F	27	GLY	-	expression tag	UNP B3PBE0
F	28	SER	-	expression tag	UNP B3PBE0
F	29	SER	-	expression tag	UNP B3PBE0
F	30	HIS	-	expression tag	UNP B3PBE0

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Chain	Residue	Modelled	Actual	Comment	Reference
F	31	HIS	-	expression tag	UNP B3PBE0
F	32	HIS	-	expression tag	UNP B3PBE0
F	33	HIS	-	expression tag	UNP B3PBE0
F	34	HIS	-	expression tag	UNP B3PBE0
F	35	HIS	-	expression tag	UNP B3PBE0
G	26	MET	-	initiating methionine	UNP B3PBE0
G	27	GLY	-	expression tag	UNP B3PBE0
G	28	SER	-	expression tag	UNP B3PBE0
G	29	SER	-	expression tag	UNP B3PBE0
G	30	HIS	-	expression tag	UNP B3PBE0
G	31	HIS	-	expression tag	UNP B3PBE0
G	32	HIS	-	expression tag	UNP B3PBE0
G	33	HIS	-	expression tag	UNP B3PBE0
G	34	HIS	-	expression tag	UNP B3PBE0
G	35	HIS	-	expression tag	UNP B3PBE0
H	26	MET	-	initiating methionine	UNP B3PBE0
H	27	GLY	-	expression tag	UNP B3PBE0
H	28	SER	-	expression tag	UNP B3PBE0
H	29	SER	-	expression tag	UNP B3PBE0
H	30	HIS	-	expression tag	UNP B3PBE0
H	31	HIS	-	expression tag	UNP B3PBE0
H	32	HIS	-	expression tag	UNP B3PBE0
H	33	HIS	-	expression tag	UNP B3PBE0
H	34	HIS	-	expression tag	UNP B3PBE0
H	35	HIS	-	expression tag	UNP B3PBE0

- Molecule 2 is SODIUM ION (three-letter code: NA) (formula: Na).

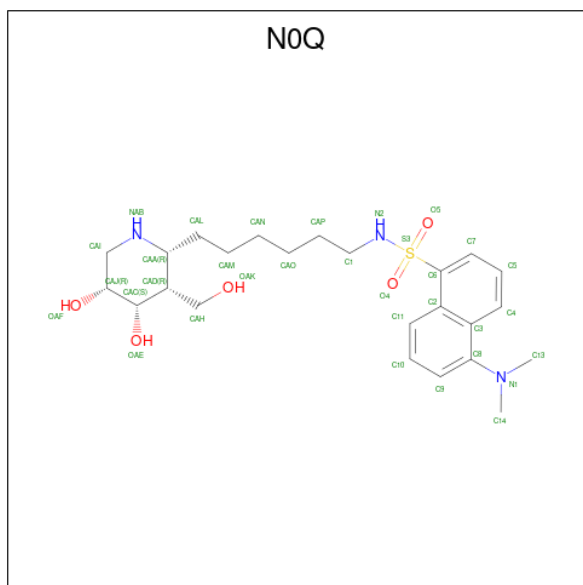
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	4	Total Na 4 4	0	0
2	B	3	Total Na 3 3	0	0
2	C	4	Total Na 4 4	0	0
2	D	5	Total Na 5 5	0	0
2	E	5	Total Na 5 5	0	0
2	F	4	Total Na 4 4	0	0
2	G	5	Total Na 5 5	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	H	2	Total	Na	0	0
			2	2		

- Molecule 3 is 5-(dimethylamino)- {N}-[6-[(2 {R},3 {R},4 {S},5 {R})-3-(hydroxymethyl)-4,5-bis(oxidanyl)piperidin-2-yl]hexyl]naphthalene-1-sulfonamide (three-letter code: N0Q) (formula: C<sub>24</sub>H<sub>37</sub>N<sub>3</sub>O<sub>5</sub>S) (labeled as "Ligand of Interest" by depositor).



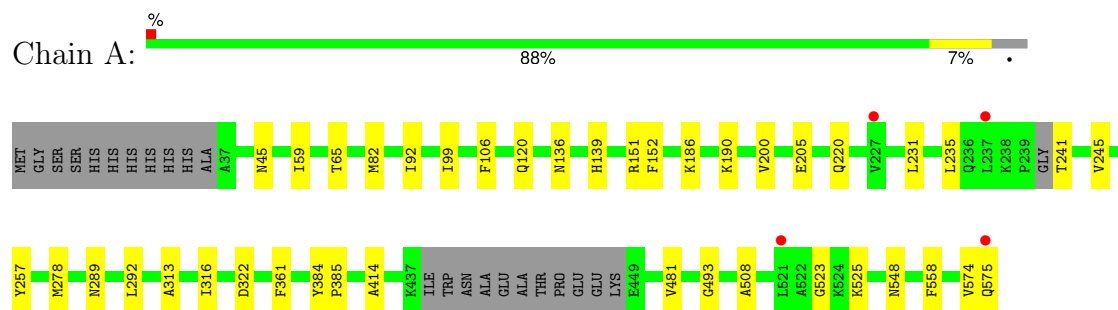
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	238	Total 238	O 238	0	0
4	B	300	Total 300	O 300	0	0
4	C	286	Total 286	O 286	0	0
4	D	344	Total 344	O 344	0	0
4	E	359	Total 359	O 359	0	0
4	F	308	Total 308	O 308	0	0
4	G	390	Total 390	O 390	0	0
4	H	277	Total 277	O 277	0	0



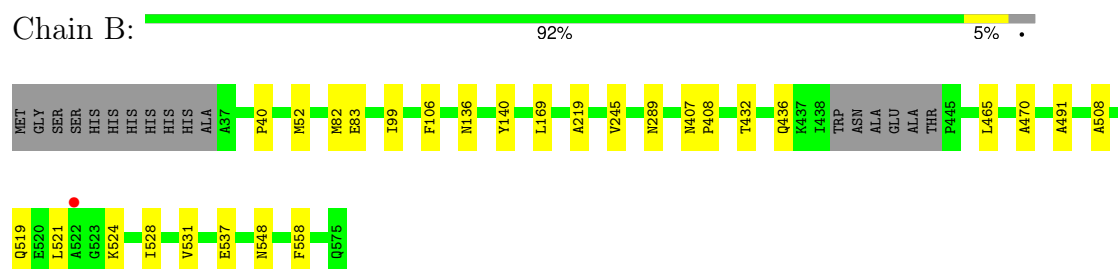
### 3 Residue-property plots [i](#)

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.

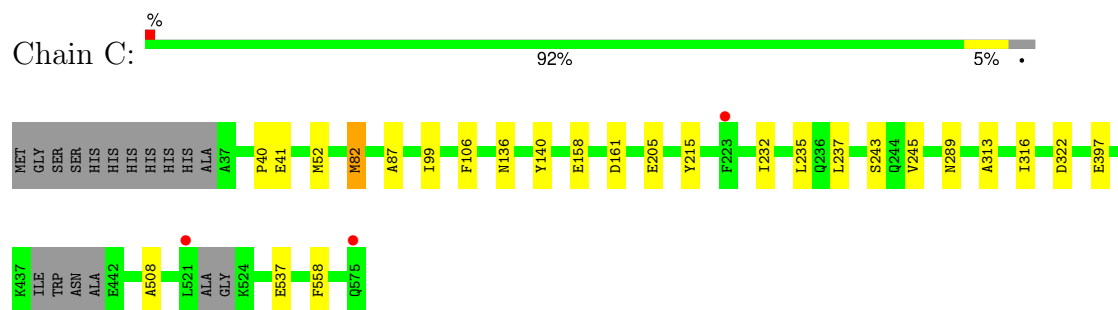
- Molecule 1: Beta-galactosidase, putative, bgl35A



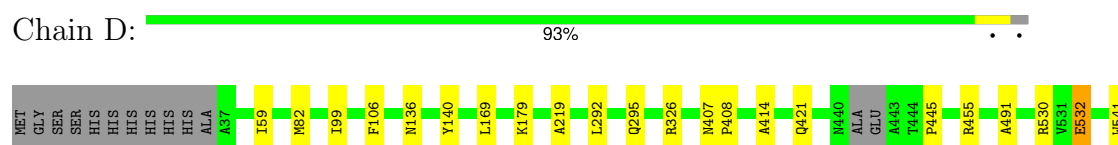
- Molecule 1: Beta-galactosidase, putative, bgl35A



- Molecule 1: Beta-galactosidase, putative, bgl35A



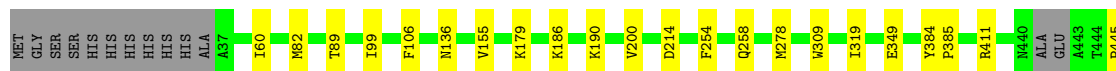
- Molecule 1: Beta-galactosidase, putative, bgl35A





- Molecule 1: Beta-galactosidase, putative, bgl35A

Chain E: 93% 5% .



