



wwPDB X-ray Structure Validation Summary Report ⓘ

Sep 14, 2020 – 02:15 PM BST

PDB ID : 6WEW
Title : Crystal structures of human E-NPP 1: bound to N-{4-[(7-methoxyquinolin-4-yl)oxy]phenyl}sulfuric diamide
Authors : Peat, T.S.; Dennis, M.; Newman, J.
Deposited on : 2020-04-03
Resolution : 2.73 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 ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.14.4.dev1
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) : 2.14.4.dev1

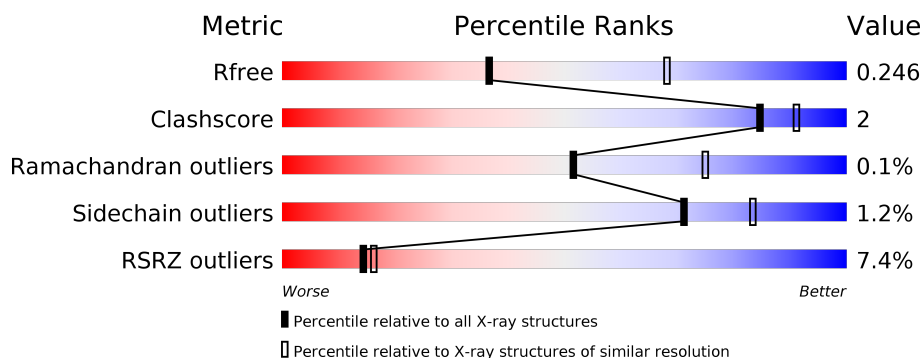
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.73 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.



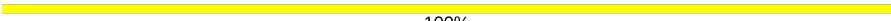
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1271 (2.76-2.72)
Clashscore	141614	1322 (2.76-2.72)
Ramachandran outliers	138981	1297 (2.76-2.72)
Sidechain outliers	138945	1298 (2.76-2.72)
RSRZ outliers	127900	1243 (2.76-2.72)

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 $\leq 5\%$. 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	AbA	925	<div> <div>4%</div> <div>88%</div> <div>12%</div> </div>
1	BaB	925	<div> <div>9%</div> <div>85%</div> <div>14%</div> </div>
2	AdA	4	<div> <div>100%</div> </div>
3	AhA	3	<div> <div>100%</div> </div>
4	AlA	2	<div> <div>100%</div> </div>
4	BeB	2	<div> <div>100%</div> </div>

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Mol	Chain	Length	Quality of chain
5	BbB	3	 100%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	BMA	AdA	4	X	-	-	-
4	NAG	BeB	2	X	-	-	-
8	NAG	BaB	1002	-	-	-	X

2 Entry composition [i](#)

There are 11 unique types of molecules in this entry. The entry contains 13249 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 Ectonucleotide pyrophosphatase/phosphodiesterase family member 1.

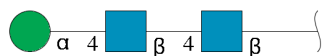
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	AbA	817	Total	C	N	O	S	0	5	0
			6572	4194	1117	1211	50			
1	BaB	795	Total	C	N	O	S	0	2	0
			6180	3937	1049	1147	47			

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



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	AdA	4	Total	C	N	O	0	0	0
			50	28	2	20			

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



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	AhA	3	Total	C	N	O	0	0	0
			39	22	2	15			

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



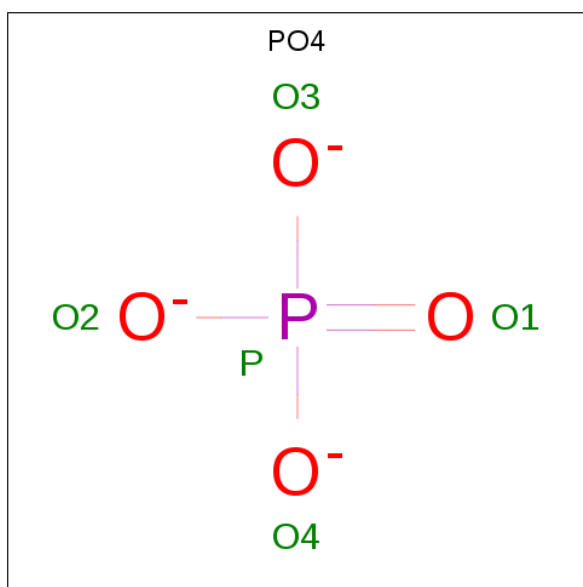
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	AlA	2	Total	C	N	O	0	0	0
			28	16	2	10			
4	BeB	2	Total	C	N	O	0	0	0
			28	16	2	10			

