



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 06:28 PM UTC

PDB ID : 6W8C / pdb_00006w8c
Title : K2P2.1 (TREK-1):ML335 complex, 1 mM K+
Authors : Lolicato, M.; Minor, D.L.
Deposited on : 2020-03-20
Resolution : 2.60 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

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

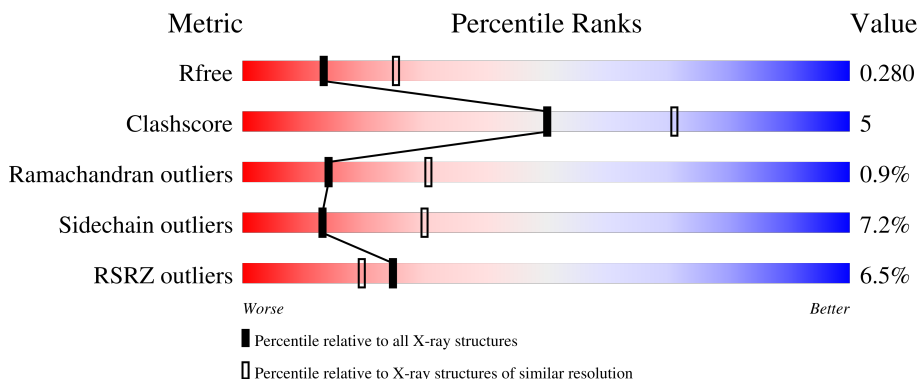
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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}	180053	4008 (2.60-2.60)
Clashscore	190562	4347 (2.60-2.60)
Ramachandran outliers	187476	4277 (2.60-2.60)
Sidechain outliers	187428	4277 (2.60-2.60)
RSRZ outliers	180081	4008 (2.60-2.60)

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 ≥ 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	312	 6% 73% 14% • 12%
1	B	312	 6% 75% 13% • 10%

2 Entry composition

There are 13 unique types of molecules in this entry. The entry contains 4741 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 Potassium channel subfamily K member 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	276	Total	C	N	O	S	0	0	0
			2159	1438	341	375	5			
1	B	281	Total	C	N	O	S	0	0	0
			2182	1453	345	379	5			

There are 46 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	20	MET	-	expression tag	UNP P97438
A	84	ARG	LYS	engineered mutation	UNP P97438
A	85	GLU	GLN	engineered mutation	UNP P97438
A	86	LYS	THR	engineered mutation	UNP P97438
A	88	LEU	ILE	engineered mutation	UNP P97438
A	89	ARG	ALA	engineered mutation	UNP P97438
A	90	ALA	GLN	engineered mutation	UNP P97438
A	92	PRO	ALA	engineered mutation	UNP P97438
A	95	SER	ASN	engineered mutation	UNP P97438
A	96	ASP	SER	engineered mutation	UNP P97438
A	97	GLN	THR	engineered mutation	UNP P97438
A	119	ALA	ASN	engineered mutation	UNP P97438
A	300	ALA	SER	engineered mutation	UNP P97438
A	306	ALA	GLU	engineered mutation	UNP P97438
A	323	SER	-	expression tag	UNP P97438
A	324	ASN	-	expression tag	UNP P97438
A	325	SER	-	expression tag	UNP P97438
A	326	LEU	-	expression tag	UNP P97438
A	327	GLU	-	expression tag	UNP P97438
A	328	VAL	-	expression tag	UNP P97438
A	329	LEU	-	expression tag	UNP P97438
A	330	PHE	-	expression tag	UNP P97438
A	331	GLN	-	expression tag	UNP P97438
B	20	MET	-	expression tag	UNP P97438
B	84	ARG	LYS	engineered mutation	UNP P97438

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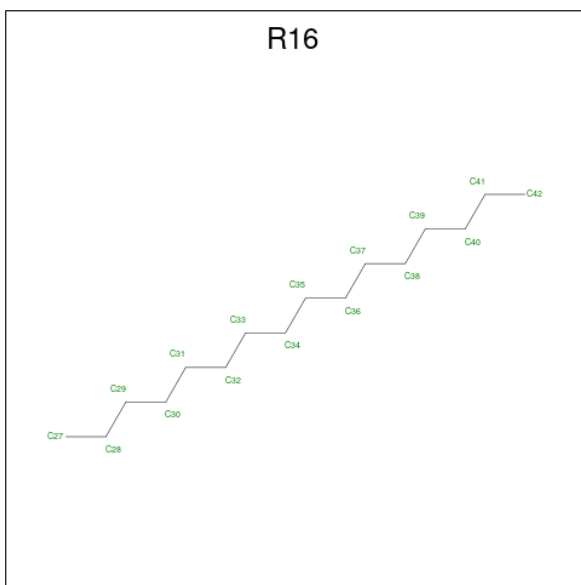
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Chain	Residue	Modelled	Actual	Comment	Reference
B	85	GLU	GLN	engineered mutation	UNP P97438
B	86	LYS	THR	engineered mutation	UNP P97438
B	88	LEU	ILE	engineered mutation	UNP P97438
B	89	ARG	ALA	engineered mutation	UNP P97438
B	90	ALA	GLN	engineered mutation	UNP P97438
B	92	PRO	ALA	engineered mutation	UNP P97438
B	95	SER	ASN	engineered mutation	UNP P97438
B	96	ASP	SER	engineered mutation	UNP P97438
B	97	GLN	THR	engineered mutation	UNP P97438
B	119	ALA	ASN	engineered mutation	UNP P97438
B	300	ALA	SER	engineered mutation	UNP P97438
B	306	ALA	GLU	engineered mutation	UNP P97438
B	323	SER	-	expression tag	UNP P97438
B	324	ASN	-	expression tag	UNP P97438
B	325	SER	-	expression tag	UNP P97438
B	326	LEU	-	expression tag	UNP P97438
B	327	GLU	-	expression tag	UNP P97438
B	328	VAL	-	expression tag	UNP P97438
B	329	LEU	-	expression tag	UNP P97438
B	330	PHE	-	expression tag	UNP P97438
B	331	GLN	-	expression tag	UNP P97438

- Molecule 2 is POTASSIUM ION (CCD ID: K) (formula: K).

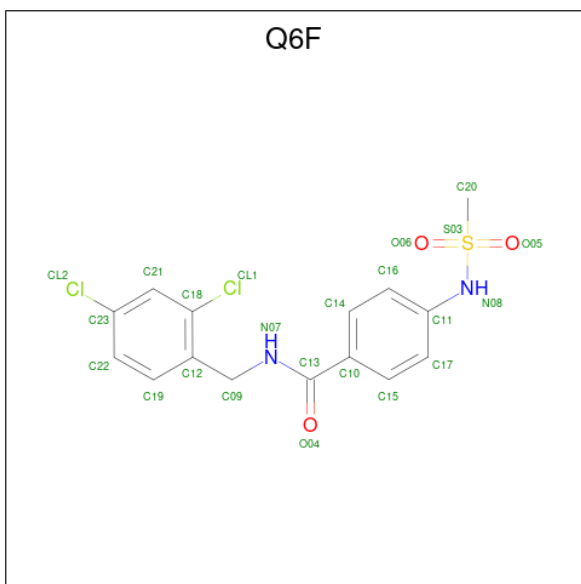
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	5	Total K 5 5	0	0
2	B	1	Total K 1 1	0	0

- Molecule 3 is HEXADECANE (CCD ID: R16) (formula: C₁₆H₃₄).



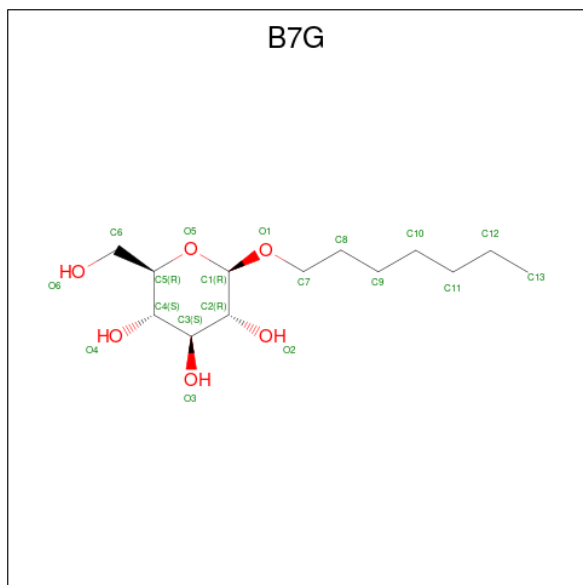
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C 16 16	0	0
3	A	1	Total C 16 16	0	0
3	A	1	Total C 16 16	0	0

- Molecule 4 is N-[(2,4-dichlorophenyl)methyl]-4-[(methylsulfonyl)amino]benzamide (CCD ID: Q6F) (formula: $C_{15}H_{14}Cl_2N_2O_3S$).