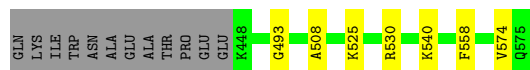
- Molecule 1: Beta-galactosidase, putative, bgl35A

Chain F: 92% 5% .



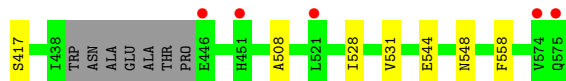
- Molecule 1: Beta-galactosidase, putative, bgl35A

Chain G: 90% 6% .



- Molecule 1: Beta-galactosidase, putative, bgl35A

Chain H: 91% 6% .



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	98.95Å 116.05Å 115.58Å 89.84° 90.07° 89.98°	Depositor
Resolution (Å)	63.20 – 1.60 63.16 – 1.60	Depositor EDS
% Data completeness (in resolution range)	95.8 (63.20-1.60) 95.8 (63.16-1.60)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.48 (at 1.60Å)	Xtriage
Refinement program	REFMAC 5.8.0253	Depositor
R, $R_{free}$	0.152 , 0.212 0.163 , 0.218	Depositor DCC
$R_{free}$ test set	32511 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	23.6	Xtriage
Anisotropy	0.249	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 44.3	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.45$ , $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	0.076 for h,l,-k 0.076 for h,-l,k 0.048 for h,-k,-l 0.032 for -h,-k,l 0.034 for -h,k,-l 0.036 for -h,-l,-k 0.033 for -h,l,k	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	36143	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.05% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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 [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: N0Q, NA

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	0.95	2/4249 (0.0%)	1.00	1/5792 (0.0%)
1	B	0.94	0/4297	1.02	0/5857
1	C	0.96	2/4264 (0.0%)	1.02	0/5816
1	D	0.94	1/4339 (0.0%)	0.99	1/5914 (0.0%)
1	E	0.96	1/4322 (0.0%)	1.04	1/5893 (0.0%)
1	F	0.99	3/4360 (0.1%)	1.05	3/5940 (0.1%)
1	G	0.92	2/4280 (0.0%)	1.03	1/5832 (0.0%)
1	H	0.96	2/4285 (0.0%)	1.01	0/5843
All	All	0.95	13/34396 (0.0%)	1.02	7/46887 (0.0%)

The worst 5 of 13 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	F	336	GLU	CD-OE2	-8.55	1.16	1.25
1	C	397	GLU	CD-OE1	7.55	1.33	1.25
1	G	349	GLU	CD-OE2	7.14	1.33	1.25
1	A	575	GLN	C-O	6.91	1.36	1.23
1	H	544	GLU	CD-OE2	-6.38	1.18	1.25

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	530	ARG	NE-CZ-NH2	-7.26	116.67	120.30
1	D	530	ARG	NE-CZ-NH2	-6.65	116.98	120.30
1	F	455	ARG	NE-CZ-NH1	-5.55	117.53	120.30
1	G	530	ARG	NE-CZ-NH2	-5.41	117.60	120.30
1	E	411	ARG	NE-CZ-NH1	5.09	122.84	120.30

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	4138	0	3969	17	0
1	B	4182	0	4008	11	0
1	C	4153	0	3950	14	0
1	D	4227	0	4051	13	0
1	E	4207	0	4028	10	0
1	F	4245	0	4068	19	0
1	G	4162	0	4026	14	0
1	H	4170	0	3990	14	0
2	A	4	0	0	0	0
2	B	3	0	0	0	0
2	C	4	0	0	0	0
2	D	5	0	0	0	0
2	E	5	0	0	0	0
2	F	4	0	0	0	0
2	G	5	0	0	0	0
2	H	2	0	0	0	0
3	A	21	0	0	0	0
3	B	14	0	0	0	0
3	C	13	0	0	0	0
3	D	21	0	0	0	0
3	E	13	0	0	1	0
3	F	15	0	0	0	0
3	G	15	0	0	0	0
3	H	13	0	0	0	0
4	A	238	0	0	1	0
4	B	300	0	0	0	0
4	C	286	0	0	0	0
4	D	344	0	0	3	0
4	E	359	0	0	0	0
4	F	308	0	0	8	0
4	G	390	0	0	1	0
4	H	277	0	0	2	0
All	All	36143	0	32090	107	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 2.

The worst 5 of 107 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:F:241:THR:OG1	1:F:244:GLN:HG3	1.79	0.81
1:F:179:LYS:HE2	4:F:742:HOH:O	1.81	0.78
1:H:169:LEU:HD12	1:H:219:ALA:HA	1.66	0.77
1:F:415[C]:ARG:HH21	1:F:415[C]:ARG:HG3	1.55	0.72
1:A:139:HIS:HB2	4:A:899:HOH:O	1.89	0.71

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	521/550 (95%)	503 (96%)	18 (4%)	0	100	100
1	B	530/550 (96%)	515 (97%)	14 (3%)	1 (0%)	47	26
1	C	527/550 (96%)	507 (96%)	20 (4%)	0	100	100
1	D	536/550 (98%)	516 (96%)	18 (3%)	2 (0%)	34	15
1	E	535/550 (97%)	517 (97%)	16 (3%)	2 (0%)	34	15
1	F	537/550 (98%)	519 (97%)	18 (3%)	0	100	100
1	G	526/550 (96%)	510 (97%)	16 (3%)	0	100	100
1	H	530/550 (96%)	511 (96%)	19 (4%)	0	100	100
All	All	4242/4400 (96%)	4098 (97%)	139 (3%)	5 (0%)	51	29

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	445	PRO
1	B	491	ALA
1	D	491	ALA
1	E	491	ALA

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Mol	Chain	Res	Type
1	D	445	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	425/461 (92%)	418 (98%)	7 (2%)	62	41
1	B	427/461 (93%)	420 (98%)	7 (2%)	62	41
1	C	421/461 (91%)	415 (99%)	6 (1%)	67	47
1	D	433/461 (94%)	430 (99%)	3 (1%)	84	73
1	E	430/461 (93%)	425 (99%)	5 (1%)	71	54
1	F	435/461 (94%)	430 (99%)	5 (1%)	73	57
1	G	429/461 (93%)	424 (99%)	5 (1%)	71	54
1	H	426/461 (92%)	419 (98%)	7 (2%)	62	41
All	All	3426/3688 (93%)	3381 (99%)	45 (1%)	69	50

5 of 45 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	F	63	SER
1	G	179	LYS
1	F	83	GLU
1	F	520	GLU
1	G	540	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 15 such sidechains are listed below:

Mol	Chain	Res	Type
1	F	64	GLN
1	H	289	ASN
1	F	224	ASN
1	H	421	GLN

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	G	289	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 ⓘ

There are no monosaccharides in this entry.

