wwPDB X-ray Structure Validation Summary Report (i)

Sep 20, 2023 – 02:36 AM EDT

PDB ID	:	5KMH
Title	:	Structure of CavAb in complex with Br-verapamil
Authors	:	Tang, L.; Gamal EL-Din, T.M.; Swanson, T.M.; Pryde, D.C.; Scheuer, T.; Zheng, N.; Catterall, W.A.
Deposited on	:	2016-06-27
Resolution	:	3.20 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

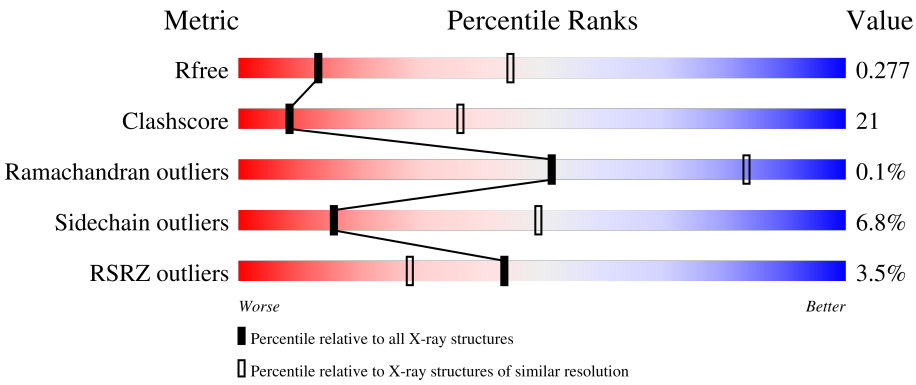
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35.1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35.1

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 3.20 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	1133 (3.20-3.20)
Clashscore	141614	1253 (3.20-3.20)
Ramachandran outliers	138981	1234 (3.20-3.20)
Sidechain outliers	138945	1233 (3.20-3.20)
RSRZ outliers	127900	1095 (3.20-3.20)

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 <=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	285	2% 49% 25% • 23%
1	B	285	2% 45% 29% • 23%
1	C	285	2% 41% 32% • 23%
1	D	285	4% 43% 31% • 23%

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 7366 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 Ion transport protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	219	1800	1227	269	294	10	0	0	0
1	B	219	1800	1227	269	294	10	0	0	0
1	C	219	1800	1227	269	294	10	0	0	0
1	D	219	1800	1227	269	294	10	0	0	0

There are 84 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	983	MET	-	initiating methionine	UNP A8EVM5
A	984	ASP	-	expression tag	UNP A8EVM5
A	985	TYR	-	expression tag	UNP A8EVM5
A	986	LYS	-	expression tag	UNP A8EVM5
A	987	ASP	-	expression tag	UNP A8EVM5
A	988	ASP	-	expression tag	UNP A8EVM5
A	989	ASP	-	expression tag	UNP A8EVM5
A	990	ASP	-	expression tag	UNP A8EVM5
A	991	LYS	-	expression tag	UNP A8EVM5
A	992	GLY	-	expression tag	UNP A8EVM5
A	993	SER	-	expression tag	UNP A8EVM5
A	994	LEU	-	expression tag	UNP A8EVM5
A	995	VAL	-	expression tag	UNP A8EVM5
A	996	PRO	-	expression tag	UNP A8EVM5
A	997	ARG	-	expression tag	UNP A8EVM5
A	998	GLY	-	expression tag	UNP A8EVM5
A	999	SER	-	expression tag	UNP A8EVM5
A	1000	HIS	-	expression tag	UNP A8EVM5
A	1177	ASP	GLU	conflict	UNP A8EVM5
A	1178	ASP	SER	conflict	UNP A8EVM5
A	1181	ASN	MET	conflict	UNP A8EVM5

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Chain	Residue	Modelled	Actual	Comment	Reference
B	983	MET	-	initiating methionine	UNP A8EVM5
B	984	ASP	-	expression tag	UNP A8EVM5
B	985	TYR	-	expression tag	UNP A8EVM5
B	986	LYS	-	expression tag	UNP A8EVM5
B	987	ASP	-	expression tag	UNP A8EVM5
B	988	ASP	-	expression tag	UNP A8EVM5
B	989	ASP	-	expression tag	UNP A8EVM5
B	990	ASP	-	expression tag	UNP A8EVM5
B	991	LYS	-	expression tag	UNP A8EVM5
B	992	GLY	-	expression tag	UNP A8EVM5
B	993	SER	-	expression tag	UNP A8EVM5
B	994	LEU	-	expression tag	UNP A8EVM5
B	995	VAL	-	expression tag	UNP A8EVM5
B	996	PRO	-	expression tag	UNP A8EVM5
B	997	ARG	-	expression tag	UNP A8EVM5
B	998	GLY	-	expression tag	UNP A8EVM5
B	999	SER	-	expression tag	UNP A8EVM5
B	1000	HIS	-	expression tag	UNP A8EVM5
B	1177	ASP	GLU	conflict	UNP A8EVM5
B	1178	ASP	SER	conflict	UNP A8EVM5
B	1181	ASN	MET	conflict	UNP A8EVM5
C	983	MET	-	initiating methionine	UNP A8EVM5
C	984	ASP	-	expression tag	UNP A8EVM5
C	985	TYR	-	expression tag	UNP A8EVM5
C	986	LYS	-	expression tag	UNP A8EVM5
C	987	ASP	-	expression tag	UNP A8EVM5
C	988	ASP	-	expression tag	UNP A8EVM5
C	989	ASP	-	expression tag	UNP A8EVM5
C	990	ASP	-	expression tag	UNP A8EVM5
C	991	LYS	-	expression tag	UNP A8EVM5
C	992	GLY	-	expression tag	UNP A8EVM5
C	993	SER	-	expression tag	UNP A8EVM5
C	994	LEU	-	expression tag	UNP A8EVM5
C	995	VAL	-	expression tag	UNP A8EVM5
C	996	PRO	-	expression tag	UNP A8EVM5
C	997	ARG	-	expression tag	UNP A8EVM5
C	998	GLY	-	expression tag	UNP A8EVM5
C	999	SER	-	expression tag	UNP A8EVM5
C	1000	HIS	-	expression tag	UNP A8EVM5
C	1177	ASP	GLU	conflict	UNP A8EVM5
C	1178	ASP	SER	conflict	UNP A8EVM5
C	1181	ASN	MET	conflict	UNP A8EVM5

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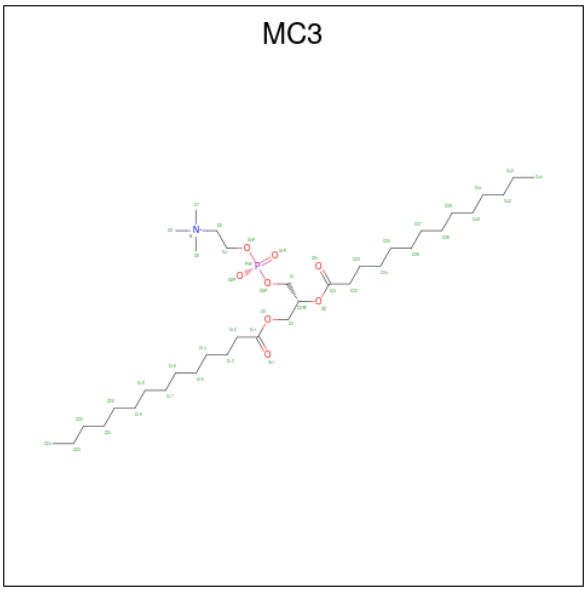
Chain	Residue	Modelled	Actual	Comment	Reference
D	983	MET	-	initiating methionine	UNP A8EVM5
D	984	ASP	-	expression tag	UNP A8EVM5
D	985	TYR	-	expression tag	UNP A8EVM5
D	986	LYS	-	expression tag	UNP A8EVM5
D	987	ASP	-	expression tag	UNP A8EVM5
D	988	ASP	-	expression tag	UNP A8EVM5
D	989	ASP	-	expression tag	UNP A8EVM5
D	990	ASP	-	expression tag	UNP A8EVM5
D	991	LYS	-	expression tag	UNP A8EVM5
D	992	GLY	-	expression tag	UNP A8EVM5
D	993	SER	-	expression tag	UNP A8EVM5
D	994	LEU	-	expression tag	UNP A8EVM5
D	995	VAL	-	expression tag	UNP A8EVM5
D	996	PRO	-	expression tag	UNP A8EVM5
D	997	ARG	-	expression tag	UNP A8EVM5
D	998	GLY	-	expression tag	UNP A8EVM5
D	999	SER	-	expression tag	UNP A8EVM5
D	1000	HIS	-	expression tag	UNP A8EVM5
D	1177	ASP	GLU	conflict	UNP A8EVM5
D	1178	ASP	SER	conflict	UNP A8EVM5
D	1181	ASN	MET	conflict	UNP A8EVM5

- Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca).

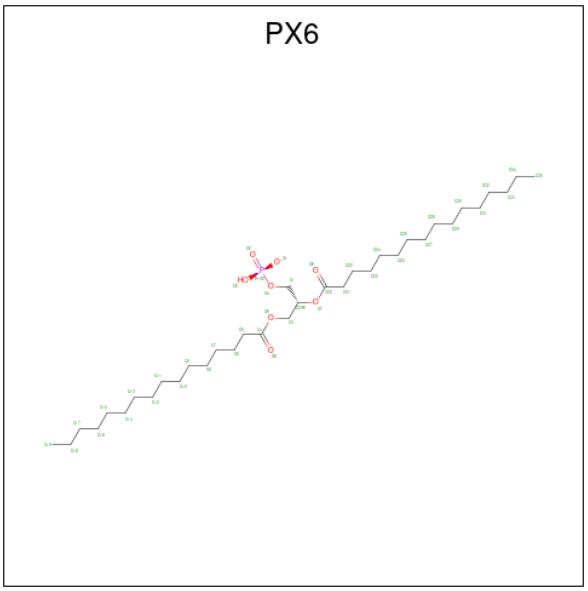
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Ca		
2	A	2	2	2	0	0
			Total	Ca		
2	D	1	1	1	0	0

- Molecule 3 is 1,2-DIMYRISTOYL-RAC-GLYCERO-3-PHOSPHOCHOLINE (three-letter code: MC3) (formula: $C_{36}H_{72}NO_8P$).