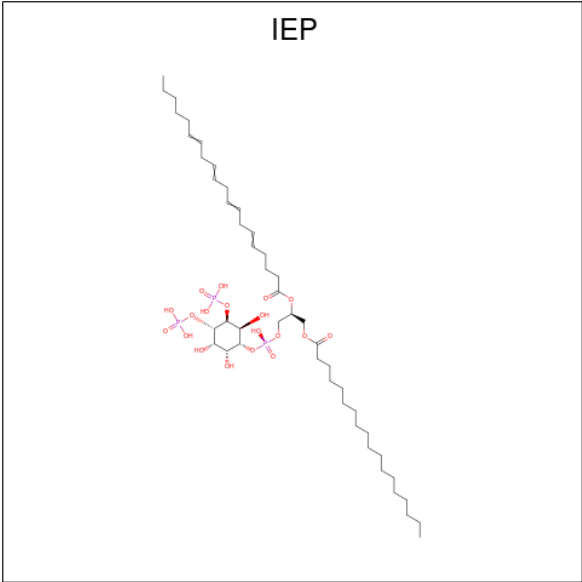
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	Cl	N	O	S	
			23	15	2	2	3	1	
4	B	1	Total	C	Cl	N	O	S	
			23	15	2	2	3	1	

- Molecule 5 is heptyl beta-D-glucopyranoside (CCD ID: B7G) (formula: C₁₃H₂₆O₆).



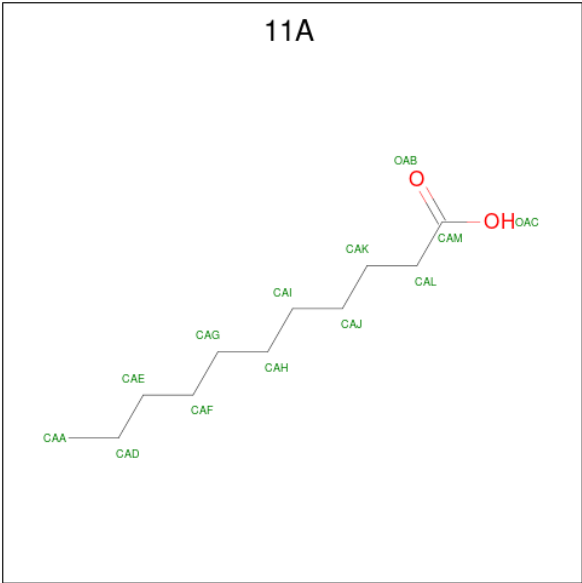
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O		
			19	13	6	0	0
5	B	1	Total	C	O		
			19	13	6	0	0
5	B	1	Total	C	O		
			19	13	6	0	0
5	B	1	Total	C	O		
			19	13	6	0	0

- Molecule 6 is [(2 {S})-1-octadecanoyloxy-3-[oxidanyl-[(1 {R},2 {R},3 {S},4 {S},5 {S},6 {S})-2,3,6-tris(oxidanyl)-4,5-diphosphonoxy-cyclohexyl]oxy-phosphoryl]oxy-propan-2-yl] icos-5,8,11,14-tetraenoate (CCD ID: IEP) (formula: C₄₇H₈₅O₁₉P₃).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	A	1	Total	C	O	P	0	0
			69	47	19	3		
6	B	1	Total	C	O	P	0	0
			69	47	19	3		

- Molecule 7 is UNDECANOIC ACID (CCD ID: 11A) (formula: C₁₁H₂₂O₂).

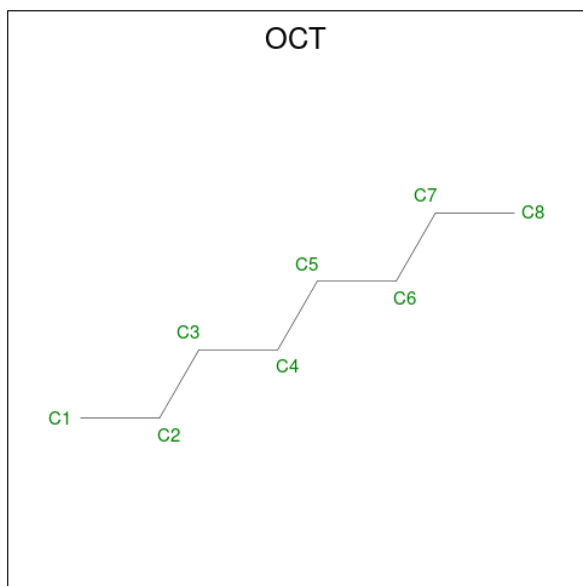


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	1	Total	C	O	0	0
			13	11	2		
7	B	1	Total	C	O	0	0
			13	11	2		

- Molecule 8 is CADMIUM ION (CCD ID: CD) (formula: Cd).

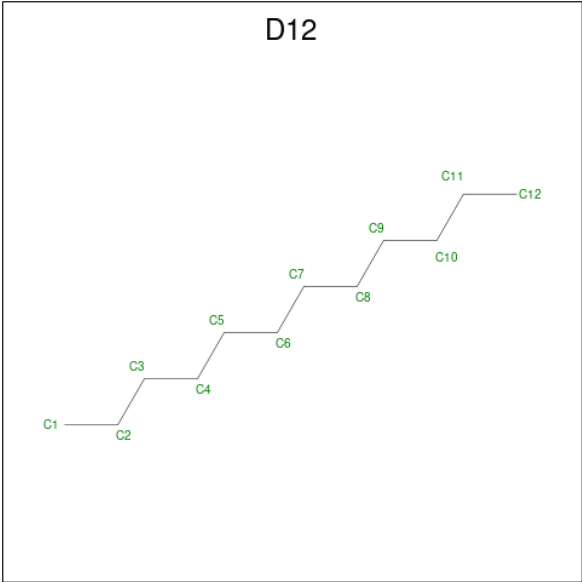
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	B	3	Total	Cd	0	0
			3	3		

- Molecule 9 is N-OCTANE (CCD ID: OCT) (formula: C₈H₁₈).



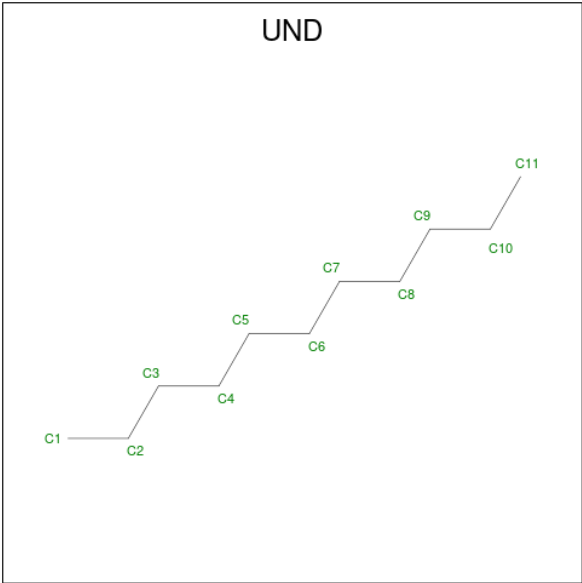
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	B	1	Total	C	0	0
			8	8		
9	B	1	Total	C	0	0
			8	8		

- Molecule 10 is DODECANE (CCD ID: D12) (formula: C₁₂H₂₆).



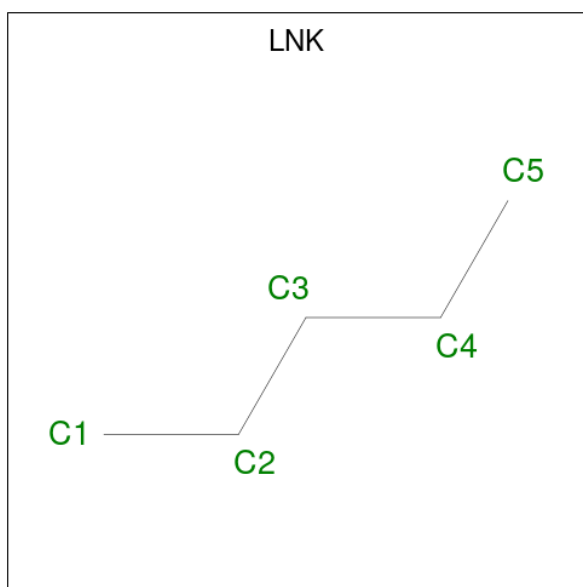
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	B	1	Total	C	0	0
			12	12		
10	B	1	Total	C	0	0
			12	12		

- Molecule 11 is UNDECANE (CCD ID: UND) (formula: C₁₁H₂₄).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
11	B	1	Total	C	0	0
			11	11		

- Molecule 12 is PENTANE (CCD ID: LNK) (formula: C₅H₁₂).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
12	B	1	Total C 5 5	0	0