## 5.6 Ligand geometry ⓘ

Of 40 ligands modelled in this entry, 32 are monoatomic - leaving 8 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	$\# Z  > 2$
3	N0Q	H	603	-	13,13,35	1.73	2 (15%)	10,17,49	1.47	2 (20%)
3	N0Q	C	605	-	13,13,35	0.93	1 (7%)	10,17,49	1.81	2 (20%)
3	N0Q	F	605	-	15,15,35	3.01	5 (33%)	13,19,49	1.23	1 (7%)
3	N0Q	A	605	-	21,21,35	1.91	5 (23%)	21,28,49	2.43	8 (38%)
3	N0Q	B	604	-	14,14,35	1.69	4 (28%)	12,18,49	1.81	3 (25%)
3	N0Q	D	606	-	21,21,35	2.37	7 (33%)	21,28,49	1.98	6 (28%)
3	N0Q	E	606	-	13,13,35	1.53	3 (23%)	10,17,49	1.57	3 (30%)
3	N0Q	G	606	-	15,15,35	2.13	4 (26%)	13,19,49	1.52	3 (23%)

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	N0Q	H	603	-	-	2/5/22/40	0/1/1/3
3	N0Q	C	605	-	-	2/5/22/40	0/1/1/3
3	N0Q	F	605	-	-	4/7/24/40	0/1/1/3
3	N0Q	A	605	-	-	8/13/30/40	0/1/1/3
3	N0Q	B	604	-	-	3/6/23/40	0/1/1/3
3	N0Q	D	606	-	-	7/13/30/40	0/1/1/3
3	N0Q	E	606	-	-	3/5/22/40	0/1/1/3
3	N0Q	G	606	-	-	3/7/24/40	0/1/1/3

The worst 5 of 31 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	F	605	N0Q	CAI-NAB	-6.62	1.38	1.47
3	D	606	N0Q	C6-S3	-6.37	1.61	1.75
3	F	605	N0Q	CAD-CAC	-6.36	1.46	1.53
3	A	605	N0Q	C6-S3	-5.65	1.62	1.75
3	F	605	N0Q	CAJ-CAC	-5.32	1.44	1.52

The worst 5 of 28 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	605	N0Q	O5-S3-O4	-6.88	109.65	118.87
3	D	606	N0Q	O5-S3-O4	-4.87	112.34	118.87
3	C	605	N0Q	CAI-CAJ-CAC	4.36	115.58	110.25
3	B	604	N0Q	CAM-CAL-CAA	-4.15	106.03	113.94
3	A	605	N0Q	O4-S3-N2	3.77	112.58	107.33

There are no chirality outliers.

5 of 32 torsion outliers are listed below:

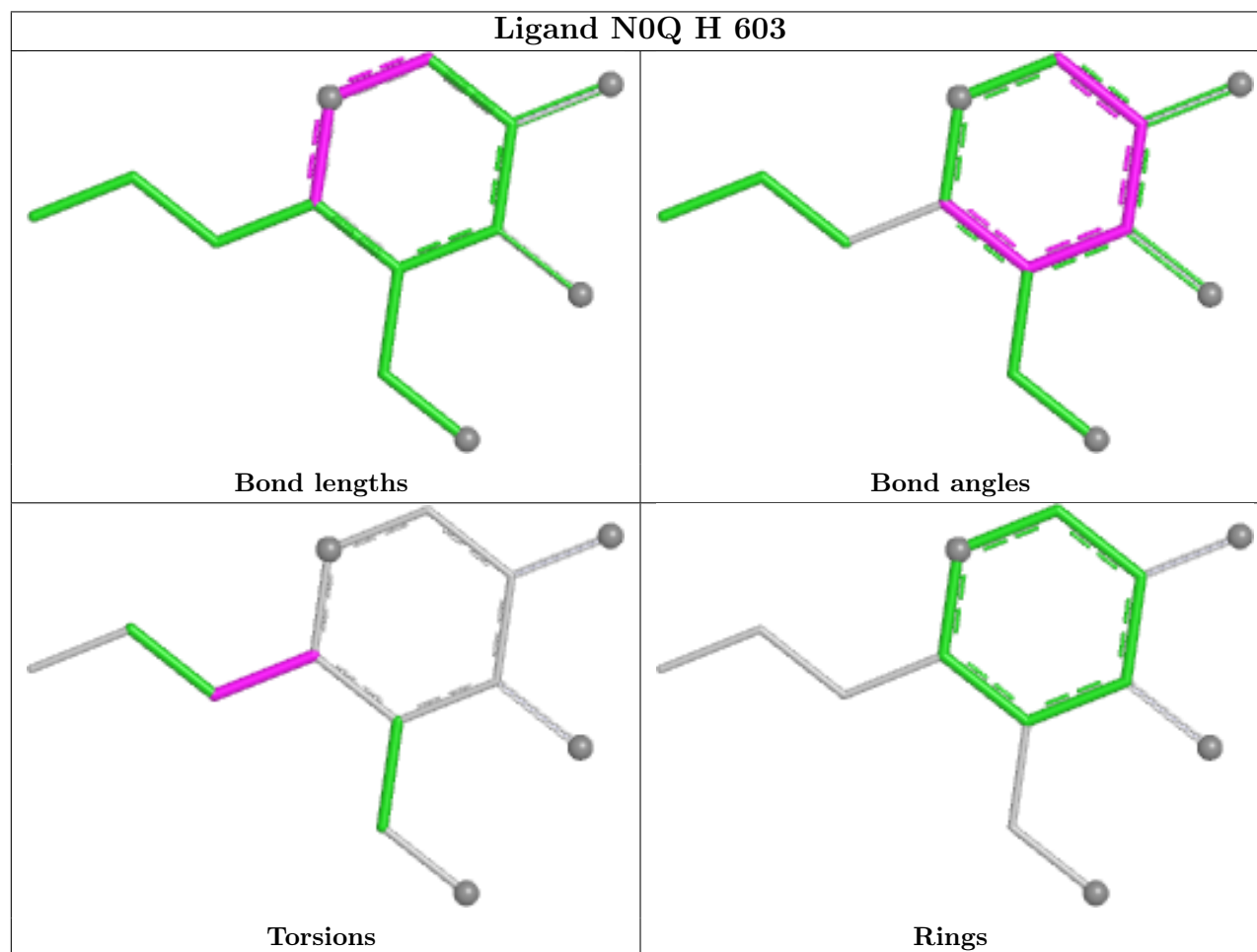
Mol	Chain	Res	Type	Atoms
3	A	605	N0Q	C1-N2-S3-C6
3	A	605	N0Q	C1-N2-S3-O4
3	A	605	N0Q	C1-N2-S3-O5
3	A	605	N0Q	N2-C1-CAP-CAO
3	A	605	N0Q	NAB-CAA-CAL-CAM

There are no ring outliers.

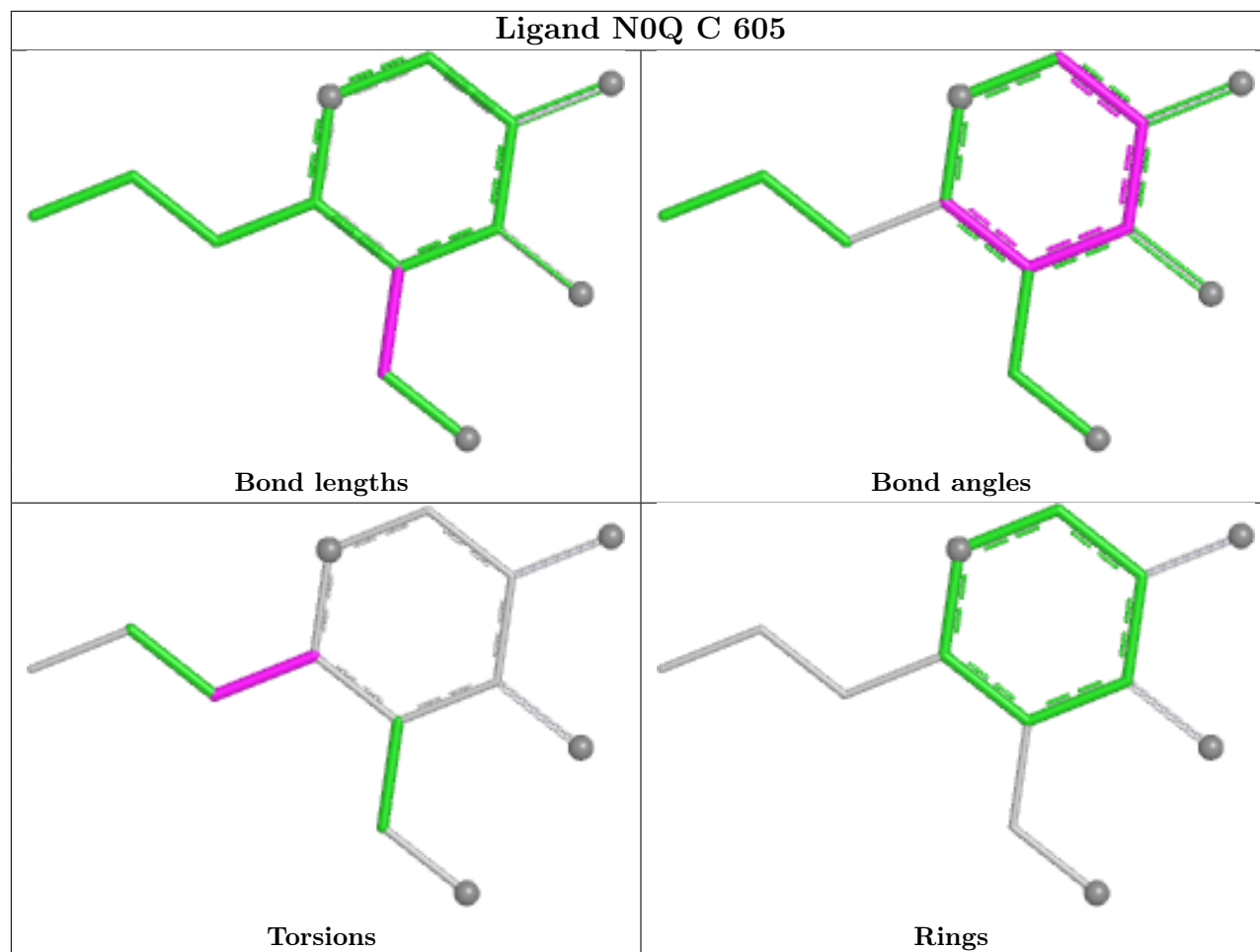
1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	E	606	N0Q	1	0