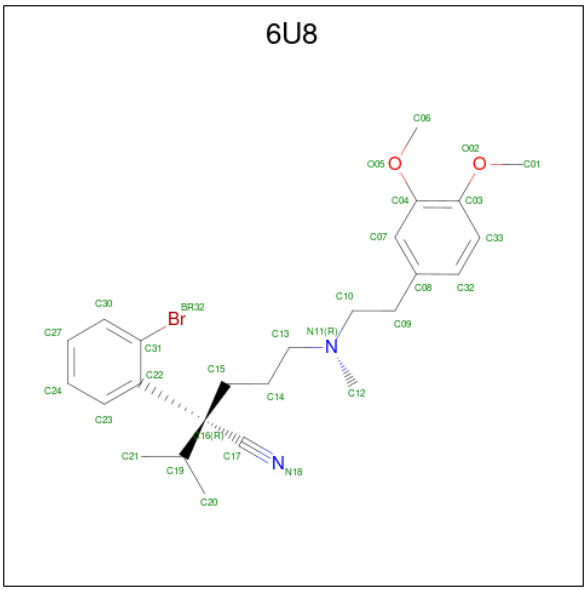
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	O	P		
3	A	1	21	13	7	1	0	0
			Total	C	O	P		
3	A	1	21	13	7	1	0	0
			Total	C	O	P		
3	A	1	10	3	6	1	0	0
			Total	C	O	P		
3	B	1	10	3	6	1	0	0
			Total	C	O	P		
3	D	1	21	13	7	1	0	0
			Total	C	O	P		
3	D	1	10	3	6	1	0	0

- Molecule 4 is 1,2-DIPALMITOYL-SN-GLYCERO-3-PHOSPHATE (three-letter code: PX6) (formula: $C_{35}H_{68}O_8P$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	O	P		
4	A	1	10	3	6	1	0	0
			Total	C	O	P		
4	B	1	10	3	6	1	0	0
			Total	C	O	P		
4	C	1	10	3	6	1	0	0
			Total	C	O	P		
4	D	1	10	3	6	1	0	0

- Molecule 5 is (2 {R})-2-(2-bromophenyl)-5-[2-(3,4-dimethoxyphenyl)ethyl-methyl-amino]-2-propan-2-yl-pentanenitrile (three-letter code: 6U8) (formula: $C_{25}H_{33}BrN_2O_2$).



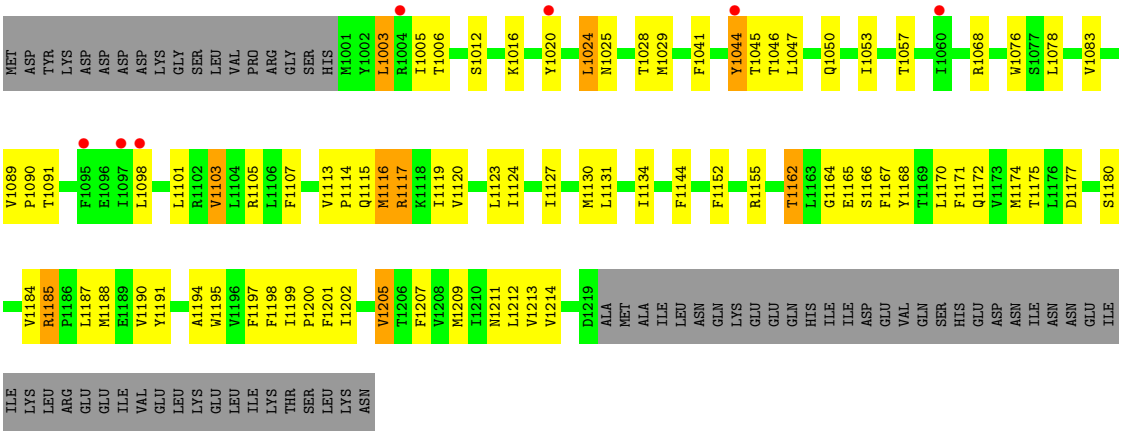
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	Br	C	N	O		
5	C	1	30	1	25	2	2	0	0

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.

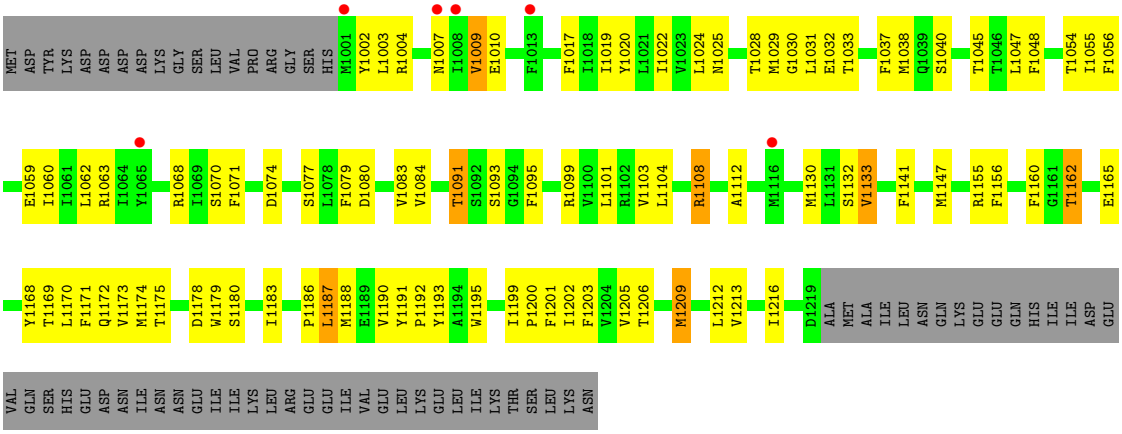
• Molecule 1: Ion transport protein

Chain A:



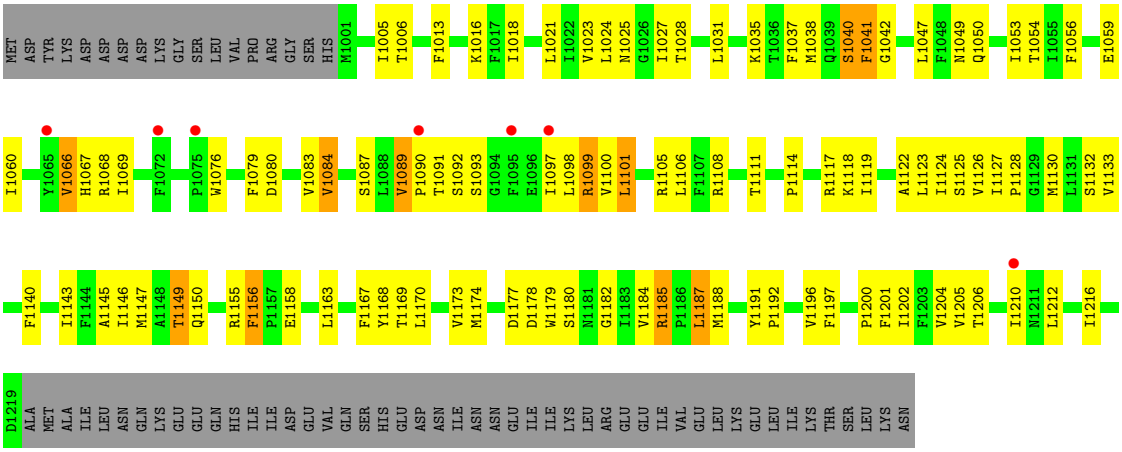
• Molecule 1: Ion transport protein

Chain B:



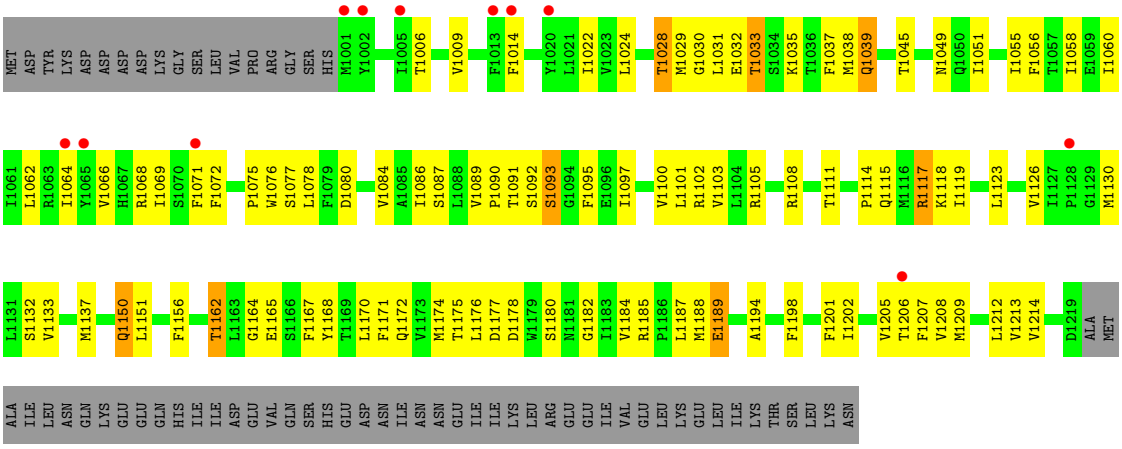
• Molecule 1: Ion transport protein

Chain C:



- Molecule 1: Ion transport protein

Chain D:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 2 21	Depositor
Cell constants a, b, c, α, β, γ	125.53Å 125.53Å 191.96Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.83 – 3.20 29.83 – 3.20	Depositor EDS
% Data completeness (in resolution range)	77.3 (29.83-3.20) 77.3 (29.83-3.20)	Depositor EDS
R_{merge}	0.19	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.06 (at 3.18Å)	Xtriage
Refinement program	REFMAC 5.8.0073, PHENIX	Depositor
R, R_{free}	0.251 , 0.294 0.225 , 0.277	Depositor DCC
R_{free} test set	1956 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å^2)	80.4	Xtriage
Anisotropy	0.469	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.29 , 53.1	EDS
L-test for twinning[2]	$< \|L\| > = 0.42$, $< L^2 > = 0.24$	Xtriage
Estimated twinning fraction	0.447 for k,h,-l	Xtriage
Reported twinning fraction	0.545 for H, K, L 0.455 for K, H, -L	Depositor
Outliers	0 of 39187 reflections	Xtriage
F_o,F_c correlation	0.90	EDS
Total number of atoms	7366	wwPDB-VP
Average B, all atoms (Å^2)	114.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.82% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: PX6, 6U8, CA, MC3

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	0.67	0/1851	0.90	1/2520 (0.0%)
1	B	0.60	0/1851	0.83	0/2520
1	C	0.69	1/1851 (0.1%)	0.87	0/2520
1	D	0.63	0/1851	0.83	0/2520
All	All	0.65	1/7404 (0.0%)	0.86	1/10080 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	1158	GLU	CB-CG	5.01	1.61	1.52

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	1185	ARG	NE-CZ-NH2	-6.41	117.10	120.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

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	1800	0	1869	100	0
1	B	1800	0	1869	76	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	1800	0	1869	87	0
1	D	1800	0	1869	78	0
2	A	2	0	0	0	0
2	D	1	0	0	0	0
3	A	52	0	43	5	0
3	B	10	0	5	1	0
3	D	31	0	24	2	0
4	A	10	0	6	0	0
4	B	10	0	6	0	0
4	C	10	0	6	0	0
4	D	10	0	6	2	0
5	C	30	0	0	2	0
All	All	7366	0	7572	312	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 21.