- Molecule 5 is an oligosaccharide called beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
5	BbB	3	Total	C	N	O	0	0	0
			39	22	2	15			

- Molecule 6 is PHOSPHATE ION (three-letter code: PO4) (formula: O₄P).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	AbA	1	Total	O	P	0	0
			4	3	1		

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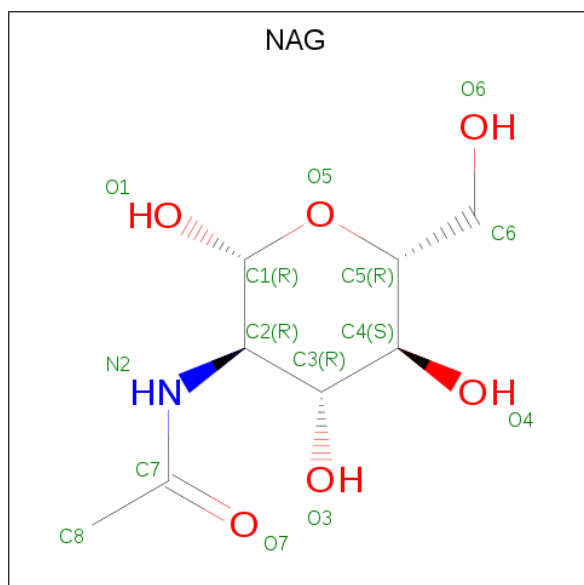
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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	BaB	1	Total	O	P	0	0
			5	4	1		

- Molecule 7 is ZINC ION (three-letter code: ZN) (formula: Zn).

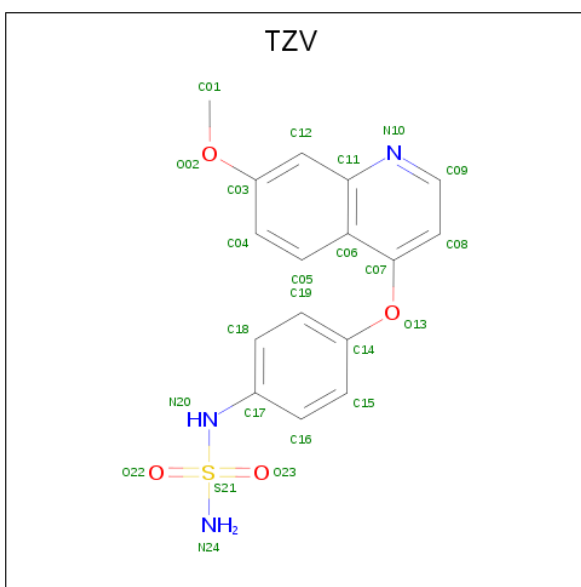
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	AbA	2	Total	Zn	0	0
			2	2		
7	BaB	1	Total	Zn	0	0
			1	1		

- Molecule 8 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: C₈H₁₅NO₆).



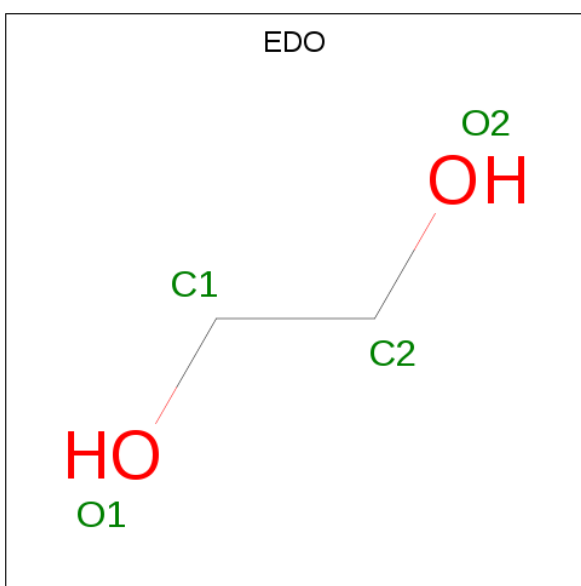
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
8	AbA	1	Total	C	N	O	0	0
			14	8	1	5		
8	AbA	1	Total	C	N	O	0	0
			14	8	1	5		
8	BaB	1	Total	C	N	O	0	0
			14	8	1	5		
8	BaB	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 9 is N-{4-[(7-methoxyquinolin-4-yl)oxy]phenyl}sulfuric diamide (three-letter code: TZV) (formula: C₁₆H₁₅N₃O₄S) (labeled as "Ligand of Interest" by author).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
9	AbA	1	Total	C	N	O	S	0	0
			24	16	3	4	1		
9	BaB	1	Total	C	N	O	S	0	0
			24	16	3	4	1		