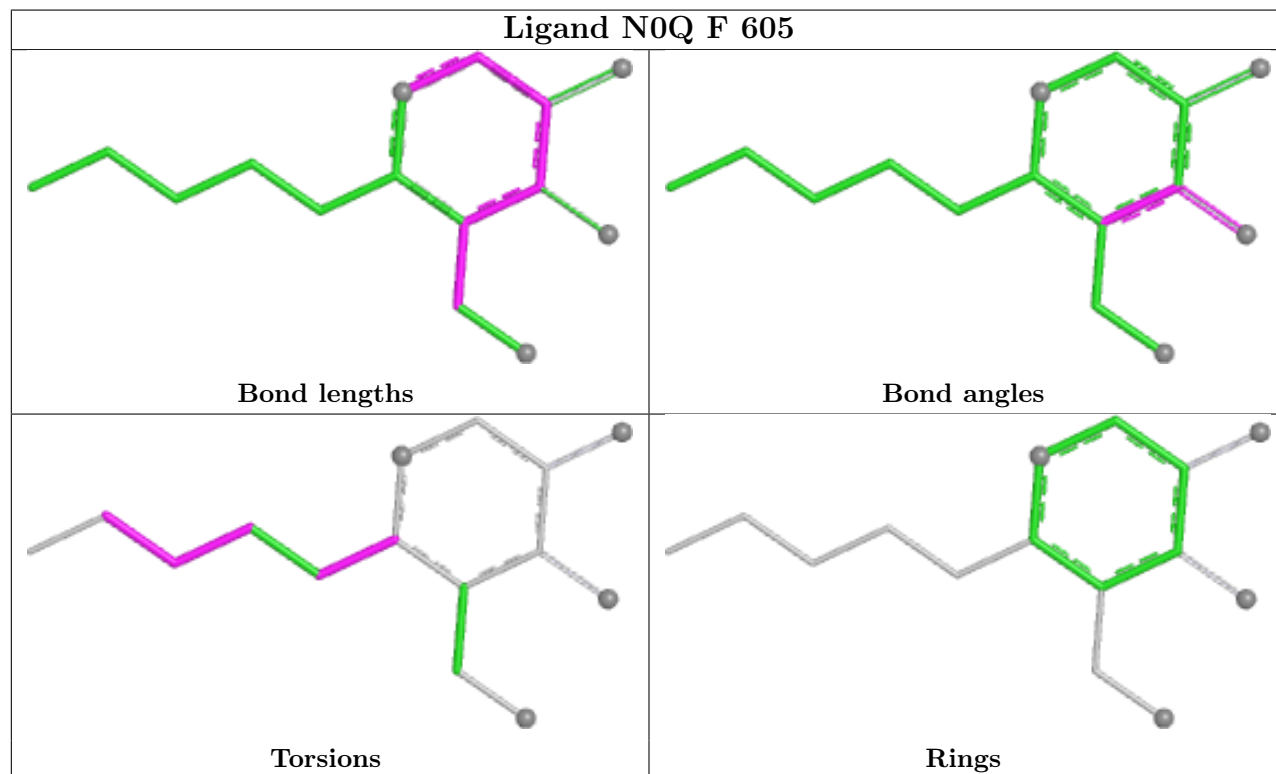
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

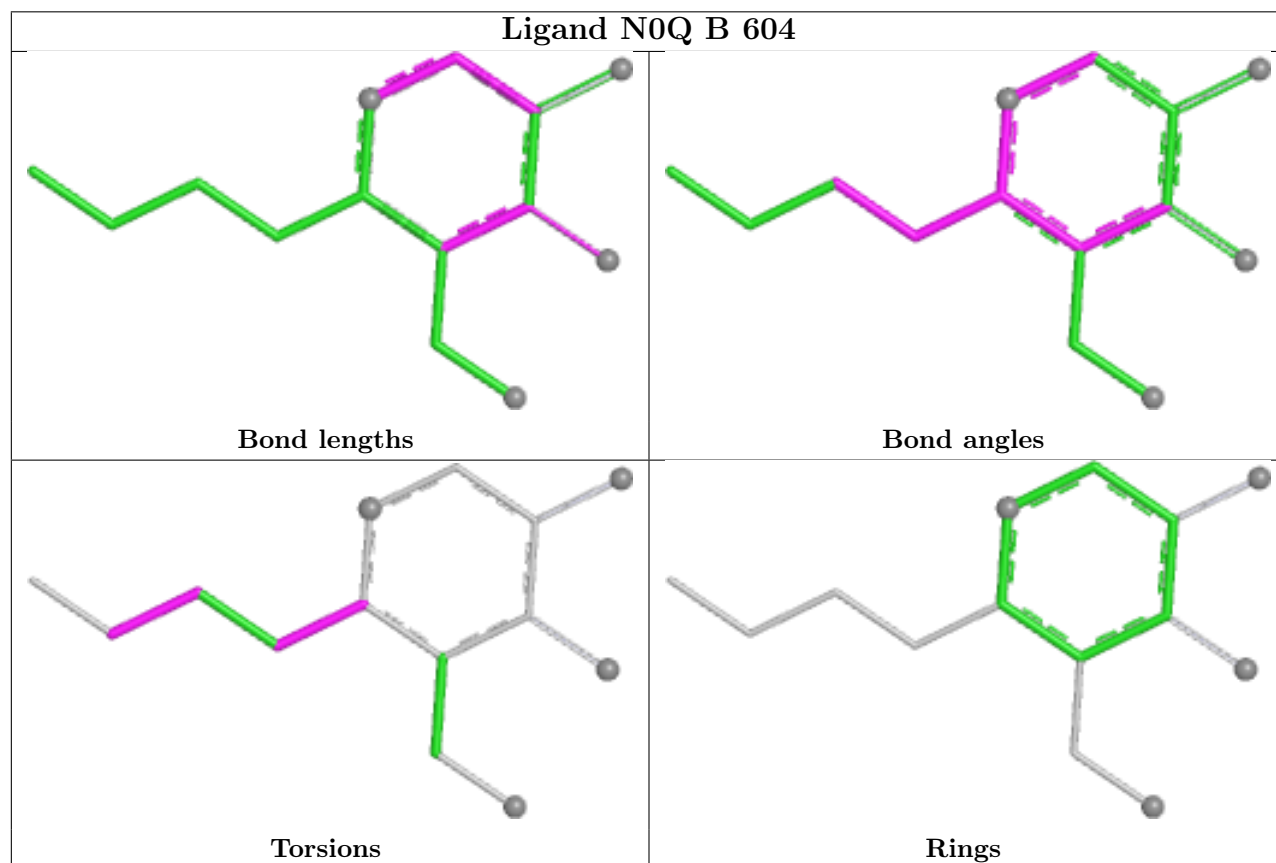
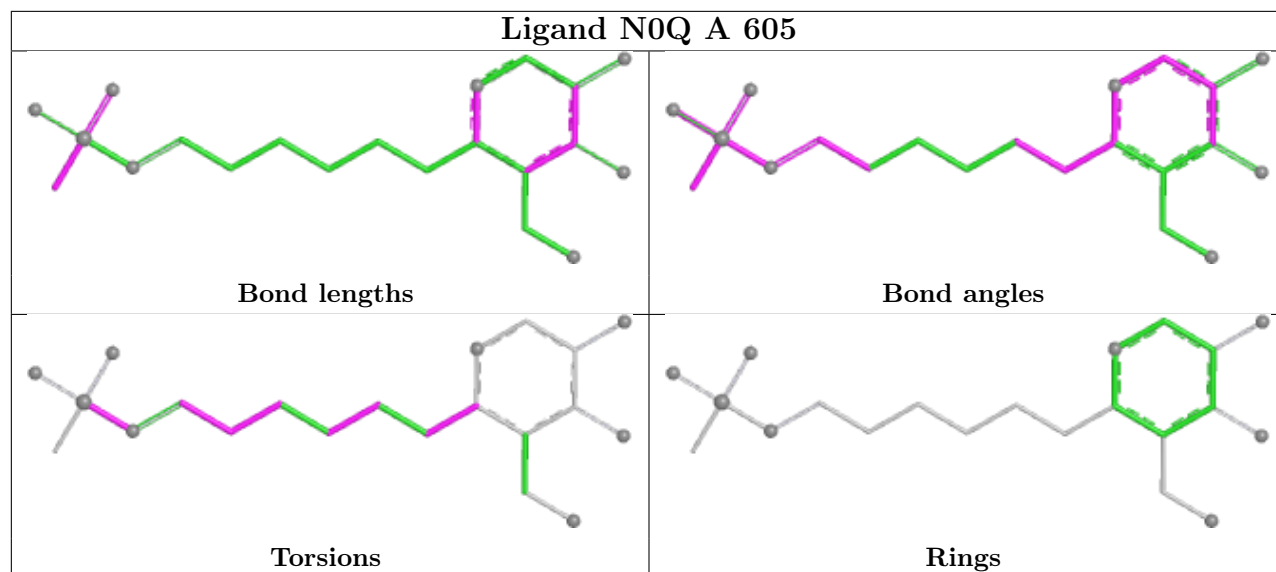