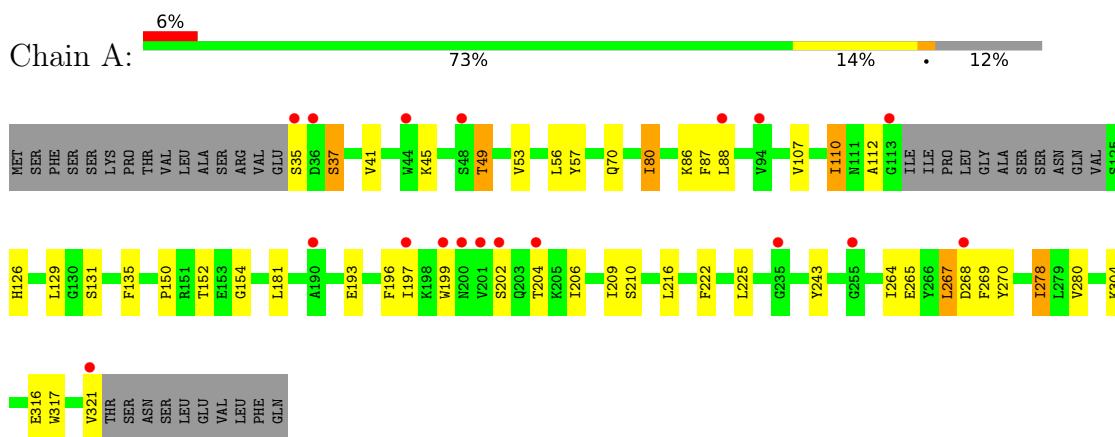
- Molecule 13 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
13	A	1	Total O 1 1	0	0

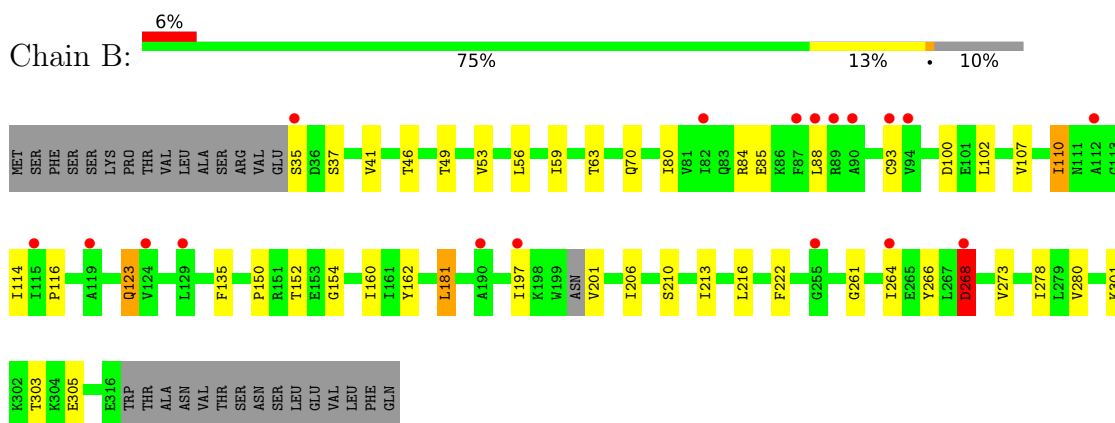
3 Residue-property plots [i](#)

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: Potassium channel subfamily K member 2



- Molecule 1: Potassium channel subfamily K member 2



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	67.13Å 119.78Å 128.87Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	14.97 – 2.60 14.97 – 2.60	Depositor EDS
% Data completeness (in resolution range)	100.0 (14.97-2.60) 99.3 (14.97-2.60)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.13 (at 2.61Å)	Xtriage
Refinement program	BUSTER 2.10.3 (6-FEB-2020)	Depositor
R, R_{free}	0.251 , 0.263 0.261 , 0.280	Depositor DCC
R_{free} test set	1591 reflections (4.87%)	wwPDB-VP
Wilson B-factor (Å ²)	81.9	Xtriage
Anisotropy	0.299	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.27 , 92.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	4741	wwPDB-VP
Average B, all atoms (Å ²)	122.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.09% 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: R16, OCT, UND, Q6F, K, CD, B7G, D12, IEP, 11A, LNK

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	0.86	0/2212	1.05	3/3008 (0.1%)
1	B	0.82	0/2234	1.03	0/3037
All	All	0.84	0/4446	1.04	3/6045 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	B	0	1
All	All	0	2

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	202	SER	N-CA-C	6.65	114.23	108.78
1	A	264	ILE	N-CA-C	-5.74	100.33	109.17
1	A	270	TYR	N-CA-C	5.19	117.35	111.02

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	268	ASP	Peptide
1	B	268	ASP	Peptide

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	2159	0	2207	27	0
1	B	2182	0	2242	27	0
2	A	5	0	0	0	0
2	B	1	0	0	0	0
3	A	48	0	102	0	0
4	A	23	0	0	1	0
4	B	23	0	0	1	0
5	A	19	0	26	0	0
5	B	57	0	78	1	0
6	A	69	0	0	1	0
6	B	69	0	0	3	0
7	A	13	0	21	0	0
7	B	13	0	21	1	0
8	B	3	0	0	0	0
9	B	16	0	36	0	0
10	B	24	0	52	2	0
11	B	11	0	24	0	0
12	B	5	0	12	0	0
13	A	1	0	0	1	0
All	All	4741	0	4821	51	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 5.

The worst 5 of 51 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:317:TRP:NE1	13:A:501:HOH:O	1.96	0.77
6:B:413:IEP:O46	6:B:413:IEP:O43	2.09	0.70
1:A:107:VAL:HG22	1:B:110:ILE:HD11	1.77	0.65
1:B:273:VAL:HG12	10:B:408:D12:H22	1.79	0.65
1:A:197:ILE:HD11	1:A:206:ILE:HD13	1.82	0.61

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	272/312 (87%)	254 (93%)	15 (6%)	3 (1%)	11	25
1	B	277/312 (89%)	255 (92%)	20 (7%)	2 (1%)	18	38
All	All	549/624 (88%)	509 (93%)	35 (6%)	5 (1%)	14	30

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	112	ALA
1	B	266	TYR
1	A	204	THR
1	B	264	ILE
1	A	199	TRP

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	227/260 (87%)	208 (92%)	19 (8%)	10	23
1	B	230/260 (88%)	216 (94%)	14 (6%)	17	37
All	All	457/520 (88%)	424 (93%)	33 (7%)	13	30

5 of 33 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	216	LEU

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Mol	Chain	Res	Type
1	B	268	ASP
1	B	305	GLU
1	A	225	LEU
1	A	216	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	83	GLN
1	B	40	ASN
1	B	123	GLN

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 28 ligands modelled in this entry, 9 are monoatomic - leaving 19 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	$\# Z > 2$
7	11A	A	411	-	12,12,12	0.75	0	12,12,12	0.77	0
3	R16	A	407	-	15,15,15	0.39	0	14,14,14	0.58	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
10	D12	B	408	-	11,11,11	0.41	0	10,10,10	0.51	0
5	B7G	A	409	-	19,19,19	1.22	2 (10%)	24,24,24	0.96	1 (4%)
10	D12	B	407	-	11,11,11	0.42	0	10,10,10	0.55	0
3	R16	A	406	-	15,15,15	0.35	0	14,14,14	0.71	0
9	OCT	B	405	-	7,7,7	0.44	0	6,6,6	0.40	0
6	IEP	A	410	-	69,69,69	1.00	3 (4%)	84,87,87	1.31	8 (9%)
6	IEP	B	413	-	69,69,69	1.12	5 (7%)	84,87,87	1.40	13 (15%)
5	B7G	B	411	-	19,19,19	1.27	3 (15%)	24,24,24	1.59	2 (8%)
11	UND	B	412	-	10,10,10	0.42	0	9,9,9	0.56	0
5	B7G	B	409	-	19,19,19	1.22	2 (10%)	24,24,24	1.20	1 (4%)
7	11A	B	414	-	12,12,12	0.82	0	12,12,12	1.00	1 (8%)
9	OCT	B	406	-	7,7,7	0.41	0	6,6,6	0.58	0
12	LNK	B	416	-	4,4,4	0.47	0	3,3,3	0.34	0
5	B7G	B	410	-	19,19,19	1.33	3 (15%)	24,24,24	2.42	8 (33%)
3	R16	A	405	-	15,15,15	0.38	0	14,14,14	0.72	0
4	Q6F	B	415	-	24,24,24	1.69	5 (20%)	34,34,34	2.68	6 (17%)
4	Q6F	A	408	-	24,24,24	1.68	5 (20%)	34,34,34	2.99	11 (32%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	11A	A	411	-	-	4/10/10/10	-
3	R16	A	407	-	-	7/13/13/13	-
10	D12	B	408	-	-	6/9/9/9	-
5	B7G	A	409	-	-	6/10/30/30	0/1/1/1
10	D12	B	407	-	-	4/9/9/9	-
3	R16	A	406	-	-	7/13/13/13	-
9	OCT	B	405	-	-	3/5/5/5	-
6	IEP	A	410	-	-	19/66/90/90	0/1/1/1
6	IEP	B	413	-	-	38/66/90/90	0/1/1/1
5	B7G	B	411	-	-	5/10/30/30	0/1/1/1
11	UND	B	412	-	-	2/8/8/8	-
5	B7G	B	409	-	-	3/10/30/30	0/1/1/1
7	11A	B	414	-	-	4/10/10/10	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
9	OCT	B	406	-	-	1/5/5/5	-
12	LNK	B	416	-	-	2/2/2/2	-
5	B7G	B	410	-	-	6/10/30/30	0/1/1/1
3	R16	A	405	-	-	6/13/13/13	-
4	Q6F	B	415	-	-	3/14/14/14	0/2/2/2
4	Q6F	A	408	-	-	1/14/14/14	0/2/2/2