- Molecule 10 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C₂H₆O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
10	AbA	1	Total	C	O	0	0
			4	2	2		
10	AbA	1	Total	C	O	0	0
			4	2	2		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
10	AbA	1	Total	C	O	0	0
			4	2	2		

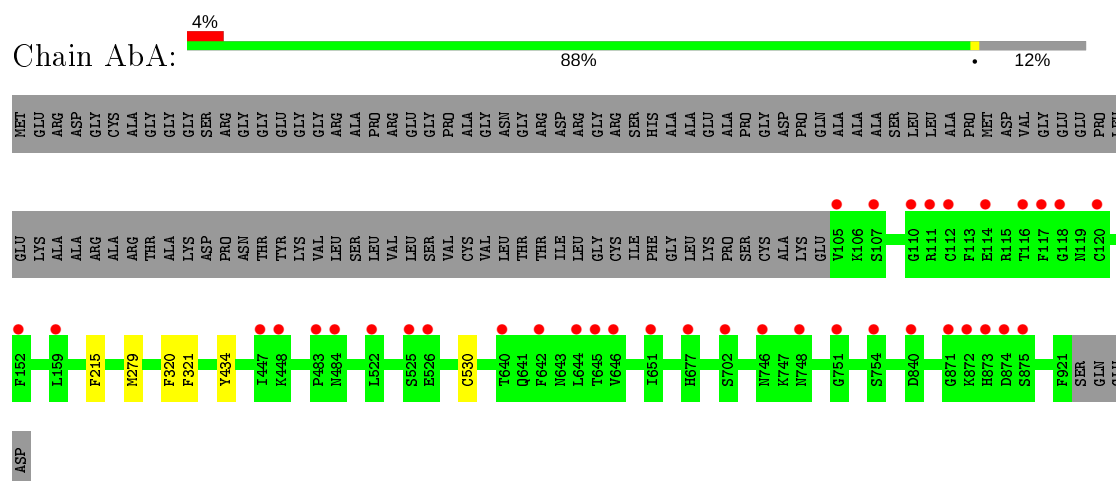
- Molecule 11 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
11	AbA	126	Total	O	0	0
			126	126		
11	BaB	59	Total	O	0	0
			59	59		