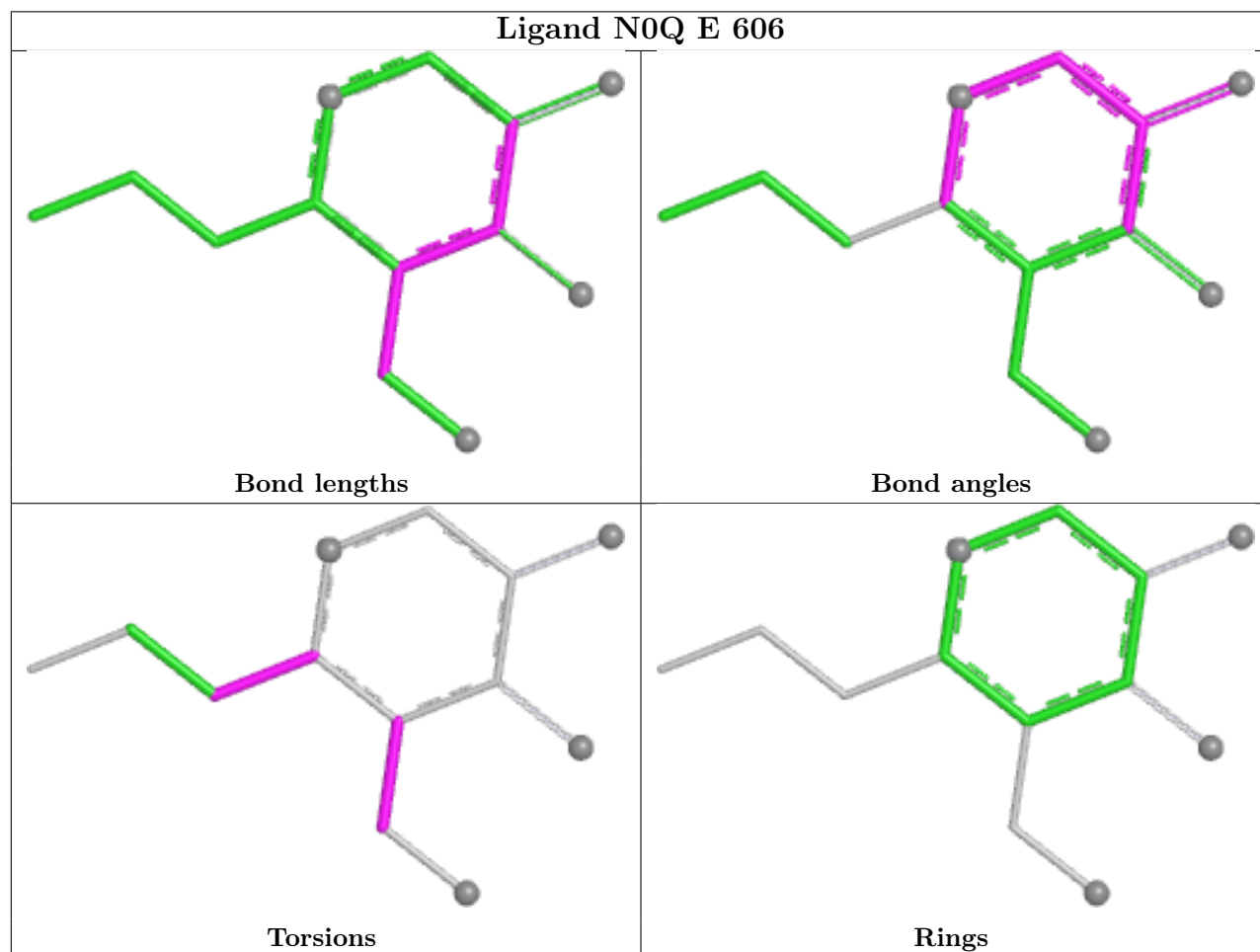
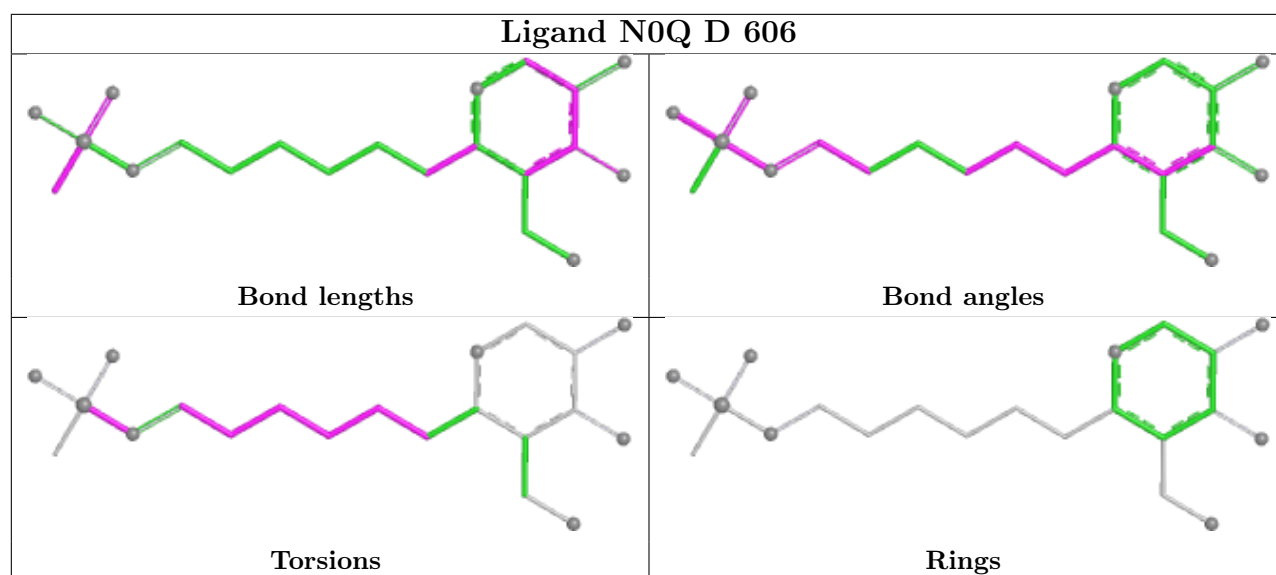
## Ligand N0Q C 605

