wwPDB X-ray Structure Validation Summary Report (i)

Mar 6, 2026 – 08:09 PM UTC

PDB ID	:	8W07 / pdb_00008w07
Title	:	Crystal Structure of the ER-alpha Ligand-binding Domain (L372S, L536S) in complex with k-402
Authors	:	Min, C.K.; Nwachukwu, J.C.; Hou, Y.; Russo, R.J.; Papa, A.; Min, J.; Peng, R.; Kim, S.H.; Ziegler, Y.; Rangarajan, E.S.; Izard, T.; Katzenellenbogen, B.S.; Katzenellenbogen, J.K.; Nettles, K.W.
Deposited on	:	2024-02-13
Resolution	:	1.83 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 (1)) were used in the production of this report:

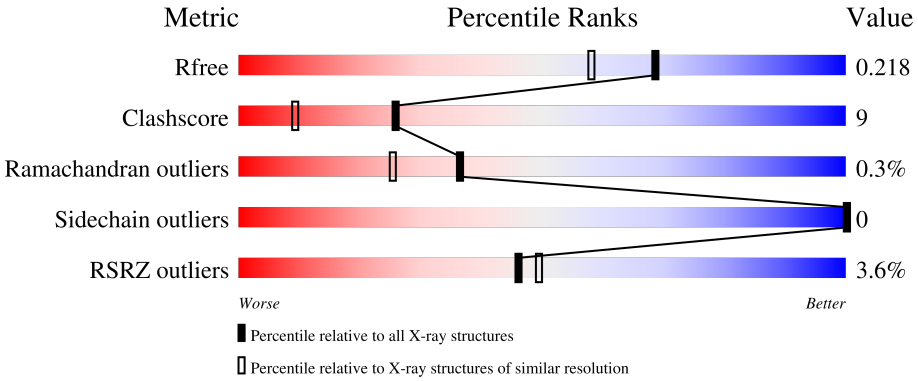
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal 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 (i)

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

The reported resolution of this entry is 1.83 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	1296 (1.84-1.84)
Clashscore	190562	1329 (1.84-1.84)
Ramachandran outliers	187476	1318 (1.84-1.84)
Sidechain outliers	187428	1318 (1.84-1.84)
RSRZ outliers	180081	1296 (1.84-1.84)

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	242	5% 79% 16%
1	B	242	2% 81% 13% 5%
1	C	242	2% 83% 13%
1	D	242	5% 73% 17% 9%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 15119 atoms, of which 7425 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.

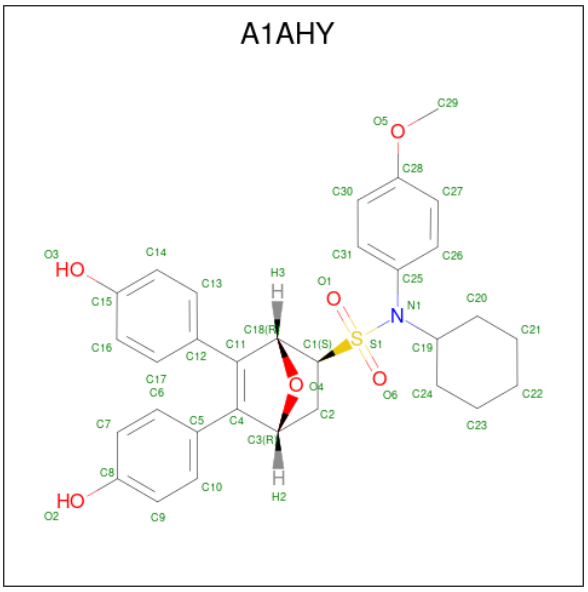
- Molecule 1 is a protein called Estrogen receptor.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	233	Total	C	H	N	O	S	0	2	0
			3691	1177	1853	314	330	17			
1	B	229	Total	C	H	N	O	S	0	0	0
			3622	1150	1826	306	323	17			
1	C	232	Total	C	H	N	O	S	0	2	0
			3690	1174	1855	315	329	17			
1	D	221	Total	C	H	N	O	S	0	0	0
			3498	1115	1759	297	310	17			

There are 8 discrepancies between the modelled and reference sequences:

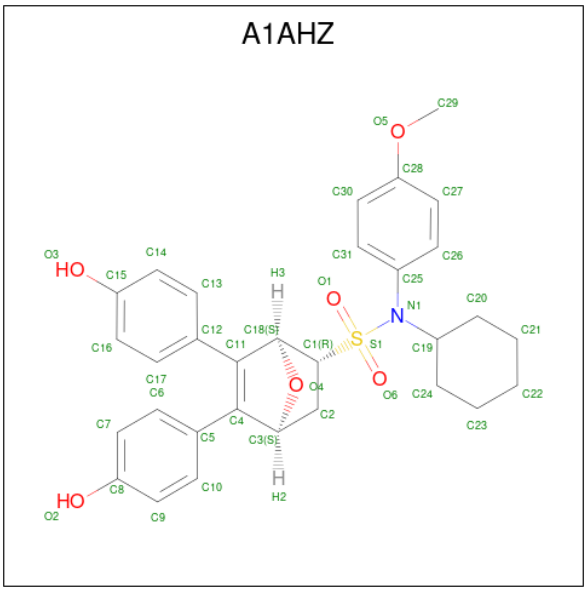
Chain	Residue	Modelled	Actual	Comment	Reference
A	372	SER	LEU	engineered mutation	UNP P03372
A	536	SER	LEU	engineered mutation	UNP P03372
B	372	SER	LEU	engineered mutation	UNP P03372
B	536	SER	LEU	engineered mutation	UNP P03372
C	372	SER	LEU	engineered mutation	UNP P03372
C	536	SER	LEU	engineered mutation	UNP P03372
D	372	SER	LEU	engineered mutation	UNP P03372
D	536	SER	LEU	engineered mutation	UNP P03372

- Molecule 2 is (1R,2S,4R)-N-cyclohexyl-5,6-bis(4-hydroxyphenyl)-N-(4-methoxyphenyl)-7-oxabicyclo[2.2.1]hept-5-ene-2-sulfonamide (CCD ID: A1AHY) (formula: $C_{31}H_{33}NO_6S$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	A	1	Total	C	H	N	O	S	0	0
			72	31	33	1	6	1		

- Molecule 3 is (1S,2R,4S)-N-cyclohexyl-5,6-bis(4-hydroxyphenyl)-N-(4-methoxyphenyl)-7-oxabicyclo[2.2.1]hept-5-ene-2-sulfonamide (CCD ID: A1AHZ) (formula: $C_{31}H_{33}NO_6S$).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
3	B	1	Total	C	H	N	O	S	0	0
			72	31	33	1	6	1		
3	C	1	Total	C	H	N	O	S	0	0
			72	31	33	1	6	1		

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Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
3	D	1	Total	C	H	N	O	S	0	0
			72	31	33	1	6	1		

- Molecule 4 is water.