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	415	Q6F	C13-N07	4.91	1.44	1.33
4	A	408	Q6F	C13-N07	4.82	1.44	1.33
6	B	413	IEP	P42-O41	4.62	1.67	1.59
6	B	413	IEP	O20-C18	4.41	1.46	1.33
6	A	410	IEP	O20-C18	4.19	1.45	1.33

The worst 5 of 51 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	408	Q6F	C20-S03-N08	10.91	118.84	106.56
4	B	415	Q6F	O06-S03-O05	-10.44	104.88	118.87
4	B	415	Q6F	C20-S03-N08	7.74	115.28	106.56
4	A	408	Q6F	O06-S03-O05	-7.23	109.17	118.87
4	A	408	Q6F	C17-C11-N08	-5.99	107.41	120.02

There are no chirality outliers.

5 of 127 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	B	415	Q6F	C11-N08-S03-O06
5	A	409	B7G	O5-C1-O1-C7
5	B	409	B7G	C8-C7-O1-C1
5	B	411	B7G	C8-C7-O1-C1
6	A	410	IEP	C30-C29-O28-P25

There are no ring outliers.

7 monomers are involved in 10 short contacts:

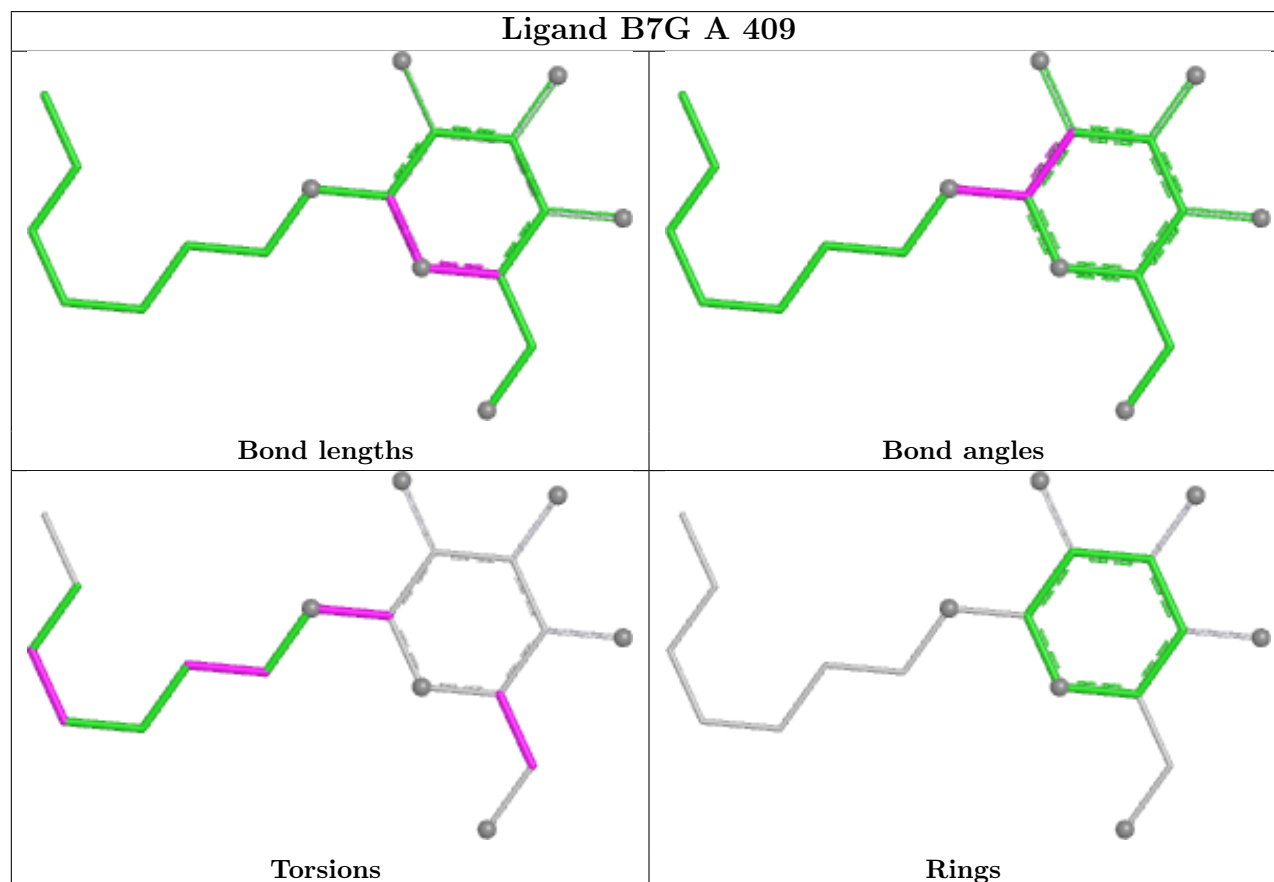
Mol	Chain	Res	Type	Clashes	Symm-Clashes
10	B	408	D12	2	0