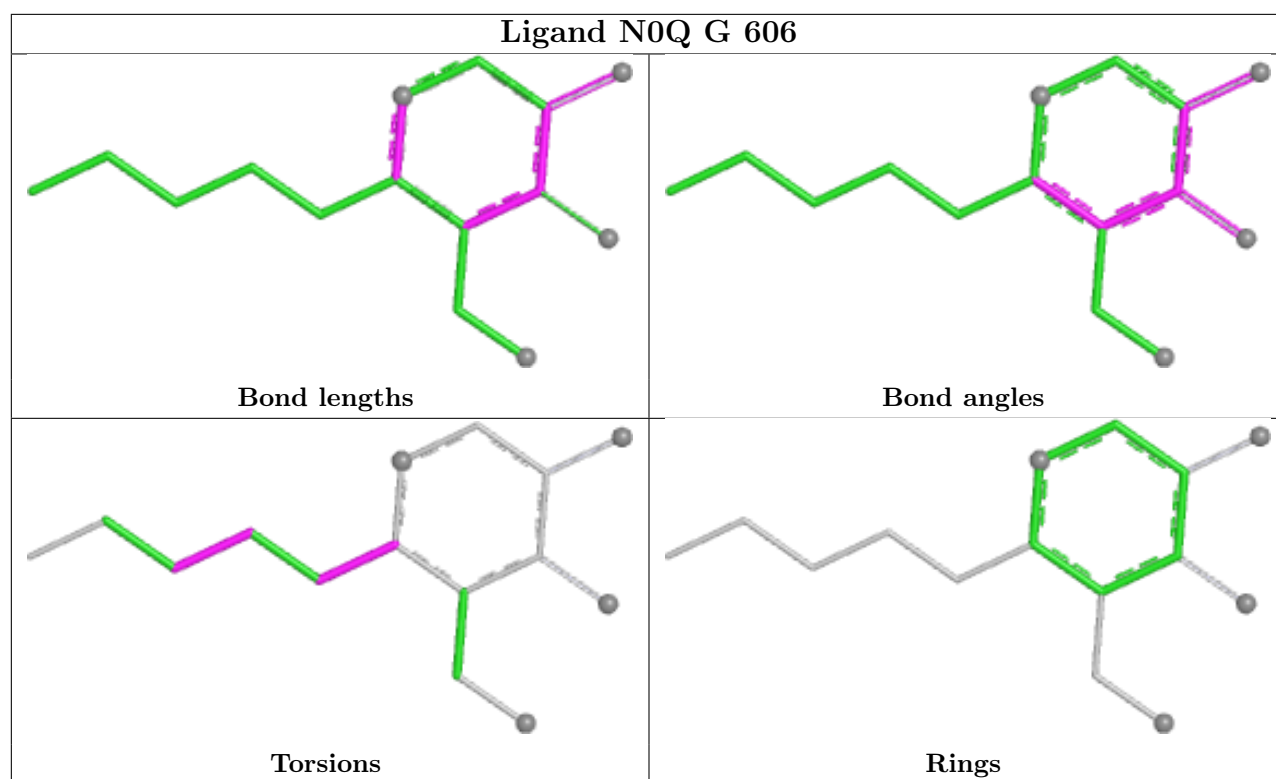


## Ligand N0Q F 605









## 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q < 0.9
1	A	527/550 (95%)	-0.24	4 (0%) 86 86	20, 30, 53, 83	25 (4%)
1	B	533/550 (96%)	-0.32	1 (0%) 95 94	20, 26, 46, 62	20 (3%)
1	C	533/550 (96%)	-0.19	3 (0%) 89 89	20, 28, 50, 67	32 (6%)
1	D	537/550 (97%)	-0.27	1 (0%) 95 94	16, 25, 43, 59	23 (4%)
1	E	537/550 (97%)	-0.27	1 (0%) 95 94	16, 25, 46, 61	17 (3%)
1	F	535/550 (97%)	-0.21	2 (0%) 92 92	17, 28, 51, 67	30 (5%)
1	G	526/550 (95%)	-0.29	1 (0%) 95 94	17, 25, 46, 65	12 (2%)
1	H	532/550 (96%)	-0.28	6 (1%) 80 80	20, 28, 46, 70	24 (4%)
All	All	4260/4400 (96%)	-0.26	19 (0%) 92 92	16, 27, 48, 83	183 (4%)

The worst 5 of 19 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	522	ALA	6.6
1	C	575	GLN	4.2
1	H	575	GLN	3.9
1	F	226	ALA	3.7
1	A	521	LEU	3.1

### 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](#)

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<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
2	NA	A	602	1/1	0.93	0.08	40,40,40,40	0
2	NA	C	603	1/1	0.95	0.05	47,47,47,47	0
2	NA	C	604	1/1	0.95	0.06	50,50,50,50	0
3	N0Q	C	605	13/33	0.95	0.08	19,24,31,40	0
3	N0Q	H	603	13/33	0.95	0.08	20,22,28,32	0
3	N0Q	D	606	21/33	0.96	0.10	18,22,52,61	8
3	N0Q	E	606	13/33	0.96	0.09	18,19,28,32	1
3	N0Q	A	605	21/33	0.96	0.10	22,25,50,64	9
2	NA	C	602	1/1	0.97	0.08	39,39,39,39	0
2	NA	E	604	1/1	0.97	0.06	35,35,35,35	0
2	NA	A	604	1/1	0.97	0.06	39,39,39,39	0
3	N0Q	F	605	15/33	0.97	0.08	20,22,38,41	3
3	N0Q	G	606	15/33	0.97	0.08	17,22,33,37	2
3	N0Q	B	604	14/33	0.97	0.07	19,22,32,35	1
2	NA	D	605	1/1	0.98	0.07	29,29,29,29	0
2	NA	E	601	1/1	0.98	0.08	30,30,30,30	0
2	NA	A	601	1/1	0.98	0.09	37,37,37,37	0
2	NA	F	602	1/1	0.98	0.07	29,29,29,29	0
2	NA	F	603	1/1	0.98	0.09	35,35,35,35	0
2	NA	G	602	1/1	0.98	0.06	35,35,35,35	0
2	NA	G	605	1/1	0.98	0.07	33,33,33,33	0
2	NA	H	601	1/1	0.98	0.05	42,42,42,42	0
2	NA	G	603	1/1	0.99	0.08	29,29,29,29	0
2	NA	G	604	1/1	0.99	0.08	34,34,34,34	0
2	NA	D	603	1/1	0.99	0.12	31,31,31,31	0
2	NA	D	604	1/1	0.99	0.12	33,33,33,33	0
2	NA	H	602	1/1	0.99	0.06	30,30,30,30	0
2	NA	B	603	1/1	0.99	0.13	36,36,36,36	0
2	NA	C	601	1/1	0.99	0.08	33,33,33,33	0
2	NA	A	603	1/1	0.99	0.11	33,33,33,33	0
2	NA	E	605	1/1	0.99	0.10	29,29,29,29	0
2	NA	B	601	1/1	0.99	0.11	38,38,38,38	0
2	NA	B	602	1/1	0.99	0.14	34,34,34,34	0
2	NA	F	604	1/1	0.99	0.07	32,32,32,32	0
2	NA	D	601	1/1	0.99	0.07	33,33,33,33	0
2	NA	G	601	1/1	1.00	0.09	26,26,26,26	0
2	NA	F	601	1/1	1.00	0.09	29,29,29,29	0