The worst 5 of 312 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:1089:VAL:HG12	1:A:1090:PRO:HD2	1.27	1.16
1:A:1076:TRP:CG	1:A:1117:ARG:HD2	1.99	0.97
1:A:1076:TRP:CD2	1:A:1117:ARG:CD	2.47	0.96
1:A:1076:TRP:CZ3	1:A:1117:ARG:HG3	2.02	0.95
1:A:1144:PHE:CD2	1:A:1197:PHE:CZ	2.57	0.91

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	217/285 (76%)	206 (95%)	11 (5%)	0	100	100
1	B	217/285 (76%)	208 (96%)	9 (4%)	0	100	100
1	C	217/285 (76%)	207 (95%)	10 (5%)	0	100	100
1	D	217/285 (76%)	210 (97%)	6 (3%)	1 (0%)	29	67
All	All	868/1140 (76%)	831 (96%)	36 (4%)	1 (0%)	51	83

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	1093	SER

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	202/264 (76%)	189 (94%)	13 (6%)	17	52
1	B	202/264 (76%)	190 (94%)	12 (6%)	19	54
1	C	202/264 (76%)	187 (93%)	15 (7%)	13	46
1	D	202/264 (76%)	187 (93%)	15 (7%)	13	46
All	All	808/1056 (76%)	753 (93%)	55 (7%)	16	49

5 of 55 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	1049	ASN
1	C	1111	THR
1	D	1189	GLU
1	D	1117	ARG
1	C	1059	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	C	1181	ASN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

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	$\#\|Z\| > 2$
5	6U8	C	1302	-	29,31,31	1.70	8 (27%)	31,42,42	6.23	12 (38%)
3	MC3	D	1304	-	9,9,45	0.86	0	11,12,53	0.61	0
3	MC3	A	1304	-	20,20,45	1.96	4 (20%)	22,24,53	1.26	2 (9%)
3	MC3	B	1302	-	9,9,45	0.89	0	11,12,53	0.88	0
3	MC3	A	1306	-	9,9,45	1.08	1 (11%)	11,12,53	1.39	2 (18%)
4	PX6	A	1305	-	9,9,43	1.27	1 (11%)	11,12,48	1.60	2 (18%)
3	MC3	D	1302	-	20,20,45	1.89	4 (20%)	22,24,53	1.65	2 (9%)
4	PX6	B	1301	-	9,9,43	1.00	1 (11%)	11,12,48	1.08	0
4	PX6	D	1303	-	9,9,43	1.23	1 (11%)	11,12,48	1.22	1 (9%)
3	MC3	A	1303	-	20,20,45	1.75	4 (20%)	22,24,53	1.71	3 (13%)
4	PX6	C	1301	-	9,9,43	1.33	1 (11%)	11,12,48	1.44	2 (18%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	6U8	C	1302	-	-	17/28/31/31	0/2/2/2
3	MC3	D	1304	-	-	4/8/8/49	-
3	MC3	A	1304	-	-	10/22/22/49	-
3	MC3	B	1302	-	-	5/8/8/49	-
3	MC3	A	1306	-	-	2/8/8/49	-
4	PX6	A	1305	-	-	4/8/8/45	-
3	MC3	D	1302	-	-	14/22/22/49	-
4	PX6	B	1301	-	-	5/8/8/45	-
4	PX6	D	1303	-	-	5/8/8/45	-
3	MC3	A	1303	-	-	12/22/22/49	-
4	PX6	C	1301	-	-	7/8/8/45	-

The worst 5 of 25 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1304	MC3	O11-C11	6.77	1.42	1.22
3	D	1302	MC3	O11-C11	6.46	1.41	1.22
3	A	1303	MC3	O11-C11	5.86	1.40	1.22
5	C	1302	6U8	O02-C03	4.06	1.43	1.37
5	C	1302	6U8	C16-C17	3.70	1.55	1.47

The worst 5 of 26 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	C	1302	6U8	C16-C17-N18	-31.69	124.04	177.45
3	A	1303	MC3	O3-C11-O11	-6.54	107.08	123.59
5	C	1302	6U8	O05-C04-C03	6.49	124.45	115.41
5	C	1302	6U8	O02-C03-C04	6.34	124.25	115.41
3	D	1302	MC3	O3-C11-O11	-6.29	107.73	123.59

There are no chirality outliers.

5 of 85 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	1303	MC3	O2-C2-C3-O3

Continued on next page...

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Mol	Chain	Res	Type	Atoms
3	A	1304	MC3	O3P-C1-C2-C3
3	A	1304	MC3	O11-C11-O3-C3
3	A	1304	MC3	C1-O3P-P-O1P
3	A	1304	MC3	C1-O3P-P-O2P

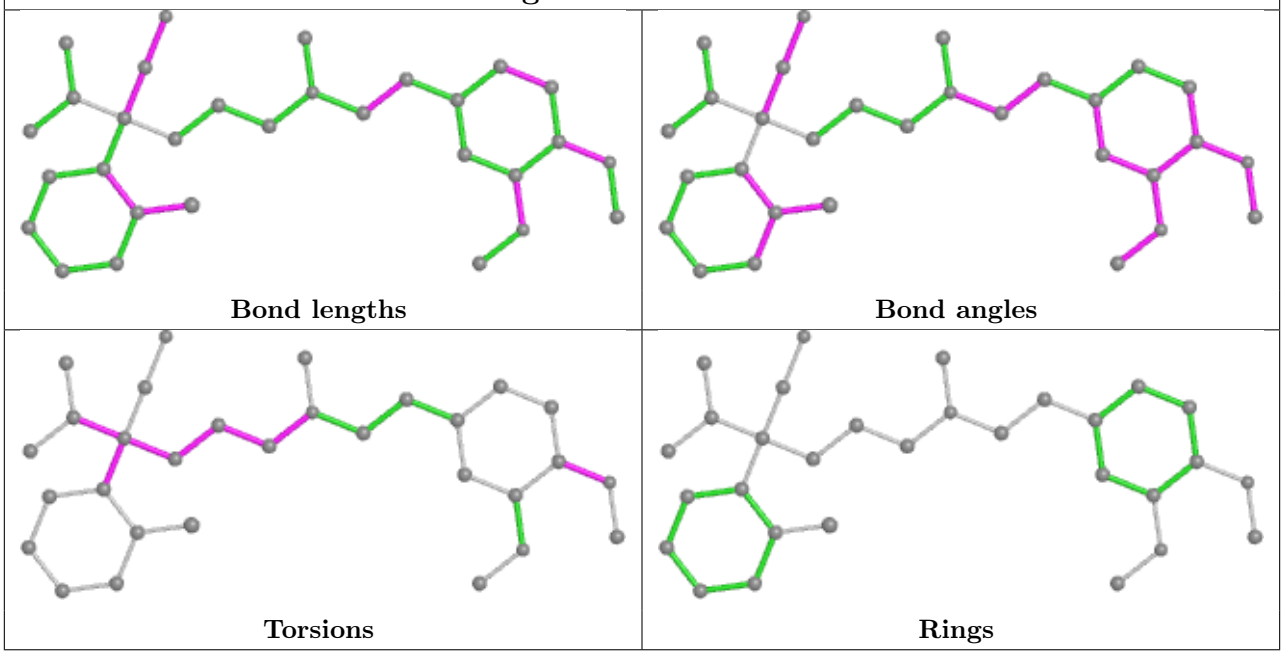
There are no ring outliers.

6 monomers are involved in 12 short contacts:

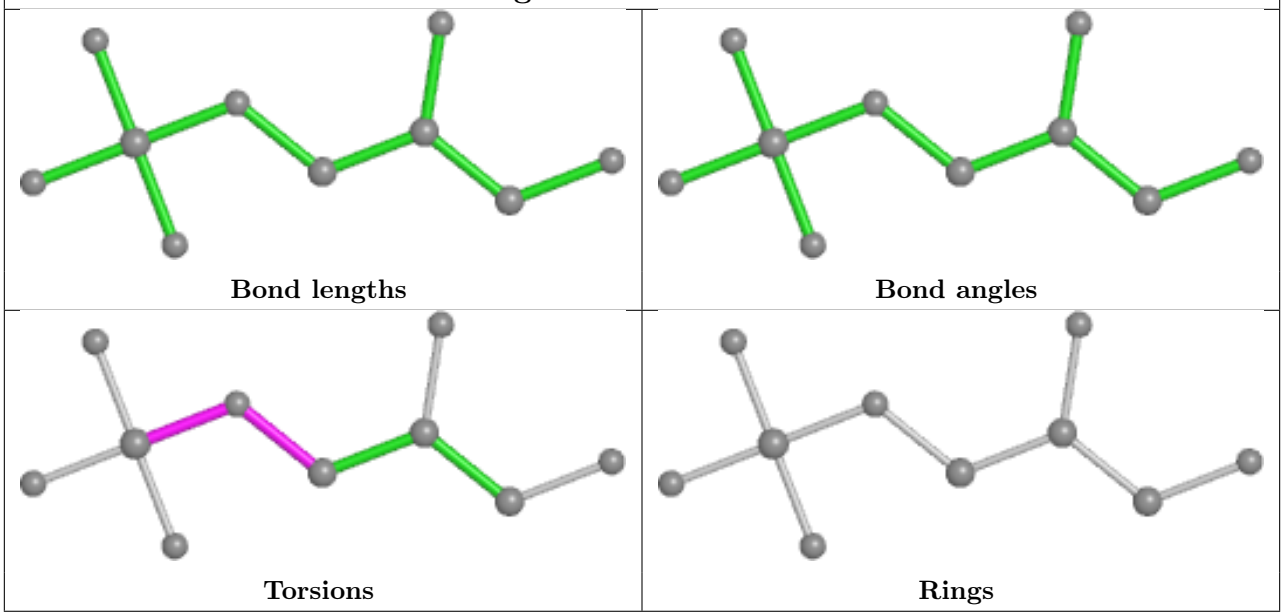
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	C	1302	6U8	2	0
3	A	1304	MC3	4	0
3	B	1302	MC3	1	0
3	D	1302	MC3	2	0
4	D	1303	PX6	2	0
3	A	1303	MC3	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