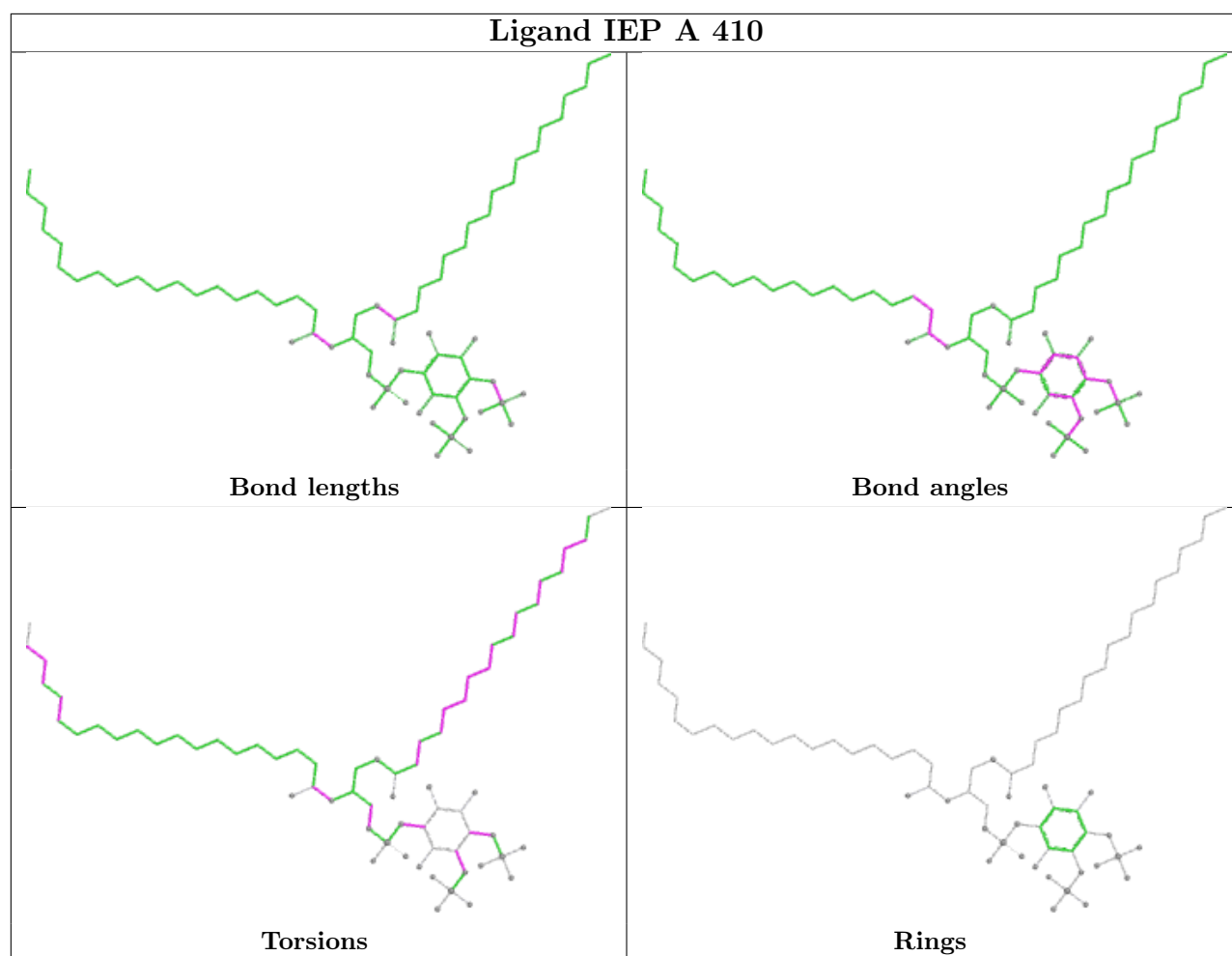
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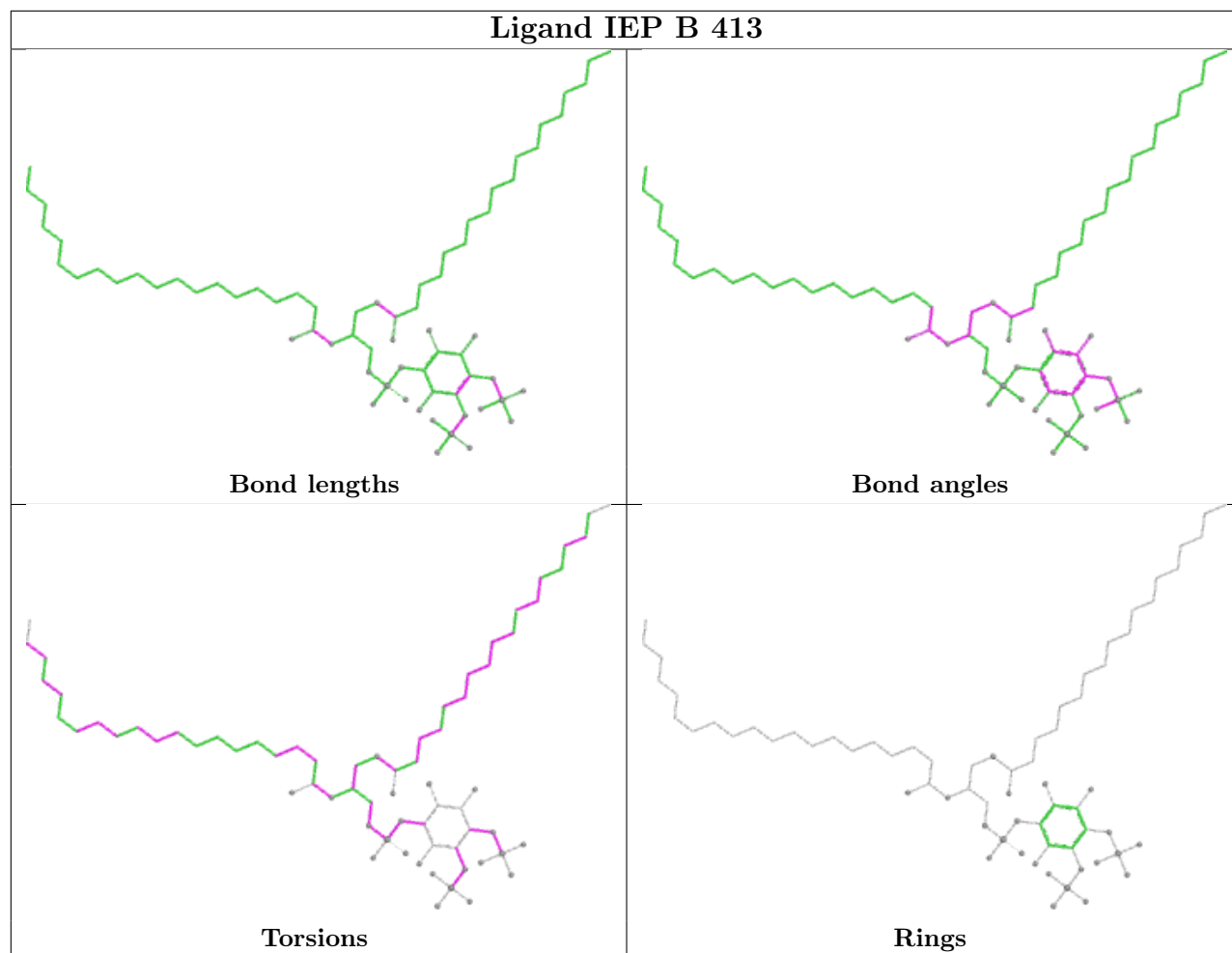
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Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	410	IEP	1	0
6	B	413	IEP	3	0
5	B	411	B7G	1	0
7	B	414	11A	1	0
4	B	415	Q6F	1	0
4	A	408	Q6F	1	0

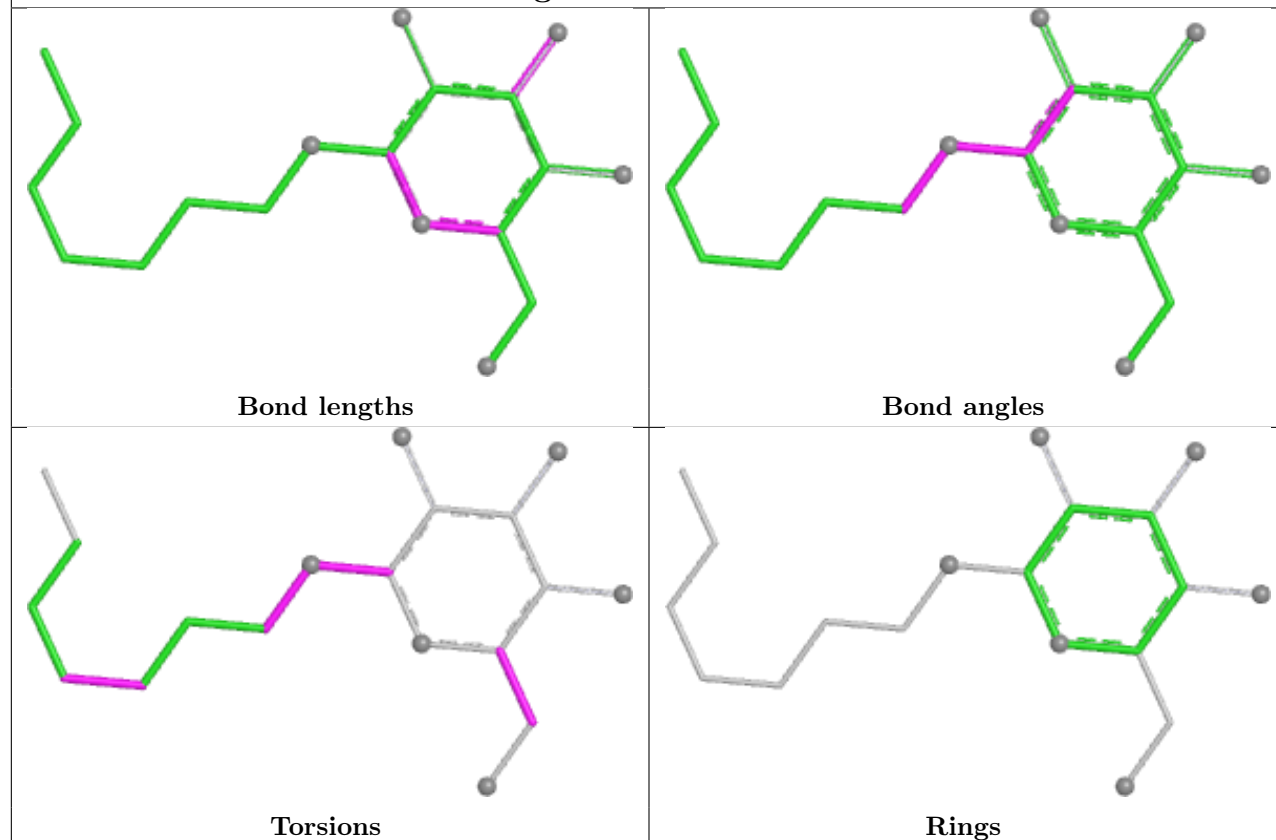
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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