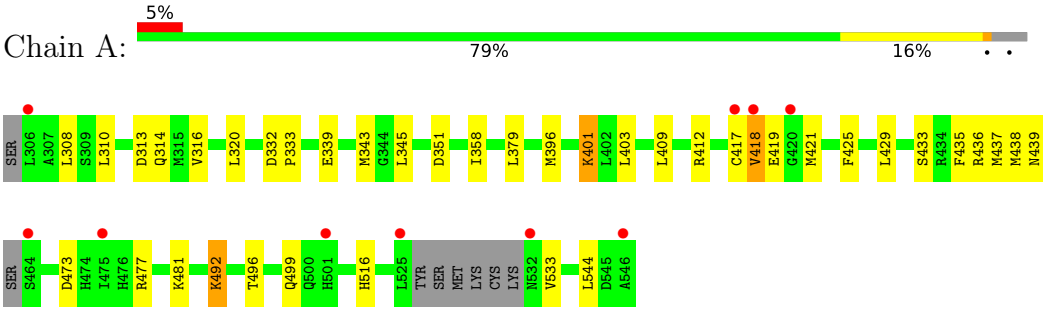
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	88	Total	O	0	0
			88	88		
4	B	87	Total	O	0	0
			87	87		
4	C	77	Total	O	0	0
			77	77		
4	D	78	Total	O	0	0
			78	78		

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.

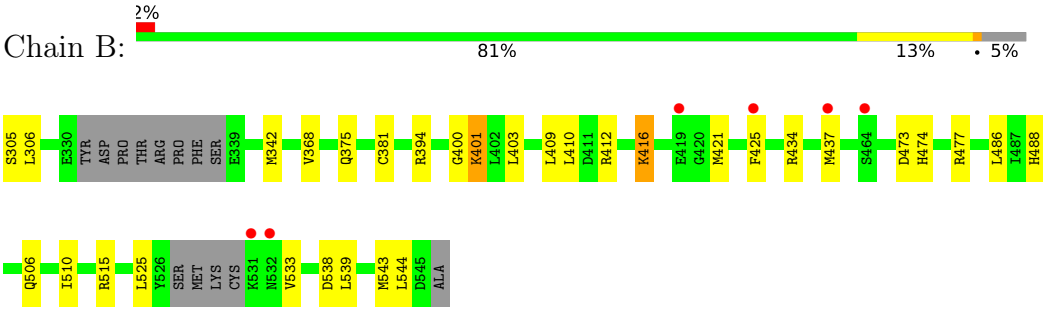
• Molecule 1: Estrogen receptor

Chain A:



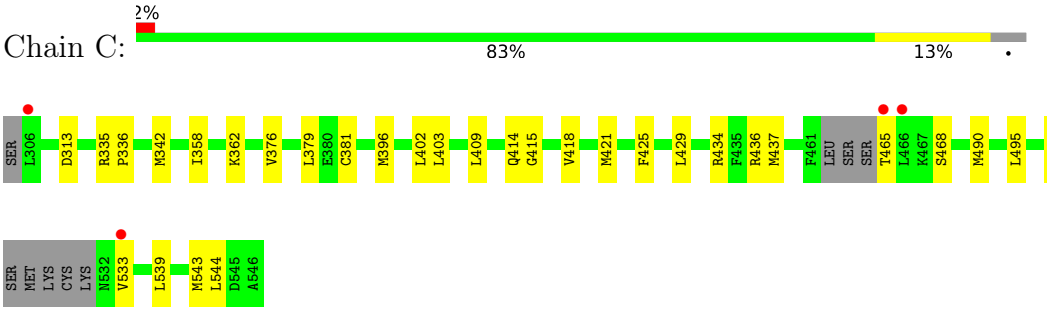
• Molecule 1: Estrogen receptor

Chain B:



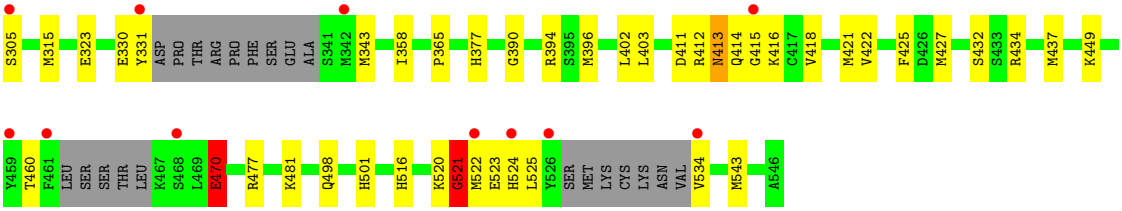
• Molecule 1: Estrogen receptor

Chain C:



• Molecule 1: Estrogen receptor

Chain D:


S305
M315
E323
E330
Y331
ASP
PRO
THR
ARG
PRO
PHE
SER
GLU
ALA
S341
M342
M343
I358
P365
H377
G390
R394
S395
M396
L402
L403
D411
R412
N413
Q414
G415
K416
C417
V418
M421
V422
F425
D426
M427
S432
S433
R434
M437
K449
Y459
T460
F461
LEU
SER
SER
THR
LEU
K467
S468
L469
E470
R477
K481
Q498
H501
H516
K520
G521
M522
E523
H524
L525
Y526
SER
MET
LYS
CYS
LYS
ASN
VAL
V534
M543
A546