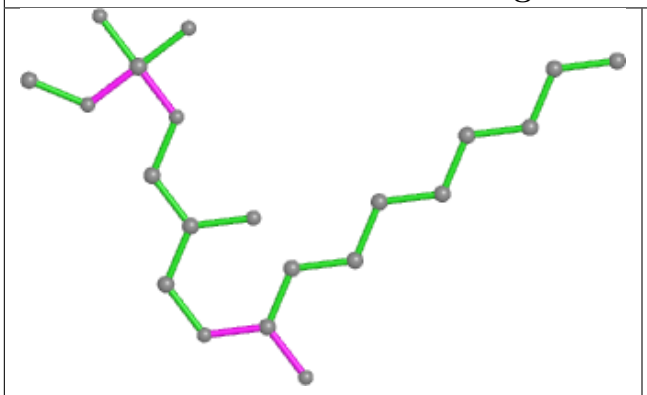
Ligand 6U8 C 1302



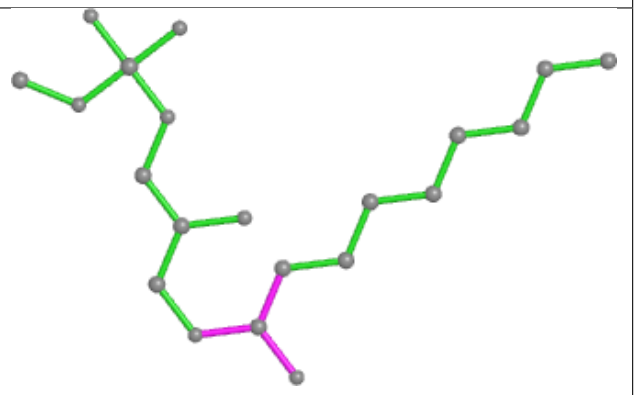
Ligand MC3 D 1304



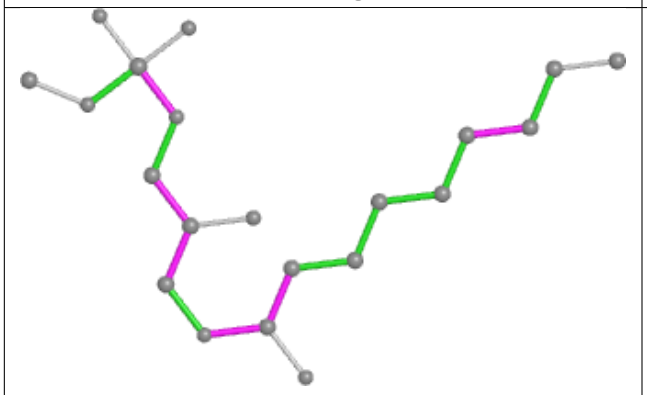
Ligand MC3 A 1304



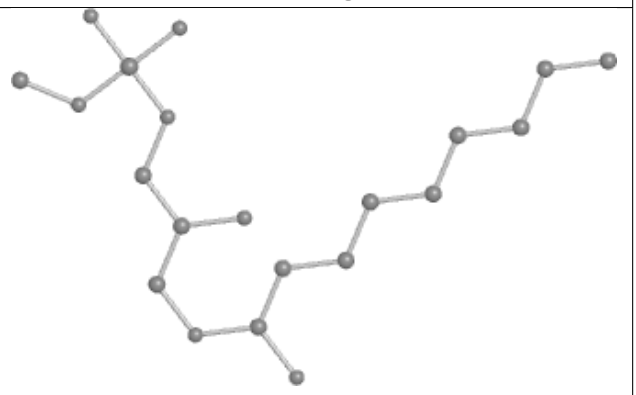
Bond lengths



Bond angles

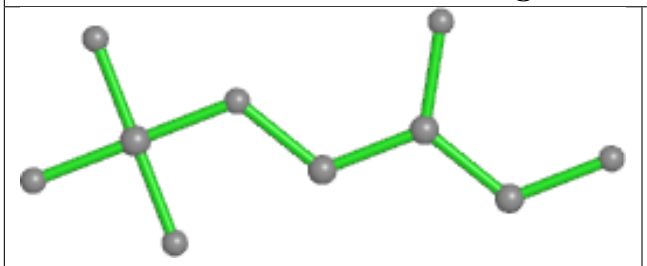


Torsions

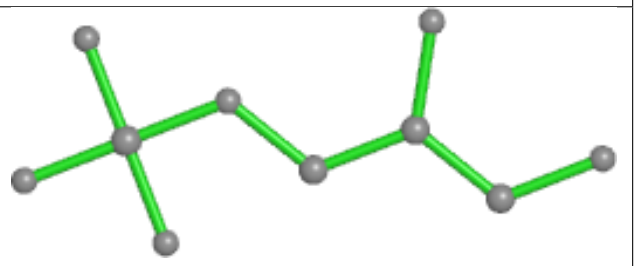


Rings

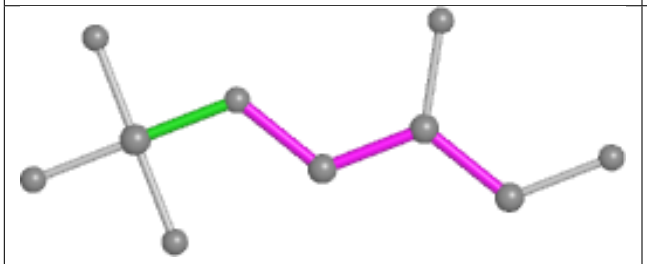
Ligand MC3 B 1302



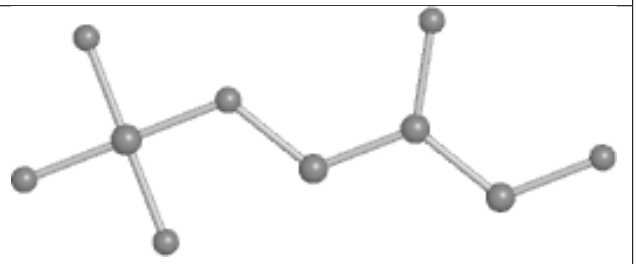
Bond lengths



Bond angles

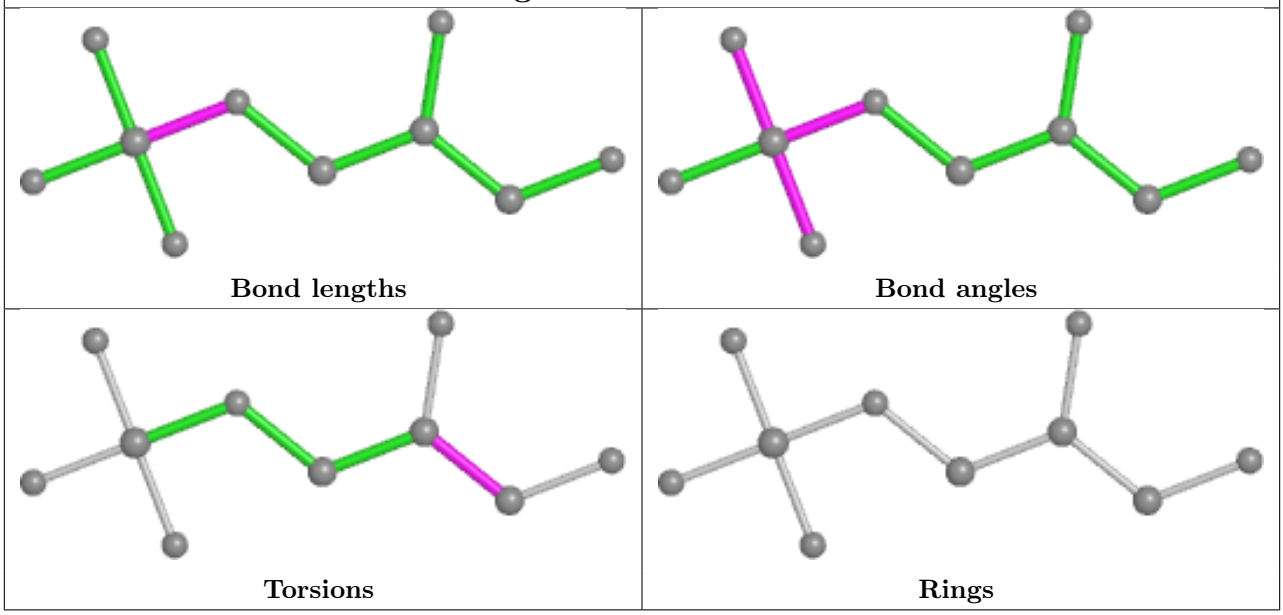


Torsions

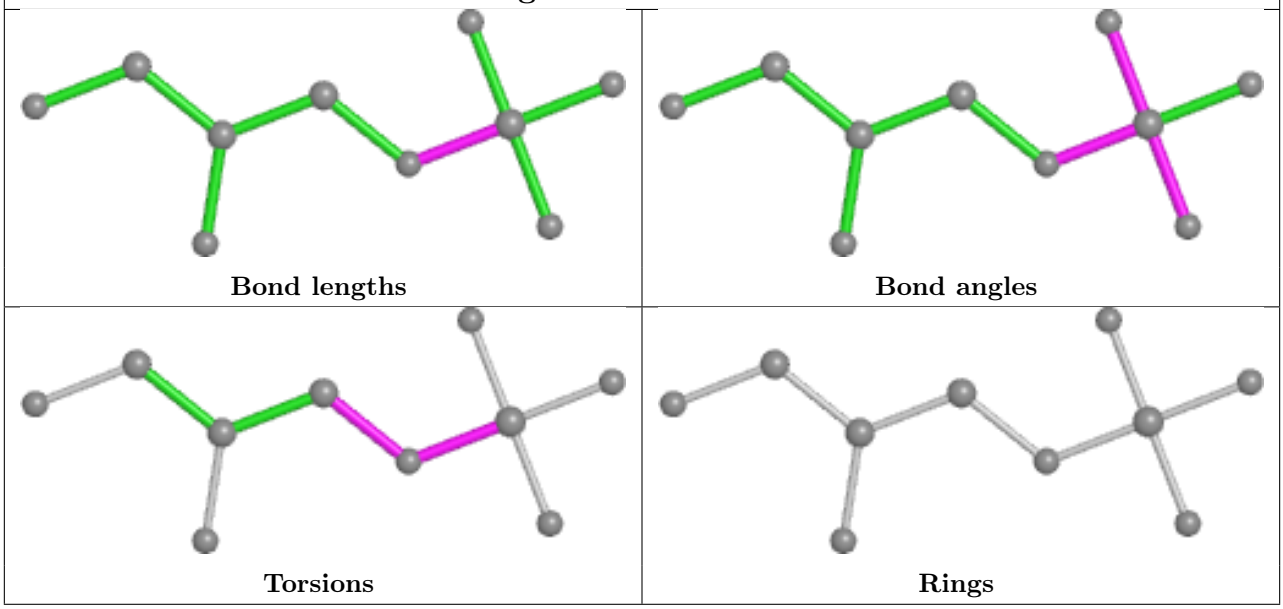


Rings

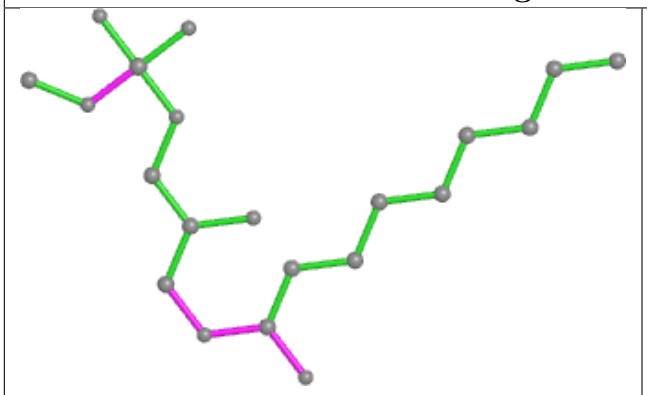
Ligand MC3 A 1306



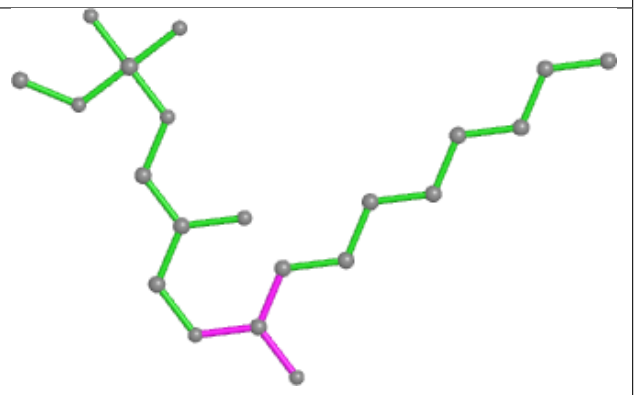
Ligand PX6 A 1305



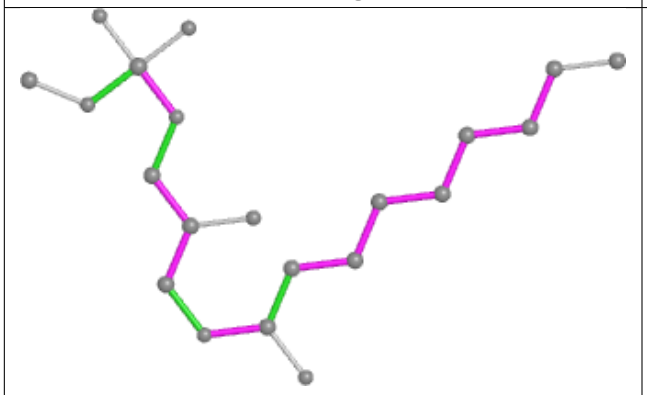
Ligand MC3 D 1302



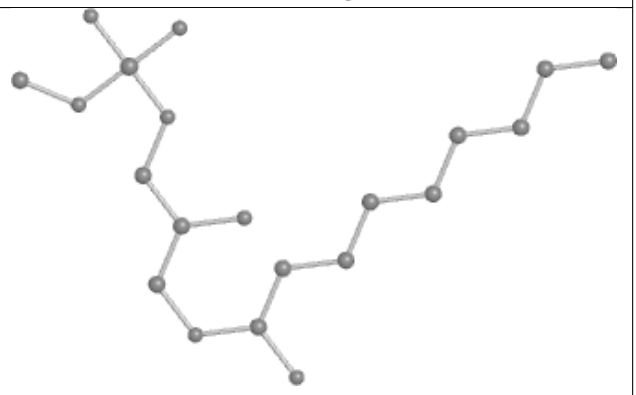
Bond lengths



Bond angles

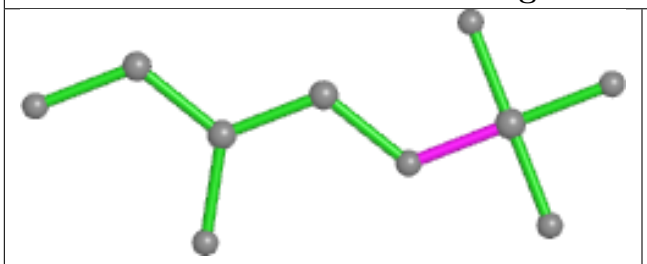


Torsions

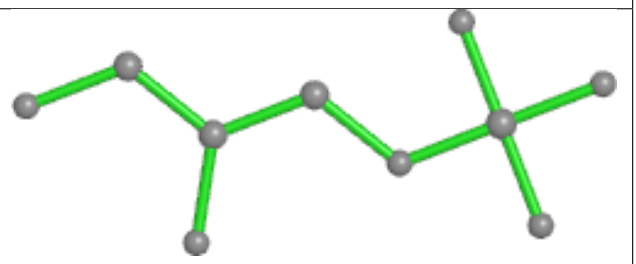


Rings