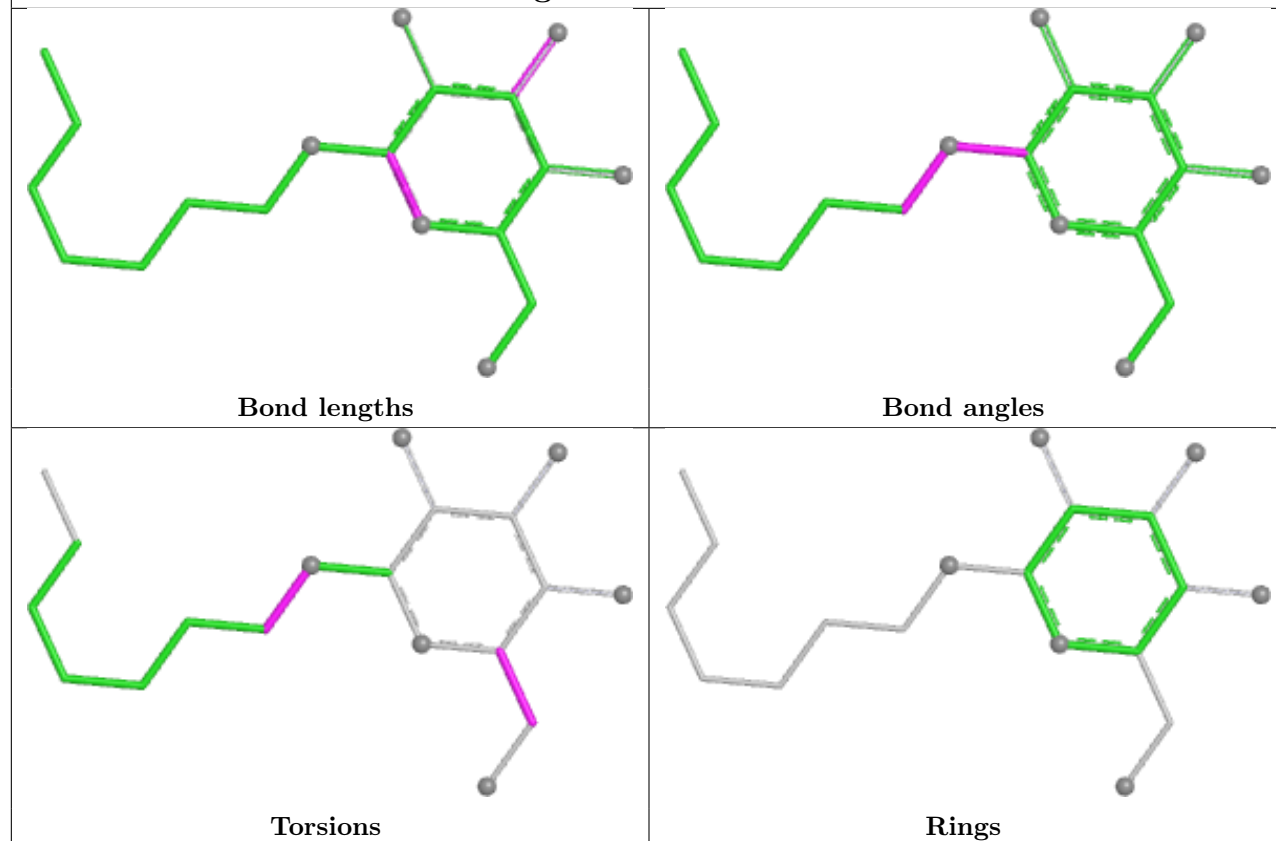


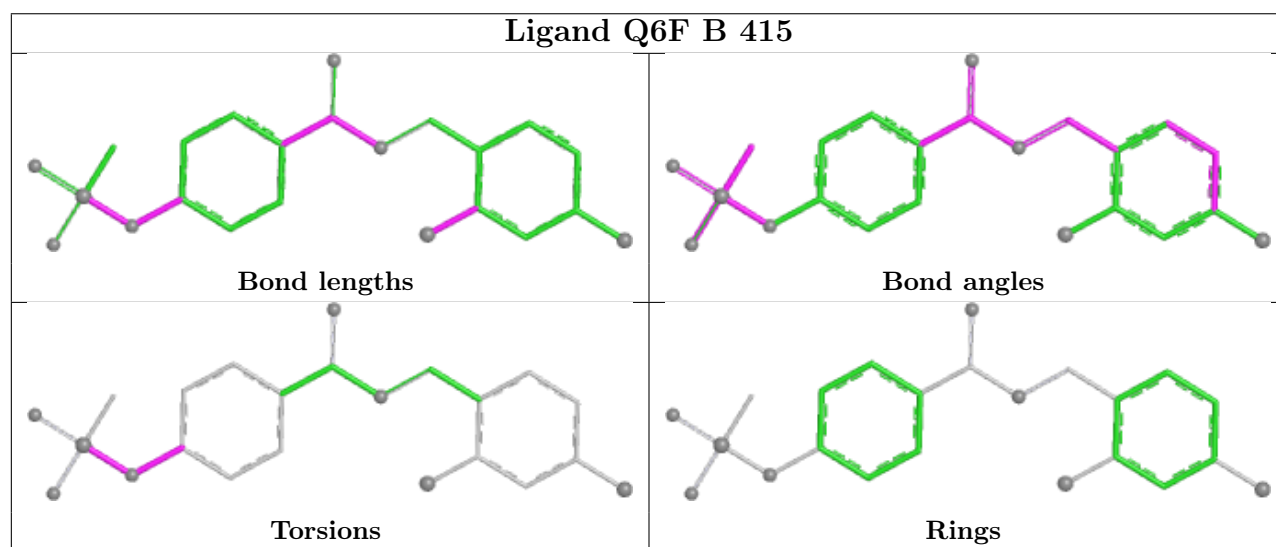
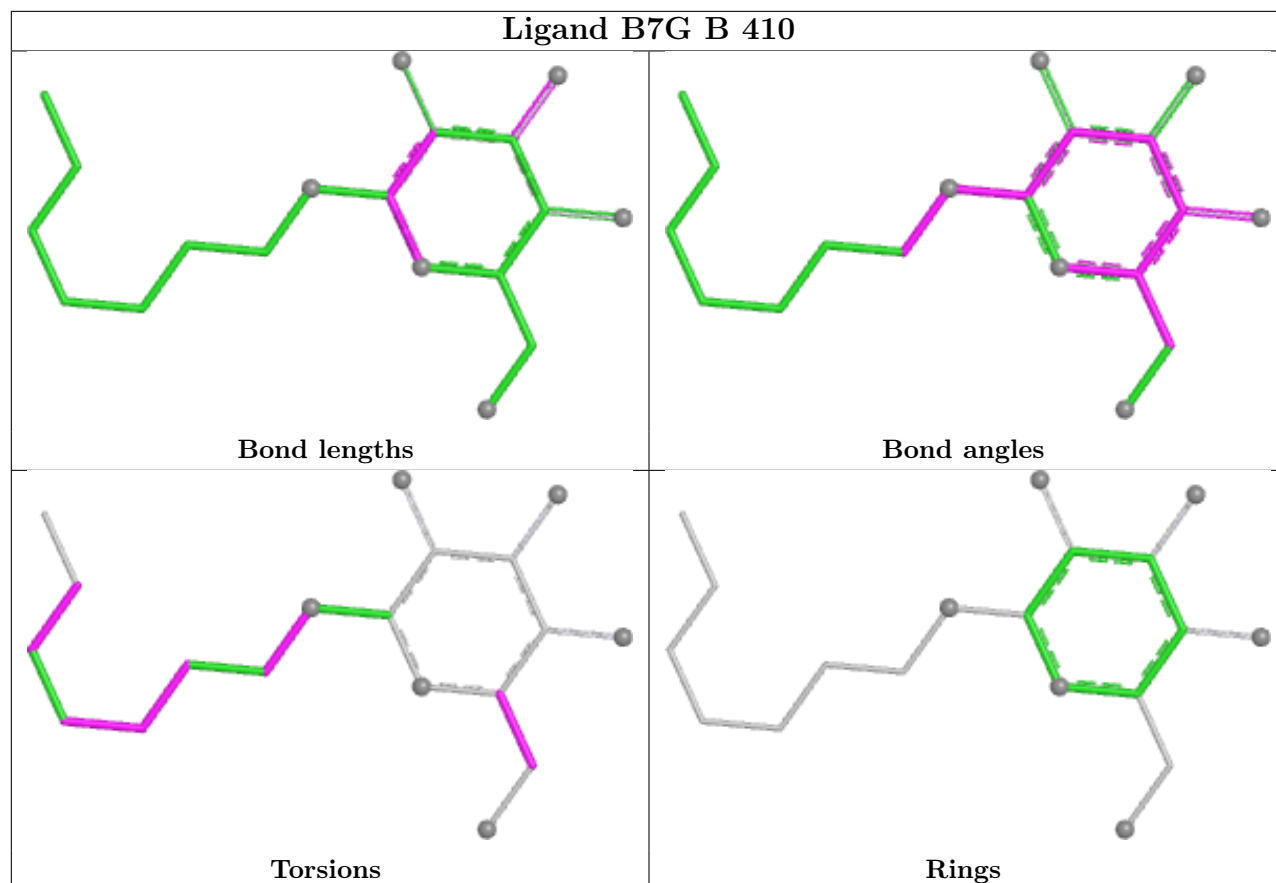


