



wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 8, 2020 – 05:42 AM BST

PDB ID : 4RZ8
Title : Crystal structure of HIV-1 gp120 core in complex with NBD-11021, a small molecule CD4-antagonist
Authors : Kwon, Y.D.; Debnath, A.K.; Kwong, P.D.
Deposited on : 2014-12-18
Resolution : 1.90 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) 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 : 2.13.1
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) : 2.13.1

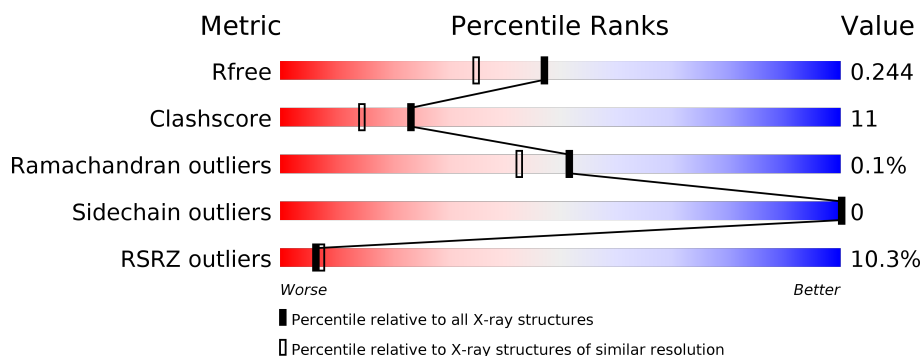
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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	6207 (1.90-1.90)
Clashscore	141614	6847 (1.90-1.90)
Ramachandran outliers	138981	6760 (1.90-1.90)
Sidechain outliers	138945	6760 (1.90-1.90)
RSRZ outliers	127900	6082 (1.90-1.90)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	353	<div> <div>18%</div> <div>72%</div> <div>24%</div> <div>.</div> </div>
1	B	353	<div> <div>14%</div> <div>74%</div> <div>21%</div> <div>5%</div> </div>
1	C	353	<div> <div>4%</div> <div>75%</div> <div>21%</div> <div>.</div> </div>
1	D	353	<div> <div>4%</div> <div>76%</div> <div>20%</div> <div>.</div> </div>

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 crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	NAG	A	504	-	-	-	X
2	NAG	C	502	-	-	-	X
2	NAG	D	502	-	-	-	X

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 12111 atoms, of which 100 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 Envelope glycoprotein gp120.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	339	Total	C	N	O	S	0	0	0
			2654	1666	460	507	21			
1	B	334	Total	C	N	O	S	0	0	0
			2617	1645	453	499	20			
1	C	339	Total	C	N	O	S	0	0	0
			2654	1666	460	507	21			
1	D	339	Total	C	N	O	S	0	0	0
			2654	1666	460	507	21			

There are 36 discrepancies between the modelled and reference sequences:

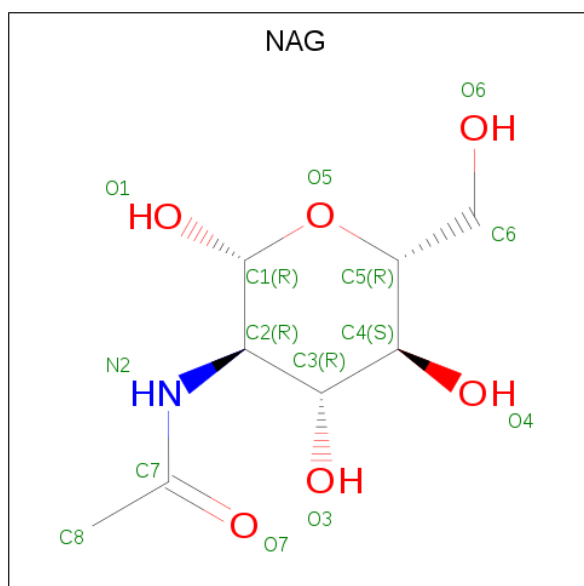
Chain	Residue	Modelled	Actual	Comment	Reference
A	124	GLY	-	linker	UNP Q0ED31
A	198	GLY	-	linker	UNP Q0ED31
A	318	GLY	-	linker	UNP Q0ED31
A	319	GLY	-	linker	UNP Q0ED31
A	320	SER	-	linker	UNP Q0ED31
A	321	GLY	-	linker	UNP Q0ED31
A	322	SER	-	linker	UNP Q0ED31
A	323	GLY	-	linker	UNP Q0ED31
A	375	SER	HIS	engineered mutation	UNP Q0ED31
B	124	GLY	-	linker	UNP Q0ED31
B	198	GLY	-	linker	UNP Q0ED31
B	318	GLY	-	linker	UNP Q0ED31
B	319	GLY	-	linker	UNP Q0ED31
B	320	SER	-	linker	UNP Q0ED31
B	321	GLY	-	linker	UNP Q0ED31
B	322	SER	-	linker	UNP Q0ED31
B	323	GLY	-	linker	UNP Q0ED31
B	375	SER	HIS	engineered mutation	UNP Q0ED31
C	124	GLY	-	linker	UNP Q0ED31
C	198	GLY	-	linker	UNP Q0ED31
C	318	GLY	-	linker	UNP Q0ED31

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Chain	Residue	Modelled	Actual	Comment	Reference
C	319	GLY	-	linker	UNP Q0ED31
C	320	SER	-	linker	UNP Q0ED31
C	321	GLY	-	linker	UNP Q0ED31
C	322	SER	-	linker	UNP Q0ED31
C	323	GLY	-	linker	UNP Q0ED31
C	375	SER	HIS	engineered mutation	UNP Q0ED31
D	124	GLY	-	linker	UNP Q0ED31
D	198	GLY	-	linker	UNP Q0ED31
D	318	GLY	-	linker	UNP Q0ED31
D	319	GLY	-	linker	UNP Q0ED31
D	320	SER	-	linker	UNP Q0ED31
D	321	GLY	-	linker	UNP Q0ED31
D	322	SER	-	linker	UNP Q0ED31
D	323	GLY	-	linker	UNP Q0ED31
D	375	SER	HIS	engineered mutation	UNP Q0ED31

- Molecule 2 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	A	1	Total	C	N	O	0	0
			14	8	1	5		