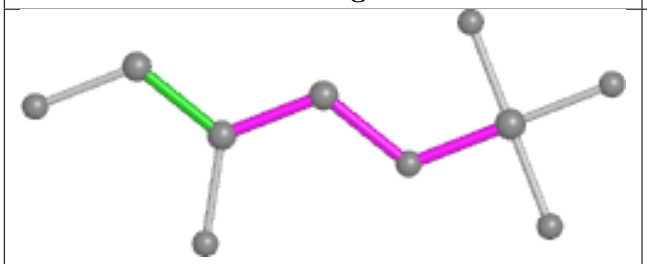
Ligand PX6 B 1301



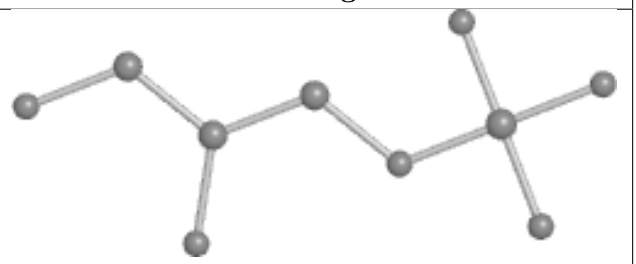
Bond lengths



Bond angles

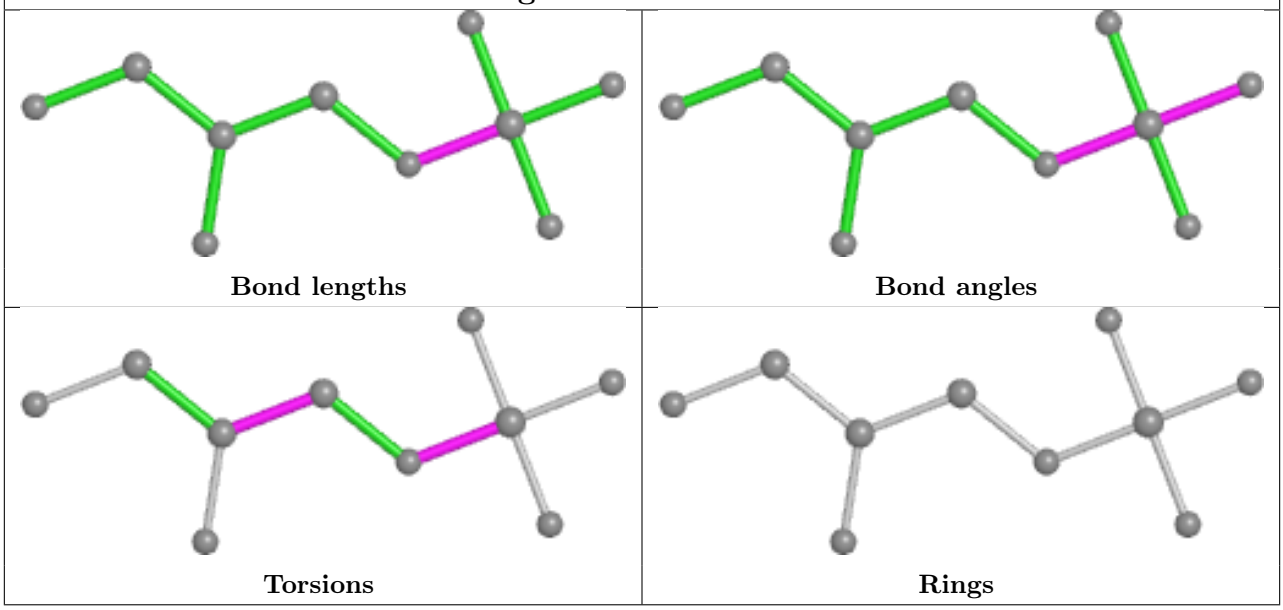


Torsions

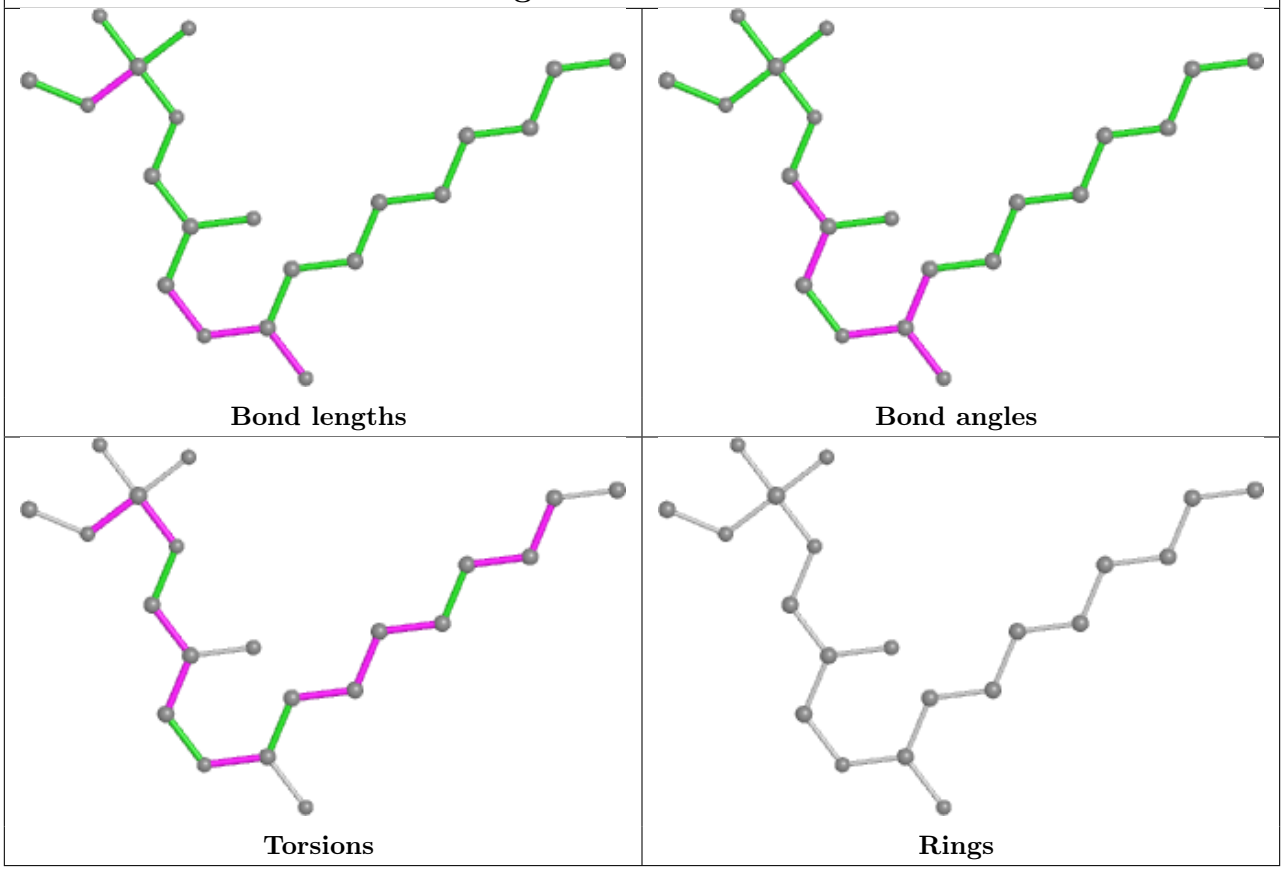


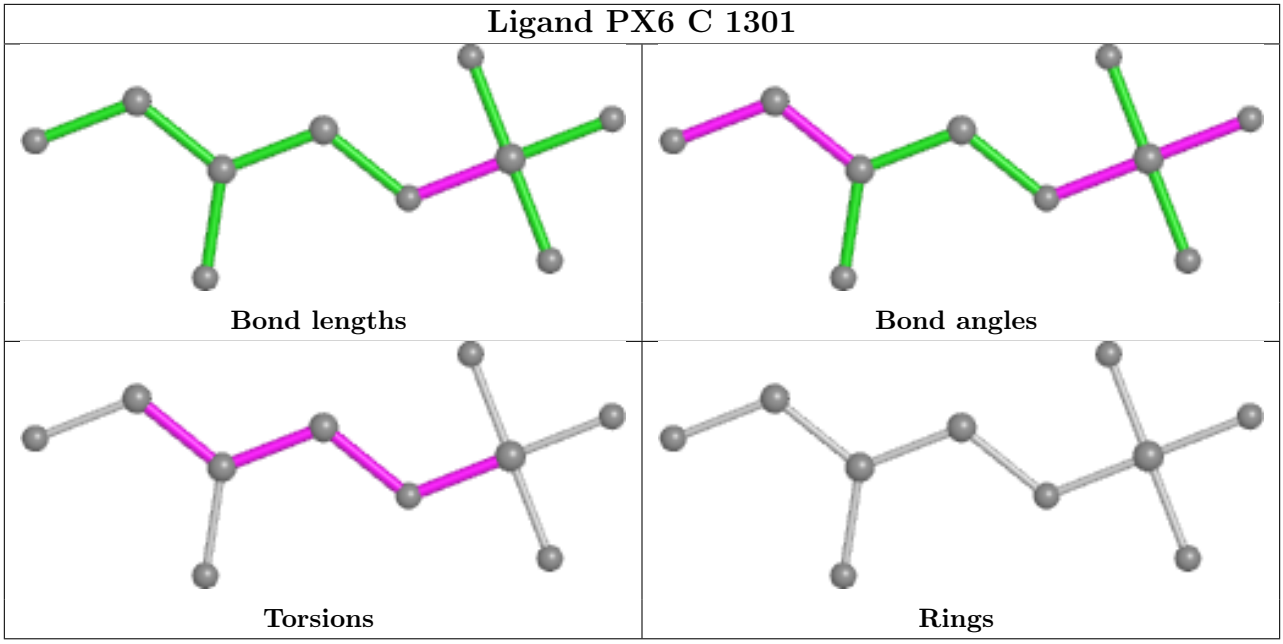
Rings

Ligand PX6 D 1303



Ligand MC3 A 1303





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	219/285 (76%)	0.16	7 (3%)	47	31	35, 109, 175, 248	0
1	B	219/285 (76%)	0.17	6 (2%)	54	39	44, 118, 183, 268	0
1	C	219/285 (76%)	0.18	7 (3%)	47	31	30, 112, 193, 225	0
1	D	219/285 (76%)	0.24	11 (5%)	28	16	38, 118, 186, 241	0
All	All	876/1140 (76%)	0.19	31 (3%)	44	28	30, 114, 185, 268	0

The worst 5 of 31 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	1001	MET	5.7
1	C	1065	TYR	5.0
1	D	1013	PHE	4.4
1	C	1090	PRO	3.7
1	B	1007	ASN	2.9

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 (i)

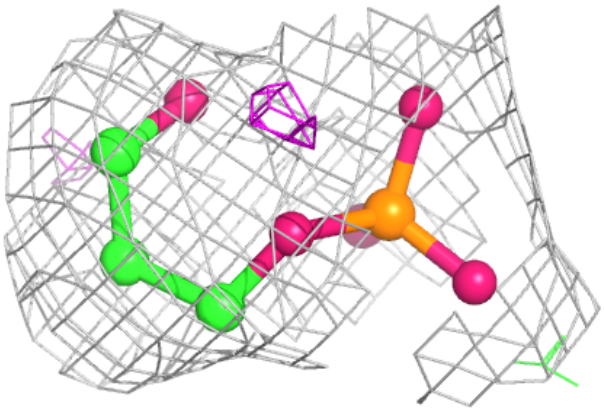
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