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α, β, γ	53.58Å 59.03Å 93.75Å 86.59° 75.01° 63.14°	Depositor
Resolution (Å)	37.54 – 1.83 37.54 – 1.83	Depositor EDS
% Data completeness (in resolution range)	71.4 (37.54-1.83) 71.4 (37.54-1.83)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.51 (at 1.83Å)	Xtriage
Refinement program	PHENIX 1.18.2_3874	Depositor
R, R_{free}	0.179 , 0.218 0.180 , 0.218	Depositor DCC
R_{free} test set	3117 reflections (3.59%)	wwPDB-VP
Wilson B-factor (Å^2)	30.9	Xtriage
Anisotropy	0.012	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.43 , 49.5	EDS
L-test for twinning[2]	$< \|L\| > = 0.51$, $< L^2 > = 0.34$	Xtriage
Estimated twinning fraction	0.110 for h,h-k,h-l	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	15119	wwPDB-VP
Average B, all atoms (Å^2)	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.26% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: A1AHZ, A1AHY

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	0.39	2/1883 (0.1%)	0.65	2/2549 (0.1%)
1	B	0.51	5/1826 (0.3%)	0.72	5/2467 (0.2%)
1	C	0.36	0/1880	0.61	0/2545
1	D	0.54	4/1768 (0.2%)	0.81	13/2387 (0.5%)
All	All	0.45	11/7357 (0.1%)	0.70	20/9948 (0.2%)

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	C	0	1
1	D	0	4
All	All	0	5

The worst 5 of 11 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	416	LYS	CE-NZ	10.56	1.81	1.49
1	D	521	GLY	C-N	-8.08	1.21	1.33
1	D	522	MET	CG-SD	7.69	2.00	1.80
1	B	401	LYS	CB-CG	-7.07	1.31	1.52
1	A	401	LYS	CE-NZ	-6.84	1.28	1.49

The worst 5 of 20 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	416	LYS	CD-CE-NZ	-10.38	78.67	111.90
1	D	522	MET	CG-SD-CE	-10.29	78.26	100.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	D	522	MET	CA-CB-CG	8.93	131.96	114.10
1	B	416	LYS	CA-CB-CG	-7.68	98.73	114.10
1	D	522	MET	N-CA-CB	-6.91	99.14	110.40

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	313	ASP	Sidechain
1	D	412	ARG	Peptide
1	D	413	ASN	Sidechain
1	D	470	GLU	Sidechain
1	D	521	GLY	Mainchain

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	1838	1853	1843	47	1
1	B	1796	1826	1826	36	1
1	C	1835	1855	1845	26	0
1	D	1739	1759	1767	29	0
2	A	39	33	0	6	0
3	B	39	33	0	2	0
3	C	39	33	0	3	0
3	D	39	33	0	3	0
4	A	88	0	0	5	0
4	B	87	0	0	4	0
4	C	77	0	0	4	0
4	D	78	0	0	1	0
All	All	7694	7425	7281	139	1

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 9.

The worst 5 of 139 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:B:401:LYS:CE	1:B:401:LYS:NZ	1.68	1.52
1:B:416:LYS:CE	1:B:416:LYS:NZ	1.81	1.40
1:B:416:LYS:NZ	1:B:416:LYS:CD	2.21	1.03
1:B:473:ASP:OD1	1:B:477:ARG:NH1	1.95	0.99
1:C:381:CYS:SG	4:C:773:HOH:O	2.23	0.94

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:481:LYS:NZ	1:B:538:ASP:OD2[1_655]	2.19	0.01

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	229/242 (95%)	226 (99%)	1 (0%)	2 (1%)	14 4
1	B	223/242 (92%)	219 (98%)	3 (1%)	1 (0%)	30 18
1	C	228/242 (94%)	227 (100%)	1 (0%)	0	100 100
1	D	213/242 (88%)	208 (98%)	5 (2%)	0	100 100
All	All	893/968 (92%)	880 (98%)	10 (1%)	3 (0%)	36 25

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	419	GLU
1	B	533	VAL
1	A	418	VAL

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	203/218 (93%)	203 (100%)	0	100	100
1	B	199/218 (91%)	199 (100%)	0	100	100
1	C	204/218 (94%)	204 (100%)	0	100	100
1	D	192/218 (88%)	192 (100%)	0	100	100
All	All	798/872 (92%)	798 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 16 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	501	HIS
1	D	474	HIS
1	C	455	ASN
1	D	413	ASN
1	C	414	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)

4 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	A1AHZ	C	601	-	42,44,44	1.67	6 (14%)	54,65,65	1.34	6 (11%)
3	A1AHZ	D	601	-	42,44,44	1.91	5 (11%)	54,65,65	1.26	5 (9%)
2	A1AHY	A	601	-	42,44,44	1.75	6 (14%)	54,65,65	1.78	11 (20%)
3	A1AHZ	B	601	-	42,44,44	1.83	5 (11%)	54,65,65	1.28	5 (9%)

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	A1AHZ	C	601	-	-	4/28/62/62	0/7/6/6
3	A1AHZ	D	601	-	-	7/28/62/62	0/7/6/6
2	A1AHY	A	601	-	-	2/28/62/62	0/7/6/6
3	A1AHZ	B	601	-	-	4/28/62/62	0/7/6/6

The worst 5 of 22 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	601	A1AHY	O6-S1	6.43	1.48	1.43
3	D	601	A1AHZ	S1-N1	5.99	1.80	1.67
3	D	601	A1AHZ	O6-S1	5.73	1.48	1.43
3	B	601	A1AHZ	S1-N1	5.47	1.79	1.67
3	B	601	A1AHZ	O6-S1	5.41	1.48	1.43

The worst 5 of 27 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	601	A1AHY	C20-C19-N1	7.14	123.38	112.02

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	B	601	A1AHZ	O6-S1-O1	4.65	122.67	119.17
3	D	601	A1AHZ	C3-C2-C1	-4.37	96.75	100.61
3	C	601	A1AHZ	O6-S1-O1	4.25	122.38	119.17
3	B	601	A1AHZ	C3-C2-C1	-3.86	97.20	100.61

There are no chirality outliers.