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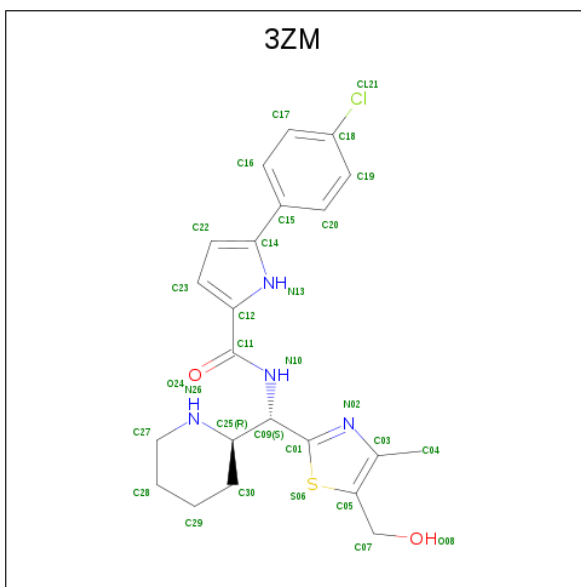
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	B	1	Total	C	N	O	0	0
			14	8	1	5		
2	B	1	Total	C	N	O	0	0
			14	8	1	5		
2	B	1	Total	C	N	O	0	0
			14	8	1	5		
2	B	1	Total	C	N	O	0	0
			14	8	1	5		
2	B	1	Total	C	N	O	0	0
			14	8	1	5		
2	B	1	Total	C	N	O	0	0
			14	8	1	5		
2	B	1	Total	C	N	O	0	0
			14	8	1	5		
2	B	1	Total	C	N	O	0	0
			14	8	1	5		
2	C	1	Total	C	N	O	0	0
			14	8	1	5		
2	C	1	Total	C	N	O	0	0
			14	8	1	5		
2	C	1	Total	C	N	O	0	0
			14	8	1	5		
2	C	1	Total	C	N	O	0	0
			14	8	1	5		
2	C	1	Total	C	N	O	0	0
			14	8	1	5		

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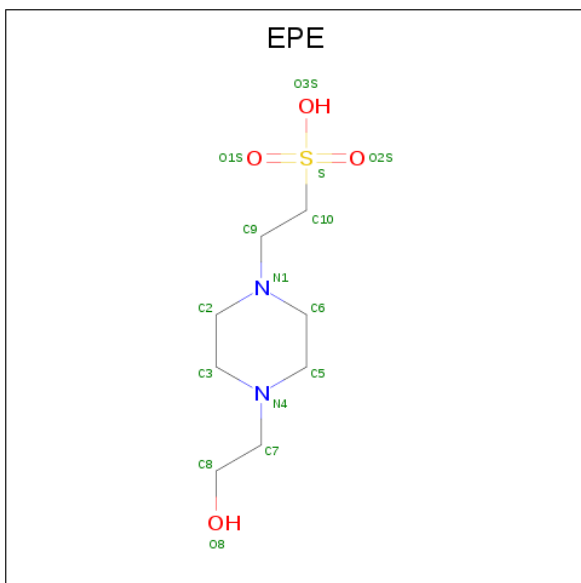
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	C	1	Total	C	N	O	0	0
			14	8	1	5		
2	C	1	Total	C	N	O	0	0
			14	8	1	5		
2	C	1	Total	C	N	O	0	0
			14	8	1	5		
2	C	1	Total	C	N	O	0	0
			14	8	1	5		
2	C	1	Total	C	N	O	0	0
			14	8	1	5		
2	D	1	Total	C	N	O	0	0
			14	8	1	5		
2	D	1	Total	C	N	O	0	0
			14	8	1	5		
2	D	1	Total	C	N	O	0	0
			14	8	1	5		
2	D	1	Total	C	N	O	0	0
			14	8	1	5		
2	D	1	Total	C	N	O	0	0
			14	8	1	5		
2	D	1	Total	C	N	O	0	0
			14	8	1	5		
2	D	1	Total	C	N	O	0	0
			14	8	1	5		
2	D	1	Total	C	N	O	0	0
			14	8	1	5		
2	D	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 3 is 5-(4-chlorophenyl)-N-{(S)-[5-(hydroxymethyl)-4-methyl-1,3-thiazol-2-yl]}[(2R)-piperidin-2-yl]methyl}-1H-pyrrole-2-carboxamide (three-letter code: 3ZM) (formula: C₂₂H₂₅ClN₄O₂S).



Mol	Chain	Residues	Atoms							ZeroOcc	AltConf
3	A	1	Total	C	Cl	H	N	O	S	0	0
			55	22	1	25	4	2	1		
3	B	1	Total	C	Cl	H	N	O	S	0	0
			55	22	1	25	4	2	1		
3	C	1	Total	C	Cl	H	N	O	S	0	0
			55	22	1	25	4	2	1		
3	D	1	Total	C	Cl	H	N	O	S	0	0
			55	22	1	25	4	2	1		

- Molecule 4 is 4-(2-HYDROXYETHYL)-1-PIPERAZINE ETHANESULFONIC ACID (three-letter code: EPE) (formula: C₈H₁₈N₂O₄S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	S	0	0
			15	8	2	4	1		
4	B	1	Total	C	N	O	S	0	0
			15	8	2	4	1		
4	C	1	Total	C	N	O	S	0	0
			15	8	2	4	1		
4	D	1	Total	C	N	O	S	0	0
			15	8	2	4	1		

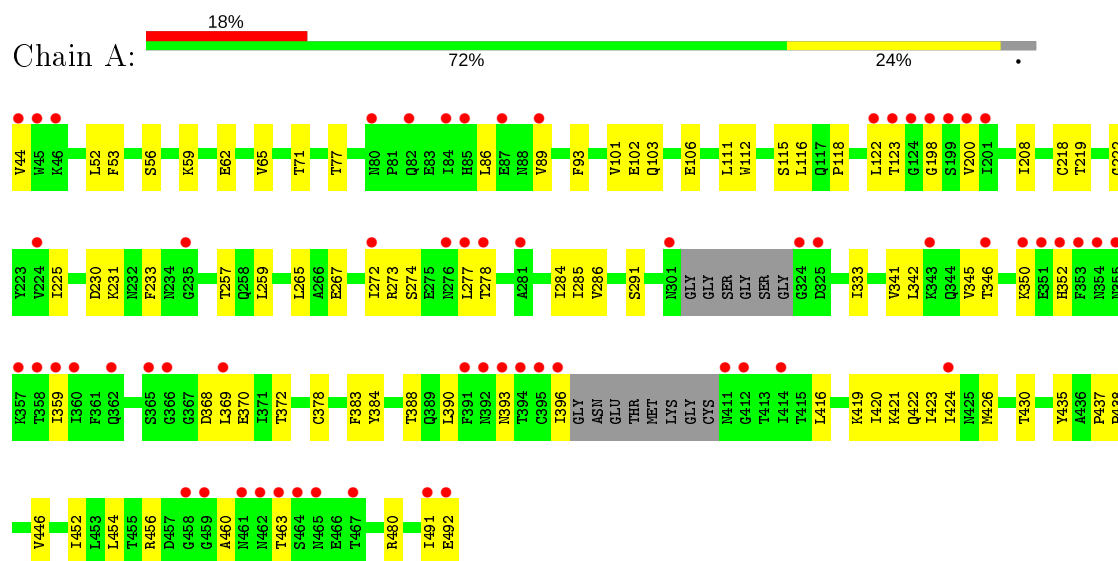
- Molecule 5 is water.

