Full wwPDB X-ray Structure Validation Report (i)

Jun 16, 2024 – 03:01 PM EDT

PDB ID	:	5CZB
Title	:	HCV NS5B IN COMPLEX WITH LIGAND IDX17119-5
Authors	:	Pierra, C.; Dousson, C.; Augustin, M.
Deposited on	:	2015-07-31
Resolution	:	1.96 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:

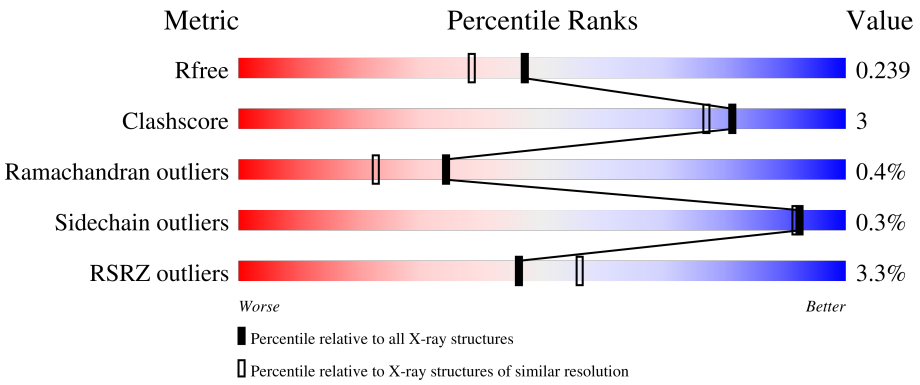
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.37.1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

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 1.96 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	2580 (1.96-1.96)
Clashscore	141614	2705 (1.96-1.96)
Ramachandran outliers	138981	2678 (1.96-1.96)
Sidechain outliers	138945	2678 (1.96-1.96)
RSRZ outliers	127900	2539 (1.96-1.96)

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	563	4% 95%
1	B	563	3% 93% 5%

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	GOL	B	604	-	-	X	-

2 Entry composition (i)

There are 7 unique types of molecules in this entry. The entry contains 9819 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.

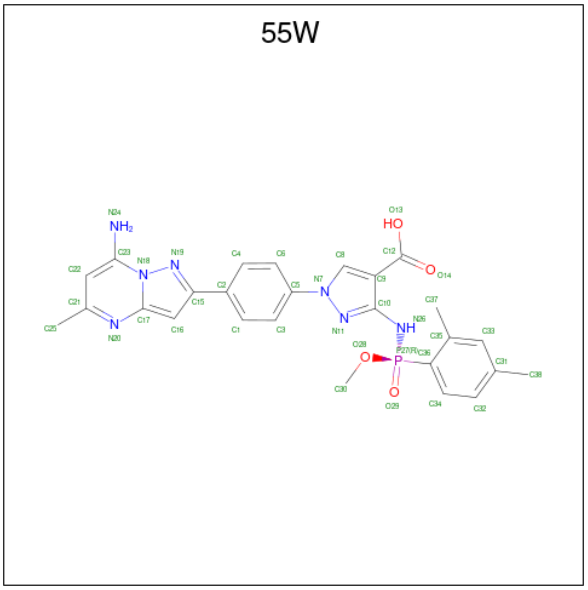
- Molecule 1 is a protein called NS5B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	555	4352	2739	771	809	33	56	3	0
1	B	557	4379	2754	778	814	33	54	5	0

There are 2 discrepancies between the modelled and reference sequences:

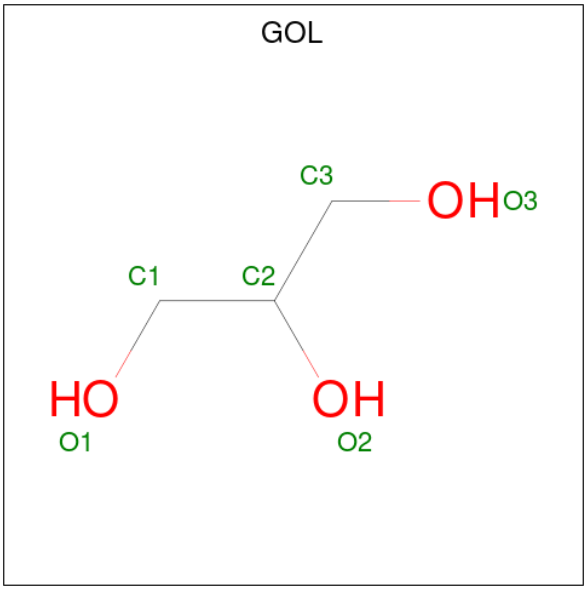
Chain	Residue	Modelled	Actual	Comment	Reference
A	0	SER	-	expression tag	UNP O92972
B	0	SER	-	expression tag	UNP O92972

- Molecule 2 is 1-[4-(7-amino-5-methylpyrazolo[1,5-a]pyrimidin-2-yl)phenyl]-3-{[(R)-(2,4-dimethylphenyl)(methoxy)phosphoryl]amino}-1H-pyrazole-4-carboxylic acid (three-letter code: 55W) (formula: $C_{26}H_{26}N_7O_4P$).



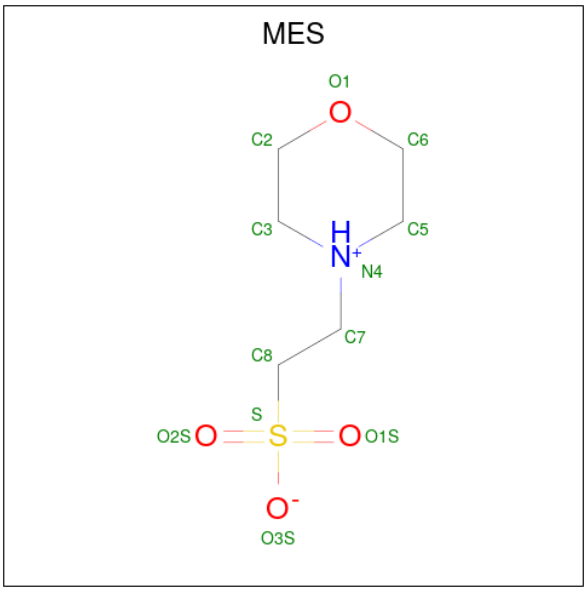
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
2	A	1	41	27	7	6	1	0	1
			Total	C	N	O	P		
2	B	1	41	27	7	6	1	0	1

