Full wwPDB X-ray Structure Validation Report (i)

Jun 17, 2024 – 06:39 PM EDT

PDB ID	:	5TM9
Title	:	Crystal Structure of the ER-alpha Ligand-binding Domain (Y537S) in Complex with the OBHS-ASC Analog, (E)-3-(4-((1R,4S,6R)-6-((3-chlorophenoxy) sulfonyl)-3-(4-hydroxyphenyl)-7-oxabicyclo[2.2.1]hept-2-en-2-yl)phenyl)acrylic acid
Authors	:	Nwachukwu, J.C.; Srinivasan, S.; Bruno, N.E.; Nowak, J.; Kojetin, D.J.; Elemento, O.; Katzenellenbogen, J.A.; Nettles, K.W.
Deposited on	:	2016-10-12
Resolution	:	2.50 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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:

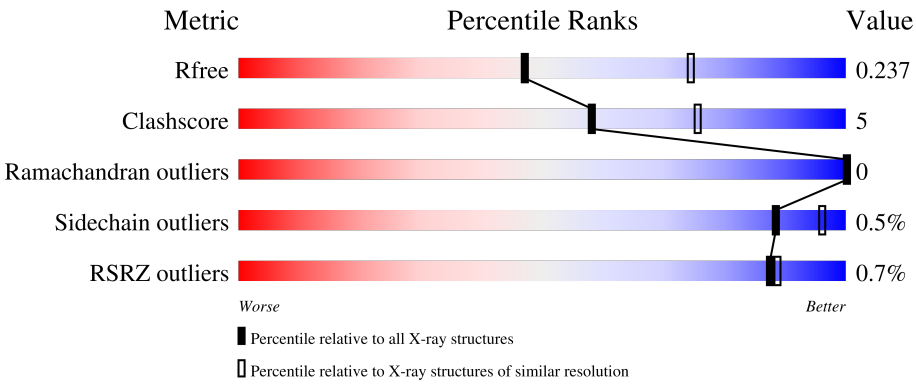
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.37.1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.50 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	4661 (2.50-2.50)
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)
RSRZ outliers	127900	4559 (2.50-2.50)

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	257	77% 6% 16%
1	B	257	% 71% 11% 18%
2	C	13	8% 54% 15% 31%

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Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.37.1

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Mol	Chain	Length	Quality of chain
2	D	13	31% 23% 46%

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 3725 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 Estrogen receptor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	215	1689	1080	289	304	16	0	1	0
1	B	211	1646	1052	287	290	17	0	1	0

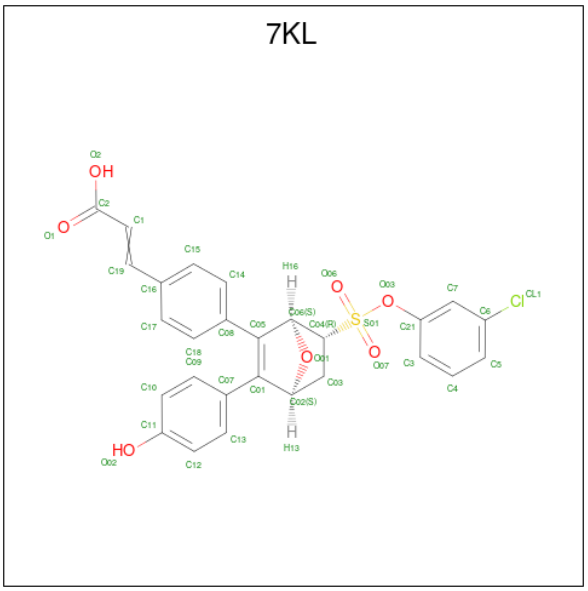
There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	537	SER	TYR	engineered mutation	UNP P03372
B	537	SER	TYR	engineered mutation	UNP P03372

- Molecule 2 is a protein called Nuclear receptor coactivator 2.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
2	C	9	66	42	12	12	0	0	0
2	D	7	49	33	9	7	0	0	0

- Molecule 3 is 3-{4-[(1S,4S,6R)-6-[(3-chlorophenoxy)sulfonyl]-3-(4-hydroxyphenyl)-7-oxabicyclo[2.2.1]hept-2-en-2-yl]phenyl}prop-2-enoic acid (three-letter code: 7KL) (formula: $C_{27}H_{21}ClO_7S$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C O S 26 20 5 1	0	0
3	A	1	Total C Cl O S 32 25 1 5 1	0	0
3	A	1	Total C Cl O S 32 25 1 5 1	0	1
3	A	1	Total C Cl O S 32 25 1 5 1	0	1
3	B	1	Total C Cl O S 32 25 1 5 1	0	0

- Molecule 4 is water.

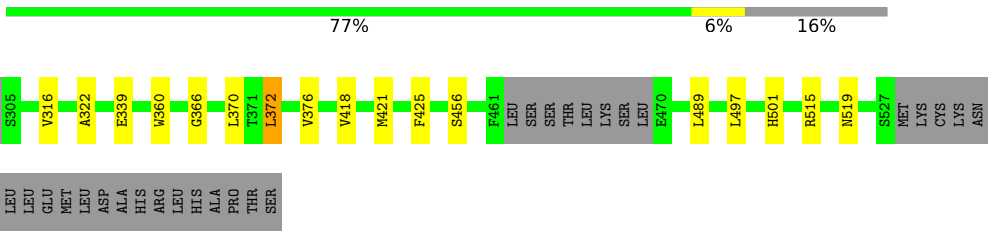
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	59	Total O 59 59	0	0
4	B	62	Total O 62 62	0	0

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.

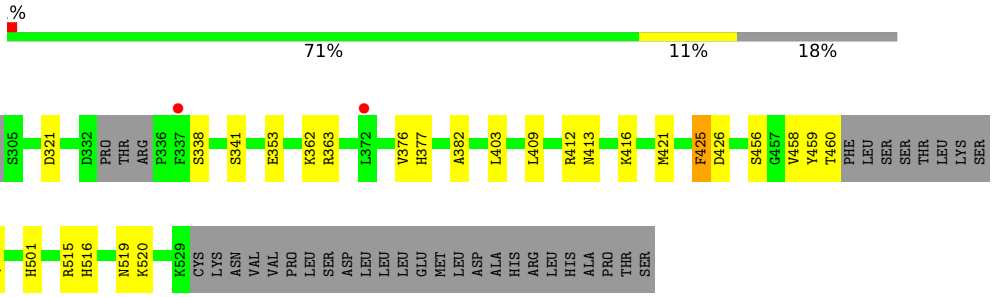
• Molecule 1: Estrogen receptor

Chain A:



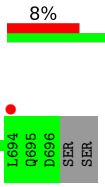
• Molecule 1: Estrogen receptor

Chain B:



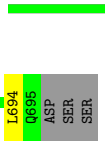
• Molecule 2: Nuclear receptor coactivator 2

Chain C:



• Molecule 2: Nuclear receptor coactivator 2

Chain D:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	58.88Å 81.98Å 61.80Å 90.00° 116.17° 90.00°	Depositor
Resolution (Å)	45.94 – 2.50 45.94 – 2.50	Depositor EDS
% Data completeness (in resolution range)	93.8 (45.94-2.50) 93.4 (45.94-2.50)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.23 (at 2.51Å)	Xtriage
Refinement program	PHENIX 1.10.1_2155	Depositor
R, R_{free}	0.196 , 0.237 0.196 , 0.237	Depositor DCC
R_{free} test set	1806 reflections (10.03%)	wwPDB-VP
Wilson B-factor (Å^2)	39.9	Xtriage
Anisotropy	0.485	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.29 , 47.6	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	0.036 for h,-k,-h-l	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	3725	wwPDB-VP
Average B, all atoms (Å^2)	53.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.44% 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: 7KL

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	0.35	0/1720	0.40	0/2328
1	B	0.28	0/1674	0.38	0/2261
2	C	0.19	0/66	0.33	0/89
2	D	0.18	0/49	0.29	0/66
All	All	0.31	0/3509	0.39	0/4744

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 (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	1689	0	1697	13	0
1	B	1646	0	1665	18	0
2	C	66	0	57	2	0
2	D	49	0	45	3	0
3	A	122	0	0	4	0
3	B	32	0	0	1	0
4	A	59	0	0	0	0
4	B	62	0	0	0	0
All	All	3725	0	3464	34	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.

All (34) 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)
3:A:602:7KL:C09	3:A:602:7KL:C14	2.30	1.08
1:A:519:ASN:HD22	1:B:519:ASN:HD22	1.21	0.85
1:B:376:VAL:HG13	2:D:690:LEU:HD23	1.72	0.71
1:B:403:LEU:HD12	1:B:409:LEU:HD13	1.79	0.65
1:A:497:LEU:O	1:A:501:HIS:ND1	2.30	0.64
1:A:370:LEU:HD12	1:A:370:LEU:N	2.17	0.59
1:B:498:GLN:HA	1:B:501[B]:HIS:CE1	2.39	0.57
1:A:366:GLY:O	1:A:370:LEU:CD1	2.54	0.56
1:B:338:SER:HB2	1:B:341:SER:H	1.71	0.56
1:B:456:SER:HA	1:B:515:ARG:NH2	2.22	0.55
1:A:456:SER:HA	1:A:515:ARG:NH2	2.23	0.53
1:B:353:GLU:OE1	3:B:601:7KL:O02	2.27	0.52
1:B:421:MET:O	1:B:425:PHE:HB2	2.10	0.51
1:A:370:LEU:N	1:A:370:LEU:CD1	2.75	0.50
1:A:316:VAL:HG21	1:A:489:LEU:HD21	1.93	0.50
1:B:362:LYS:HE3	2:D:694:LEU:HA	1.97	0.47
1:A:366:GLY:O	1:A:370:LEU:HD13	2.16	0.45
1:B:516:HIS:O	1:B:520:LYS:HG2	2.17	0.45
1:A:376:VAL:HG13	2:C:690:LEU:HD23	1.99	0.44
1:B:382:ALA:HB2	1:B:456:SER:HB2	1.99	0.44
1:B:412:ARG:NH1	1:B:426:ASP:OD2	2.51	0.44
1:B:376:VAL:HG21	2:D:691:HIS:CE1	2.53	0.43
1:A:372:LEU:CD1	2:C:691:HIS:CD2	3.01	0.43
1:A:339:GLU:HG3	1:A:418:VAL:HG22	2.00	0.42
3:A:603[A]:7KL:C3	3:A:603[A]:7KL:C04	2.98	0.41
3:A:604[B]:7KL:C15	3:A:604[B]:7KL:CL1	3.06	0.41
1:A:421:MET:HG2	1:A:425:PHE:CD1	2.55	0.41
1:B:497:LEU:O	1:B:501[A]:HIS:ND1	2.53	0.41
1:A:322:ALA:O	1:A:360:TRP:HD1	2.04	0.41
1:B:321:ASP:OD2	1:B:363:ARG:NH2	2.54	0.41
1:B:413:ASN:HA	1:B:416:LYS:HD2	2.03	0.40
3:A:602:7KL:C3	3:A:602:7KL:O07	2.69	0.40
1:B:377:HIS:NE2	1:B:460:THR:HG23	2.36	0.40
1:B:458:VAL:HG13	1:B:459:TYR:CD1	2.56	0.40

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	212/257 (82%)	210 (99%)	2 (1%)	0	100	100
1	B	206/257 (80%)	204 (99%)	2 (1%)	0	100	100
2	C	7/13 (54%)	7 (100%)	0	0	100	100
2	D	5/13 (38%)	5 (100%)	0	0	100	100
All	All	430/540 (80%)	426 (99%)	4 (1%)	0	100	100

There are no Ramachandran outliers to report.

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	185/232 (80%)	184 (100%)	1 (0%)	88	96
1	B	179/232 (77%)	178 (99%)	1 (1%)	86	95
2	C	6/13 (46%)	6 (100%)	0	100	100
2	D	4/13 (31%)	4 (100%)	0	100	100
All	All	374/490 (76%)	372 (100%)	2 (0%)	88	96

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	372	LEU
1	B	425	PHE

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	359	ASN
1	B	519	ASN
2	C	691	HIS

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

5 ligands 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	$\#\|Z\| > 2$
3	7KL	A	601	-	28,29,40	3.97	13 (46%)	35,44,59	1.61	7 (20%)
3	7KL	A	604[B]	-	35,36,40	4.19	12 (34%)	45,54,59	1.54	8 (17%)
3	7KL	A	603[A]	-	35,36,40	4.37	12 (34%)	45,54,59	1.54	7 (15%)
3	7KL	B	601	-	35,36,40	3.80	10 (28%)	45,54,59	1.10	4 (8%)
3	7KL	A	602	-	35,36,40	3.84	12 (34%)	45,54,59	1.66	8 (17%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the

Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	7KL	A	601	-	-	2/15/41/48	0/5/4/5
3	7KL	A	604[B]	-	-	1/17/43/48	0/6/5/5
3	7KL	A	603[A]	-	-	2/17/43/48	0/6/5/5
3	7KL	B	601	-	-	3/17/43/48	0/6/5/5
3	7KL	A	602	-	-	0/17/43/48	0/6/5/5

All (59) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	603[A]	7KL	C6-CL1	-12.48	1.47	1.74
3	B	601	7KL	C06-C05	-11.85	1.37	1.50
3	A	601	7KL	C06-C05	-11.00	1.38	1.50
3	A	603[A]	7KL	C06-C05	-10.96	1.38	1.50
3	A	604[B]	7KL	C06-C05	-10.94	1.38	1.50
3	A	602	7KL	C06-C05	-10.41	1.39	1.50
3	A	604[B]	7KL	C6-CL1	-10.23	1.52	1.74
3	A	603[A]	7KL	C07-C01	-8.80	1.31	1.48
3	A	604[B]	7KL	C07-C01	-8.76	1.32	1.48
3	A	602	7KL	C07-C01	-8.73	1.32	1.48
3	A	603[A]	7KL	C08-C05	-8.58	1.32	1.48
3	A	604[B]	7KL	C08-C05	-8.53	1.32	1.48
3	A	602	7KL	C08-C05	-8.49	1.32	1.48
3	A	601	7KL	C07-C01	-8.45	1.32	1.48
3	B	601	7KL	C02-C01	-8.38	1.39	1.51
3	A	604[B]	7KL	O03-S01	-8.36	1.46	1.60
3	A	603[A]	7KL	O03-S01	-8.33	1.46	1.60
3	A	601	7KL	C08-C05	-8.28	1.32	1.48
3	B	601	7KL	C08-C05	-8.04	1.33	1.48
3	A	602	7KL	C02-C01	-7.86	1.40	1.51
3	B	601	7KL	C07-C01	-7.66	1.34	1.48
3	A	602	7KL	C6-CL1	-7.20	1.58	1.74
3	A	604[B]	7KL	C02-C01	-7.12	1.41	1.51
3	A	601	7KL	C02-C01	-7.08	1.41	1.51
3	A	603[A]	7KL	C02-C01	-7.04	1.41	1.51
3	B	601	7KL	C04-S01	6.96	1.94	1.79
3	B	601	7KL	O06-S01	6.46	1.53	1.43
3	A	602	7KL	O03-S01	-6.32	1.50	1.60
3	B	601	7KL	O07-S01	6.27	1.53	1.43
3	A	603[A]	7KL	O03-C21	-5.68	1.33	1.42
3	A	604[B]	7KL	O03-C21	-5.58	1.33	1.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	602	7KL	C04-S01	5.58	1.91	1.79
3	A	601	7KL	O03-S01	-5.58	1.49	1.57
3	A	604[B]	7KL	C04-S01	5.30	1.90	1.79
3	A	603[A]	7KL	C04-S01	5.27	1.90	1.79
3	A	601	7KL	C04-S01	5.07	1.90	1.79
3	A	602	7KL	O03-C21	-4.25	1.35	1.42
3	A	601	7KL	O01-C06	-4.21	1.38	1.43
3	A	602	7KL	O07-S01	4.06	1.49	1.43
3	A	603[A]	7KL	C19-C16	-3.93	1.37	1.51
3	A	604[B]	7KL	C19-C16	-3.93	1.37	1.51
3	B	601	7KL	O03-S01	-3.79	1.54	1.60
3	A	602	7KL	C19-C16	-3.75	1.37	1.51
3	A	603[A]	7KL	O01-C06	-3.73	1.38	1.43
3	A	604[B]	7KL	O01-C06	-3.70	1.38	1.43
3	A	601	7KL	C19-C16	-3.58	1.38	1.51
3	B	601	7KL	O03-C21	-3.42	1.37	1.42
3	A	602	7KL	O06-S01	3.38	1.48	1.43
3	B	601	7KL	C19-C16	-3.29	1.39	1.51
3	A	603[A]	7KL	O01-C02	-3.24	1.37	1.44
3	A	604[B]	7KL	O01-C02	-3.22	1.37	1.44
3	A	601	7KL	O01-C02	-3.20	1.37	1.44
3	A	601	7KL	O07-S01	2.78	1.47	1.43
3	A	601	7KL	O06-S01	2.55	1.47	1.43
3	A	603[A]	7KL	O06-S01	2.35	1.47	1.43
3	A	604[B]	7KL	O06-S01	2.33	1.47	1.43
3	A	602	7KL	O01-C02	-2.27	1.39	1.44
3	A	601	7KL	C10-C11	-2.09	1.34	1.38
3	A	601	7KL	O02-C11	-2.04	1.32	1.37

All (34) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	A	602	7KL	O01-C02-C03	-5.42	93.98	104.64
3	A	601	7KL	O01-C02-C03	-5.02	94.77	104.64
3	A	603[A]	7KL	O01-C02-C03	-4.94	94.93	104.64
3	A	604[B]	7KL	O01-C02-C03	-4.90	95.01	104.64
3	A	602	7KL	O07-S01-O06	-4.24	106.55	118.01
3	A	603[A]	7KL	O07-S01-O06	-4.05	107.06	118.01
3	A	604[B]	7KL	O07-S01-O06	-4.01	107.17	118.01
3	A	602	7KL	C07-C01-C02	3.11	126.52	121.44
3	A	602	7KL	C09-C07-C01	-2.97	117.06	120.91
3	A	601	7KL	O07-S01-O06	-2.97	109.97	118.01

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	A	602	7KL	O06-S01-C04	-2.83	105.65	109.33
3	B	601	7KL	O07-S01-O06	-2.67	110.78	118.01
3	A	601	7KL	C09-C07-C01	-2.62	117.52	120.91
3	A	604[B]	7KL	C09-C07-C01	-2.58	117.57	120.91
3	A	603[A]	7KL	C09-C07-C01	-2.51	117.66	120.91
3	A	603[A]	7KL	C21-O03-S01	-2.51	113.74	119.85
3	B	601	7KL	O01-C02-C03	-2.49	99.75	104.64
3	A	601	7KL	C18-C17-C16	-2.47	118.07	121.38
3	A	601	7KL	O03-S01-O06	2.42	112.65	106.99
3	A	604[B]	7KL	C7-C6-CL1	-2.40	116.15	119.15
3	A	601	7KL	C07-C01-C02	2.37	125.30	121.44
3	B	601	7KL	C09-C07-C01	-2.32	117.91	120.91
3	A	602	7KL	C18-C17-C16	-2.31	118.28	121.38
3	A	602	7KL	C21-O03-S01	-2.25	114.37	119.85
3	A	604[B]	7KL	C07-C01-C02	2.25	125.10	121.44
3	A	602	7KL	C02-C03-C04	2.21	102.57	100.61
3	A	603[A]	7KL	C07-C01-C02	2.21	125.04	121.44
3	A	604[B]	7KL	C21-O03-S01	-2.18	114.54	119.85
3	B	601	7KL	C21-C7-C6	2.09	120.58	118.14
3	A	603[A]	7KL	C7-C6-CL1	-2.03	116.61	119.15
3	A	604[B]	7KL	C08-C05-C01	2.02	134.04	128.81
3	A	603[A]	7KL	C08-C05-C01	2.02	134.03	128.81
3	A	604[B]	7KL	C12-C13-C07	-2.01	118.44	120.78
3	A	601	7KL	O07-S01-C04	-2.01	106.71	109.33

There are no chirality outliers.