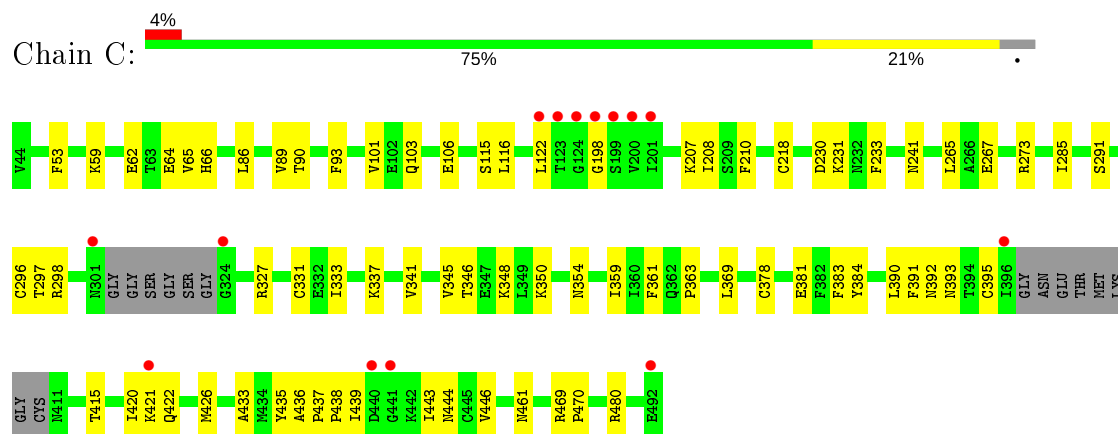
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	92	Total	O	0	0
			92	92		
5	B	126	Total	O	0	0
			126	126		
5	C	232	Total	O	0	0
			232	232		
5	D	242	Total	O	0	0
			242	242		

3 Residue-property plots [i](#)

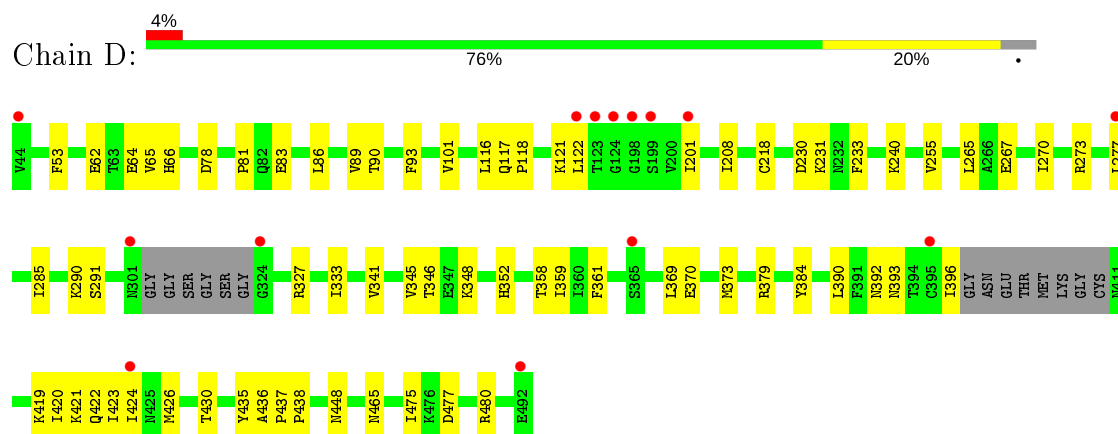
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: Envelope glycoprotein gp120





• Molecule 1: Envelope glycoprotein gp120



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	113.62Å 68.84Å 116.19Å 90.00° 110.59° 90.00°	Depositor
Resolution (Å)	44.03 – 1.90 44.03 – 1.82	Depositor EDS
% Data completeness (in resolution range)	93.8 (44.03-1.90) 83.1 (44.03-1.82)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.30 (at 1.82Å)	Xtriage
Refinement program	PHENIX (phenix.refine: dev_1839)	Depositor
R, R_{free}	0.227 , 0.243 0.229 , 0.244	Depositor DCC
R_{free} test set	2002 reflections (1.52%)	wwPDB-VP
Wilson B-factor (Å ²)	34.2	Xtriage
Anisotropy	0.375	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 54.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.026 for l,-k,h	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	12111	wwPDB-VP
Average B, all atoms (Å ²)	58.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 72.06 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 2.3531e-06. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹ Intensities estimated from amplitudes.

² Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: EPE, NAG, 3ZM

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	0.20	0/2709	0.37	0/3678
1	B	0.20	0/2672	0.37	0/3627
1	C	0.21	0/2709	0.38	0/3678
1	D	0.20	0/2709	0.37	0/3678
All	All	0.20	0/10799	0.37	0/14661

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	2654	0	2591	74	0
1	B	2617	0	2556	56	0
1	C	2654	0	2589	58	0
1	D	2654	0	2589	58	0
2	A	126	0	117	2	0
2	B	126	0	117	1	0
2	C	154	0	143	8	0
2	D	154	0	143	9	0
3	A	30	25	25	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	30	25	25	1	0
3	C	30	25	25	0	0
3	D	30	25	25	0	0
4	A	15	0	17	4	0
4	B	15	0	17	6	0
4	C	15	0	17	2	0
4	D	15	0	17	0	0
5	A	92	0	0	3	0
5	B	126	0	0	9	0
5	C	232	0	0	12	0
5	D	242	0	0	12	0
All	All	12011	100	11013	253	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 11.

The worst 5 of 253 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:D:240:LYS:HB2	2:D:502:NAG:H82	1.43	0.98
1:D:480:ARG:NH2	5:D:805:HOH:O	2.05	0.88
1:C:395:CYS:SG	5:C:819:HOH:O	2.32	0.86
2:D:508:NAG:H83	2:D:508:NAG:H3	1.55	0.86
1:C:480:ARG:NH2	5:C:764:HOH:O	2.10	0.85

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	333/353 (94%)	319 (96%)	14 (4%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	328/353 (93%)	316 (96%)	12 (4%)	0	100	100
1	C	333/353 (94%)	320 (96%)	12 (4%)	1 (0%)	41	31
1	D	333/353 (94%)	322 (97%)	11 (3%)	0	100	100
All	All	1327/1412 (94%)	1277 (96%)	49 (4%)	1 (0%)	51	43

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	198	GLY

5.3.2 Protein sidechains ⓘ

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	303/311 (97%)	303 (100%)	0	100	100
1	B	298/311 (96%)	298 (100%)	0	100	100
1	C	303/311 (97%)	303 (100%)	0	100	100
1	D	303/311 (97%)	303 (100%)	0	100	100
All	All	1207/1244 (97%)	1207 (100%)	0	100	100

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

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

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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](#)