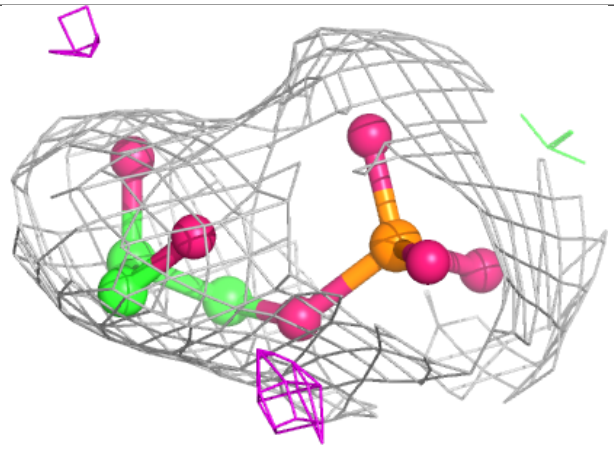
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
4	PX6	B	1301	10/44	0.83	0.23	88,127,144,150	0
4	PX6	D	1303	10/44	0.83	0.32	54,103,130,136	0
3	MC3	B	1302	10/46	0.88	0.15	127,152,169,182	0
3	MC3	A	1303	21/46	0.90	0.25	59,90,108,118	0
4	PX6	A	1305	10/44	0.90	0.25	66,111,117,126	0
5	6U8	C	1302	30/30	0.90	0.26	50,86,128,259	0
3	MC3	D	1302	21/46	0.91	0.27	62,101,120,154	0
3	MC3	D	1304	10/46	0.91	0.22	77,98,110,110	0
3	MC3	A	1304	21/46	0.91	0.29	55,82,98,107	0
4	PX6	C	1301	10/44	0.93	0.19	58,78,121,125	0
2	CA	A	1301	1/1	0.94	0.32	99,99,99,99	0
3	MC3	A	1306	10/46	0.95	0.21	80,103,106,122	0
2	CA	A	1302	1/1	0.97	0.27	88,88,88,88	0
2	CA	D	1301	1/1	0.98	0.26	43,43,43,43	0

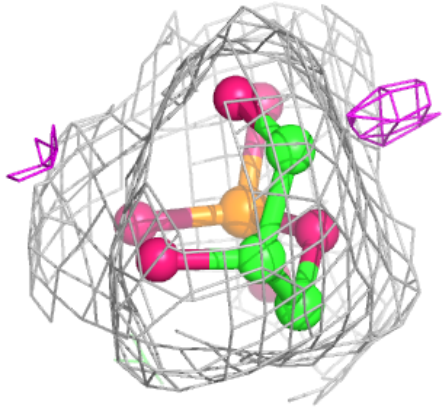
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around PX6 B 1301:

2mF$_o$-DF$_c$ (at 0.7 rmsd) in gray
mF$_o$-DF$_c$ (at 3 rmsd) in purple (negative) and green (positive)