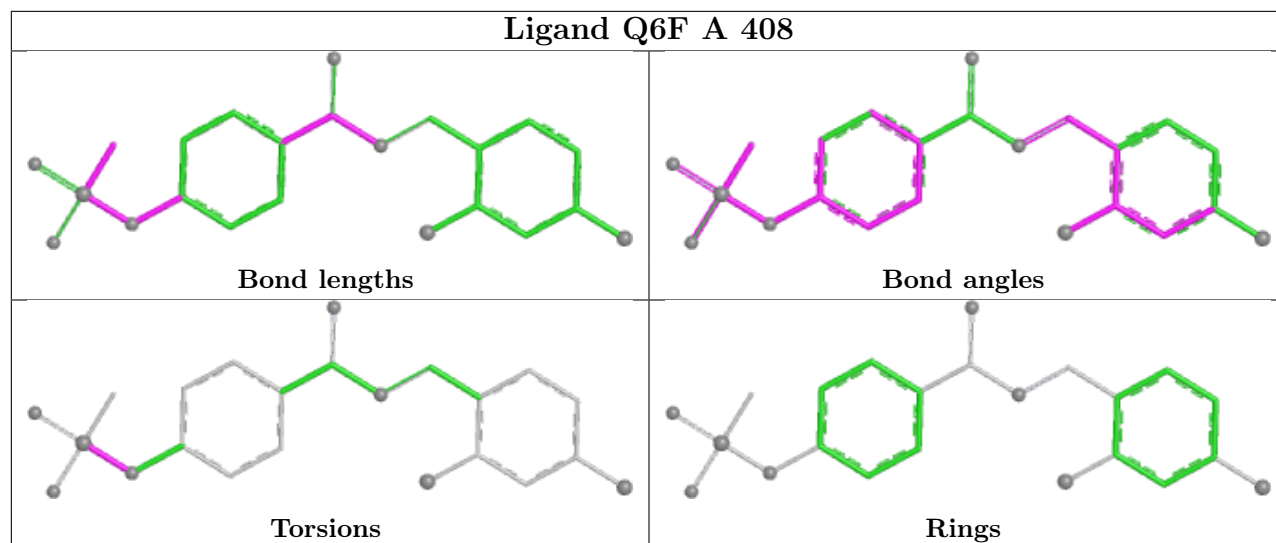
Ligand B7G B 411



Ligand B7G B 409







5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	276/312 (88%)	0.37	18 (6%) 25 19	69, 104, 197, 255	0
1	B	281/312 (90%)	0.38	18 (6%) 25 20	69, 107, 212, 262	0
All	All	557/624 (89%)	0.37	36 (6%) 25 19	69, 106, 206, 262	0

The worst 5 of 36 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	268	ASP	4.6
1	A	197	ILE	4.2
1	B	35	SER	3.8
1	B	190	ALA	3.8
1	B	129	LEU	3.5

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 oligosaccharides in this entry.

6.4 Ligands [i](#)

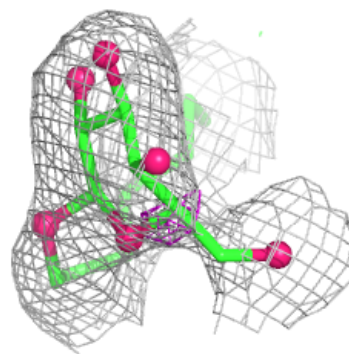
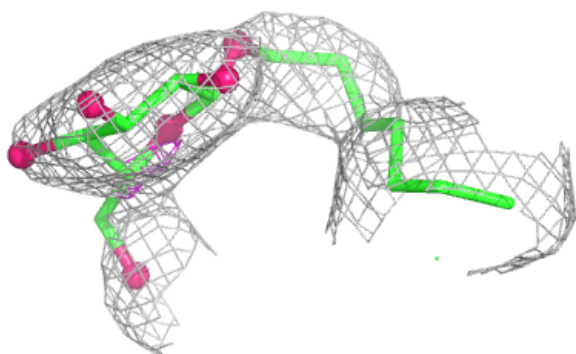
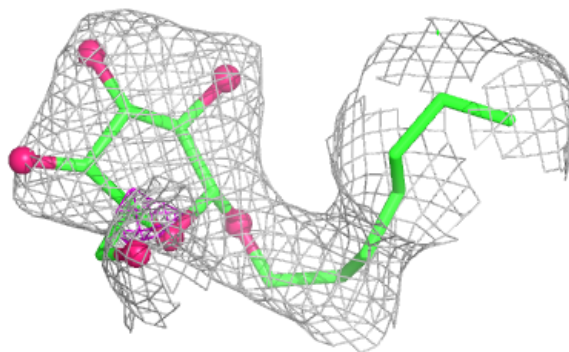
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
5	B7G	B	410	19/19	0.52	0.16	133,135,140,142	0
5	B7G	B	411	19/19	0.53	0.13	134,146,148,148	0
5	B7G	B	409	19/19	0.71	0.10	136,141,160,160	0
6	IEP	A	410	69/69	0.71	0.16	109,143,228,235	0
6	IEP	B	413	69/69	0.71	0.22	99,141,205,211	0
5	B7G	A	409	19/19	0.75	0.13	146,151,156,157	0
9	OCT	B	405	8/8	0.77	0.16	121,121,122,123	0
7	11A	B	414	13/13	0.78	0.20	114,116,120,120	0
11	UND	B	412	11/11	0.79	0.10	127,129,132,132	0
10	D12	B	407	12/12	0.81	0.13	130,131,132,132	0
2	K	B	401	1/1	0.84	0.16	157,157,157,157	0
9	OCT	B	406	8/8	0.84	0.14	117,119,122,122	0
12	LNK	B	416	5/5	0.84	0.30	96,96,96,96	0
2	K	A	401	1/1	0.86	0.08	127,127,127,127	0
7	11A	A	411	13/13	0.87	0.16	121,125,129,130	0
3	R16	A	406	16/16	0.88	0.10	111,120,133,133	0
3	R16	A	407	16/16	0.89	0.14	122,142,155,156	0
3	R16	A	405	16/16	0.92	0.10	116,124,129,129	0
4	Q6F	A	408	23/23	0.93	0.08	80,89,96,97	0
10	D12	B	408	12/12	0.93	0.14	115,132,155,158	0
8	CD	B	402	1/1	0.94	0.04	203,203,203,203	0
2	K	A	412	1/1	0.95	0.06	91,91,91,91	0
2	K	A	402	1/1	0.96	0.05	96,96,96,96	0
2	K	A	403	1/1	0.96	0.16	119,119,119,119	0
4	Q6F	B	415	23/23	0.96	0.07	78,88,104,108	0
8	CD	B	404	1/1	0.97	0.12	176,176,176,176	0
2	K	A	404	1/1	0.98	0.08	87,87,87,87	0
8	CD	B	403	1/1	0.99	0.04	124,124,124,124	0

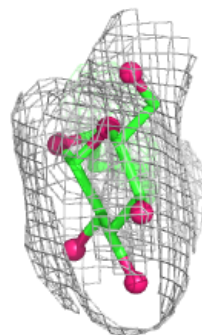
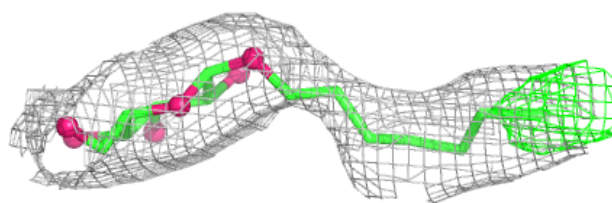
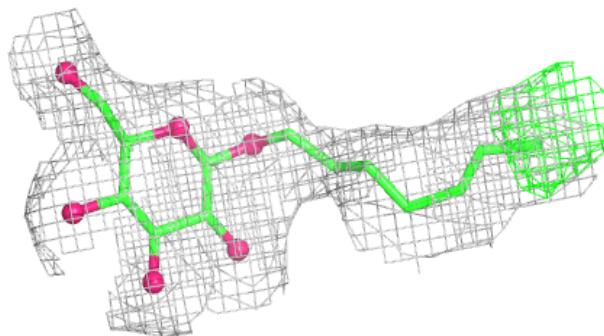
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around B7G B 410:

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

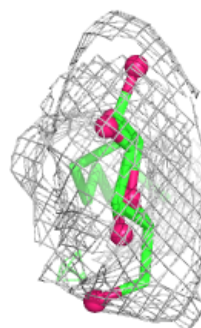
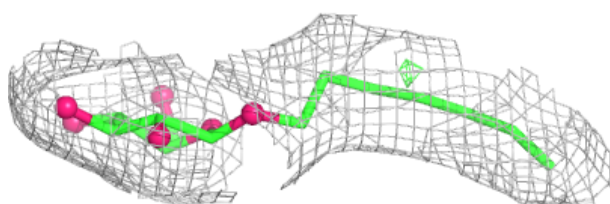
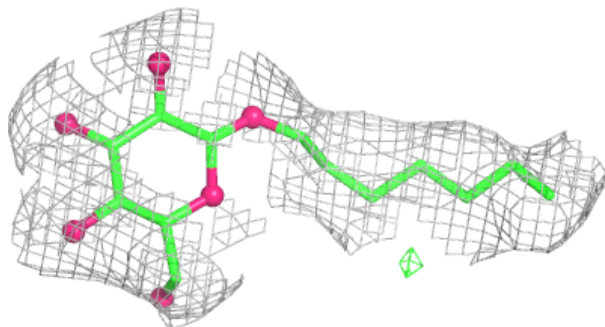
**Electron density around B7G B 411:**

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

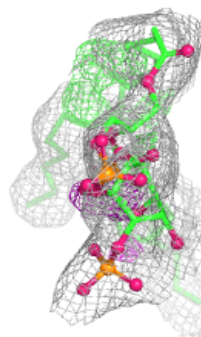
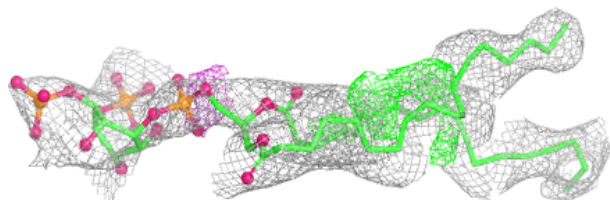
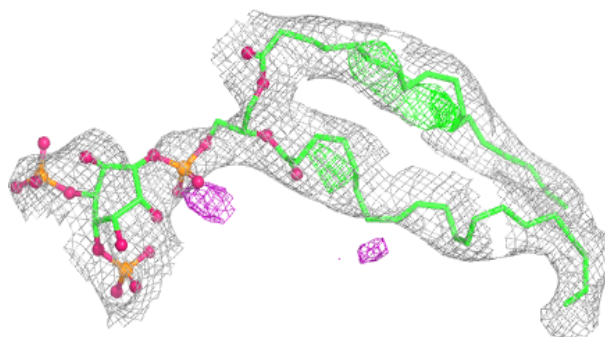


Electron density around B7G B 409:

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

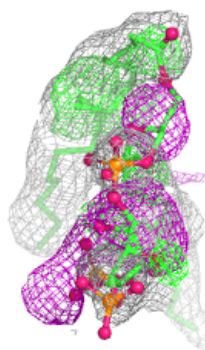
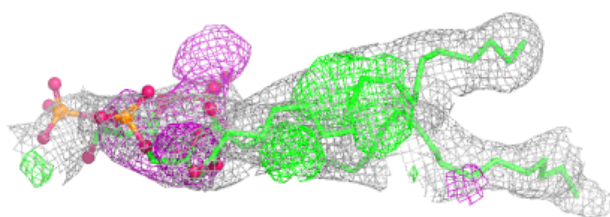
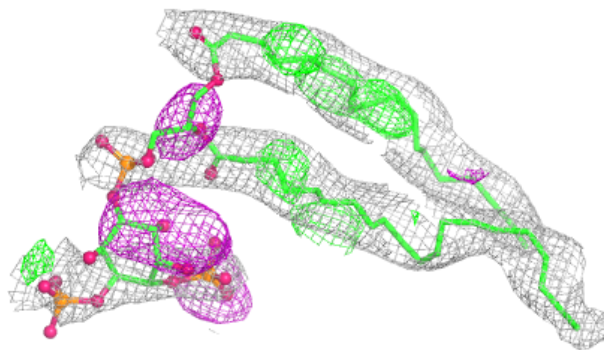
**Electron density around IEP A 410:**

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and green (positive)

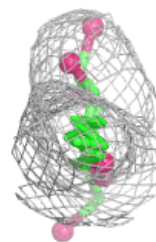
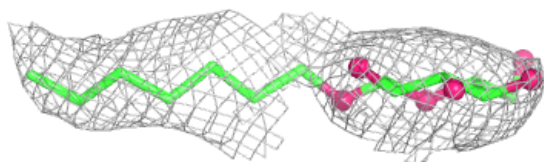
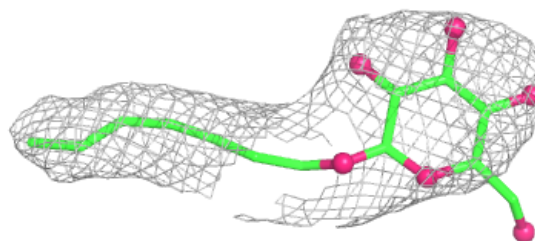


Electron density around IEP B 413:

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

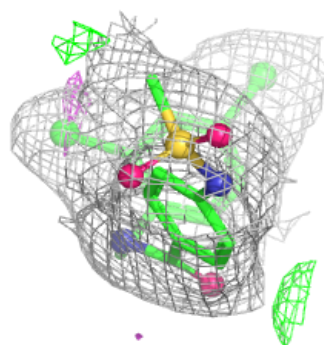
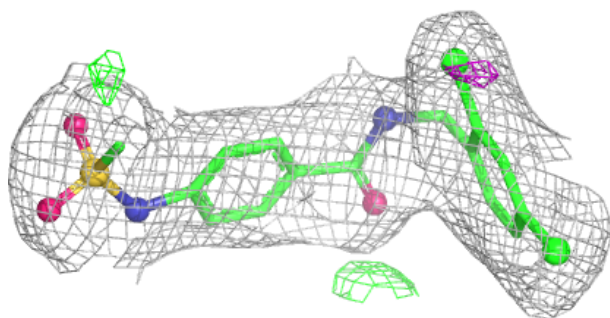
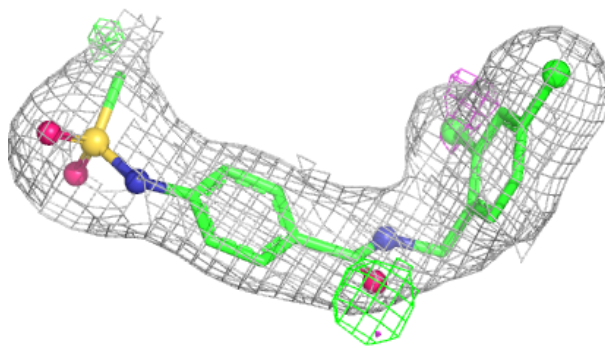
**Electron density around B7G A 409:**

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

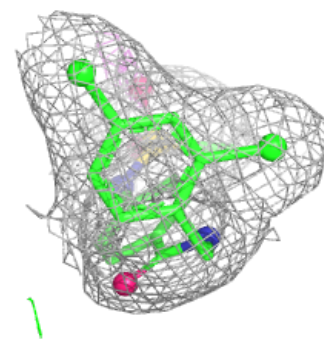
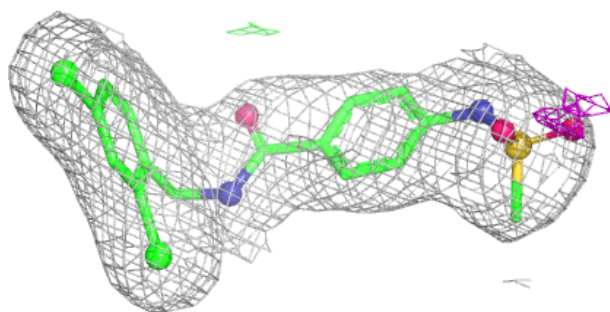
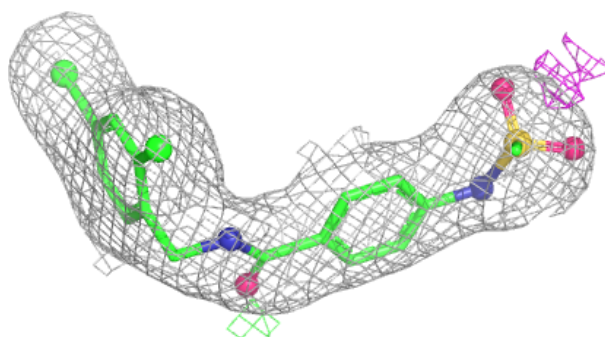


Electron density around Q6F A 408:

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

**Electron density around Q6F B 415:**

$2mF_o-DF_c$ (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.