48 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	NAG	A	506	1	14,14,15	0.24	0	17,19,21	0.46	0
2	NAG	C	509	1	14,14,15	0.25	0	17,19,21	0.43	0
2	NAG	C	505	1	14,14,15	0.26	0	17,19,21	0.45	0
2	NAG	B	505	1	14,14,15	0.22	0	17,19,21	0.42	0
2	NAG	C	511	1	14,14,15	0.22	0	17,19,21	0.46	0
3	3ZM	C	512	-	30,33,33	2.42	8 (26%)	26,46,46	2.80	11 (42%)
2	NAG	D	506	1	14,14,15	0.25	0	17,19,21	0.43	0
3	3ZM	D	512	-	30,33,33	2.43	8 (26%)	26,46,46	2.83	11 (42%)
2	NAG	C	507	1	14,14,15	0.33	0	17,19,21	0.49	0
4	EPE	B	511	-	15,15,15	0.82	1 (6%)	18,20,20	1.81	5 (27%)
4	EPE	A	511	-	15,15,15	0.82	1 (6%)	18,20,20	1.63	5 (27%)
2	NAG	D	510	1	14,14,15	0.26	0	17,19,21	0.46	0
2	NAG	A	509	1	14,14,15	0.22	0	17,19,21	0.41	0
2	NAG	A	502	1	14,14,15	0.24	0	17,19,21	0.40	0
2	NAG	A	508	1	14,14,15	0.24	0	17,19,21	0.40	0
3	3ZM	A	510	-	30,33,33	2.56	10 (33%)	26,46,46	2.97	11 (42%)
2	NAG	D	501	1	14,14,15	0.22	0	17,19,21	0.35	0
2	NAG	A	507	1	14,14,15	0.29	0	17,19,21	0.45	0
2	NAG	A	503	1	14,14,15	0.22	0	17,19,21	0.51	0
2	NAG	A	504	1	14,14,15	0.23	0	17,19,21	0.42	0
2	NAG	C	501	1	14,14,15	0.20	0	17,19,21	0.36	0
3	3ZM	B	510	-	30,33,33	2.54	10 (33%)	26,46,46	2.98	10 (38%)
4	EPE	C	513	-	15,15,15	0.84	1 (6%)	18,20,20	1.66	5 (27%)
2	NAG	D	504	1	14,14,15	0.26	0	17,19,21	0.40	0
4	EPE	D	513	-	15,15,15	0.81	1 (6%)	18,20,20	1.82	6 (33%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	NAG	D	505	1	14,14,15	0.26	0	17,19,21	0.43	0
2	NAG	A	505	1	14,14,15	0.24	0	17,19,21	0.41	0
2	NAG	B	508	1	14,14,15	0.24	0	17,19,21	0.43	0
2	NAG	C	506	1	14,14,15	0.25	0	17,19,21	0.43	0
2	NAG	A	501	1	14,14,15	0.21	0	17,19,21	0.36	0
2	NAG	B	501	1	14,14,15	0.22	0	17,19,21	0.36	0
2	NAG	C	508	1	14,14,15	0.30	0	17,19,21	0.45	0
2	NAG	C	504	1	14,14,15	0.30	0	17,19,21	0.36	0
2	NAG	D	511	1	14,14,15	0.22	0	17,19,21	0.42	0
2	NAG	C	510	1	14,14,15	0.26	0	17,19,21	0.45	0
2	NAG	D	503	1	14,14,15	0.28	0	17,19,21	0.47	0
2	NAG	D	509	1	14,14,15	0.25	0	17,19,21	0.42	0
2	NAG	C	503	1	14,14,15	0.30	0	17,19,21	0.46	0
2	NAG	D	507	1	14,14,15	0.28	0	17,19,21	0.45	0
2	NAG	B	504	1	14,14,15	0.24	0	17,19,21	0.42	0
2	NAG	C	502	1	14,14,15	0.25	0	17,19,21	0.48	0
2	NAG	B	507	1	14,14,15	0.36	0	17,19,21	0.52	0
2	NAG	D	508	1	14,14,15	0.28	0	17,19,21	0.50	0
2	NAG	D	502	1	14,14,15	0.23	0	17,19,21	0.44	0
2	NAG	B	506	1	14,14,15	0.26	0	17,19,21	0.43	0
2	NAG	B	502	1	14,14,15	0.24	0	17,19,21	0.42	0
2	NAG	B	509	1	14,14,15	0.23	0	17,19,21	0.40	0
2	NAG	B	503	1	14,14,15	0.22	0	17,19,21	0.53	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
2	NAG	A	506	1	-	2/6/23/26	0/1/1/1
2	NAG	C	509	1	-	2/6/23/26	0/1/1/1
2	NAG	C	505	1	-	0/6/23/26	0/1/1/1
2	NAG	B	505	1	-	2/6/23/26	0/1/1/1
2	NAG	C	511	1	-	4/6/23/26	0/1/1/1
3	3ZM	C	512	-	-	4/13/30/30	0/4/4/4
2	NAG	D	506	1	-	2/6/23/26	0/1/1/1
3	3ZM	D	512	-	-	1/13/30/30	0/4/4/4
2	NAG	C	507	1	-	0/6/23/26	0/1/1/1
4	EPE	B	511	-	-	6/9/19/19	0/1/1/1
4	EPE	A	511	-	-	5/9/19/19	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	D	510	1	-	4/6/23/26	0/1/1/1
2	NAG	A	509	1	-	2/6/23/26	0/1/1/1
2	NAG	A	502	1	-	1/6/23/26	0/1/1/1
2	NAG	A	508	1	-	2/6/23/26	0/1/1/1
3	3ZM	A	510	-	-	0/13/30/30	0/4/4/4
2	NAG	D	501	1	-	0/6/23/26	0/1/1/1
2	NAG	A	507	1	-	0/6/23/26	0/1/1/1
2	NAG	A	503	1	-	0/6/23/26	0/1/1/1
2	NAG	A	504	1	-	0/6/23/26	0/1/1/1
2	NAG	C	501	1	-	0/6/23/26	0/1/1/1
3	3ZM	B	510	-	-	4/13/30/30	0/4/4/4
4	EPE	C	513	-	-	3/9/19/19	0/1/1/1
2	NAG	D	504	1	-	2/6/23/26	0/1/1/1
4	EPE	D	513	-	-	6/9/19/19	0/1/1/1
2	NAG	D	505	1	-	0/6/23/26	0/1/1/1
2	NAG	A	505	1	-	0/6/23/26	0/1/1/1
2	NAG	B	508	1	-	2/6/23/26	0/1/1/1
2	NAG	C	506	1	-	2/6/23/26	0/1/1/1
2	NAG	A	501	1	-	0/6/23/26	0/1/1/1
2	NAG	B	501	1	-	2/6/23/26	0/1/1/1
2	NAG	C	508	1	-	2/6/23/26	0/1/1/1
2	NAG	C	504	1	-	2/6/23/26	0/1/1/1
2	NAG	D	511	1	-	4/6/23/26	0/1/1/1
2	NAG	C	510	1	-	4/6/23/26	0/1/1/1
2	NAG	D	503	1	-	2/6/23/26	0/1/1/1
2	NAG	D	509	1	-	2/6/23/26	0/1/1/1
2	NAG	C	503	1	-	2/6/23/26	0/1/1/1
2	NAG	D	507	1	-	0/6/23/26	0/1/1/1
2	NAG	B	504	1	-	0/6/23/26	0/1/1/1
2	NAG	C	502	1	-	2/6/23/26	0/1/1/1
2	NAG	B	507	1	-	1/6/23/26	0/1/1/1
2	NAG	D	508	1	-	3/6/23/26	0/1/1/1
2	NAG	D	502	1	-	2/6/23/26	0/1/1/1
2	NAG	B	506	1	-	0/6/23/26	0/1/1/1
2	NAG	B	502	1	-	0/6/23/26	0/1/1/1
2	NAG	B	509	1	-	2/6/23/26	0/1/1/1
2	NAG	B	503	1	-	0/6/23/26	0/1/1/1