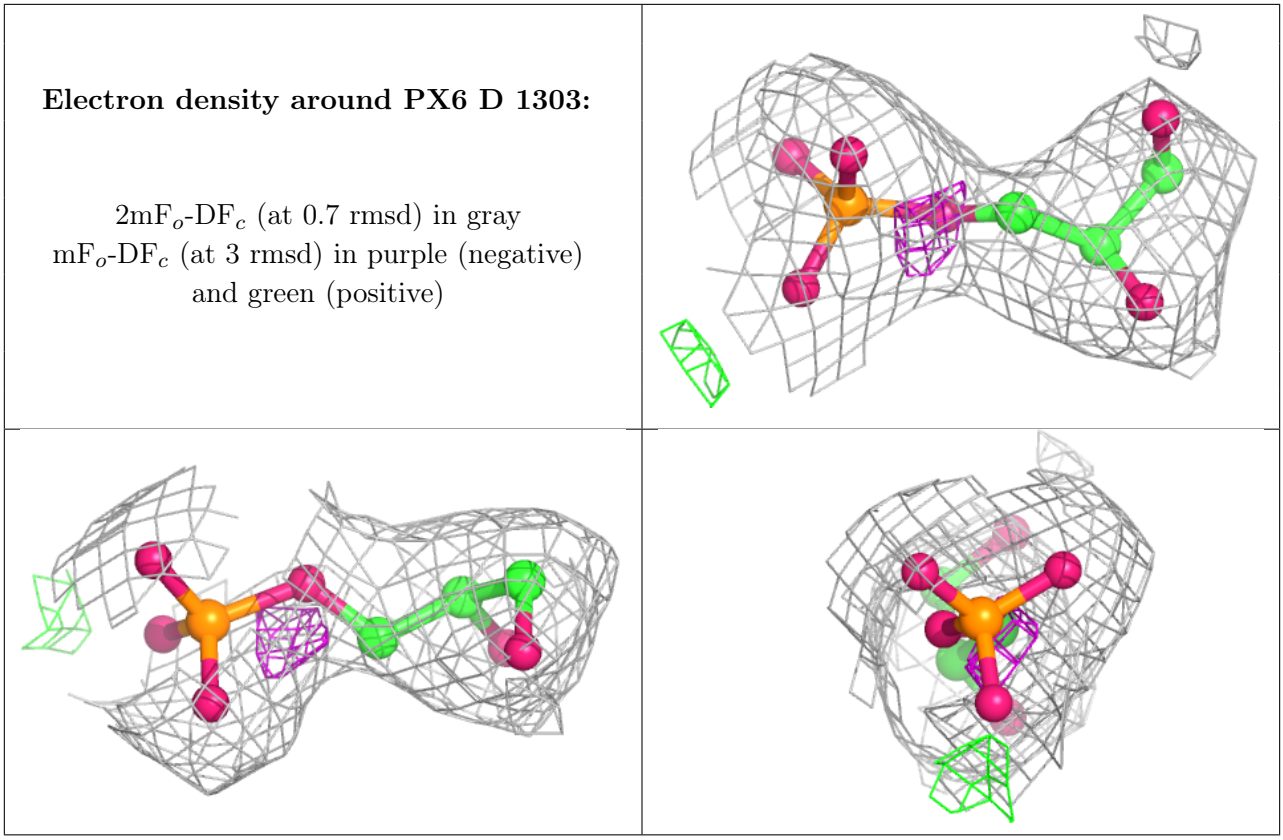






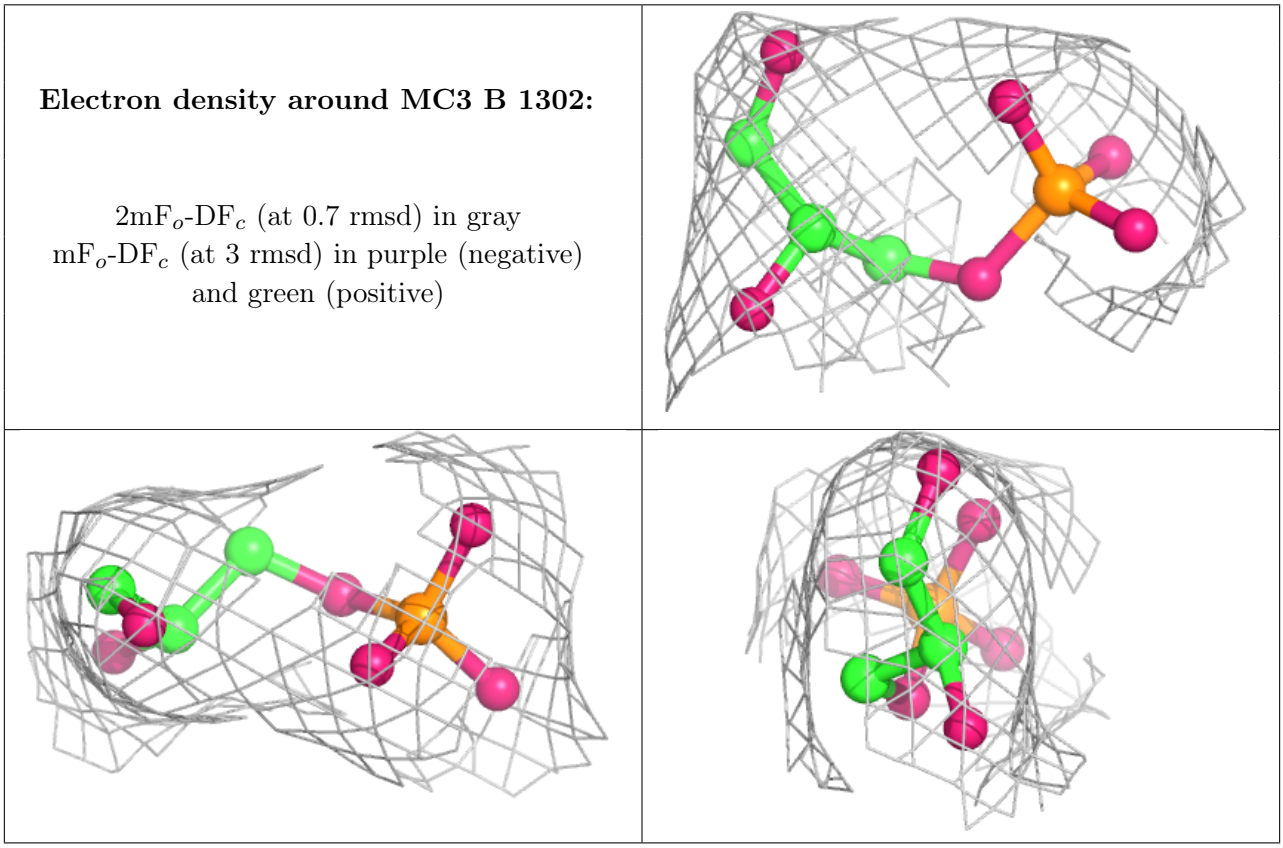
Electron density around PX6 D 1303:

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



Electron density around MC3 B 1302:

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



Electron density around MC3 A 1303:

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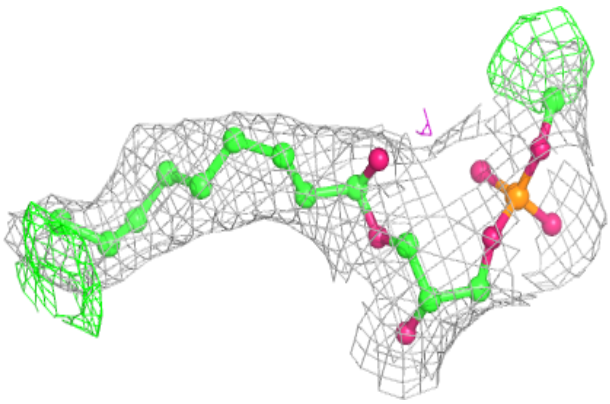
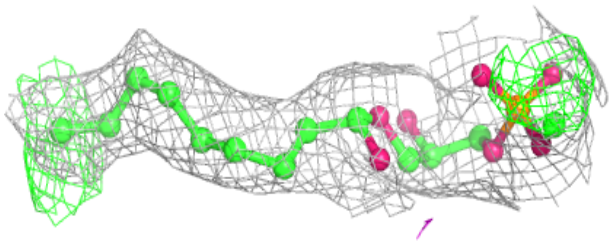
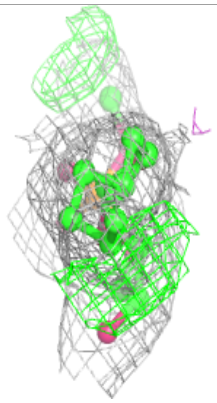
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)







Electron density around PX6 A 1305:

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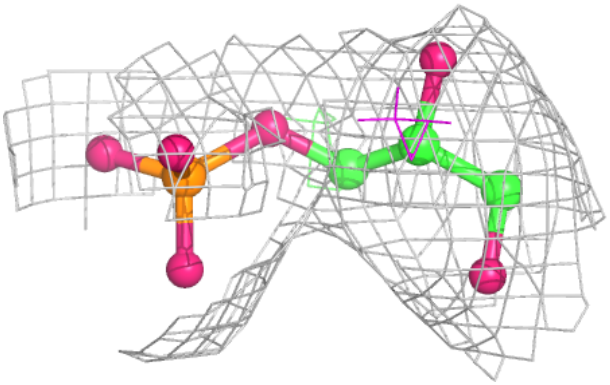
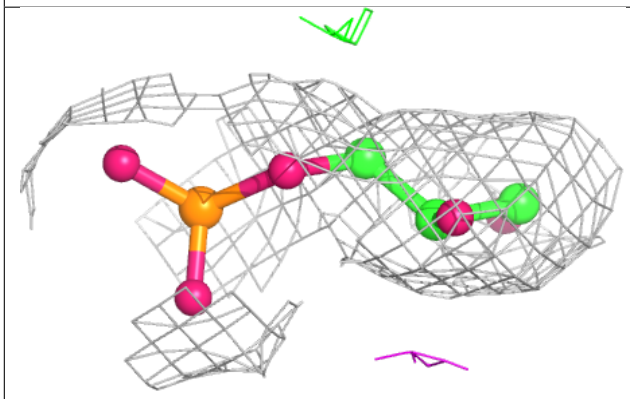
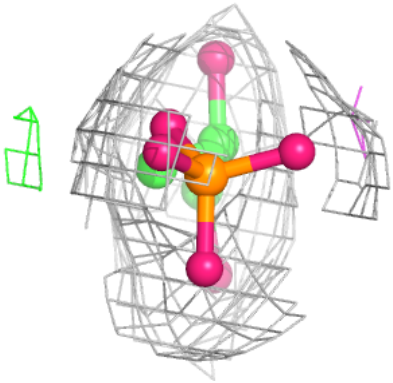
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