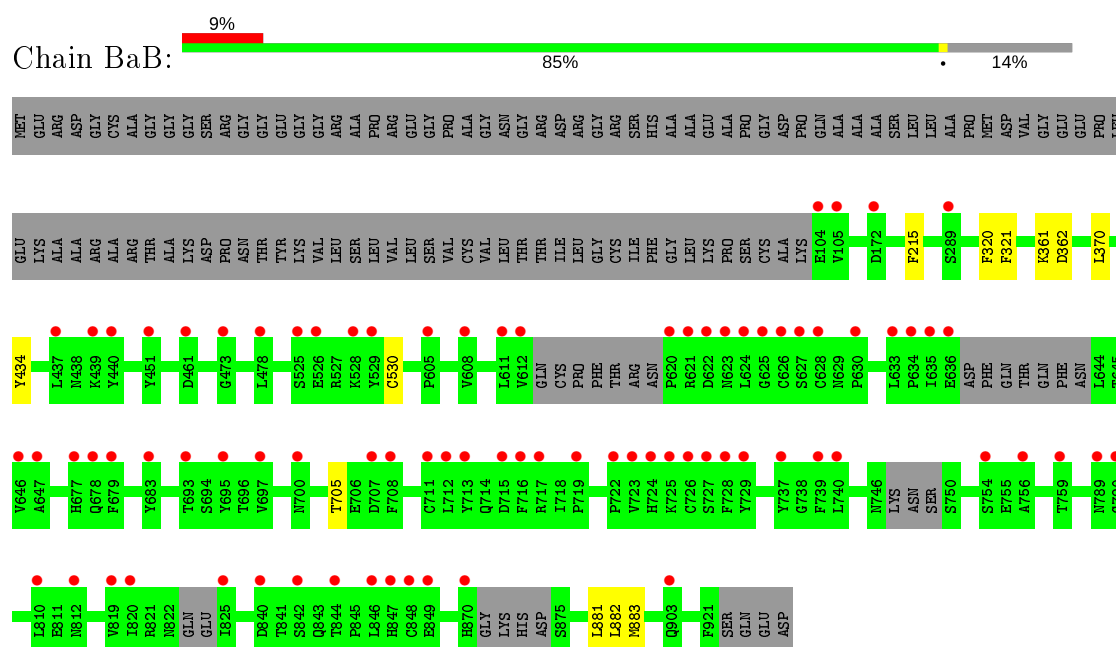
3 Residue-property plots

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: Ectonucleotide pyrophosphatase/phosphodiesterase family member 1



- Molecule 1: Ectonucleotide pyrophosphatase/phosphodiesterase family member 1




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

Chain AdA:  100%


MAG1
MAG2
BNA3
BNA4

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

Chain AhA:  100%


MAG1
MAG2
MAG3

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

Chain AlA:  100%


MAG1
MAG2

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

Chain BeB:  100%

MAG1
MAG2

- Molecule 5: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain BbB:  100%

MAG1
MAG2
BNA3

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	83.13Å 161.58Å 209.98Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.92 – 2.73 47.92 – 2.73	Depositor EDS
% Data completeness (in resolution range)	100.0 (47.92-2.73) 100.0 (47.92-2.73)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.62 (at 2.73Å)	Xtriage
Refinement program	REFMAC 5.8.0258	Depositor
R, R_{free}	0.210 , 0.241 0.217 , 0.246	Depositor DCC
R_{free} test set	3771 reflections (4.97%)	wwPDB-VP
Wilson B-factor (Å ²)	46.1	Xtriage
Anisotropy	0.063	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 35.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	13249	wwPDB-VP
Average B, all atoms (Å ²)	57.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.91% 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: ZN, BMA, NAG, TZV, PO4, EDO, MAN

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	AbA	0.63	0/6759	0.75	0/9180
1	BaB	0.64	0/6352	0.74	0/8645
All	All	0.63	0/13111	0.75	0/17825

There are no bond length outliers.

There are no bond angle outliers.

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	AbA	6572	0	6293	0	0
1	BaB	6180	0	5715	0	0
2	AdA	50	0	43	0	0
3	AhA	39	0	34	0	0
4	AlA	28	0	25	0	0
4	BeB	28	0	25	0	0
5	BbB	39	0	34	0	0
6	AbA	4	0	0	0	0
6	BaB	5	0	0	0	0
7	AbA	2	0	0	0	0
7	BaB	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	AbA	28	0	26	0	0
8	BaB	28	0	26	0	0
9	AbA	24	0	0	0	0
9	BaB	24	0	0	0	0
10	AbA	12	0	18	0	0
11	AbA	126	0	0	0	0
11	BaB	59	0	0	0	0
All	All	13249	0	12239	0	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.

There are no clashes within the asymmetric unit.

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	AbA	820/925 (89%)	782 (95%)	37 (4%)	1 (0%)	51 75
1	BaB	785/925 (85%)	745 (95%)	39 (5%)	1 (0%)	51 75
All	All	1605/1850 (87%)	1527 (95%)	76 (5%)	2 (0%)	51 75

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	AbA	321	PHE
1	BaB	321	PHE

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	AbA	733/824 (89%)	728 (99%)	5 (1%)	84	90
1	BaB	655/824 (80%)	644 (98%)	11 (2%)	60	76
All	All	1388/1648 (84%)	1372 (99%)	16 (1%)	71	83

5 of 16 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	BaB	361	LYS
1	BaB	362	ASP
1	BaB	705	THR
1	BaB	320	PHE
1	BaB	881	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 ⓘ