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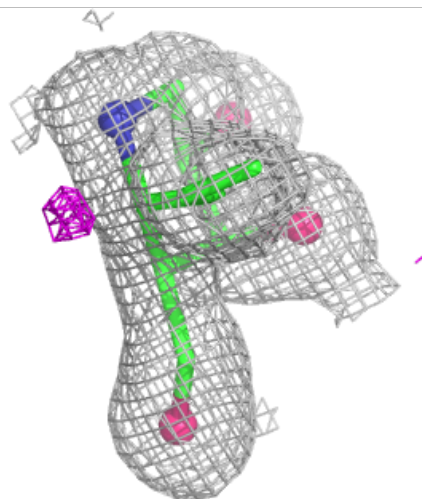
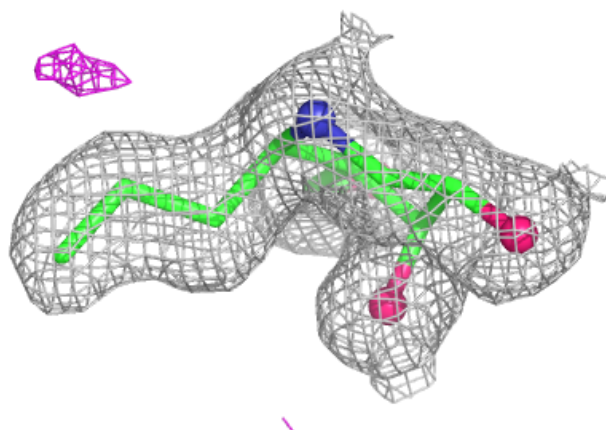
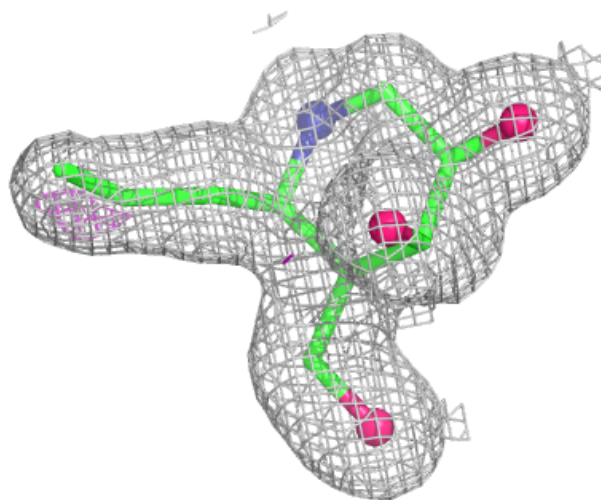
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	NA	E	603	1/1	1.00	0.07	28,28,28,28	0
2	NA	D	602	1/1	1.00	0.08	31,31,31,31	0
2	NA	E	602	1/1	1.00	0.08	27,27,27,27	0

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.

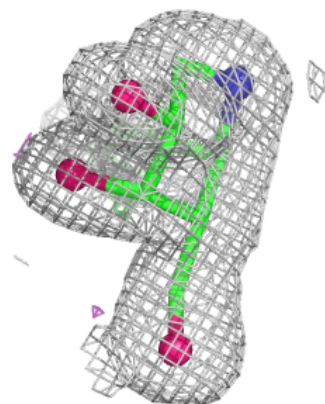
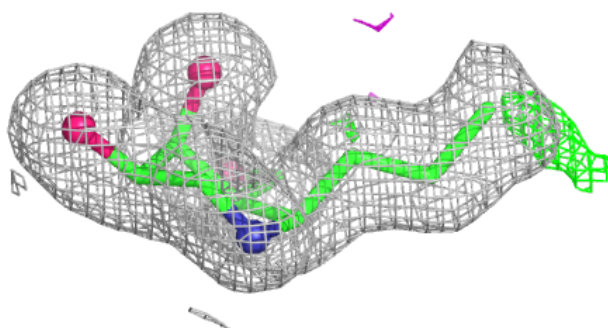
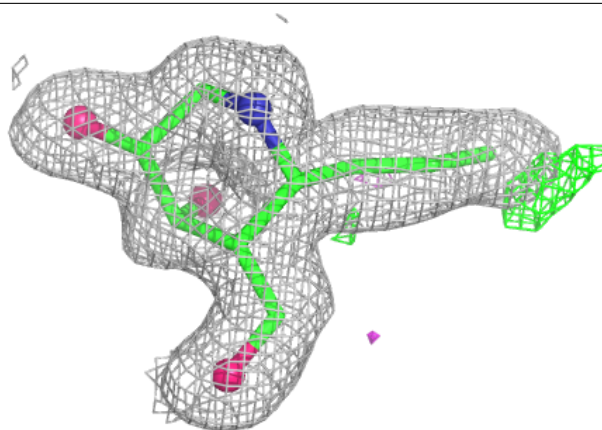
**Electron density around N0Q C 605:**

2mF<sub>o</sub>-DF<sub>c</sub> (at 0.7 rmsd) in gray  
mF<sub>o</sub>-DF<sub>c</sub> (at 3 rmsd) in purple (negative)  
and green (positive)

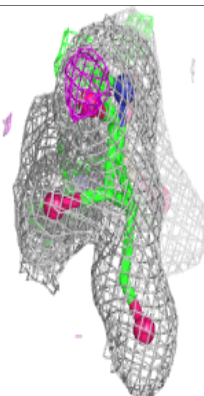
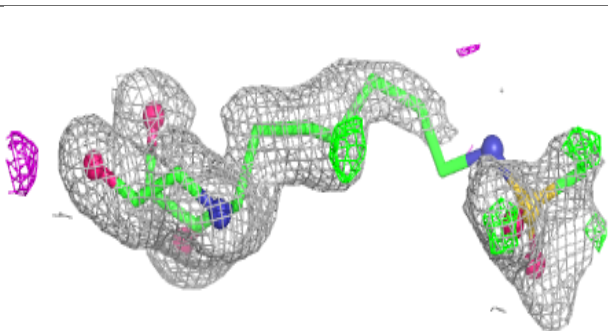
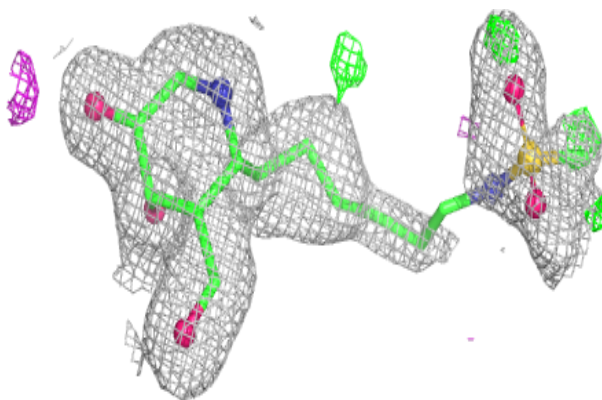


**Electron density around N0Q H 603:**

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and green (positive)

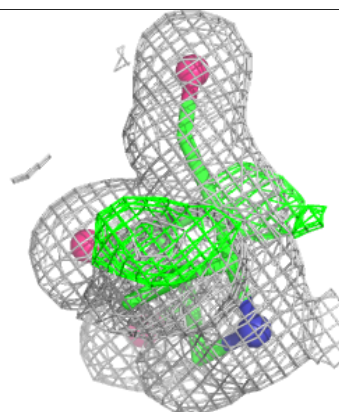
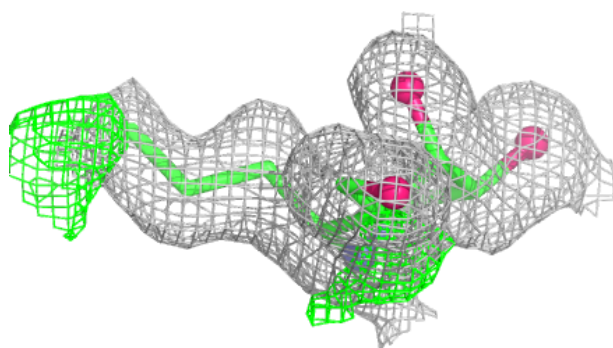
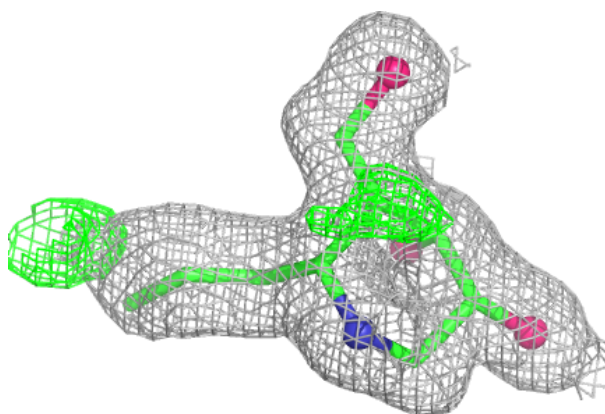
**Electron density around N0Q D 606:**