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



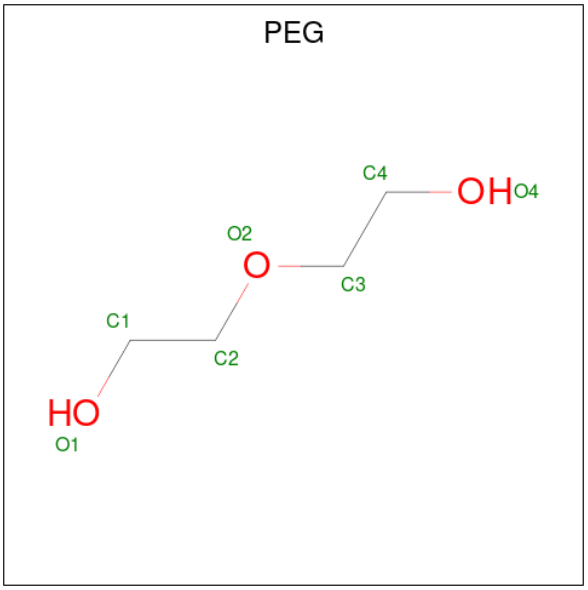
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
3	A	1	6	3	3	0	0
			Total	C	O		
3	A	1	6	3	3	0	0
			Total	C	O		
3	B	1	6	3	3	0	0
			Total	C	O		
3	B	1	6	3	3	0	0
			Total	C	O		
3	B	1	6	3	3	0	0
			Total	C	O		
3	B	1	6	3	3	0	0
			Total	C	O		
3	B	1	6	3	3	0	0

- Molecule 4 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (three-letter code: MES) (formula: $C_6H_{13}NO_4S$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	S		
4	A	1	12	6	1	4	1	0	0

- Molecule 5 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: $C_4H_{10}O_3$).



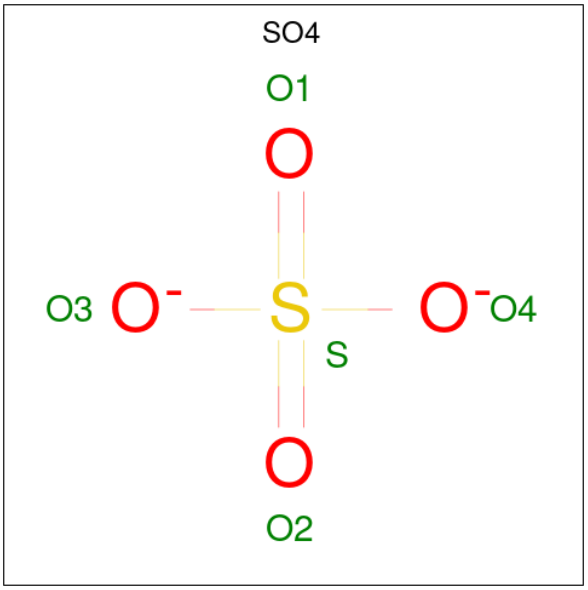
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	O				
5	A	1	7	4	3			0	0
			Total	C	O				
5	A	1	7	4	3			0	0
			Total	C	O				
5	A	1	7	4	3			0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	O			
5	A	1	7	4	3		0	0
			Total	C	O			
5	B	1	7	4	3		0	0
			Total	C	O			
5	B	1	7	4	3		0	0

- Molecule 6 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	O	S			
6	A	1	5	4	1		0	0
			Total	O	S			
6	A	1	5	4	1		0	0
			Total	O	S			
6	A	1	5	4	1		0	0
			Total	O	S			
6	A	1	5	4	1		0	0
			Total	O	S			
6	A	1	5	4	1		0	0
			Total	O	S			
6	A	1	5	4	1		0	0
			Total	O	S			
6	A	1	5	4	1		0	0
			Total	O	S			
6	A	1	5	4	1		0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	1	Total O S 5 4 1	0	0
6	A	1	Total O S 5 4 1	0	0
6	B	1	Total O S 5 4 1	0	0
6	B	1	Total O S 5 4 1	0	0
6	B	1	Total O S 5 4 1	0	0

- Molecule 7 is water.

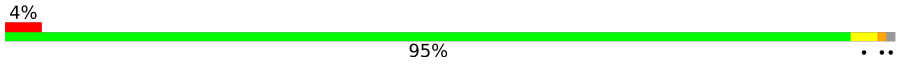
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	430	Total O 430 430	0	2
7	B	414	Total O 415 415	0	3

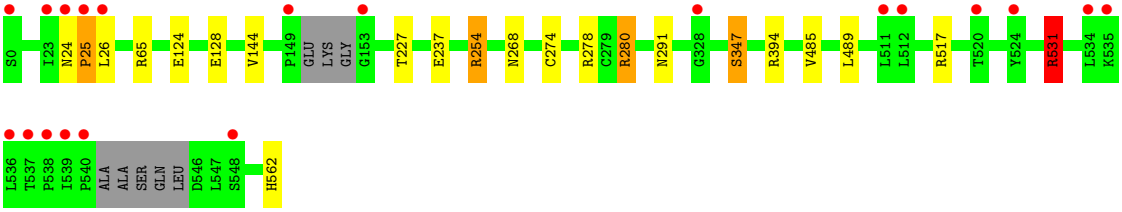
3 Residue-property plots (i)

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: NS5B

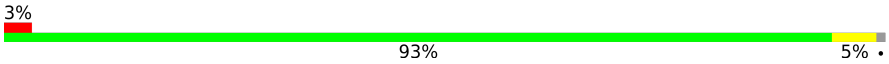
Chain A:

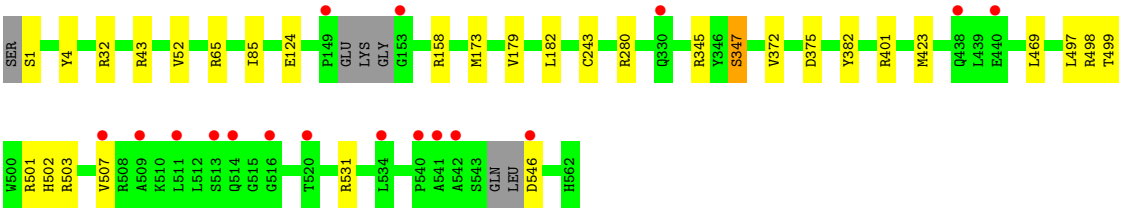




- Molecule 1: NS5B

Chain B:





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	105.36Å 108.23Å 134.76Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	84.39 – 1.96 48.14 – 1.96	Depositor EDS
% Data completeness (in resolution range)	98.0 (84.39-1.96) 98.0 (48.14-1.96)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.36 (at 1.97Å)	Xtriage
Refinement program	REFMAC 5.8.0049	Depositor
R, R_{free}	0.188 , 0.234 0.196 , 0.239	Depositor DCC
R_{free} test set	2045 reflections (1.89%)	wwPDB-VP
Wilson B-factor (Å^2)	25.7	Xtriage
Anisotropy	0.696	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 47.3	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	0.014 for k,h,-l	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	9819	wwPDB-VP
Average B, all atoms (Å^2)	37.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.42% 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: GOL, 55W, MES, PEG, SO4

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	0.58	1/4446 (0.0%)	0.79	10/6031 (0.2%)
1	B	0.58	0/4473	0.79	7/6067 (0.1%)
All	All	0.58	1/8919 (0.0%)	0.79	17/12098 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	25	PRO	N-CD	7.80	1.58	1.47

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	280	ARG	NE-CZ-NH1	11.82	126.21	120.30
1	A	280	ARG	NE-CZ-NH2	-10.72	114.94	120.30
1	A	254	ARG	NE-CZ-NH2	-9.07	115.76	120.30
1	A	531	ARG	NE-CZ-NH1	8.81	124.70	120.30
1	A	254	ARG	NE-CZ-NH1	7.87	124.24	120.30
1	B	501	ARG	NE-CZ-NH1	6.81	123.70	120.30
1	B	345	ARG	NE-CZ-NH1	6.52	123.56	120.30
1	B	158	ARG	NE-CZ-NH1	5.88	123.24	120.30
1	A	65	ARG	NE-CZ-NH1	5.71	123.16	120.30
1	A	25	PRO	CA-N-CD	-5.63	103.61	111.50
1	B	401	ARG	NE-CZ-NH1	5.60	123.10	120.30
1	B	280	ARG	NE-CZ-NH2	-5.41	117.60	120.30
1	B	375	ASP	CB-CG-OD1	5.41	123.17	118.30
1	A	65	ARG	NE-CZ-NH2	-5.36	117.62	120.30
1	A	531	ARG	CG-CD-NE	5.13	122.57	111.80
1	B	65	ARG	NE-CZ-NH2	-5.07	117.76	120.30
1	A	531	ARG	CD-NE-CZ	5.04	130.65	123.60

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	4352	0	4359	15	0
1	B	4379	0	4386	31	0
2	A	41	0	0	0	0
2	B	41	0	0	0	0
3	A	12	0	16	0	0
3	B	30	0	40	12	0
4	A	12	0	13	0	0
5	A	28	0	40	0	0
5	B	14	0	20	2	0
6	A	50	0	0	1	0
6	B	15	0	0	0	0
7	A	430	0	0	5	0
7	B	415	0	0	8	0
All	All	9819	0	8874	46	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 3.

All (46) 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:43[A]:ARG:NH1	3:B:604:GOL:H32	1.27	1.45
1:B:43[A]:ARG:NH1	3:B:604:GOL:C3	1.99	1.26
1:B:43[A]:ARG:HH12	3:B:604:GOL:C3	1.51	1.21
1:A:278[A]:ARG:NH1	7:A:701:HOH:O	1.83	1.07
1:B:43[A]:ARG:HH12	3:B:604:GOL:H32	0.70	0.81
1:A:278[A]:ARG:HG3	7:A:701:HOH:O	1.81	0.79
1:B:43[A]:ARG:HH11	3:B:604:GOL:H32	1.54	0.66
1:B:43[B]:ARG:HH21	3:B:604:GOL:C3	2.11	0.64
1:B:43[B]:ARG:HH21	3:B:604:GOL:H32	1.63	0.63
1:A:531:ARG:HD3	1:A:531:ARG:H	1.65	0.61

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:43[A]:ARG:NH1	3:B:604:GOL:O3	2.35	0.58
1:B:1:SER:HA	7:B:845:HOH:O	2.02	0.58
1:A:531:ARG:HG2	1:A:531:ARG:HH11	1.68	0.57
1:B:503:ARG:O	1:B:507:VAL:HG23	2.05	0.56
1:B:4:TYR:CE2	1:B:52:VAL:HG13	2.41	0.56
1:A:280:ARG:HD2	1:A:291:ASN:OD1	2.07	0.54
1:B:43[A]:ARG:HH11	3:B:604:GOL:H12	1.72	0.54
1:B:423:MET:SD	1:B:497:LEU:HD23	2.47	0.54
1:B:531:ARG:HD2	7:B:1034:HOH:O	2.08	0.54
1:B:347:SER:O	1:B:347:SER:OG	2.25	0.53
1:B:43[A]:ARG:HH11	3:B:604:GOL:C3	2.15	0.50
1:B:43[A]:ARG:NH1	3:B:604:GOL:C2	2.73	0.50
1:B:469:LEU:HG	5:B:608:PEG:H12	1.94	0.49
1:B:32[A]:ARG:NH2	5:B:607:PEG:O2	2.45	0.49
1:B:372:VAL:HG22	1:B:382:TYR:CD1	2.48	0.48
1:A:268:ASN:HB3	1:A:274:CYS:SG	2.54	0.47
1:A:562:HIS:NE2	7:A:704:HOH:O	2.32	0.47
1:A:278[A]:ARG:CZ	7:A:701:HOH:O	2.46	0.46
1:B:85:ILE:N	1:B:173:MET:HE3	2.31	0.46
1:B:499:THR:HG23	7:B:973:HOH:O	2.15	0.46
1:A:227:THR:HB	1:A:347:SER:O	2.16	0.45
1:B:179:VAL:HG13	7:B:763:HOH:O	2.16	0.45
1:B:372:VAL:HG22	1:B:382:TYR:CE1	2.51	0.45
1:B:498:ARG:HD3	7:B:1011:HOH:O	2.18	0.44
1:A:237:GLU:OE2	1:A:254:ARG:HD2	2.19	0.42
1:B:531:ARG:CD	7:B:1034:HOH:O	2.67	0.42
1:A:485:VAL:O	1:A:489:LEU:HG	2.19	0.42
1:B:182:LEU:HD12	1:B:243:CYS:SG	2.60	0.42
1:B:546:ASP:N	7:B:715:HOH:O	2.53	0.41
1:B:502:HIS:CE1	3:B:606:GOL:H11	2.56	0.41
1:A:124:GLU:HG2	7:A:708:HOH:O	2.21	0.41
1:A:124:GLU:O	1:A:128:GLU:HG2	2.20	0.41
1:A:517:ARG:NE	6:A:609:SO4:O1	2.51	0.41
1:B:173:MET:HE2	7:B:876:HOH:O	2.21	0.40
1:A:144:VAL:HB	1:A:394:ARG:HG2	2.04	0.40
1:B:85:ILE:HA	1:B:173:MET:HE3	2.03	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	552/563 (98%)	542 (98%)	6 (1%)	4 (1%)	22 11
1	B	556/563 (99%)	540 (97%)	16 (3%)	0	100 100
All	All	1108/1126 (98%)	1082 (98%)	22 (2%)	4 (0%)	34 22