14 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
2	NAG	AdA	1	1,2	14,14,15	0.58	0	17,19,21	1.35	2 (11%)
2	NAG	AdA	2	2	14,14,15	0.56	0	17,19,21	1.10	2 (11%)
2	BMA	AdA	3	2	11,11,12	1.05	2 (18%)	15,15,17	2.83	5 (33%)
2	BMA	AdA	4	2	11,11,12	0.31	0	15,15,17	1.53	1 (6%)
3	NAG	AhA	1	1,3	14,14,15	0.62	0	17,19,21	1.93	4 (23%)
3	NAG	AhA	2	3	14,14,15	0.44	0	17,19,21	1.00	1 (5%)
3	MAN	AhA	3	3	11,11,12	0.43	0	15,15,17	1.25	1 (6%)
4	NAG	AlA	1	1,4	14,14,15	0.55	0	17,19,21	1.09	1 (5%)
4	NAG	AlA	2	4	14,14,15	0.37	0	17,19,21	0.92	1 (5%)
5	NAG	BbB	1	1,5	14,14,15	0.72	0	17,19,21	1.54	2 (11%)
5	NAG	BbB	2	5	14,14,15	0.31	0	17,19,21	1.16	2 (11%)
5	BMA	BbB	3	5	11,11,12	0.48	0	15,15,17	1.12	1 (6%)
4	NAG	BeB	1	1,4	14,14,15	0.73	0	17,19,21	2.01	4 (23%)
4	NAG	BeB	2	4	14,14,15	0.96	2 (14%)	17,19,21	2.36	5 (29%)

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	AdA	1	1,2	-	0/6/23/26	0/1/1/1
2	NAG	AdA	2	2	-	2/6/23/26	0/1/1/1
2	BMA	AdA	3	2	-	2/2/19/22	0/1/1/1
2	BMA	AdA	4	2	1/1/4/5	2/2/19/22	0/1/1/1
3	NAG	AhA	1	1,3	-	1/6/23/26	0/1/1/1
3	NAG	AhA	2	3	-	2/6/23/26	0/1/1/1
3	MAN	AhA	3	3	-	2/2/19/22	0/1/1/1
4	NAG	AlA	1	1,4	-	2/6/23/26	0/1/1/1
4	NAG	AlA	2	4	-	2/6/23/26	0/1/1/1
5	NAG	BbB	1	1,5	-	2/6/23/26	0/1/1/1
5	NAG	BbB	2	5	-	0/6/23/26	0/1/1/1
5	BMA	BbB	3	5	-	0/2/19/22	0/1/1/1
4	NAG	BeB	1	1,4	-	4/6/23/26	0/1/1/1
4	NAG	BeB	2	4	1/1/5/7	4/6/23/26	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	AdA	3	BMA	O5-C1	2.41	1.47	1.43
4	BeB	2	NAG	C1-C2	2.41	1.55	1.52
2	AdA	3	BMA	C1-C2	2.08	1.56	1.52
4	BeB	2	NAG	O5-C1	2.02	1.46	1.43

The worst 5 of 32 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	AdA	3	BMA	C1-O5-C5	6.84	121.45	112.19
4	BeB	2	NAG	C1-O5-C5	6.48	120.98	112.19
2	AdA	3	BMA	O2-C2-C1	5.80	121.03	109.15
3	AhA	1	NAG	O5-C1-C2	-5.60	102.45	111.29
2	AdA	4	BMA	C1-O5-C5	5.16	119.18	112.19

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
4	BeB	2	NAG	C1
2	AdA	4	BMA	C1

5 of 25 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	BeB	2	NAG	C8-C7-N2-C2
4	BeB	2	NAG	O7-C7-N2-C2
4	BeB	1	NAG	C8-C7-N2-C2
4	BeB	1	NAG	O7-C7-N2-C2
3	AhA	3	MAN	C4-C5-C6-O6

There are no ring outliers.

No monomer is involved in short contacts.

5.6 Ligand geometry ⓘ

Of 14 ligands modelled in this entry, 3 are monoatomic - leaving 11 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	$\# Z > 2$
10	EDO	AbA	1008	-	3,3,3	0.08	0	2,2,2	0.26	0
10	EDO	AbA	1009	-	3,3,3	0.18	0	2,2,2	0.36	0
8	NAG	AbA	1004	1	14,14,15	0.62	0	17,19,21	1.62	4 (23%)
8	NAG	BaB	1002	1	14,14,15	0.55	0	17,19,21	1.60	5 (29%)
8	NAG	AbA	1005	1	14,14,15	0.28	0	17,19,21	0.99	0
9	TZV	BaB	1004	-	25,26,26	1.06	1 (4%)	35,37,37	1.95	5 (14%)
6	PO4	AbA	1001	1,7	0,3,4	0.00	-	0,3,6	0.00	-
9	TZV	AbA	1006	-	25,26,26	1.12	1 (4%)	35,37,37	1.87	5 (14%)
8	NAG	BaB	1003	1	14,14,15	0.43	0	17,19,21	1.14	2 (11%)
6	PO4	BaB	1005	7	4,4,4	0.68	0	6,6,6	0.44	0
10	EDO	AbA	1007	-	3,3,3	0.05	0	2,2,2	0.17	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
10	EDO	AbA	1008	-	-	1/1/1/1	-
10	EDO	AbA	1009	-	-	1/1/1/1	-
8	NAG	AbA	1004	1	-	3/6/23/26	0/1/1/1
8	NAG	BaB	1002	1	-	3/6/23/26	0/1/1/1
8	NAG	AbA	1005	1	-	2/6/23/26	0/1/1/1
9	TZV	BaB	1004	-	-	3/10/11/11	0/3/3/3
9	TZV	AbA	1006	-	-	4/10/11/11	0/3/3/3
8	NAG	BaB	1003	1	-	1/6/23/26	0/1/1/1
10	EDO	AbA	1007	-	-	1/1/1/1	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	BaB	1004	TZV	C06-C11	-3.57	1.36	1.42
9	AbA	1006	TZV	C06-C11	-3.50	1.36	1.42