All (8) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	601	7KL	C21-O03-S01-C04
3	A	601	7KL	C21-O03-S01-O07
3	A	603[A]	7KL	C21-O03-S01-C04
3	B	601	7KL	C3-C21-O03-S01
3	B	601	7KL	C7-C21-O03-S01
3	B	601	7KL	C21-O03-S01-O07
3	A	603[A]	7KL	C06-C05-C08-C14
3	A	604[B]	7KL	C06-C05-C08-C14

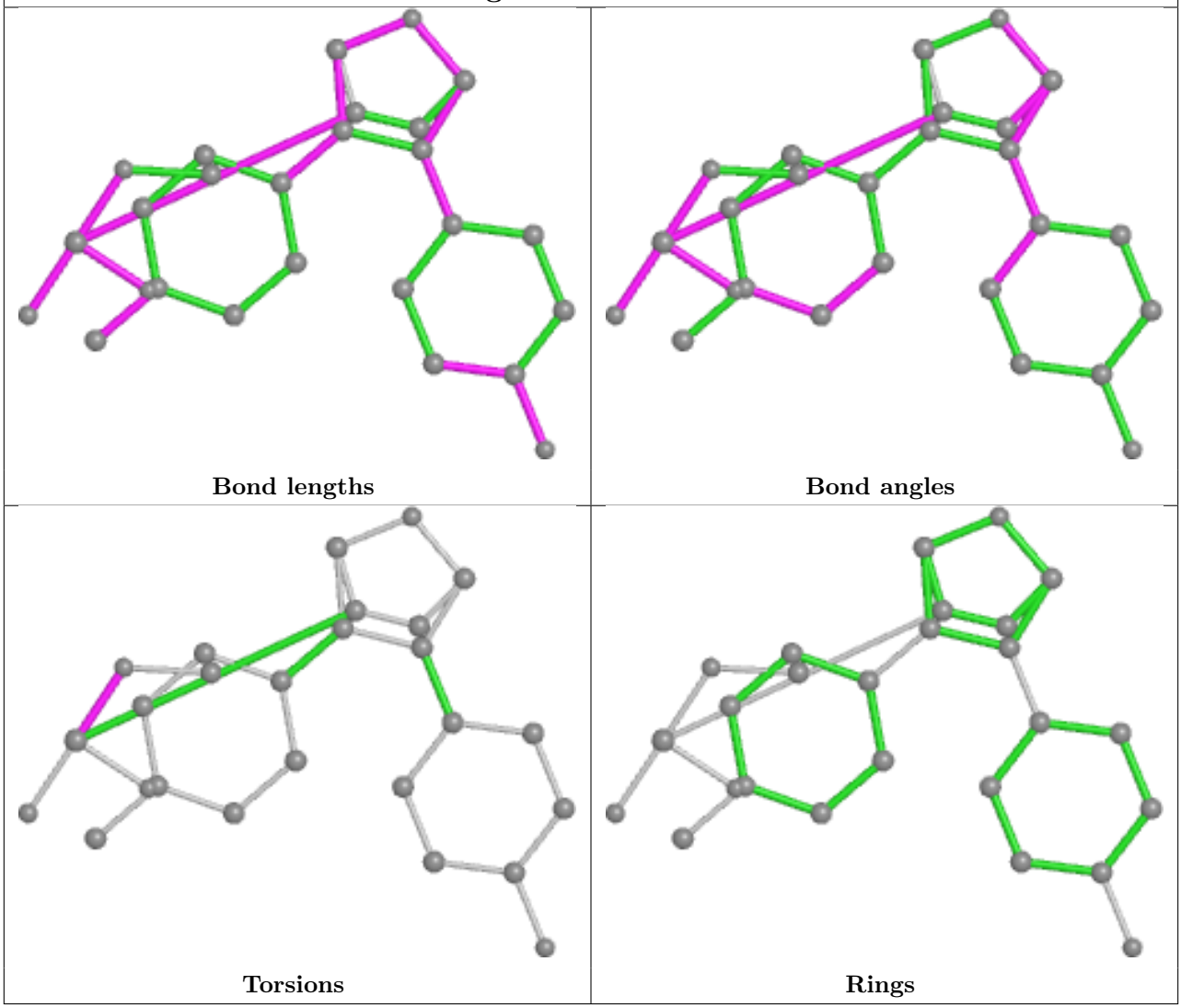
There are no ring outliers.

4 monomers are involved in 5 short contacts:

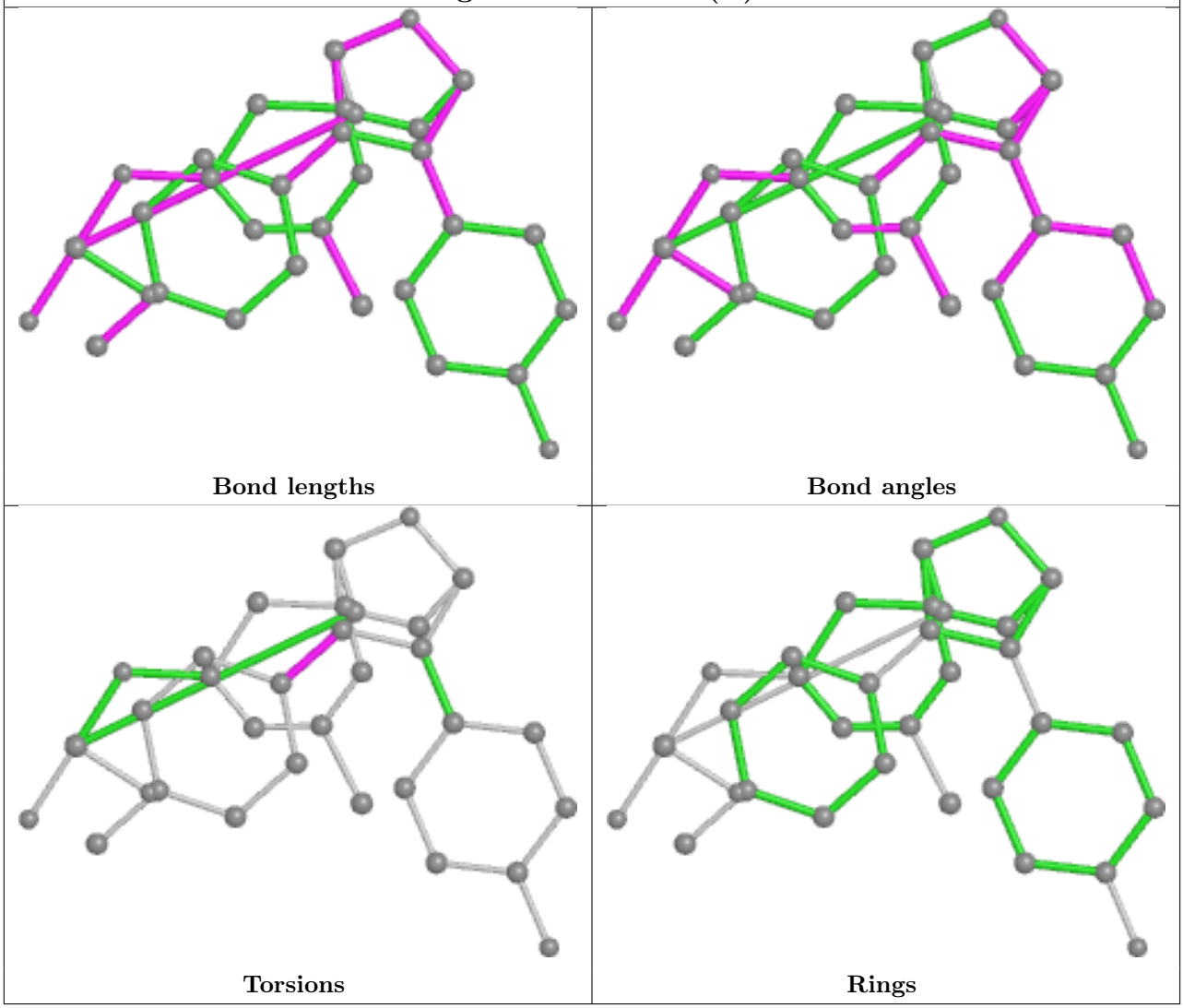
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	604[B]	7KL	1	0
3	A	603[A]	7KL	1	0
3	B	601	7KL	1	0
3	A	602	7KL	2	0

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.