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	26	LEU
1	A	25	PRO
1	A	347	SER
1	A	24	ASN

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	477/479 (100%)	476 (100%)	1 (0%)	93 93
1	B	479/479 (100%)	477 (100%)	2 (0%)	91 90
All	All	956/958 (100%)	953 (100%)	3 (0%)	92 92

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	531	ARG
1	B	124	GLU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	347	SER

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

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)

31 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	$\#\|Z\| > 2$
2	55W	B	601[B]	-	33,42,42	2.00	6 (18%)	35,63,63	1.76	6 (17%)
6	SO4	B	611	-	4,4,4	0.38	0	6,6,6	0.28	0
6	SO4	A	617	-	4,4,4	0.40	0	6,6,6	0.28	0
2	55W	A	601[B]	-	33,42,42	1.94	5 (15%)	35,63,63	1.53	4 (11%)
3	GOL	B	604	-	5,5,5	0.18	0	5,5,5	0.30	0
6	SO4	B	609	-	4,4,4	0.46	0	6,6,6	0.73	0
5	PEG	A	606	-	6,6,6	0.46	0	5,5,5	0.36	0
3	GOL	B	602	-	5,5,5	0.33	0	5,5,5	0.28	0
6	SO4	A	612	-	4,4,4	0.51	0	6,6,6	0.46	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
2	55W	B	601[A]	-	33,42,42	2.00	6 (18%)	35,63,63	1.76	6 (17%)
5	PEG	B	607	-	6,6,6	0.52	0	5,5,5	0.39	0
2	55W	A	601[A]	-	33,42,42	1.94	5 (15%)	35,63,63	1.53	4 (11%)
5	PEG	B	608	-	6,6,6	0.42	0	5,5,5	0.33	0
5	PEG	A	607	-	6,6,6	0.56	0	5,5,5	0.42	0
3	GOL	B	603	-	5,5,5	0.32	0	5,5,5	0.57	0
5	PEG	A	608	-	6,6,6	0.56	0	5,5,5	0.69	0
6	SO4	A	614	-	4,4,4	0.36	0	6,6,6	0.30	0
6	SO4	A	609	-	4,4,4	0.31	0	6,6,6	0.30	0
3	GOL	A	602	-	5,5,5	0.63	0	5,5,5	0.65	0
6	SO4	A	613	-	4,4,4	0.43	0	6,6,6	0.49	0
6	SO4	A	618	-	4,4,4	0.26	0	6,6,6	0.29	0
6	SO4	B	610	-	4,4,4	0.39	0	6,6,6	0.26	0
3	GOL	A	603	-	5,5,5	0.37	0	5,5,5	0.41	0
5	PEG	A	605	-	6,6,6	0.41	0	5,5,5	0.49	0
6	SO4	A	610	-	4,4,4	0.37	0	6,6,6	0.19	0
3	GOL	B	605	-	5,5,5	0.26	0	5,5,5	0.29	0
6	SO4	A	611	-	4,4,4	0.38	0	6,6,6	0.09	0
6	SO4	A	615	-	4,4,4	0.27	0	6,6,6	0.41	0
6	SO4	A	616	-	4,4,4	0.49	0	6,6,6	0.61	0
4	MES	A	604	-	12,12,12	2.17	1 (8%)	14,16,16	1.80	4 (28%)
3	GOL	B	606	-	5,5,5	0.46	0	5,5,5	0.78	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	PEG	A	605	-	-	3/4/4/4	-
3	GOL	B	606	-	-	0/4/4/4	-
2	55W	B	601[B]	-	-	2/16/26/26	0/5/5/5
5	PEG	A	608	-	-	2/4/4/4	-
3	GOL	B	605	-	-	1/4/4/4	-
2	55W	B	601[A]	-	-	2/16/26/26	0/5/5/5
3	GOL	A	602	-	-	0/4/4/4	-
5	PEG	B	607	-	-	2/4/4/4	-
2	55W	A	601[A]	-	-	2/16/26/26	0/5/5/5
2	55W	A	601[B]	-	-	2/16/26/26	0/5/5/5
3	GOL	B	604	-	-	2/4/4/4	-

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	PEG	B	608	-	-	0/4/4/4	-
5	PEG	A	607	-	-	4/4/4/4	-
4	MES	A	604	-	-	0/6/14/14	0/1/1/1
5	PEG	A	606	-	-	2/4/4/4	-
3	GOL	B	602	-	-	3/4/4/4	-
3	GOL	B	603	-	-	1/4/4/4	-
3	GOL	A	603	-	-	4/4/4/4	-

All (23) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	601[A]	55W	N11-N7	-7.08	1.25	1.39
2	A	601[B]	55W	N11-N7	-7.08	1.25	1.39
2	B	601[A]	55W	N11-N7	-6.95	1.26	1.39
2	B	601[B]	55W	N11-N7	-6.95	1.26	1.39
4	A	604	MES	C8-S	-6.87	1.67	1.77
2	A	601[A]	55W	P27-C36	4.86	1.85	1.79
2	A	601[B]	55W	P27-C36	4.86	1.85	1.79
2	B	601[A]	55W	C9-C10	-4.58	1.36	1.41
2	B	601[B]	55W	C9-C10	-4.58	1.36	1.41
2	A	601[A]	55W	C9-C10	-4.29	1.36	1.41
2	A	601[B]	55W	C9-C10	-4.29	1.36	1.41
2	B	601[A]	55W	P27-C36	3.67	1.83	1.79
2	B	601[B]	55W	P27-C36	3.67	1.83	1.79
2	B	601[A]	55W	C17-N20	3.63	1.38	1.34
2	B	601[B]	55W	C17-N20	3.63	1.38	1.34
2	B	601[A]	55W	C21-N20	3.29	1.39	1.33
2	B	601[B]	55W	C21-N20	3.29	1.39	1.33
2	B	601[A]	55W	C23-N24	3.14	1.42	1.35
2	B	601[B]	55W	C23-N24	3.14	1.42	1.35
2	A	601[A]	55W	C17-N20	2.67	1.37	1.34
2	A	601[B]	55W	C17-N20	2.67	1.37	1.34
2	A	601[A]	55W	C21-N20	2.43	1.38	1.33
2	A	601[B]	55W	C21-N20	2.43	1.38	1.33