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	BaB	1004	TZV	O23-S21-O22	-8.17	101.25	119.96
9	AbA	1006	TZV	O23-S21-O22	-8.09	101.45	119.96
8	AbA	1004	NAG	C1-C2-N2	-4.21	103.30	110.49
9	BaB	1004	TZV	C07-O13-C14	-3.73	111.36	118.52
8	BaB	1002	NAG	C1-C2-N2	3.59	116.62	110.49

There are no chirality outliers.

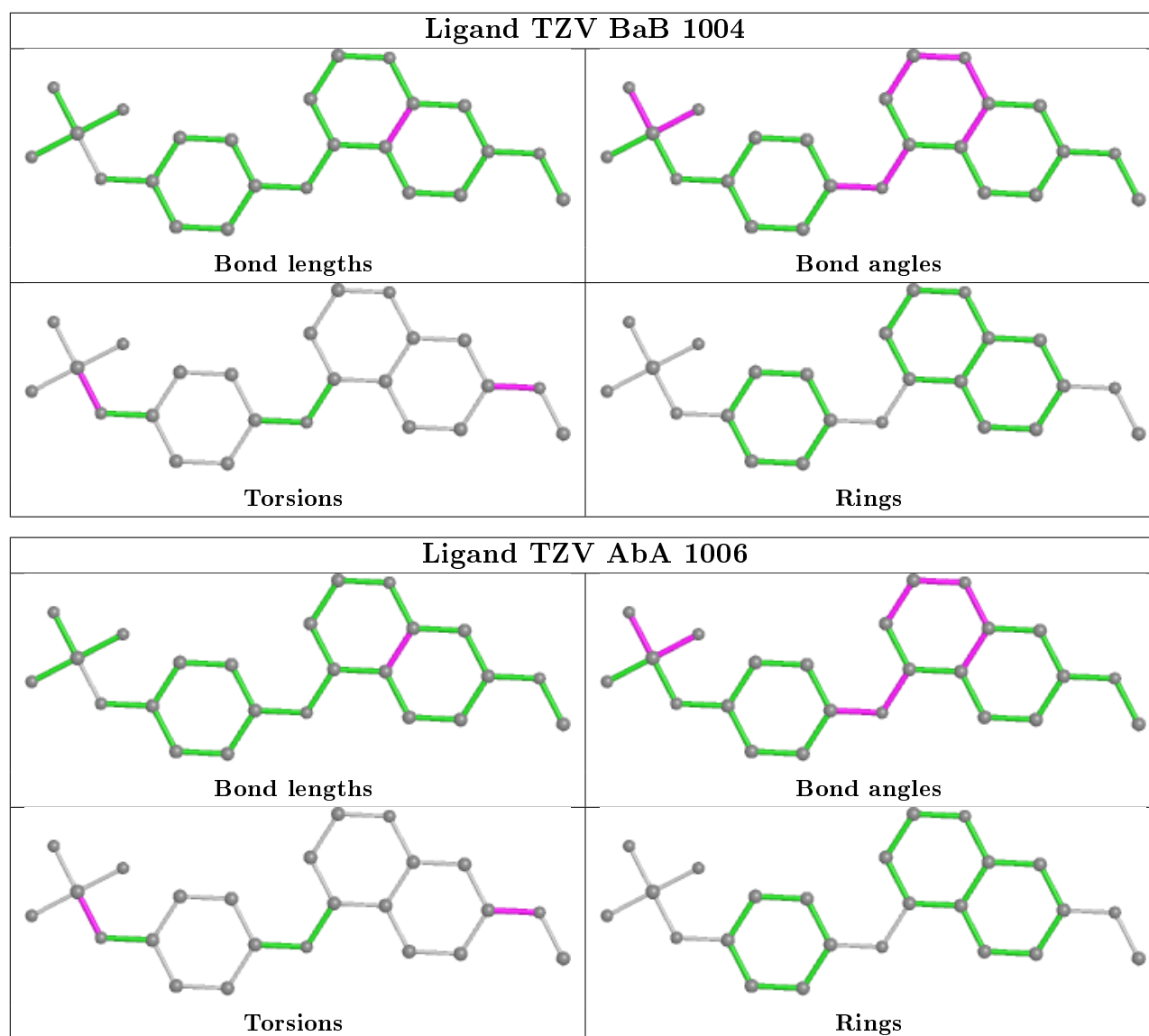
5 of 19 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
9	BaB	1004	TZV	C17-N20-S21-O22
9	AbA	1006	TZV	C17-N20-S21-O22
9	AbA	1006	TZV	C17-N20-S21-O23
9	AbA	1006	TZV	C04-C03-O02-C01
9	AbA	1006	TZV	C12-C03-O02-C01