The worst 5 of 40 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	512	3ZM	C09-C25	7.87	1.64	1.54
3	B	510	3ZM	C09-C25	7.40	1.64	1.54
3	A	510	3ZM	C09-C25	7.36	1.64	1.54
3	D	512	3ZM	C09-C25	7.18	1.64	1.54
3	A	510	3ZM	C15-C14	6.48	1.59	1.48

The worst 5 of 64 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	510	3ZM	C07-C05-C03	7.73	136.78	127.36
3	A	510	3ZM	C07-C05-C03	7.71	136.75	127.36
3	C	512	3ZM	C07-C05-C03	7.68	136.72	127.36
3	D	512	3ZM	C07-C05-C03	7.66	136.69	127.36
3	B	510	3ZM	C12-C11-N10	6.15	126.62	115.20

There are no chirality outliers.

5 of 86 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	C	512	3ZM	C01-C09-C25-N26
3	C	512	3ZM	C01-C09-C25-C30
3	C	512	3ZM	N10-C09-C25-N26
3	C	512	3ZM	N10-C09-C25-C30
3	D	512	3ZM	C01-C09-C25-C30

There are no ring outliers.

17 monomers are involved in 36 short contacts:

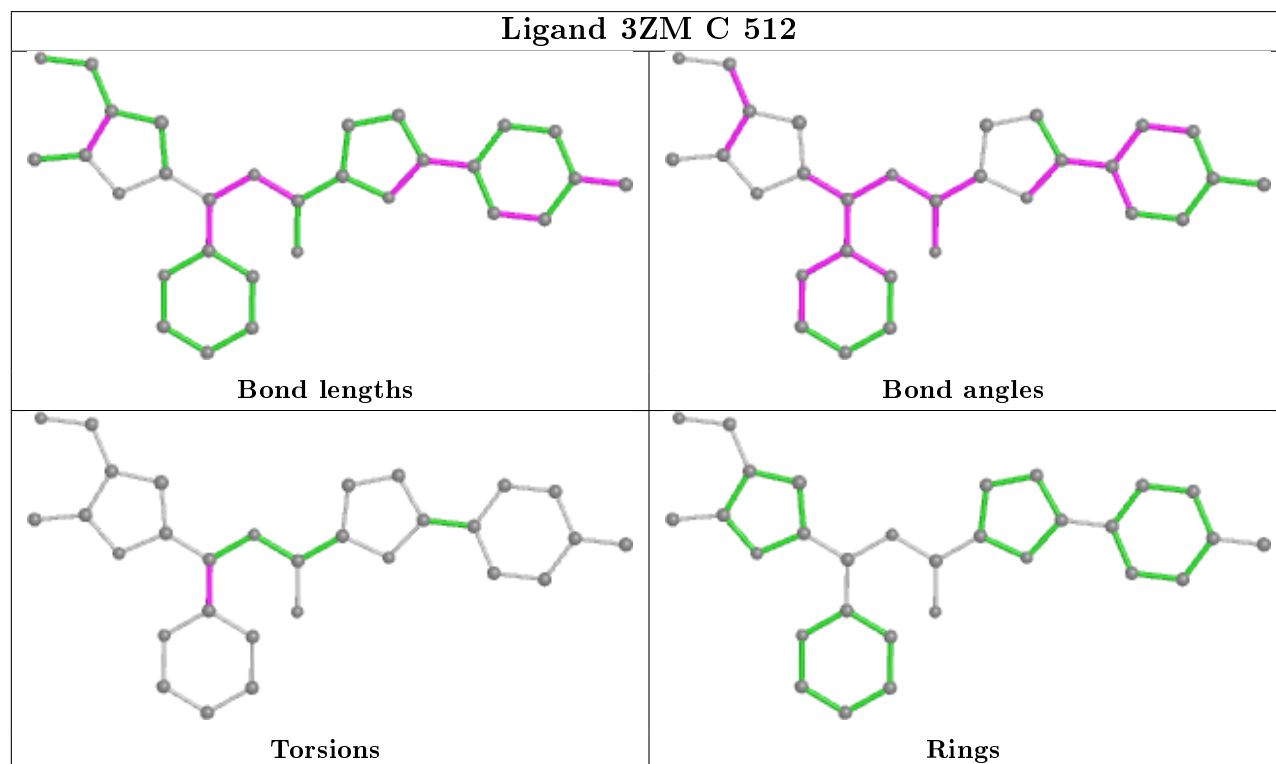
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	506	NAG	1	0
2	C	505	NAG	1	0
2	C	507	NAG	3	0
4	B	511	EPE	6	0
4	A	511	EPE	4	0
2	A	508	NAG	1	0
3	A	510	3ZM	3	0
3	B	510	3ZM	1	0
4	C	513	EPE	2	0
2	C	506	NAG	1	0
2	C	508	NAG	1	0

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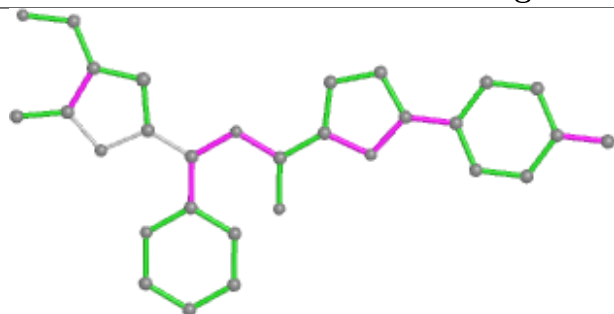
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Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	504	NAG	1	0
2	D	511	NAG	1	0
2	C	503	NAG	1	0
2	D	508	NAG	4	0
2	D	502	NAG	4	0
2	B	506	NAG	1	0

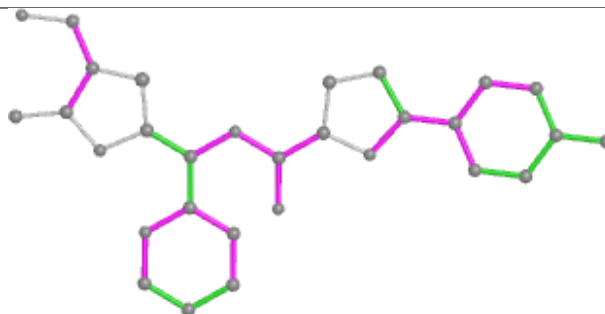
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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