All (24) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	601[A]	55W	C3-C5-N7	4.33	122.94	119.15
2	B	601[B]	55W	C3-C5-N7	4.33	122.94	119.15
2	B	601[A]	55W	C6-C5-N7	-4.16	115.52	119.15

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	601[B]	55W	C6-C5-N7	-4.16	115.52	119.15
4	A	604	MES	O1S-S-C8	4.11	111.87	106.92
2	A	601[A]	55W	C33-C35-C36	3.97	119.76	117.81
2	A	601[B]	55W	C33-C35-C36	3.97	119.76	117.81
2	A	601[A]	55W	C23-C22-C21	3.83	119.80	116.99
2	A	601[B]	55W	C23-C22-C21	3.83	119.80	116.99
2	B	601[A]	55W	C23-C22-C21	3.79	119.77	116.99
2	B	601[B]	55W	C23-C22-C21	3.79	119.77	116.99
2	B	601[A]	55W	C4-C2-C15	-3.70	115.44	121.28
2	B	601[B]	55W	C4-C2-C15	-3.70	115.44	121.28
4	A	604	MES	O2S-S-C8	3.33	110.93	106.92
2	A	601[A]	55W	C3-C5-N7	3.21	121.96	119.15
2	A	601[B]	55W	C3-C5-N7	3.21	121.96	119.15
2	B	601[A]	55W	C33-C35-C36	2.81	119.19	117.81
2	B	601[B]	55W	C33-C35-C36	2.81	119.19	117.81
2	A	601[A]	55W	C6-C5-N7	-2.60	116.88	119.15
2	A	601[B]	55W	C6-C5-N7	-2.60	116.88	119.15
4	A	604	MES	O3S-S-O1S	-2.35	105.54	111.27
4	A	604	MES	O2S-S-O1S	-2.25	106.15	113.95
2	B	601[A]	55W	C25-C21-C22	-2.21	118.43	121.81
2	B	601[B]	55W	C25-C21-C22	-2.21	118.43	121.81

There are no chirality outliers.

All (32) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	602	GOL	C1-C2-C3-O3
3	B	604	GOL	C1-C2-C3-O3
5	A	608	PEG	C1-C2-O2-C3
5	A	605	PEG	O1-C1-C2-O2
5	A	607	PEG	O1-C1-C2-O2
5	A	605	PEG	O2-C3-C4-O4
5	A	608	PEG	O2-C3-C4-O4
2	A	601[A]	55W	C3-C5-N7-C8
2	A	601[B]	55W	C3-C5-N7-C8
2	B	601[A]	55W	C3-C5-N7-C8
2	B	601[A]	55W	C6-C5-N7-C8
2	B	601[B]	55W	C3-C5-N7-C8
2	B	601[B]	55W	C6-C5-N7-C8
3	A	603	GOL	O1-C1-C2-C3
3	B	602	GOL	O2-C2-C3-O3
5	B	607	PEG	O1-C1-C2-O2

Continued on next page...

Continued from previous page...

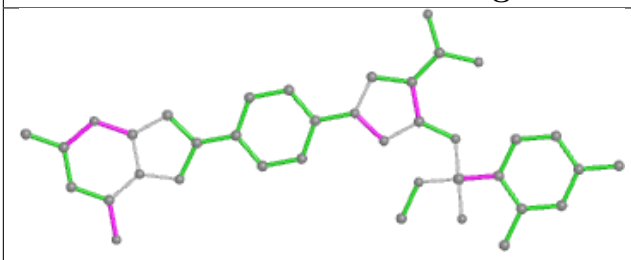
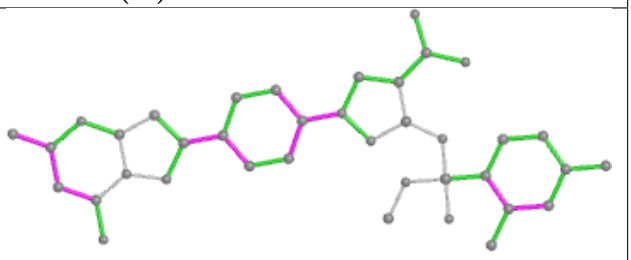
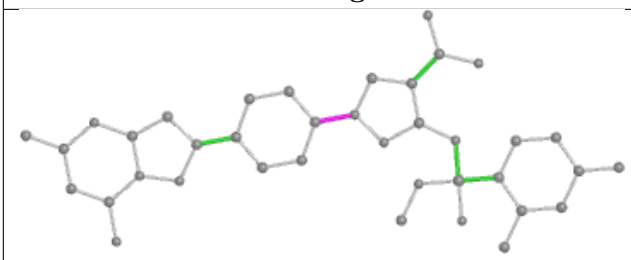
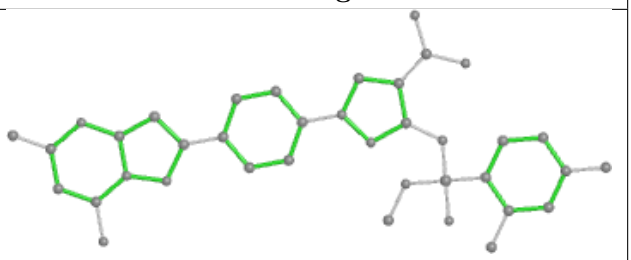
Mol	Chain	Res	Type	Atoms
5	A	607	PEG	O2-C3-C4-O4
5	A	606	PEG	O2-C3-C4-O4
2	A	601[A]	55W	C6-C5-N7-C8
2	A	601[B]	55W	C6-C5-N7-C8
3	A	603	GOL	O2-C2-C3-O3
3	B	604	GOL	O2-C2-C3-O3
3	B	605	GOL	O2-C2-C3-O3
3	A	603	GOL	C1-C2-C3-O3
5	A	607	PEG	C4-C3-O2-C2
5	A	606	PEG	C1-C2-O2-C3
5	A	605	PEG	C4-C3-O2-C2
3	B	602	GOL	O1-C1-C2-O2
3	A	603	GOL	O1-C1-C2-O2
5	B	607	PEG	C4-C3-O2-C2
3	B	603	GOL	C1-C2-C3-O3
5	A	607	PEG	C1-C2-O2-C3