5 of 17 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	C	601	A1AHZ	C25-N1-S1-O1
2	A	601	A1AHY	C30-C28-O5-C29
2	A	601	A1AHY	C27-C28-O5-C29
3	C	601	A1AHZ	C19-N1-S1-O1
3	D	601	A1AHZ	C25-N1-S1-O1

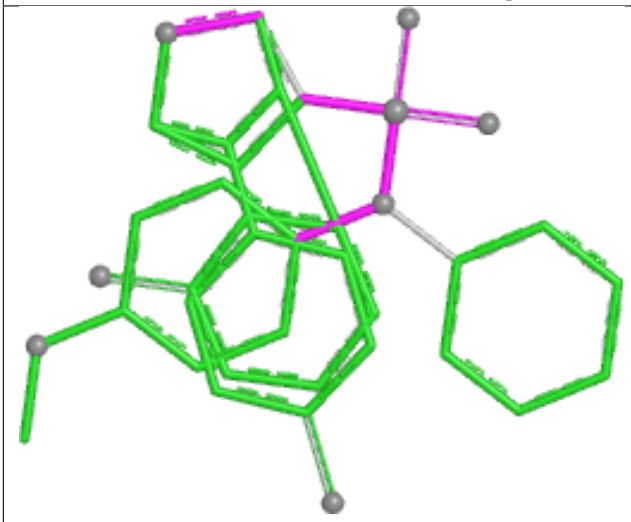
There are no ring outliers.

4 monomers are involved in 14 short contacts:

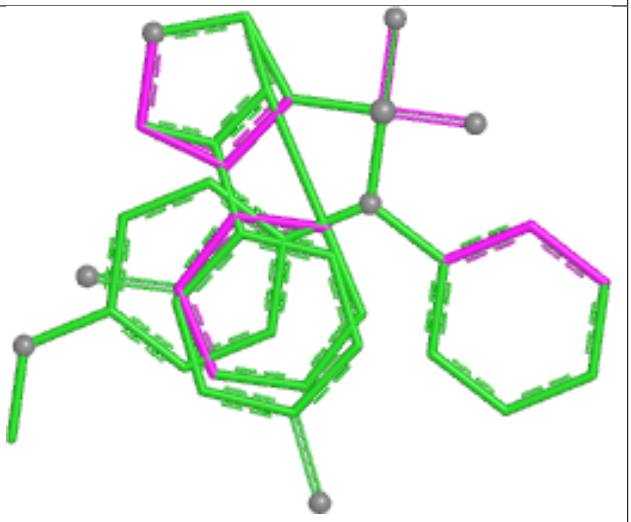
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	601	A1AHZ	3	0
3	D	601	A1AHZ	3	0
2	A	601	A1AHY	6	0
3	B	601	A1AHZ	2	0

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.