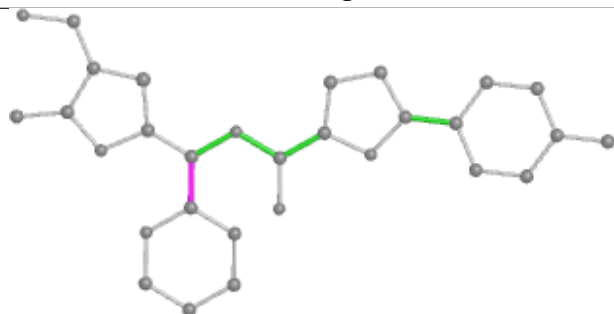
Ligand 3ZM D 512



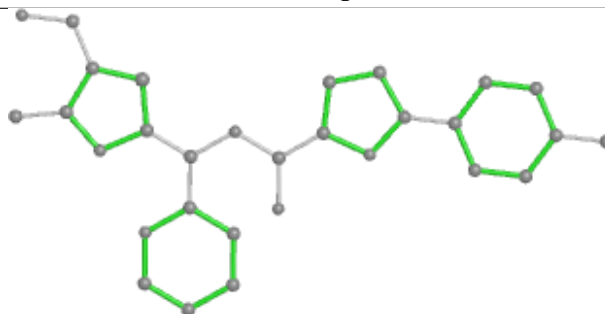
Bond lengths



Bond angles

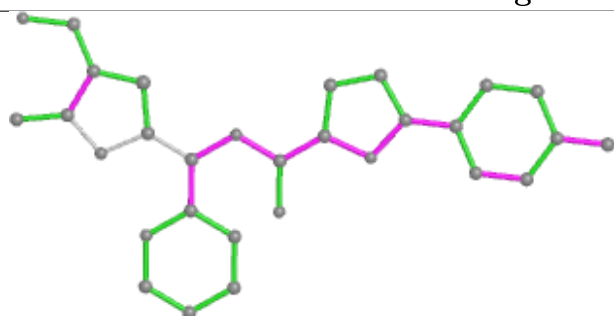


Torsions

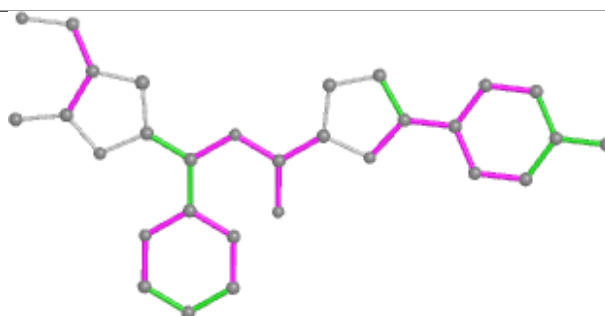


Rings

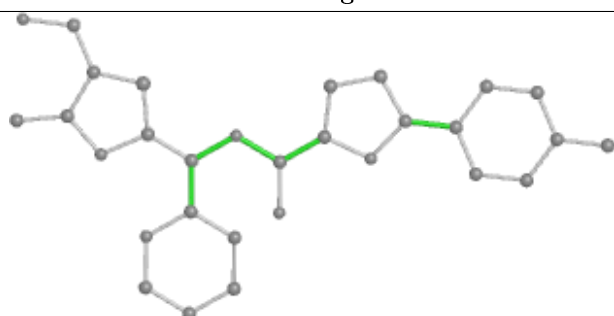
Ligand 3ZM A 510



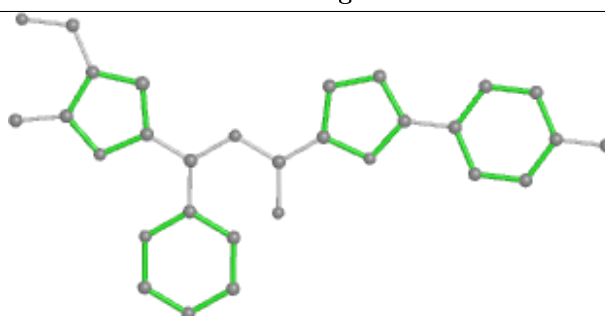
Bond lengths



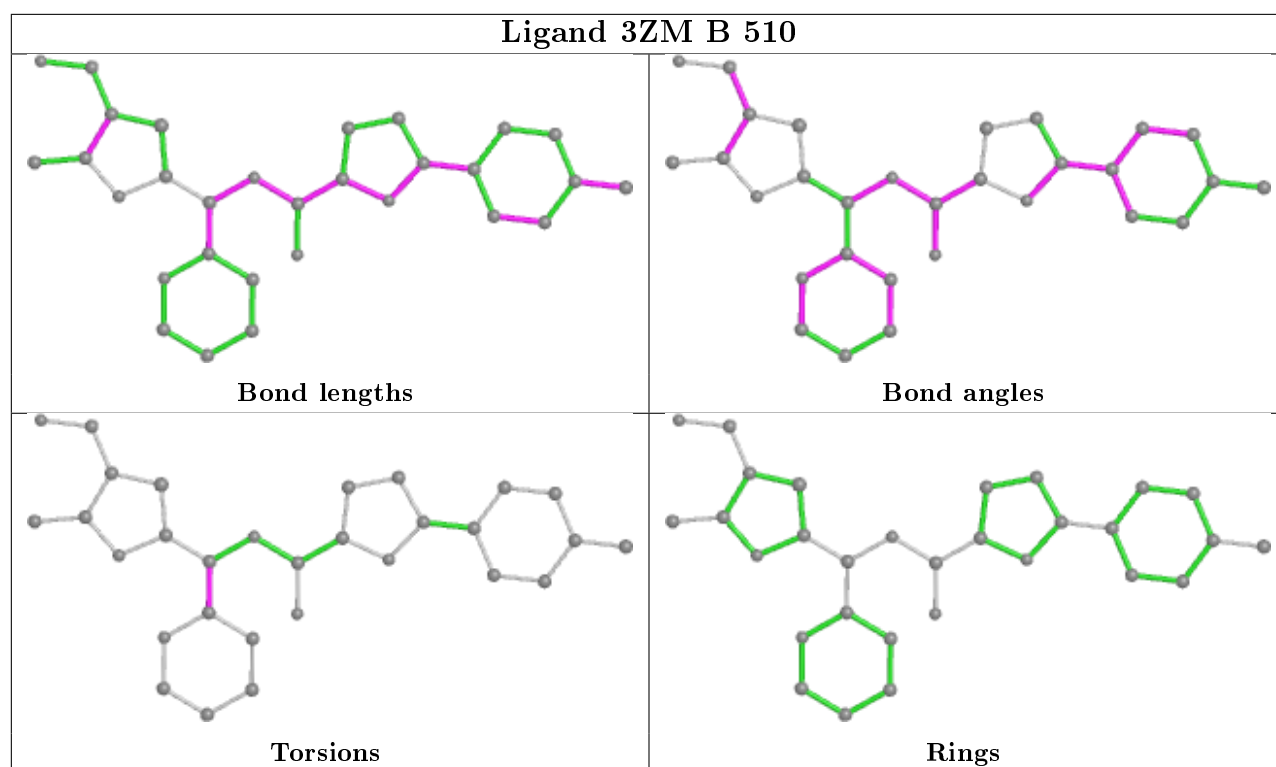
Bond angles



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 [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	339/353 (96%)	1.14	62 (18%) 1 1	36, 69, 117, 167	0
1	B	334/353 (94%)	0.98	49 (14%) 2 2	33, 63, 101, 134	0
1	C	339/353 (96%)	0.40	14 (4%) 37 40	27, 44, 78, 127	0
1	D	339/353 (96%)	0.40	14 (4%) 37 40	27, 43, 77, 112	0
All	All	1351/1412 (95%)	0.73	139 (10%) 6 7	27, 53, 101, 167	0