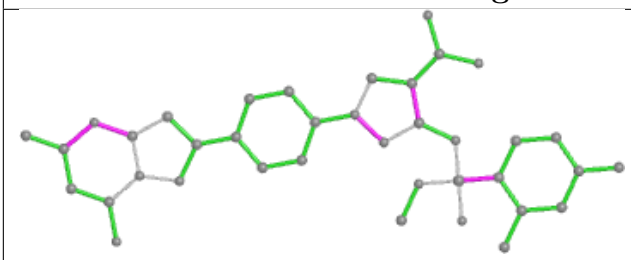
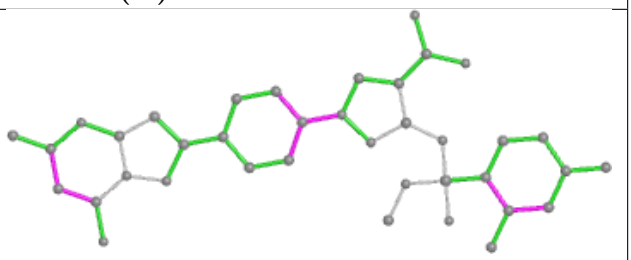
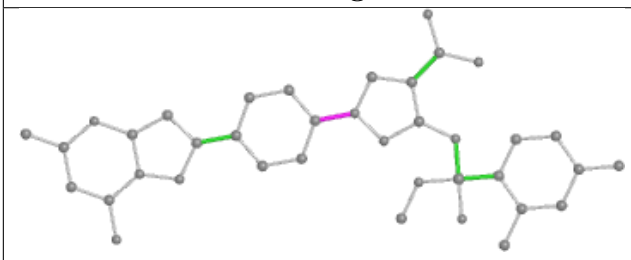
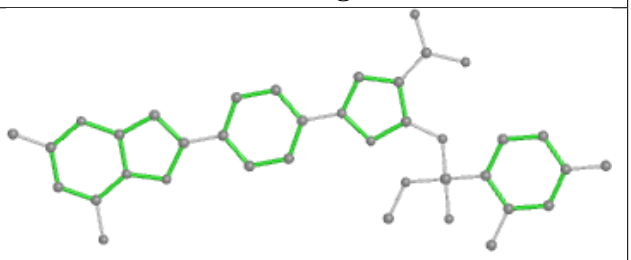
There are no ring outliers.

5 monomers are involved in 15 short contacts:

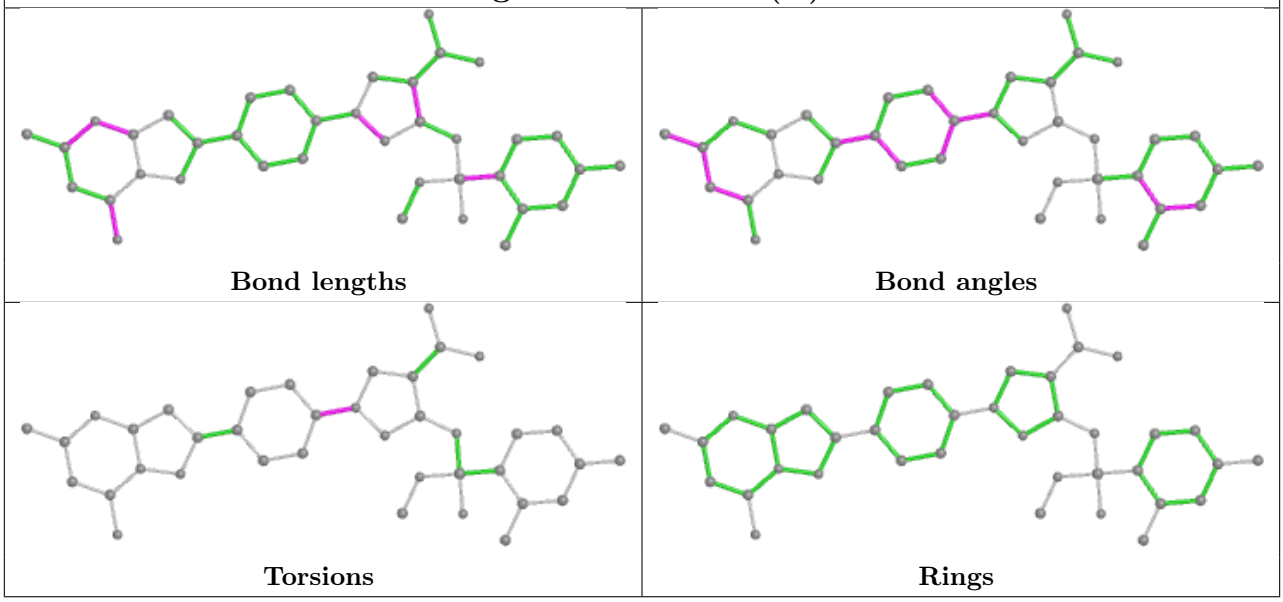
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	604	GOL	11	0
5	B	607	PEG	1	0
5	B	608	PEG	1	0
6	A	609	SO4	1	0
3	B	606	GOL	1	0

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.