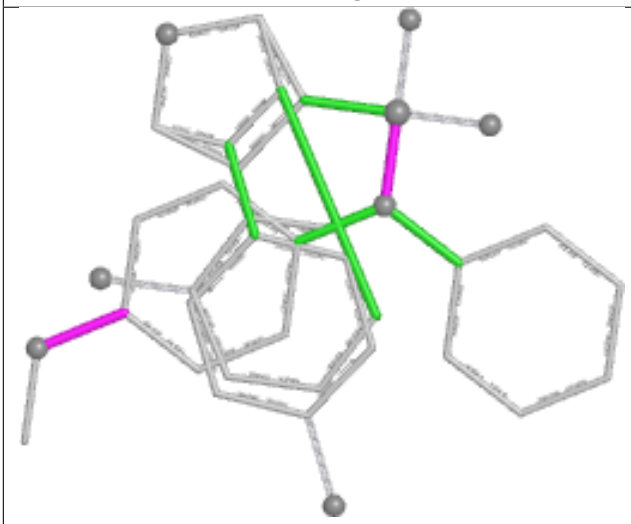
Ligand A1AHZ C 601



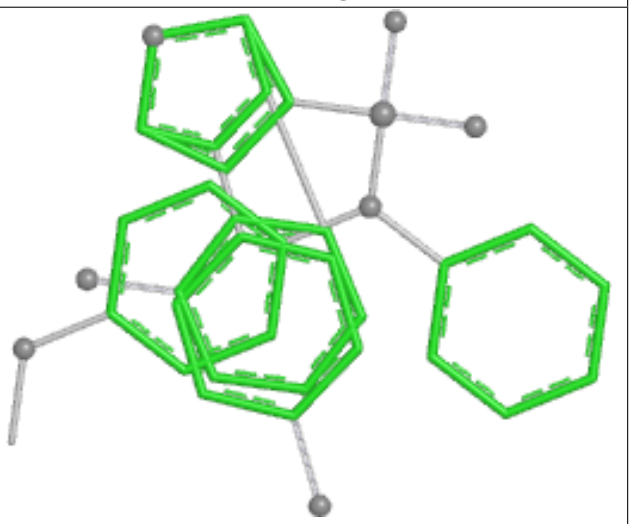
Bond lengths



Bond angles

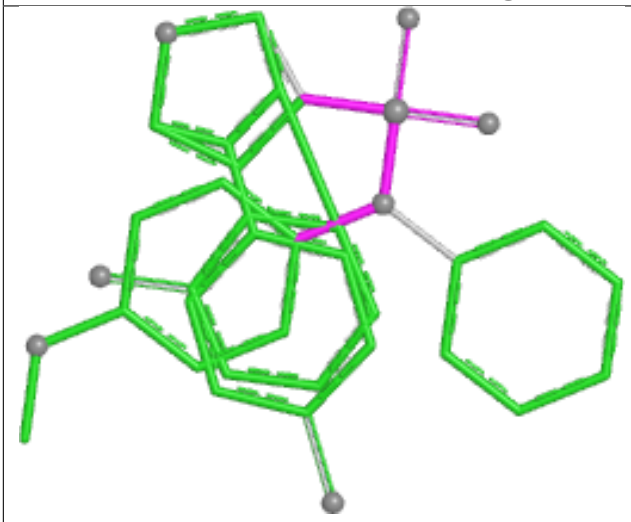


Torsions

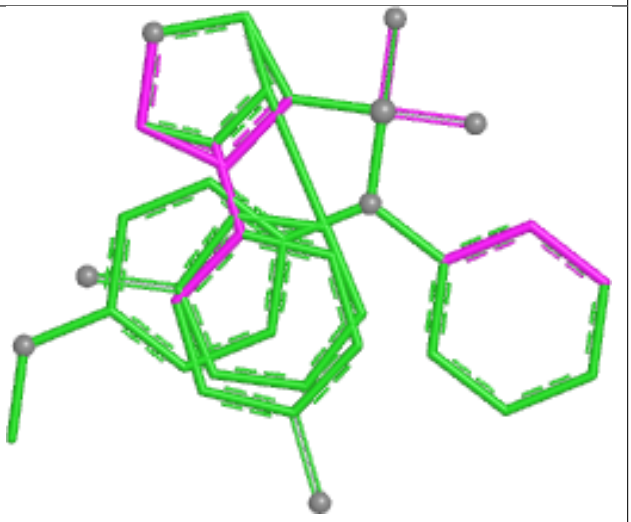


Rings

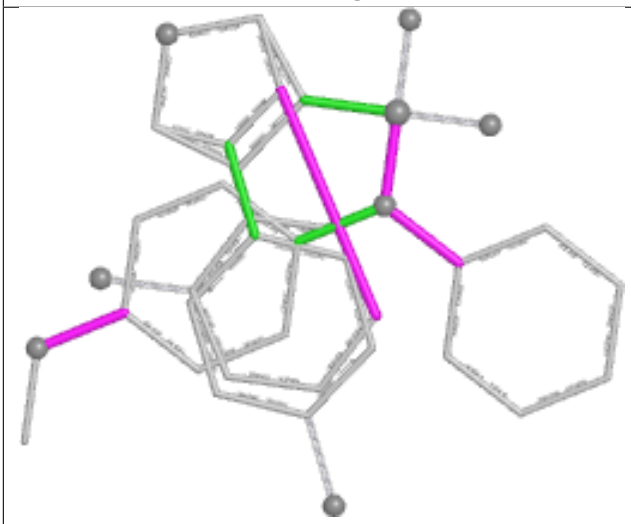
Ligand A1AHZ D 601



Bond lengths



Bond angles



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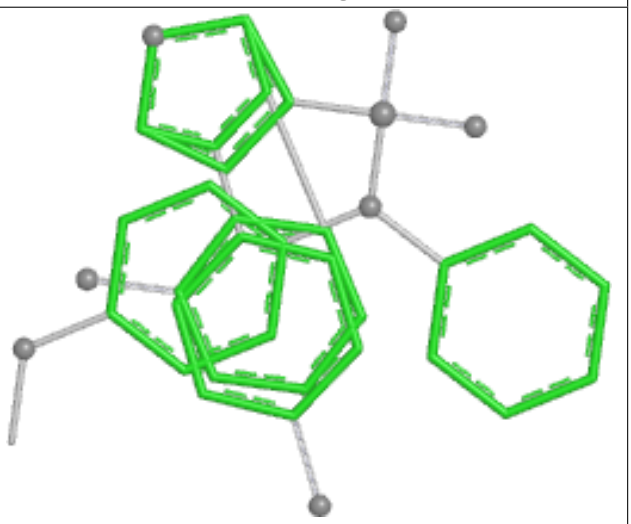
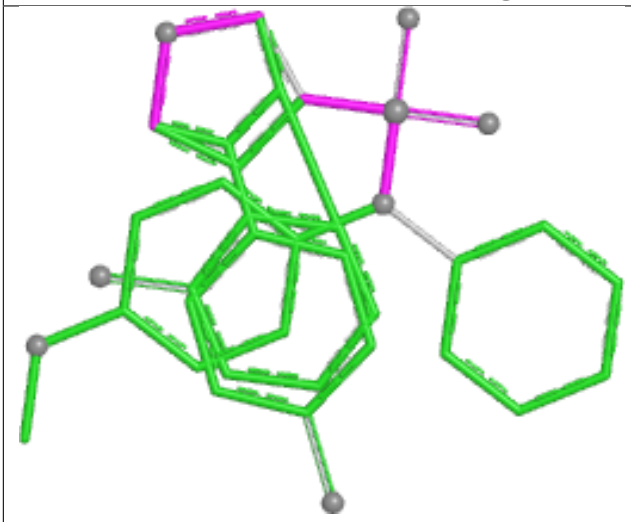
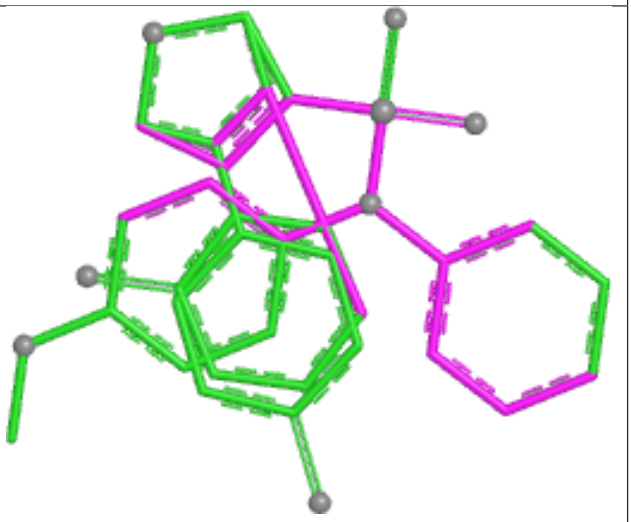