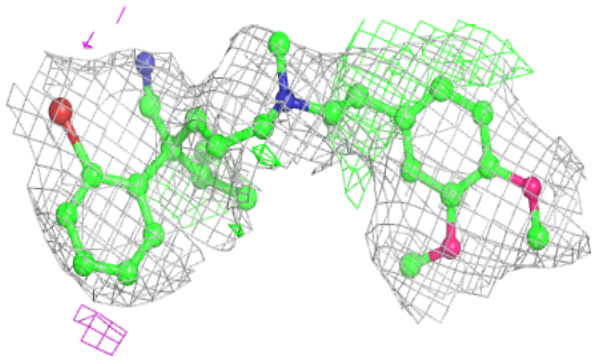


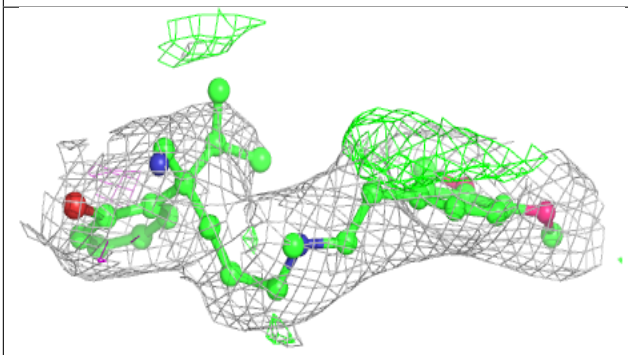


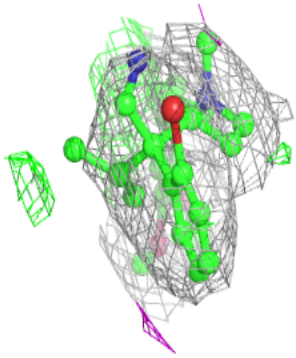


Electron density around 6U8 C 1302:

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

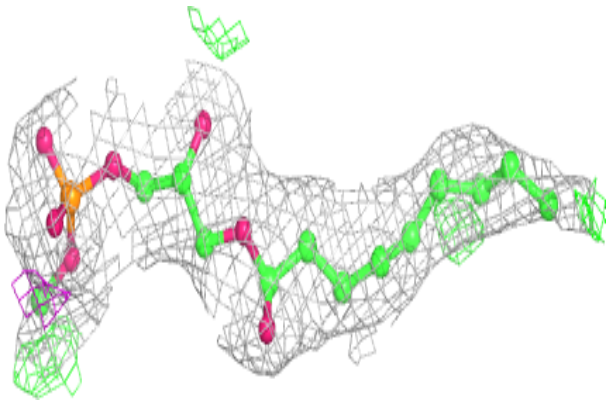


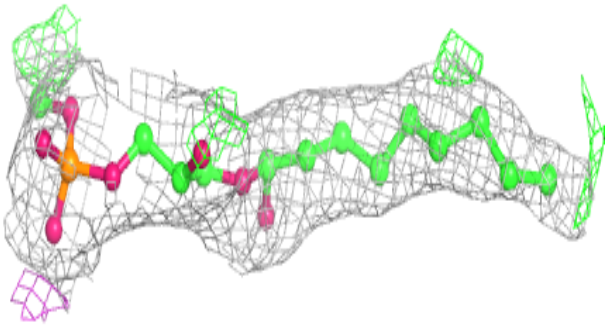


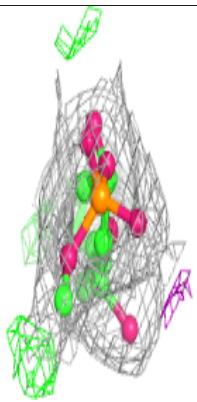


Electron density around MC3 D 1302:

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

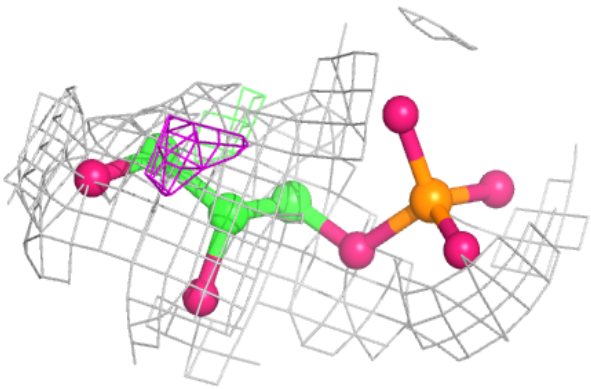


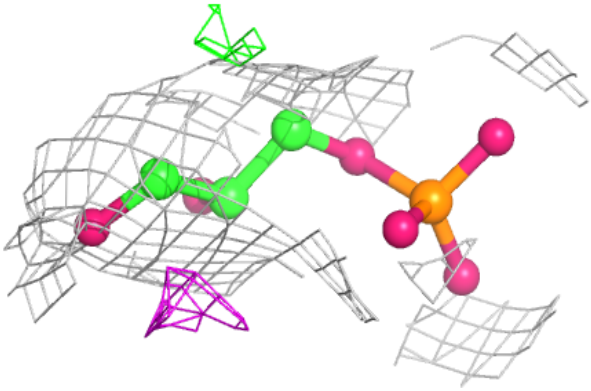


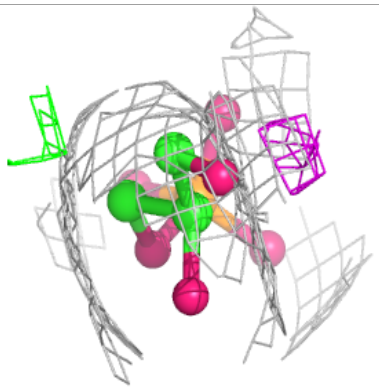


Electron density around MC3 D 1304:

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

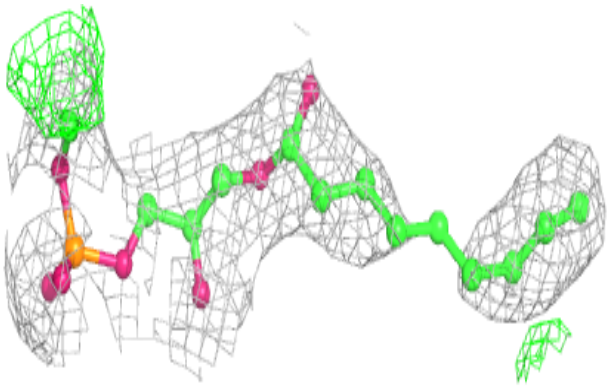


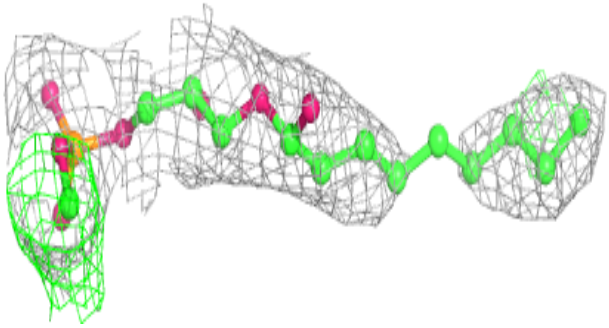


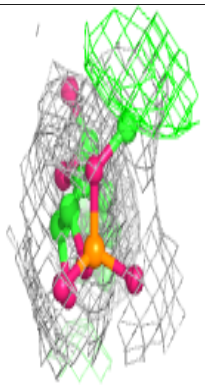


Electron density around MC3 A 1304:

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

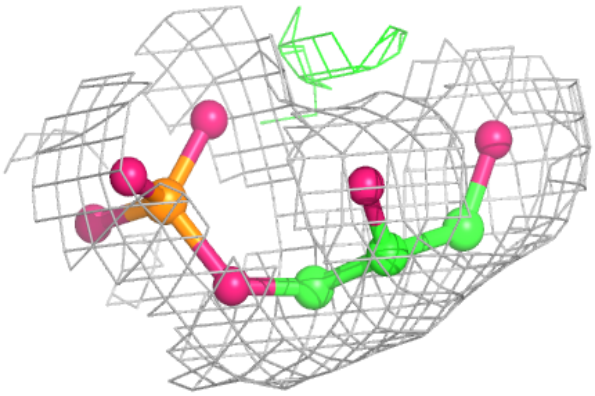


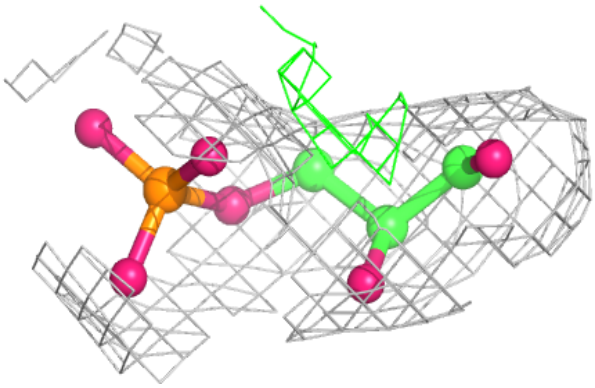


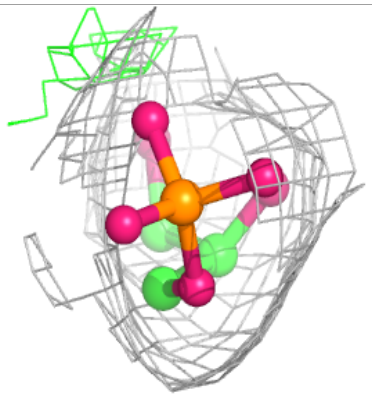


Electron density around PX6 C 1301:

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

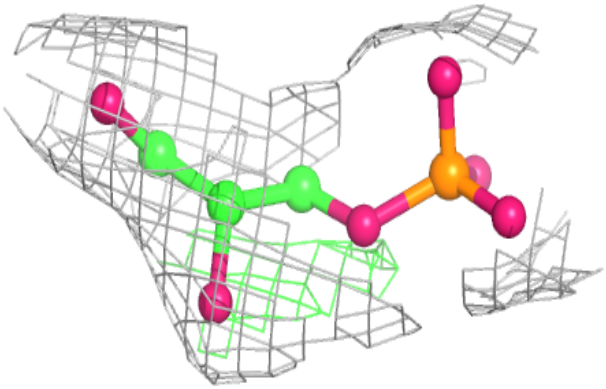


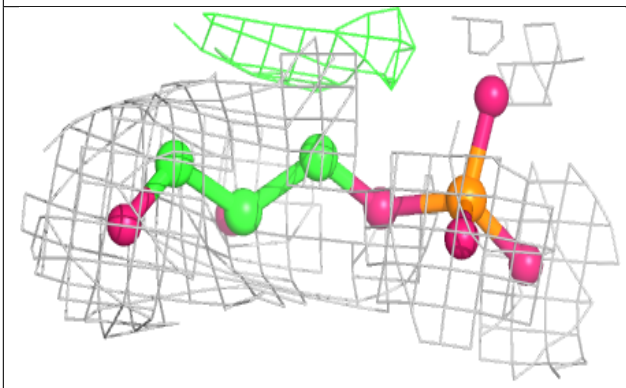




Electron density around MC3 A 1306:

$2mF_o$-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.