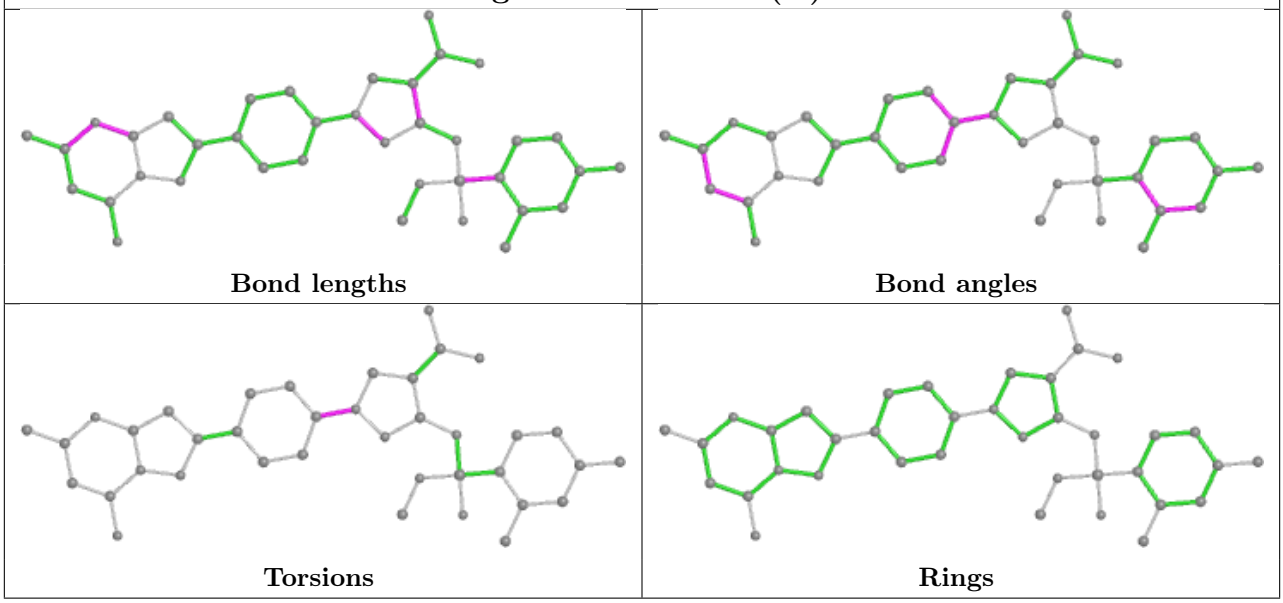
Ligand 55W B 601 (B)	
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand 55W A 601 (B)	
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand 55W B 601 (A)



Ligand 55W A 601 (A)



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	555/563 (98%)	0.23	20 (3%)	42	52	20, 33, 63, 96	20 (3%)
1	B	557/563 (98%)	0.18	17 (3%)	49	58	18, 34, 67, 90	18 (3%)
All	All	1112/1126 (98%)	0.20	37 (3%)	46	56	18, 34, 66, 96	38 (3%)

All (37) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	541	ALA	5.0
1	A	26	LEU	4.9
1	B	540	PRO	4.8
1	A	25	PRO	4.7
1	A	539	ILE	4.6
1	A	537	THR	4.4
1	A	536	LEU	4.3
1	A	23	ILE	3.9
1	A	540	PRO	3.7
1	B	153	GLY	3.6
1	B	149	PRO	3.5
1	A	538	PRO	3.4
1	A	520	THR	3.4
1	A	24	ASN	3.3
1	A	534	LEU	3.3
1	A	511	LEU	3.3
1	A	0	SER	3.3
1	A	153	GLY	3.2
1	B	534	LEU	3.2
1	A	512	LEU	3.0
1	A	149	PRO	2.8
1	B	546	ASP	2.6
1	B	542	ALA	2.6
1	A	535	LYS	2.6

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	524	TYR	2.5
1	B	514	GLN	2.4
1	B	438	GLN	2.4
1	B	330	GLN	2.4
1	B	440	GLU	2.4
1	A	548	SER	2.3
1	B	507	VAL	2.3
1	B	513	SER	2.3
1	A	328	GLY	2.2
1	B	516	GLY	2.2
1	B	509	ALA	2.1
1	B	511	LEU	2.1
1	B	520	THR	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
5	PEG	A	607	7/7	0.72	0.18	50,59,69,75	0
3	GOL	B	606	6/6	0.77	0.18	46,56,62,63	0
6	SO4	B	611	5/5	0.77	0.29	81,88,107,120	0
5	PEG	A	606	7/7	0.80	0.24	45,47,69,71	0
3	GOL	B	602	6/6	0.81	0.19	63,71,78,82	0
6	SO4	A	612	5/5	0.82	0.17	61,67,73,80	0
5	PEG	A	605	7/7	0.83	0.17	38,58,66,71	0
3	GOL	A	602	6/6	0.84	0.24	31,71,75,76	0
3	GOL	B	605	6/6	0.86	0.32	64,72,78,78	0
5	PEG	B	608	7/7	0.87	0.15	46,55,68,73	0

Continued on next page...

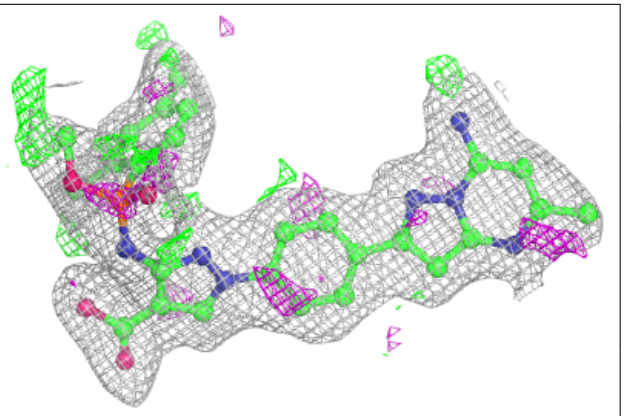
Continued from previous page...

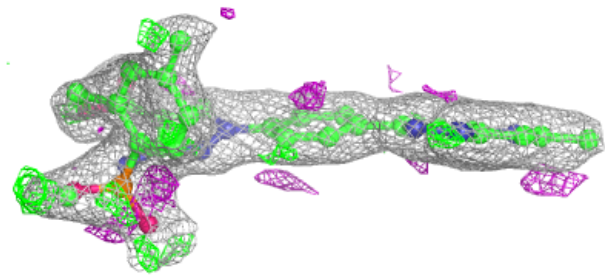
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
5	PEG	B	607	7/7	0.88	0.20	44,54,65,70	0
3	GOL	B	603	6/6	0.88	0.17	41,47,52,56	0
3	GOL	A	603	6/6	0.89	0.15	48,51,59,59	0
5	PEG	A	608	7/7	0.89	0.19	32,50,59,64	0
6	SO4	A	617	5/5	0.90	0.24	51,66,83,101	0
6	SO4	A	614	5/5	0.91	0.25	76,79,103,109	0
6	SO4	A	611	5/5	0.91	0.26	60,75,88,89	0
6	SO4	B	610	5/5	0.91	0.21	68,83,85,86	0
6	SO4	A	610	5/5	0.91	0.12	70,80,89,92	0
2	55W	B	601[A]	38/38	0.92	0.13	22,36,49,75	3
6	SO4	A	618	5/5	0.92	0.12	62,72,81,86	0
2	55W	B	601[B]	38/38	0.92	0.13	22,37,49,56	3
3	GOL	B	604	6/6	0.92	0.10	27,32,39,39	6
6	SO4	B	609	5/5	0.94	0.14	37,46,71,71	0
6	SO4	A	615	5/5	0.95	0.13	66,68,78,84	0
6	SO4	A	609	5/5	0.95	0.16	73,75,78,88	0
4	MES	A	604	12/12	0.96	0.11	36,43,46,52	0
2	55W	A	601[B]	38/38	0.96	0.10	20,26,36,38	3
2	55W	A	601[A]	38/38	0.96	0.10	20,26,36,43	3
6	SO4	A	613	5/5	0.97	0.12	41,44,50,54	0
6	SO4	A	616	5/5	0.98	0.11	38,44,73,82	0