There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for 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	AbA	817/925 (88%)	0.18	37 (4%) 33 36	22, 41, 87, 150	0
1	BaB	795/925 (85%)	0.54	82 (10%) 6 6	25, 63, 127, 152	0
All	All	1612/1850 (87%)	0.36	119 (7%) 14 16	22, 49, 117, 152	0

The worst 5 of 119 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	BaB	716	PHE	8.4
1	BaB	712	LEU	6.9
1	BaB	626	CYS	5.6
1	BaB	624	LEU	5.2
1	BaB	729	TYR	5.1

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
2	BMA	AdA	4	11/12	0.52	0.33	119,137,143,152	0
2	BMA	AdA	3	11/12	0.74	0.19	86,93,99,111	0
5	BMA	BbB	3	11/12	0.76	0.28	86,103,108,108	0
3	MAN	AhA	3	11/12	0.77	0.28	98,111,122,127	0
4	NAG	AlA	2	14/15	0.84	0.40	123,141,148,151	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
4	NAG	BeB	2	14/15	0.87	0.31	81,93,96,98	0
3	NAG	AhA	2	14/15	0.89	0.20	65,75,84,98	0
3	NAG	AhA	1	14/15	0.89	0.18	50,65,72,75	0
2	NAG	AdA	2	14/15	0.90	0.15	52,59,66,83	0
5	NAG	BbB	2	14/15	0.90	0.17	77,88,91,99	0
4	NAG	AlA	1	14/15	0.91	0.20	71,84,100,111	0
4	NAG	BeB	1	14/15	0.91	0.30	70,80,83,88	0
5	NAG	BbB	1	14/15	0.92	0.15	56,61,68,76	0
2	NAG	AdA	1	14/15	0.96	0.19	31,34,37,46	0