The worst 5 of 139 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	123	THR	13.6
1	D	324	GLY	11.2
1	D	123	THR	10.0
1	D	124	GLY	9.4
1	C	122	LEU	9.3

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(\AA^2)	Q<0.9
2	NAG	C	502	14/15	0.36	0.47	93,101,106,108	0
2	NAG	A	504	14/15	0.55	0.42	75,84,86,89	0
2	NAG	B	504	14/15	0.64	0.38	69,77,81,83	0
2	NAG	C	511	14/15	0.64	0.28	71,85,90,93	0
3	3ZM	A	510	30/30	0.68	0.35	61,119,148,152	0
2	NAG	D	511	14/15	0.69	0.29	71,83,87,90	0
2	NAG	B	508	14/15	0.71	0.28	70,80,83,85	0
2	NAG	A	505	14/15	0.72	0.24	71,80,87,87	0
2	NAG	D	510	14/15	0.73	0.32	92,96,100,101	0
3	3ZM	B	510	30/30	0.74	0.28	46,110,134,137	0
2	NAG	A	507	14/15	0.74	0.32	73,84,88,88	0
2	NAG	A	508	14/15	0.74	0.25	60,71,75,75	0
2	NAG	D	502	14/15	0.75	0.49	82,92,97,98	0
2	NAG	C	510	14/15	0.76	0.28	84,91,94,97	0
2	NAG	C	504	14/15	0.77	0.15	43,57,62,64	0
3	3ZM	D	512	30/30	0.77	0.24	48,87,111,111	0
2	NAG	B	507	14/15	0.79	0.36	71,83,91,95	0
2	NAG	A	506	14/15	0.80	0.22	49,62,74,78	0
2	NAG	A	509	14/15	0.80	0.16	53,61,64,66	0
2	NAG	C	506	14/15	0.81	0.25	54,67,73,74	0
2	NAG	B	505	14/15	0.82	0.20	56,66,70,71	0
2	NAG	B	506	14/15	0.82	0.14	49,62,71,73	0
2	NAG	C	507	14/15	0.84	0.18	44,52,61,67	0
3	3ZM	C	512	30/30	0.85	0.19	43,73,95,95	0
2	NAG	D	506	14/15	0.86	0.16	47,58,63,63	0
2	NAG	B	501	14/15	0.87	0.30	63,75,78,78	0
2	NAG	D	507	14/15	0.88	0.15	44,53,61,67	0
2	NAG	C	508	14/15	0.88	0.14	35,40,54,63	0
2	NAG	C	501	14/15	0.88	0.12	50,63,66,68	0
2	NAG	D	505	14/15	0.89	0.12	40,49,57,61	0
2	NAG	B	502	14/15	0.89	0.21	69,81,88,90	0
2	NAG	C	503	14/15	0.91	0.11	30,35,42,46	0
2	NAG	D	508	14/15	0.91	0.13	40,46,67,68	0
2	NAG	A	501	14/15	0.91	0.27	67,76,79,79	0
2	NAG	A	502	14/15	0.91	0.23	76,87,90,92	0
2	NAG	D	501	14/15	0.91	0.12	49,62,65,66	0
2	NAG	B	509	14/15	0.91	0.12	47,57,63,67	0
2	NAG	C	509	14/15	0.92	0.11	42,53,58,59	0
2	NAG	D	509	14/15	0.92	0.11	45,55,60,66	0
2	NAG	C	505	14/15	0.92	0.11	40,50,56,60	0
2	NAG	D	504	14/15	0.92	0.10	43,53,60,64	0
4	EPE	B	511	15/15	0.93	0.16	62,66,70,71	0
4	EPE	A	511	15/15	0.93	0.16	63,67,80,83	0

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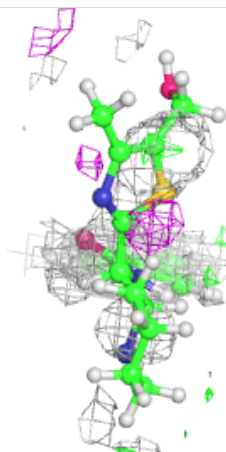
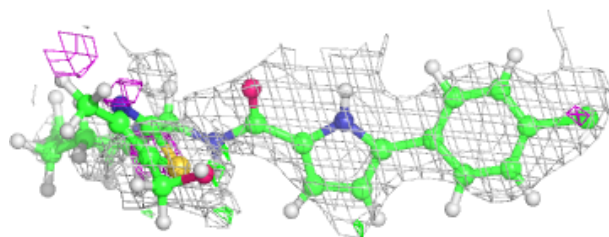
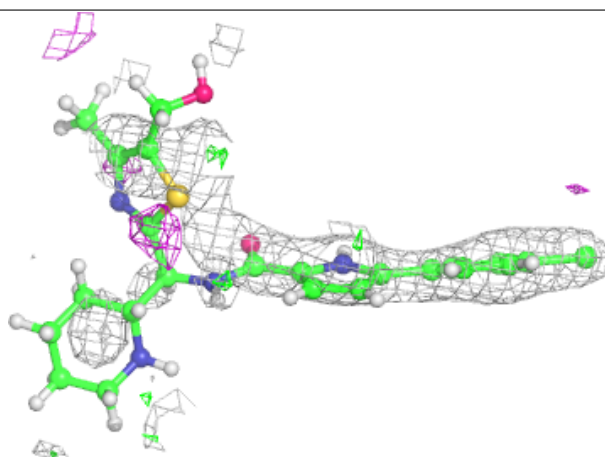
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	NAG	D	503	14/15	0.94	0.14	29,35,41,41	0
2	NAG	A	503	14/15	0.94	0.11	29,33,39,39	0
2	NAG	B	503	14/15	0.95	0.12	29,34,36,41	0
4	EPE	D	513	15/15	0.96	0.16	33,39,50,50	0
4	EPE	C	513	15/15	0.97	0.13	39,42,46,53	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.