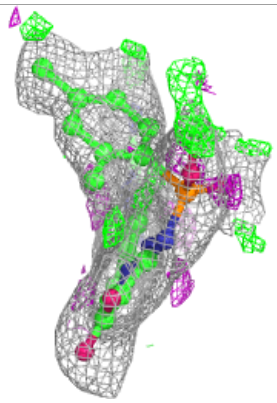
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around 55W B 601 (A):

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

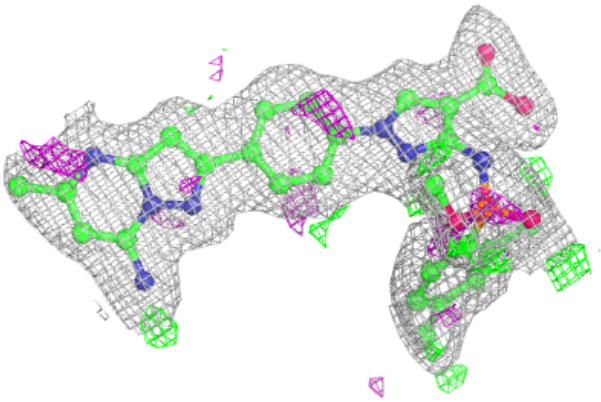


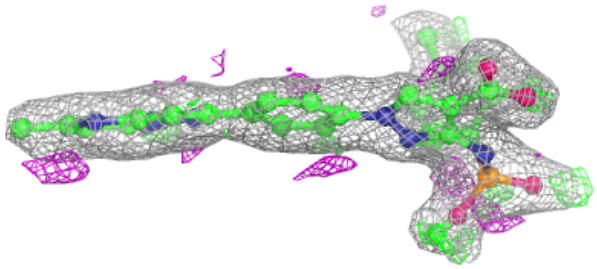


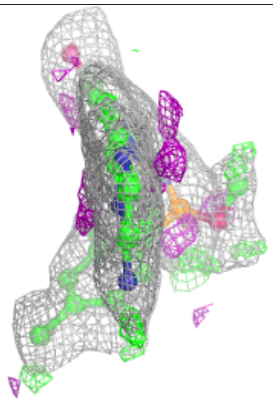


Electron density around 55W B 601 (B):

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

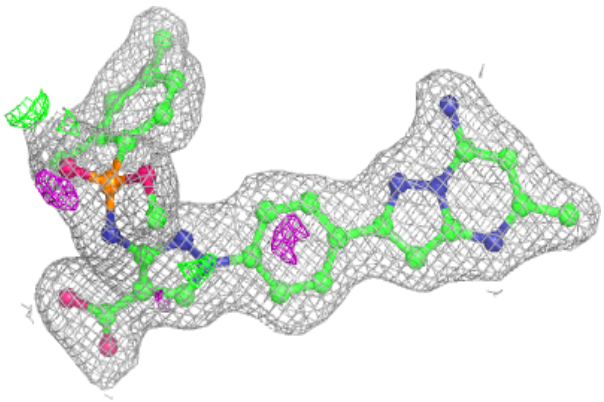


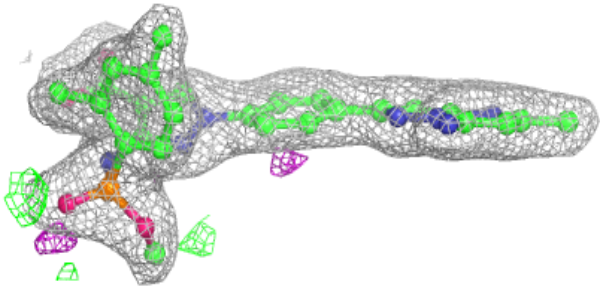


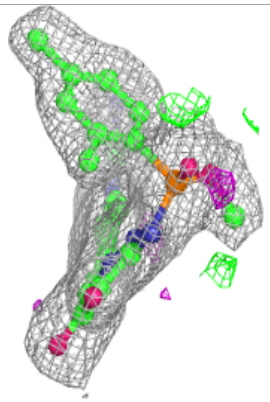


Electron density around 55W A 601 (B):

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

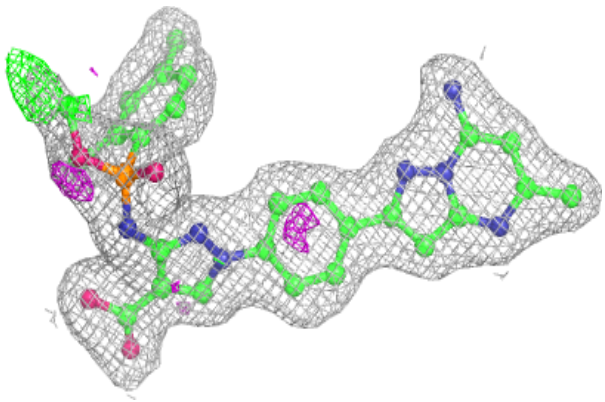


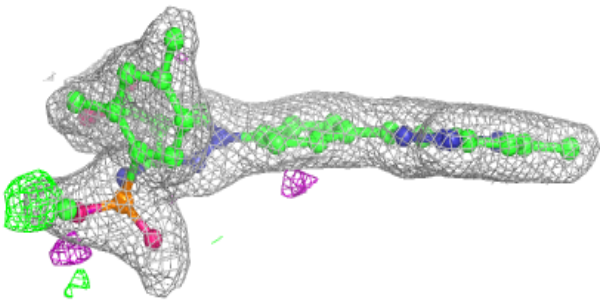




Electron density around 55W A 601 (A):

$2mF_o$-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.