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

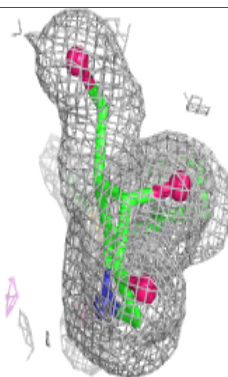
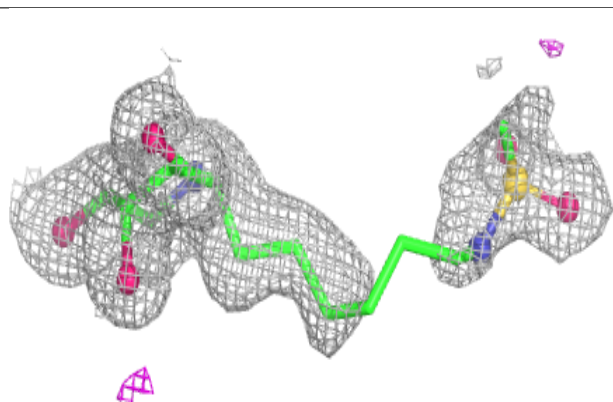
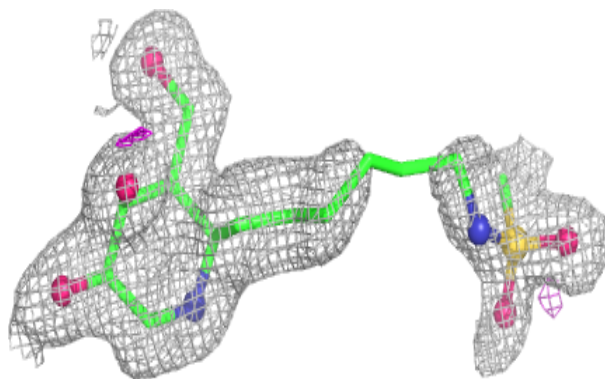


**Electron density around N0Q E 606:**

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and green (positive)

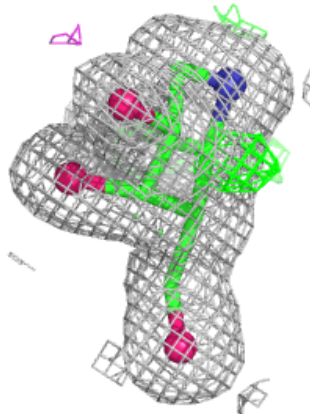
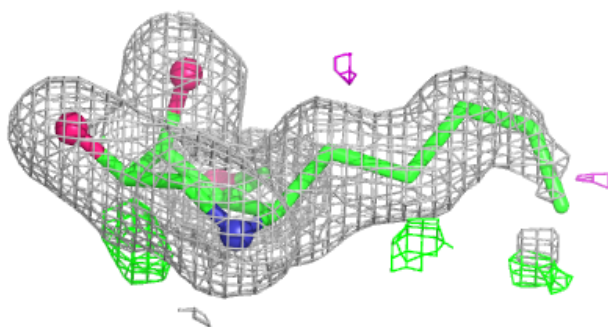
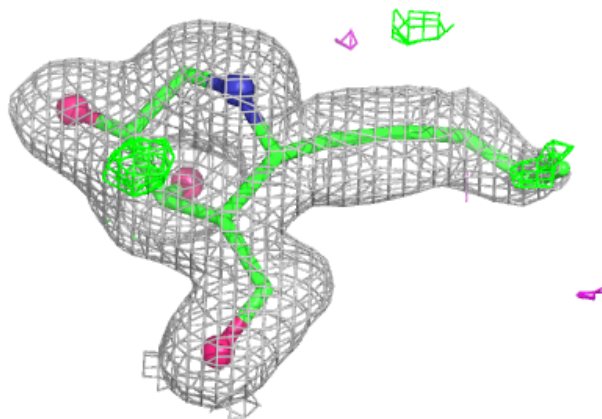
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and green (positive)



**Electron density around N0Q F 605:**

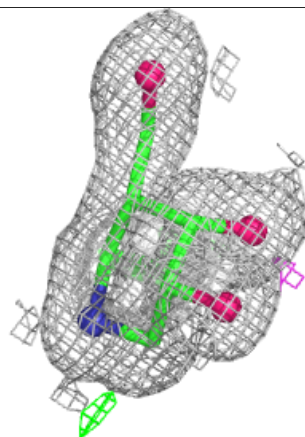
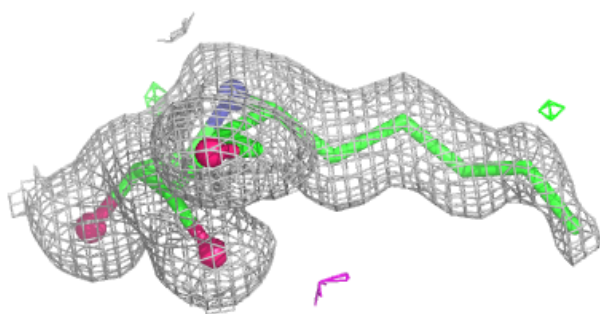
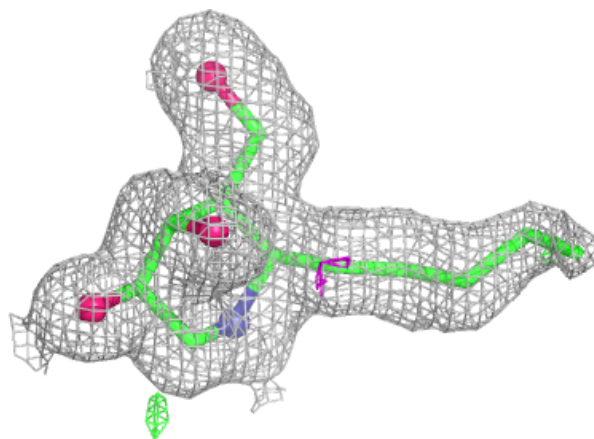
$2mF_o - DF_c$  (at 0.7 rmsd) in gray  
 $mF_o - DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





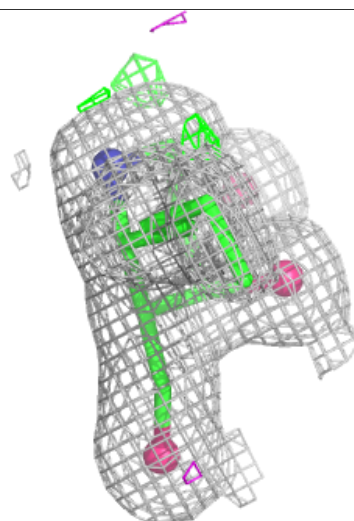
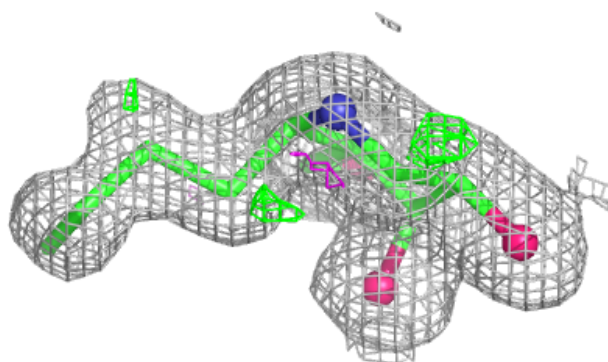
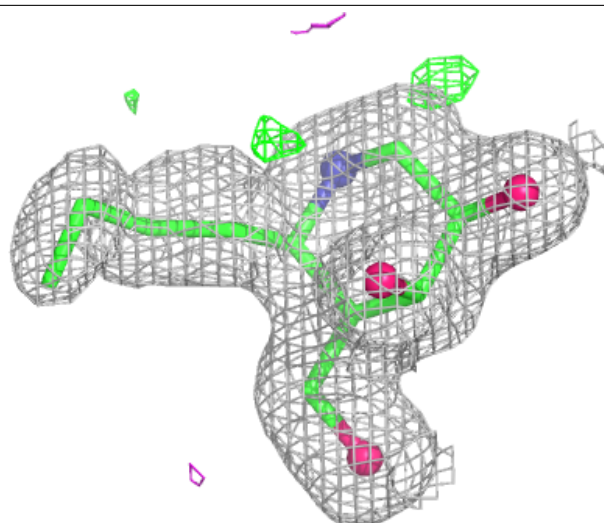
**Electron density around N0Q G 606:**

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



**Electron density around N0Q B 604:**

$2mF_o-DF_c$  (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.