Rings

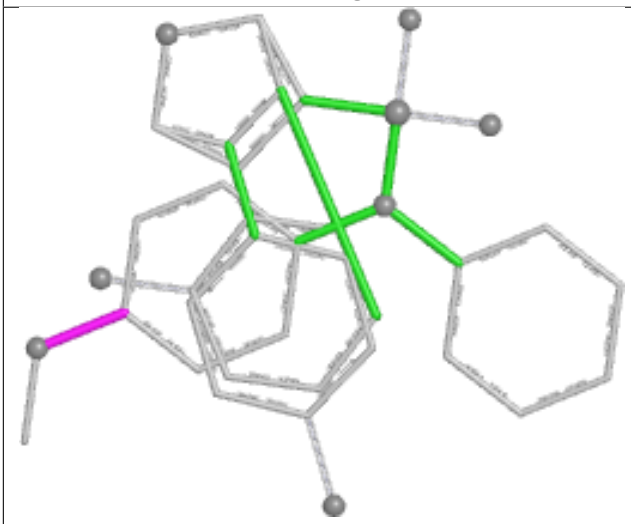
Ligand A1AHY A 601



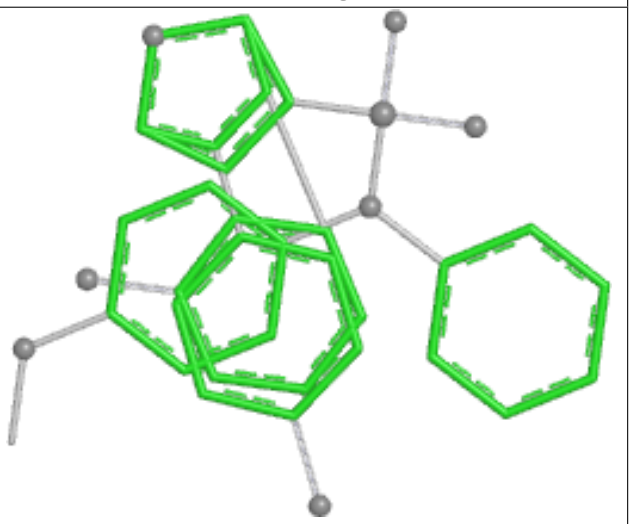
Bond lengths



Bond angles

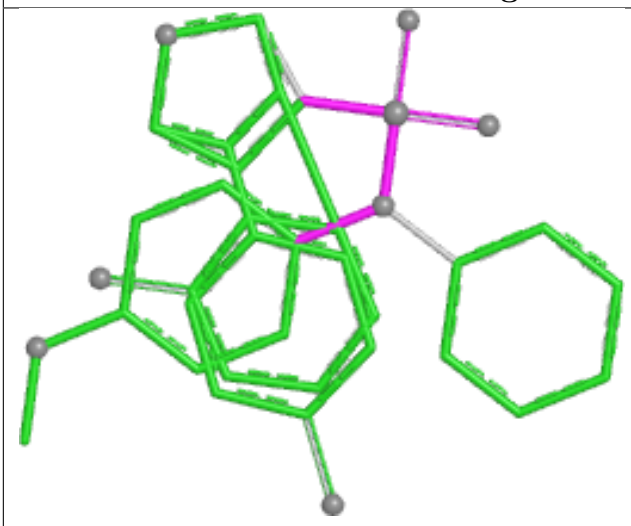


Torsions

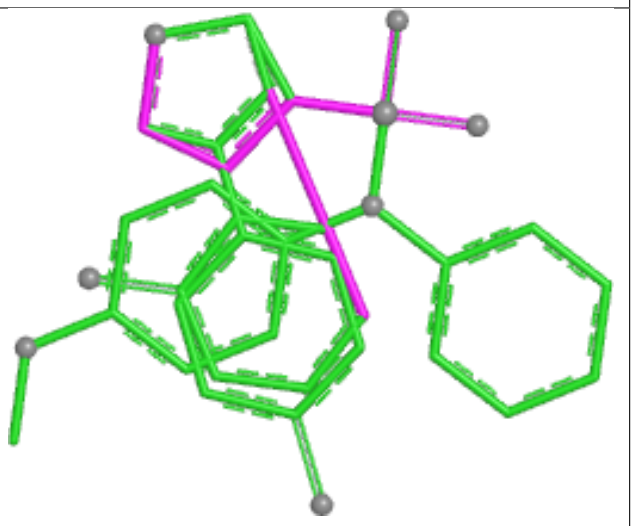


Rings

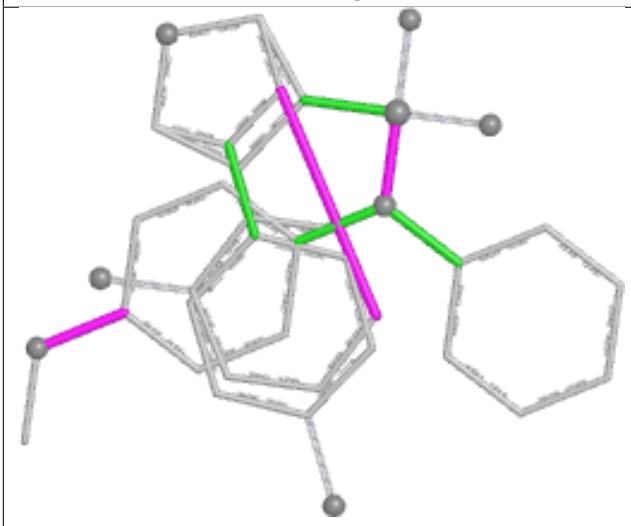
Ligand A1AHZ B 601



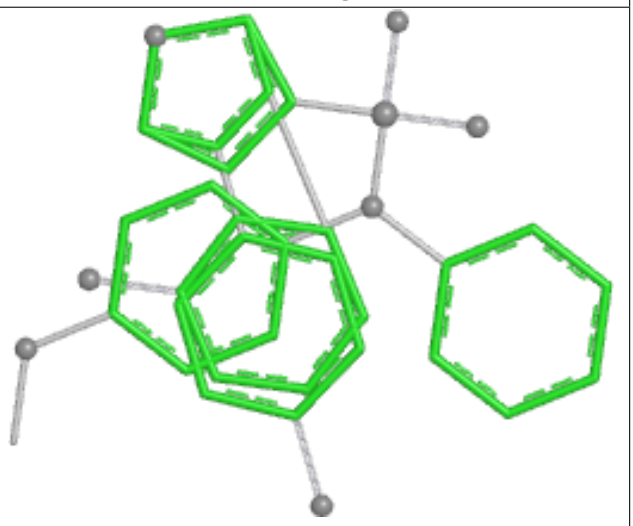
Bond lengths



Bond angles



Torsions



Rings

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

6.1 Protein, DNA and RNA chains

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95^{th} 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	233/242 (96%)	0.05	11 (4%)	36	38	19, 46, 76, 96	1 (0%)
1	B	229/242 (94%)	-0.08	6 (2%)	57	62	26, 42, 81, 103	0
1	C	232/242 (95%)	-0.11	5 (2%)	62	69	17, 41, 75, 100	1 (0%)
1	D	221/242 (91%)	0.01	11 (4%)	34	36	25, 43, 86, 116	0
All	All	915/968 (94%)	-0.03	33 (3%)	46	49	17, 43, 79, 116	2 (0%)

The worst 5 of 33 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	331	TYR	5.0
1	A	418	VAL	4.0