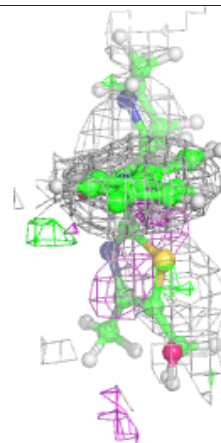
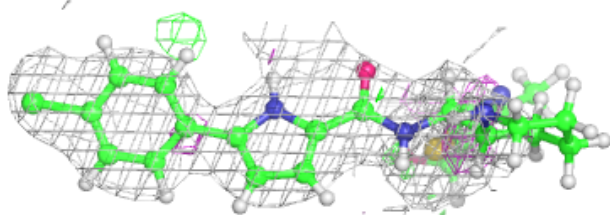
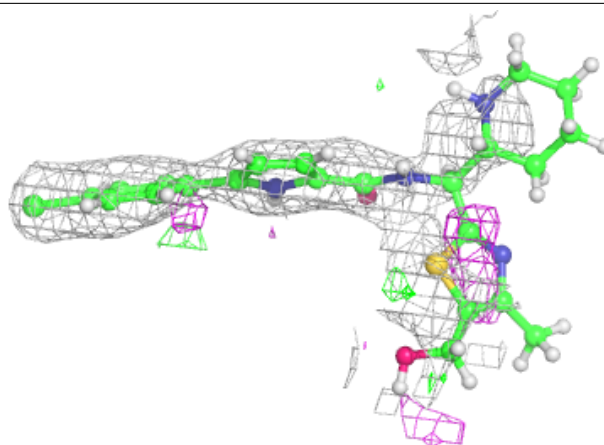
Electron density around 3ZM A 510:

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

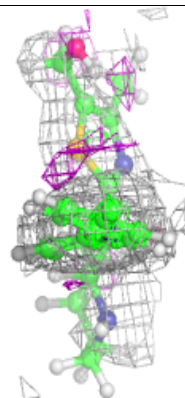
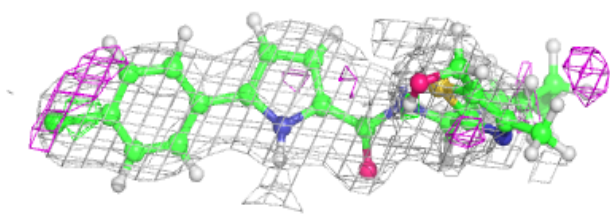
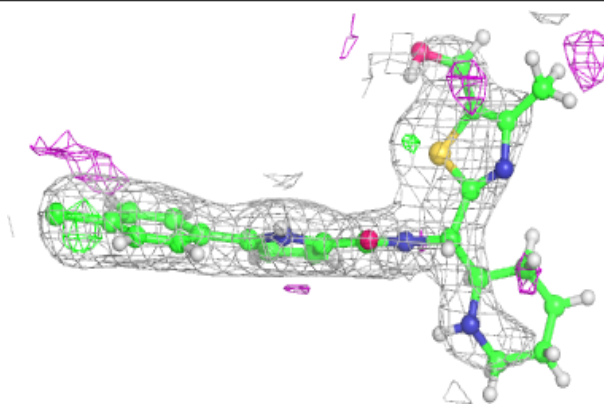


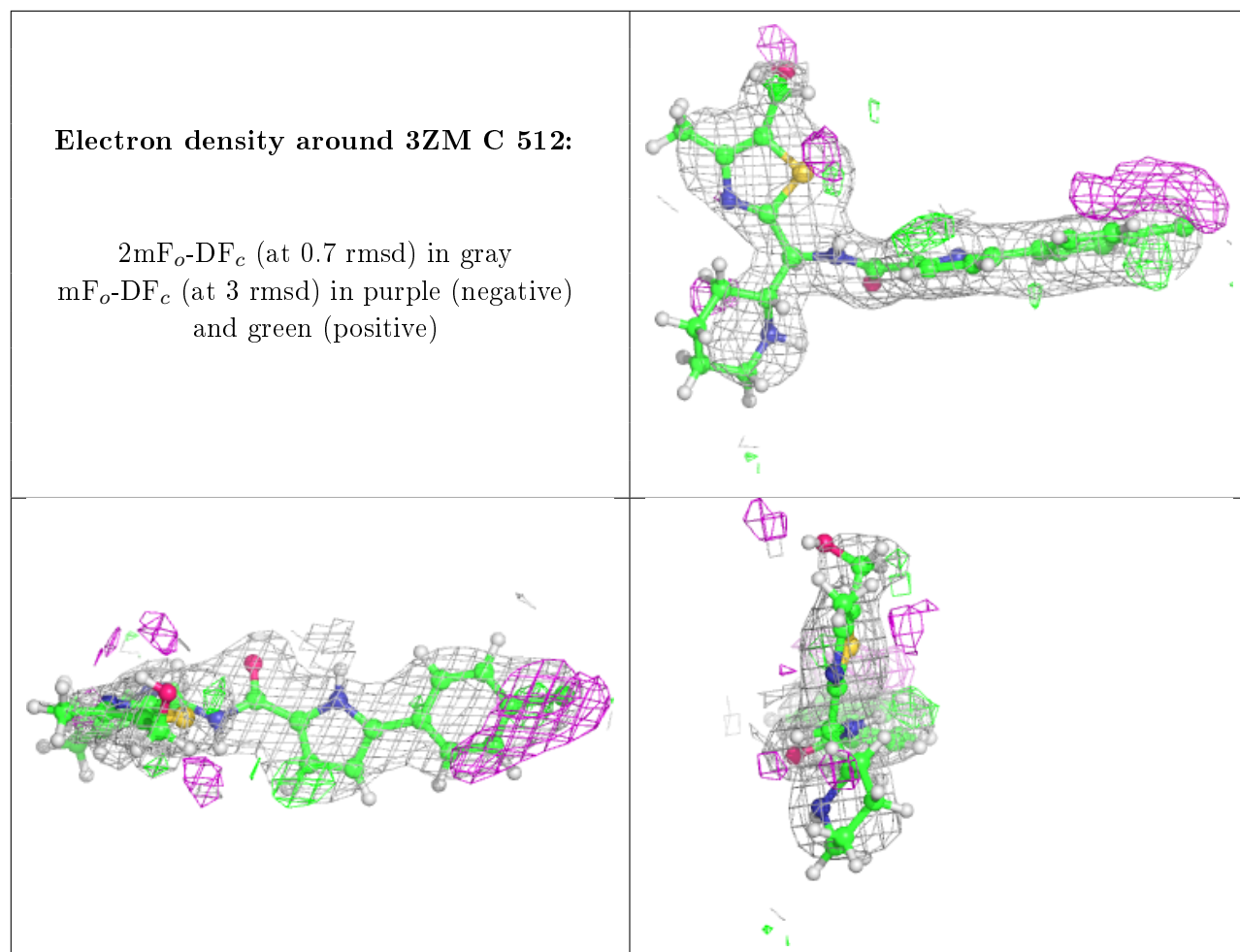
Electron density around 3ZM B 510:

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

**Electron density around 3ZM D 512:**

$2mF_o-DF_c$ (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.