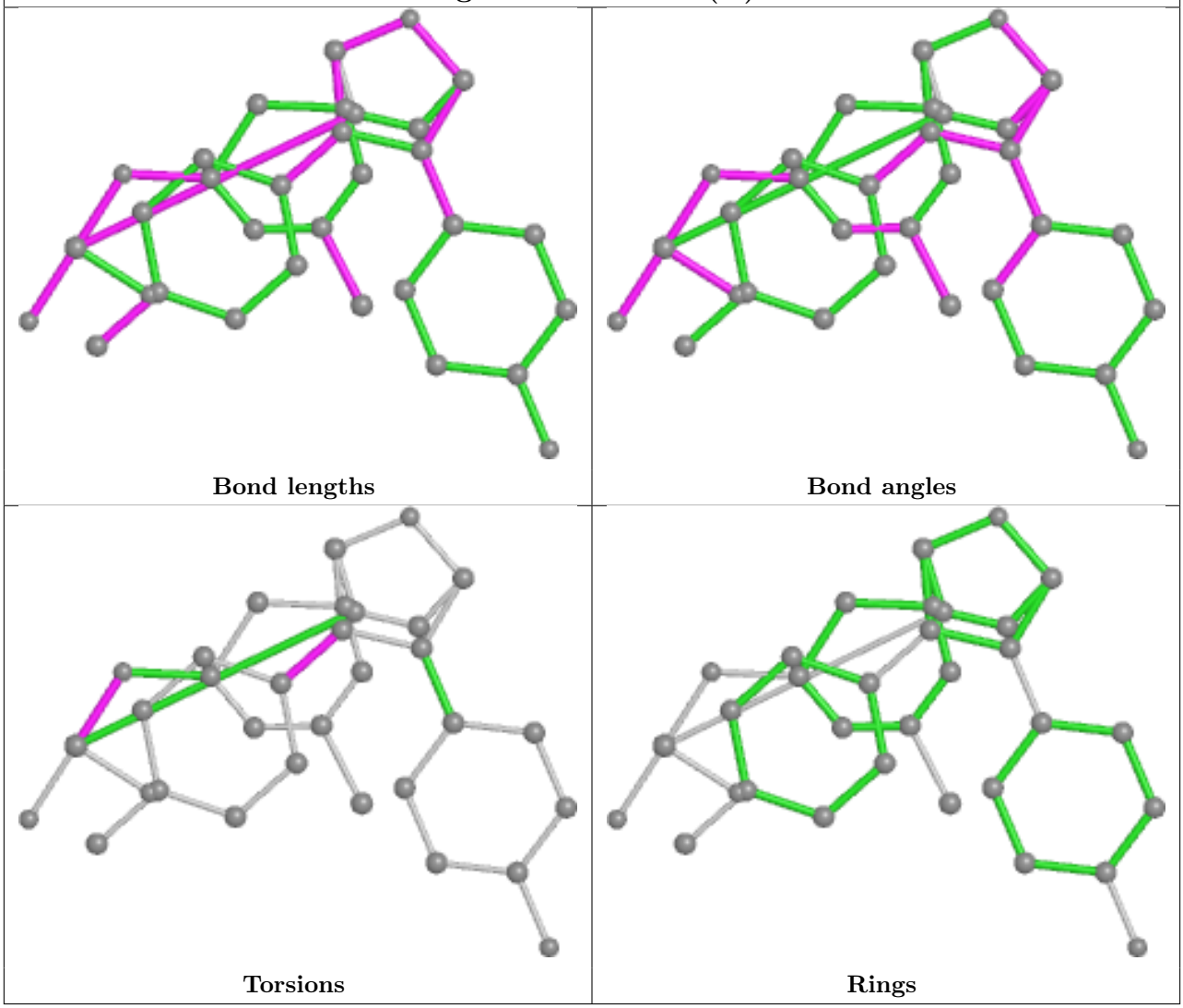
Ligand 7KL A 601



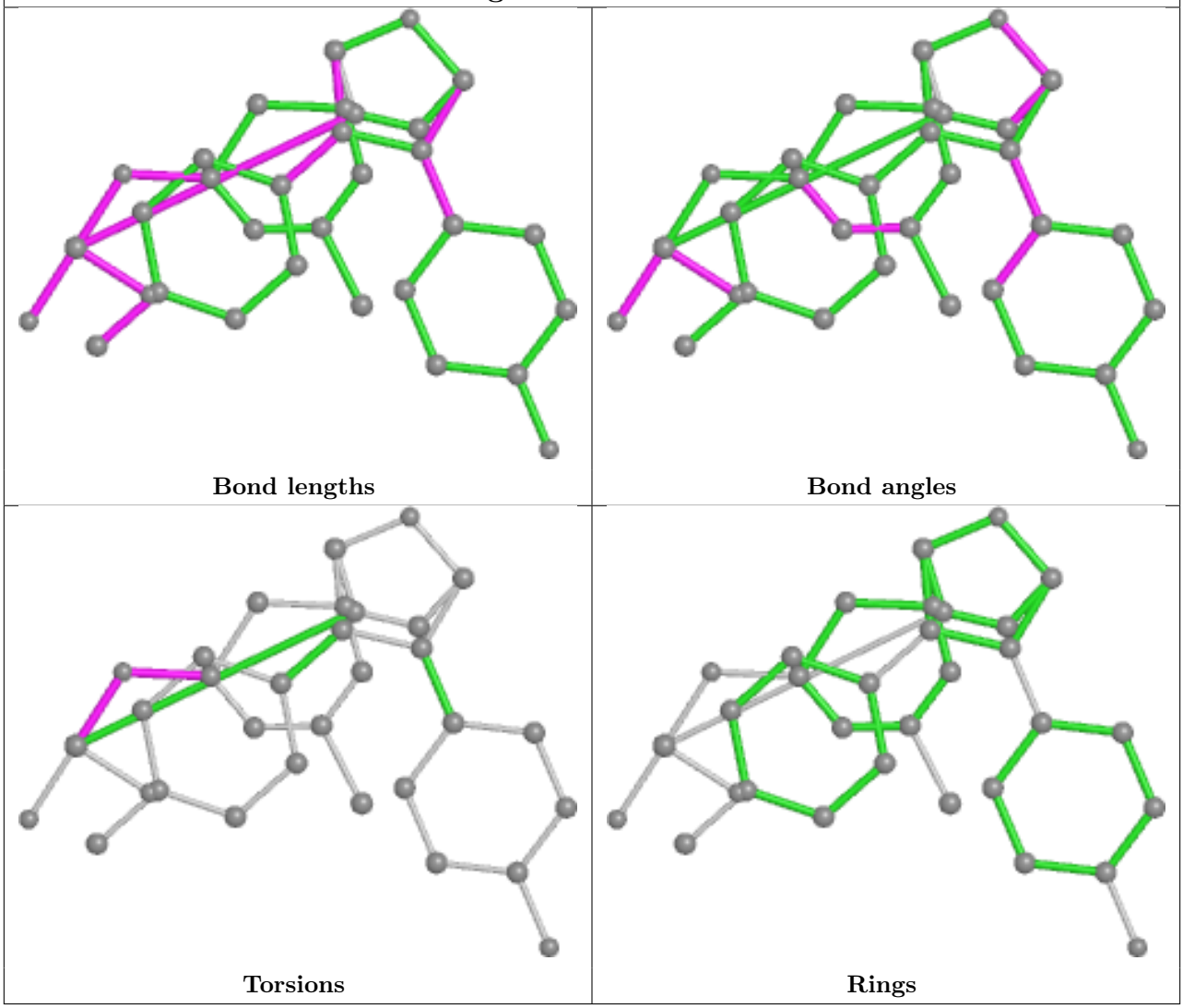
Ligand 7KL A 604 (B)



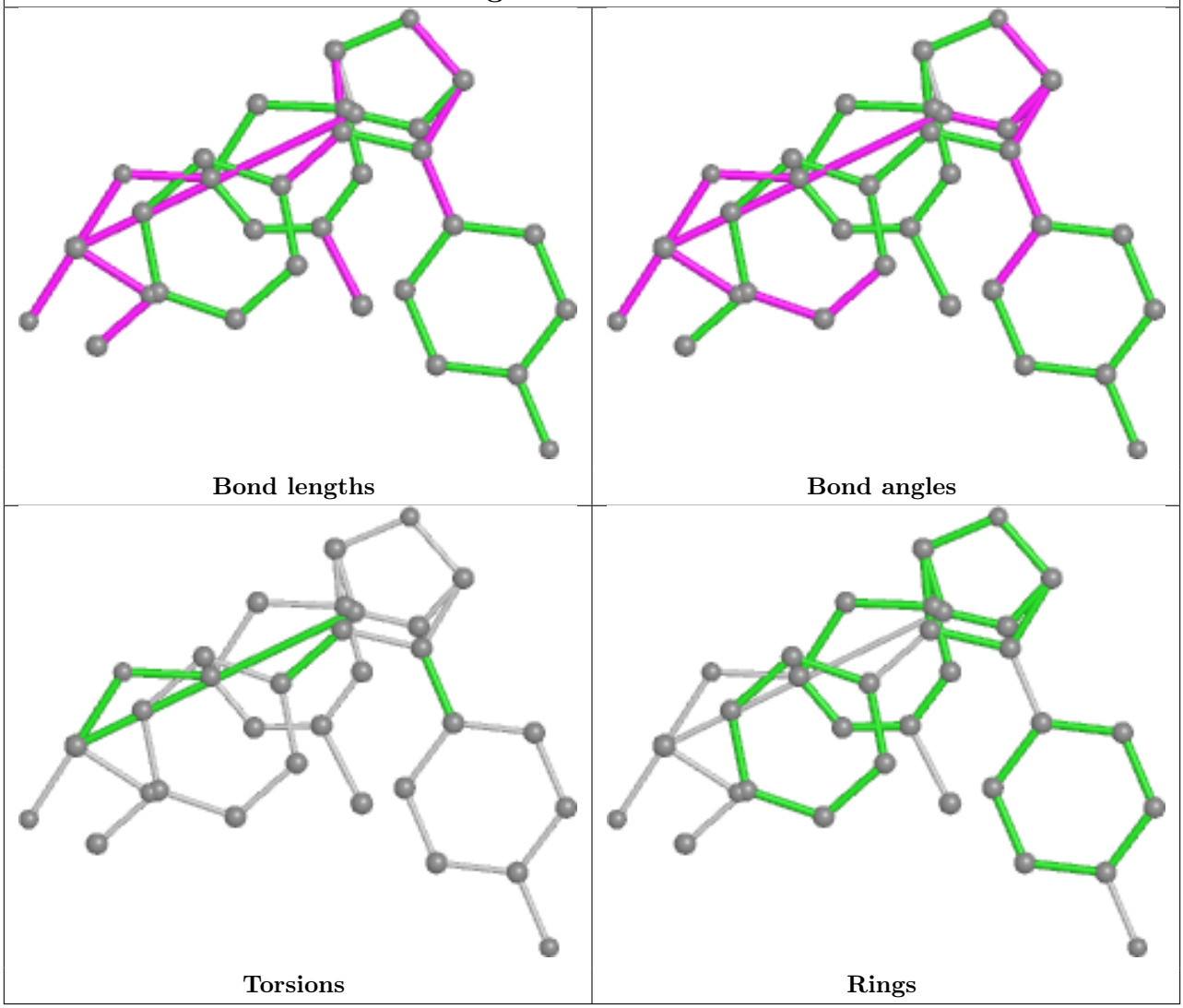
Ligand 7KL A 603 (A)