1	A	464	SER	3.9
1	C	306	LEU	3.4
1	A	306	LEU	3.3

6.2 Non-standard residues in protein, DNA, RNA chains

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

6.3 Carbohydrates

There are no oligosaccharides in this entry.

6.4 Ligands

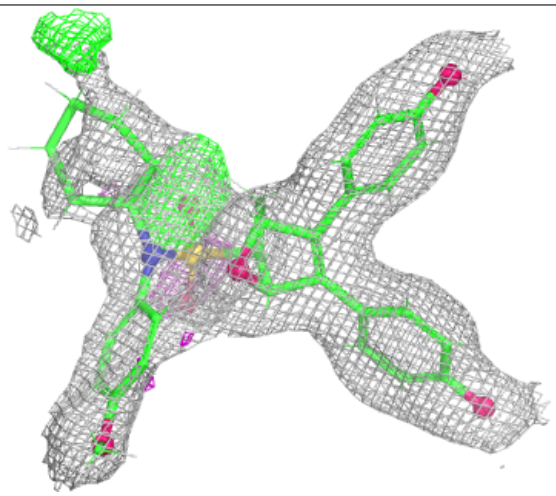
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9'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

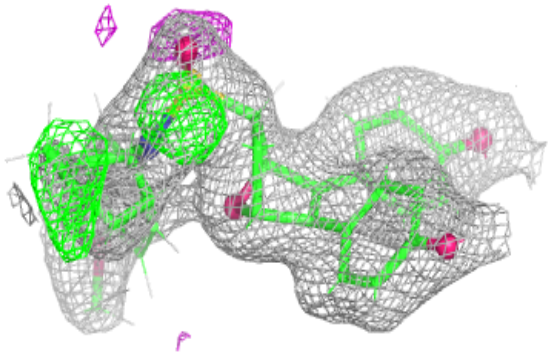
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	A1AHY	A	601	39/39	0.91	0.11	29,55,79,87	0
3	A1AHZ	B	601	39/39	0.91	0.11	29,53,83,93	0
3	A1AHZ	D	601	39/39	0.92	0.11	28,55,84,99	0
3	A1AHZ	C	601	39/39	0.94	0.10	24,50,80,96	0

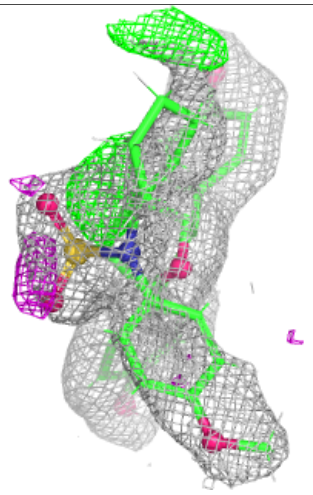
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around A1AHY 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)

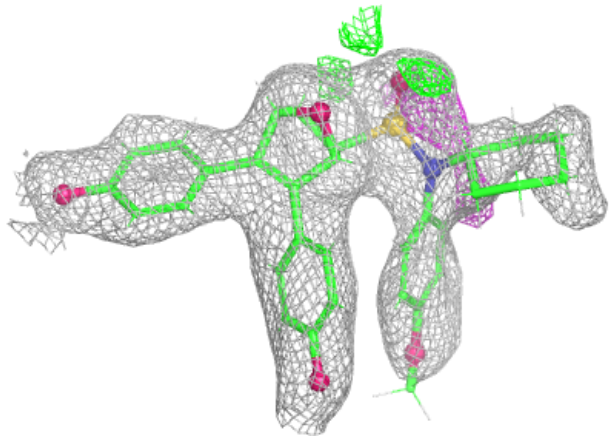


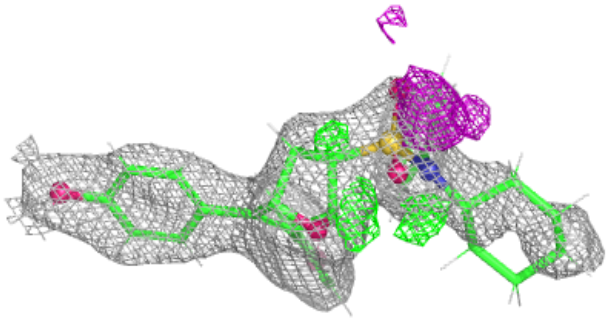


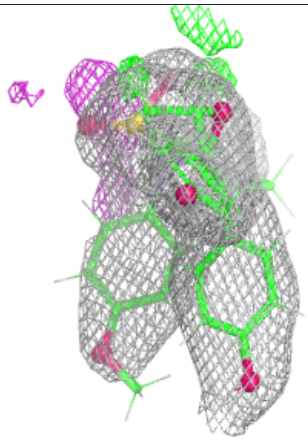


Electron density around A1AHZ B 601:

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

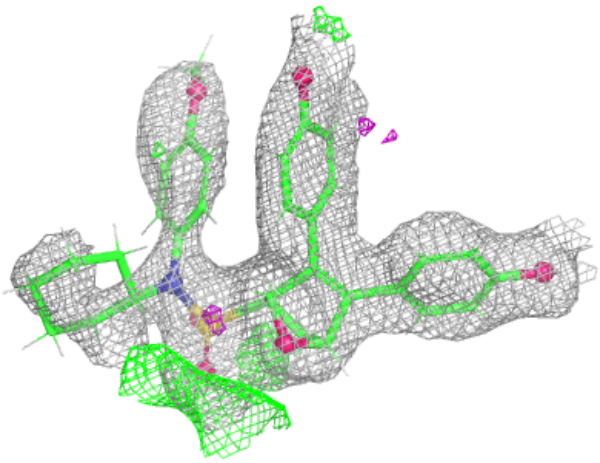


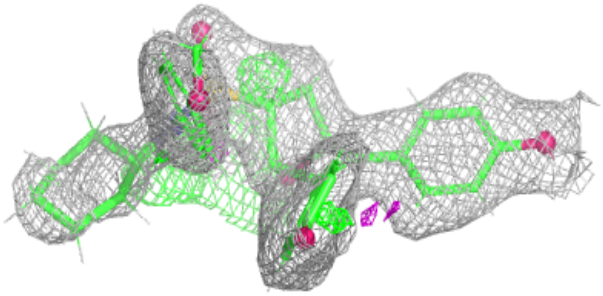


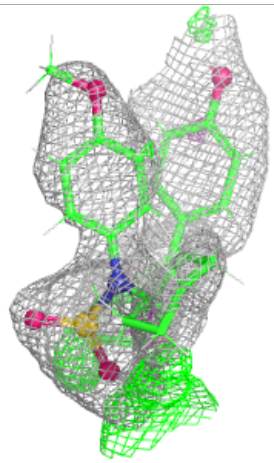


Electron density around A1AHZ D 601:

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







Electron density around A1AHZ C 601:

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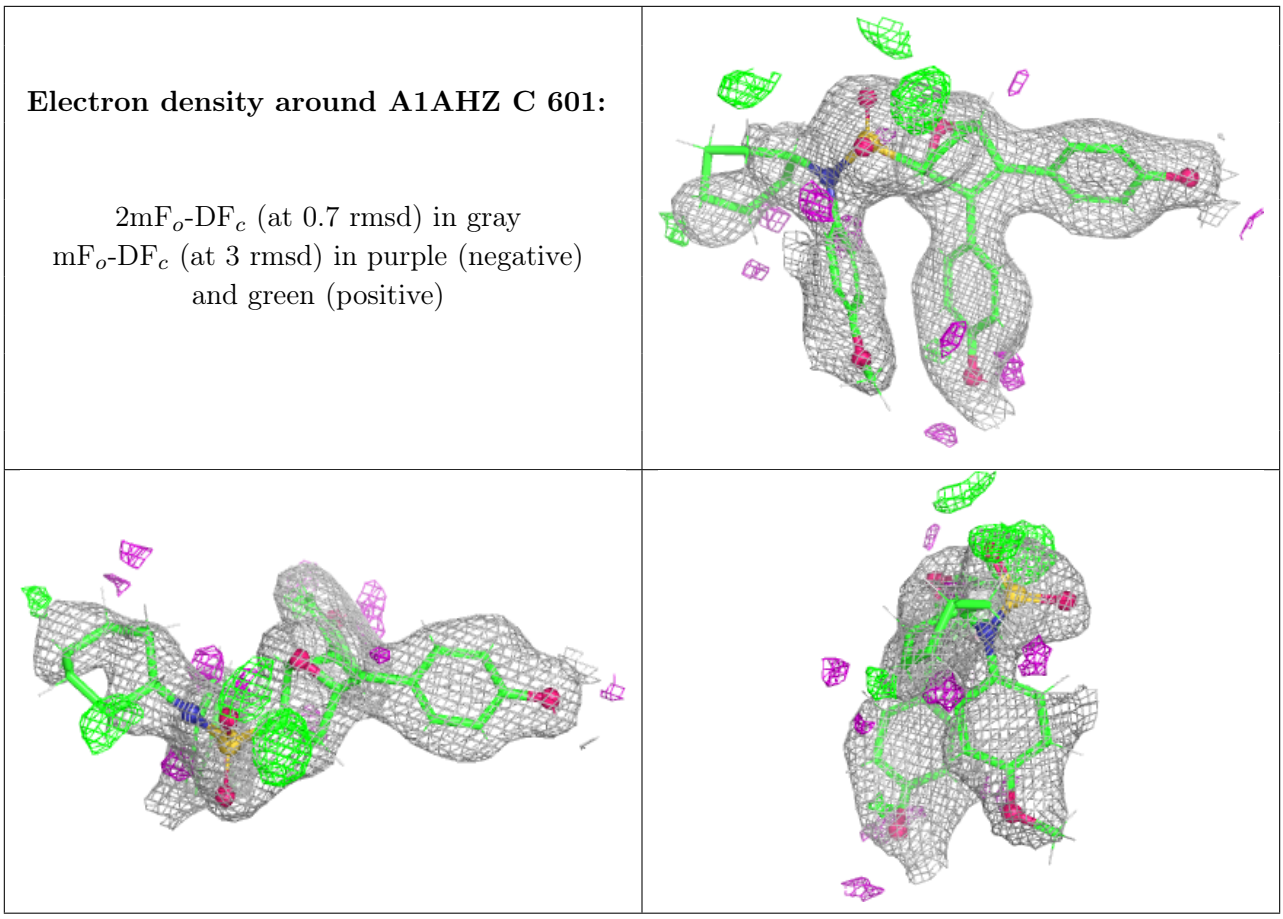
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)



6.5 Other polymers

There are no such residues in this entry.