6.4 Ligands ⓘ

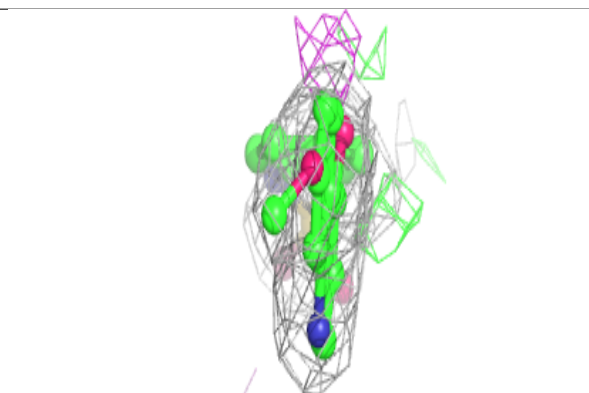
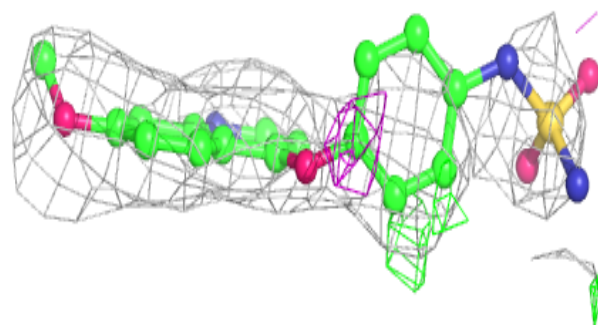
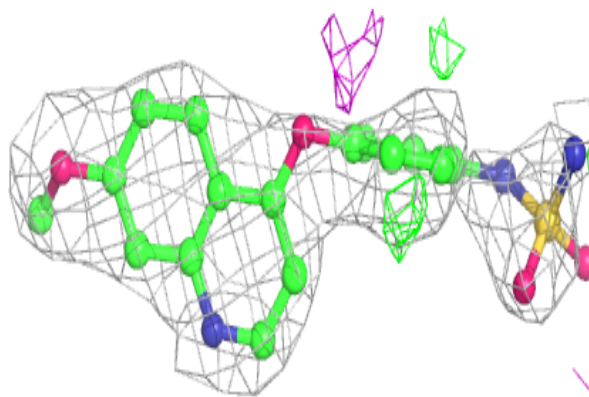
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
8	NAG	BaB	1002	14/15	0.73	0.42	118,134,143,151	0
8	NAG	AbA	1004	14/15	0.77	0.39	91,101,114,115	0
6	PO4	AbA	1001	4/5	0.82	0.28	71,82,93,95	0
10	EDO	AbA	1009	4/4	0.84	0.23	62,63,66,66	0
9	TZV	BaB	1004	24/24	0.88	0.31	48,61,112,123	0
8	NAG	AbA	1005	14/15	0.89	0.30	67,86,93,95	0
9	TZV	AbA	1006	24/24	0.89	0.29	33,41,109,117	0
8	NAG	BaB	1003	14/15	0.89	0.24	99,106,110,115	0
10	EDO	AbA	1008	4/4	0.90	0.26	58,60,61,62	0
7	ZN	AbA	1003	1/1	0.90	0.26	78,78,78,78	1
6	PO4	BaB	1005	5/5	0.90	0.20	49,49,52,52	5
10	EDO	AbA	1007	4/4	0.91	0.43	48,50,52,56	0
7	ZN	AbA	1002	1/1	0.98	0.08	44,44,44,44	0
7	ZN	BaB	1001	1/1	0.99	0.06	54,54,54,54	0

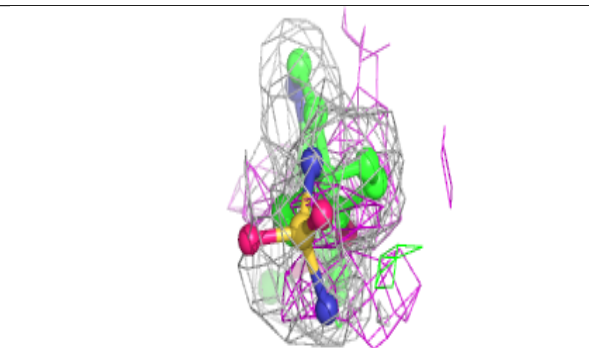
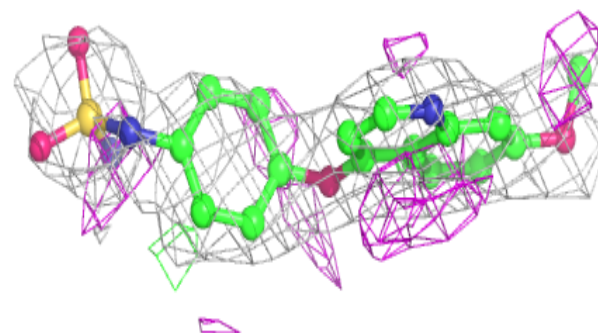
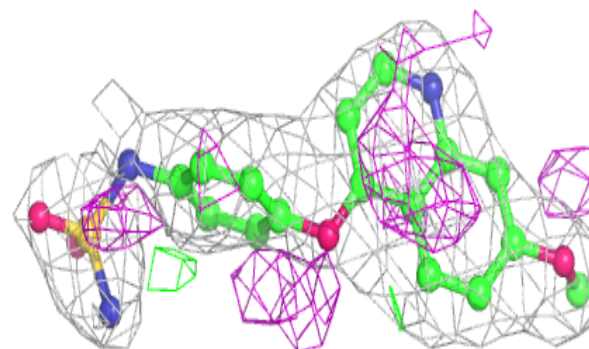
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around TZV BaB 1004:

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

**Electron density around TZV AbA 1006:**

$2mF_o-DF_c$ (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.