Ligand 7KL B 601



Ligand 7KL A 602



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	215/257 (83%)	-0.38	0 100 100	28, 50, 81, 112	1 (0%)
1	B	211/257 (82%)	-0.29	2 (0%) 84 86	27, 47, 95, 126	0
2	C	9/13 (69%)	0.36	1 (11%) 5 5	74, 91, 93, 108	0
2	D	7/13 (53%)	0.75	0 100 100	79, 88, 107, 114	0
All	All	442/540 (81%)	-0.30	3 (0%) 87 89	27, 49, 92, 126	1 (0%)

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	372	LEU	2.1
2	C	694	LEU	2.1
1	B	337	PHE	2.0

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)

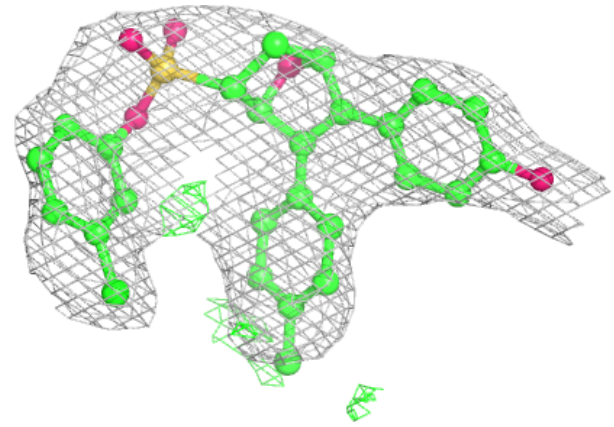
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

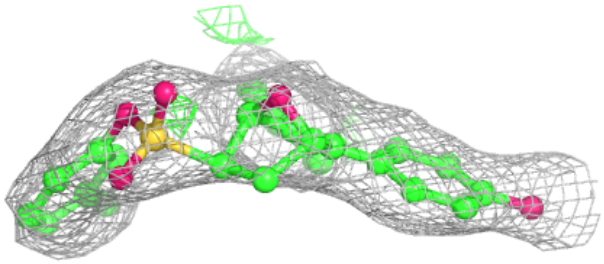
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	7KL	A	602	32/36	0.89	0.16	73,80,93,95	32
3	7KL	B	601	32/36	0.89	0.19	40,50,121,143	32
3	7KL	A	604[B]	32/36	0.93	0.13	69,75,88,89	32
3	7KL	A	603[A]	32/36	0.93	0.14	68,75,88,90	32
3	7KL	A	601	26/36	0.94	0.14	29,40,62,63	26

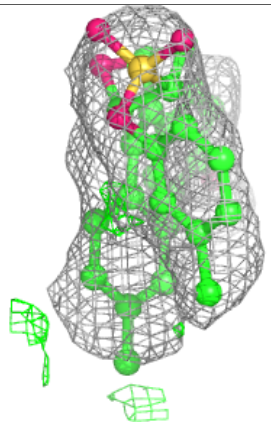
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around 7KL A 602:

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

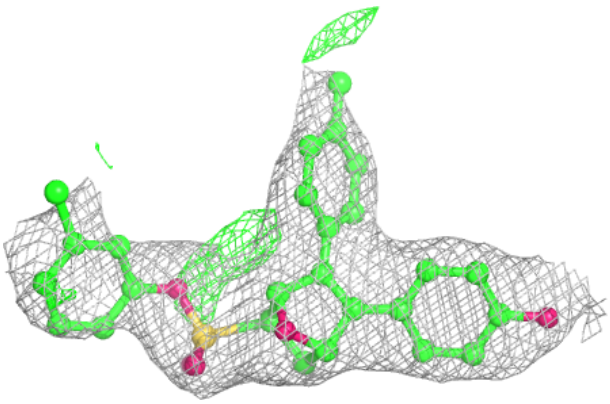


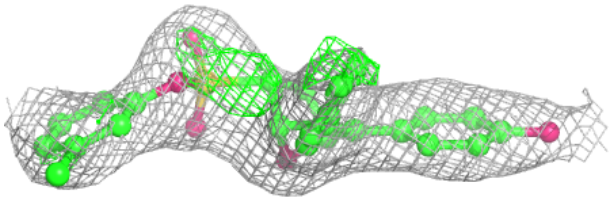


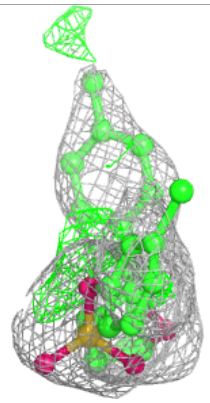


Electron density around 7KL B 601:

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

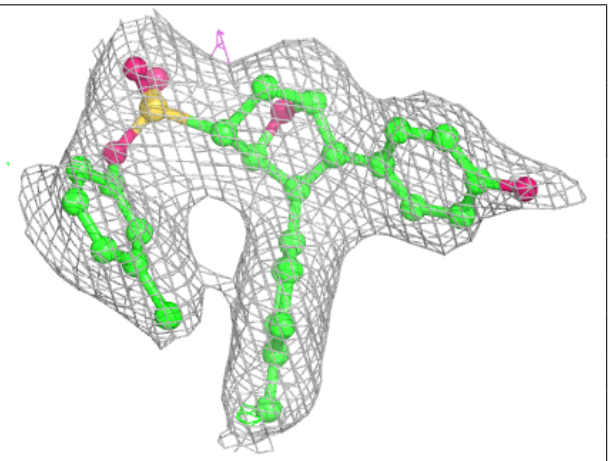


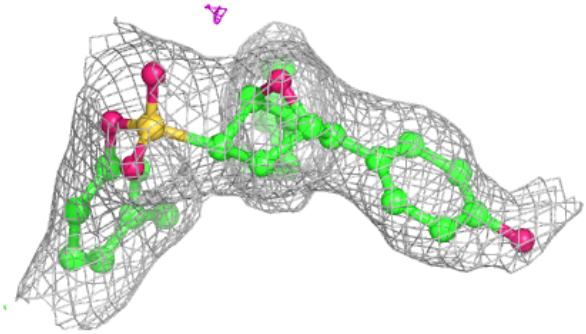




Electron density around 7KL A 604 (B):

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





Electron density around 7KL A 603 (A):

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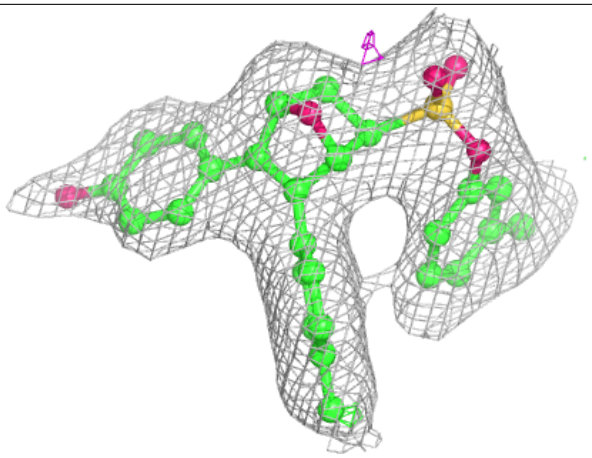
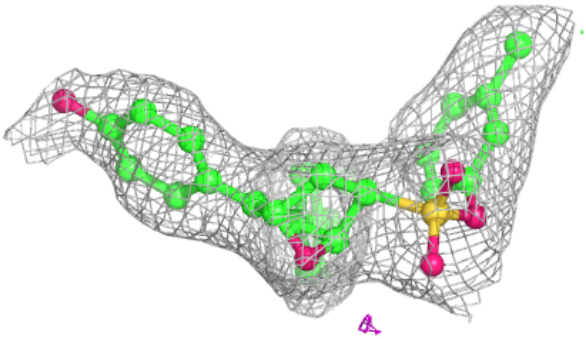
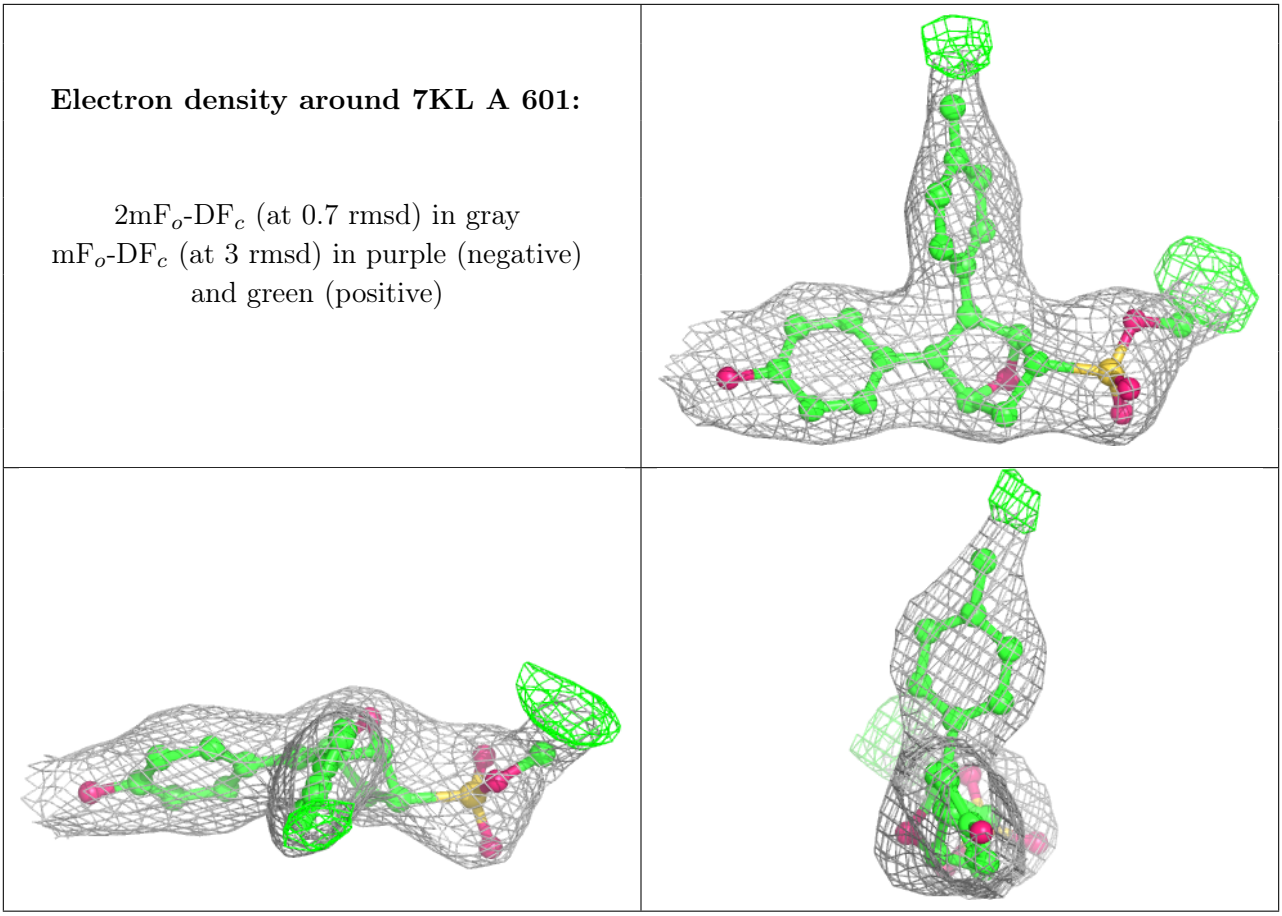
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)





Electron density around 7KL A 601:

$2mF_o$-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.