



Full wwPDB X-ray Structure Validation Report ⓘ

Sep 28, 2020 – 04:26 PM EDT

PDB ID : 6USW
Title : CRYSTAL STRUCTURE OF HIV-1 LM/HS CLADE A/E CRF01 GP120
CORE IN COMPLEX WITH (S)-MCG-IV-210
Authors : Tolbert, W.D.; Sherburn, R.; Pazgier, M.
Deposited on : 2019-10-28
Resolution : 2.50 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ 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 : 2.14.6
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) : 2.14.6

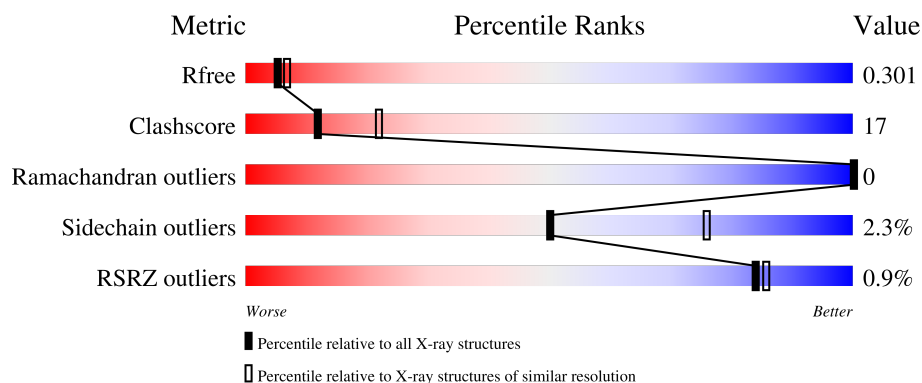
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	4661 (2.50-2.50)
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)
RSRZ outliers	127900	4559 (2.50-2.50)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments 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	355	<div> <div></div> <div>62%</div> <div>32%</div> <div>• •</div> </div>

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 2854 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 HIV-1 LM/HS clade A/E CRF01 gp120 core.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	340	Total	C	N	O	S	0	1	0
			2673	1679	461	510	23			

There are 9 discrepancies between the modelled and reference sequences:

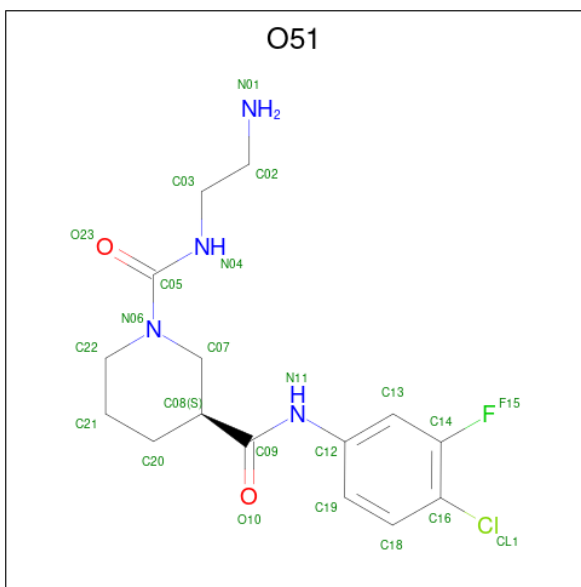
Chain	Residue	Modelled	Actual	Comment	Reference
A	42	VAL	-	expression tag	UNP A0A0M3KKW9
A	43	PRO	-	expression tag	UNP A0A0M3KKW9
A	61	TYR	HIS	engineered mutation	UNP A0A0M3KKW9
A	105	HIS	GLN	engineered mutation	UNP A0A0M3KKW9
A	108	ILE	VAL	engineered mutation	UNP A0A0M3KKW9
A	375	SER	HIS	engineered mutation	UNP A0A0M3KKW9
A	474	ASP	ASN	engineered mutation	UNP A0A0M3KKW9
A	475	MET	ILE	engineered mutation	UNP A0A0M3KKW9
A	476	ARG	LYS	engineered mutation	UNP A0A0M3KKW9

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



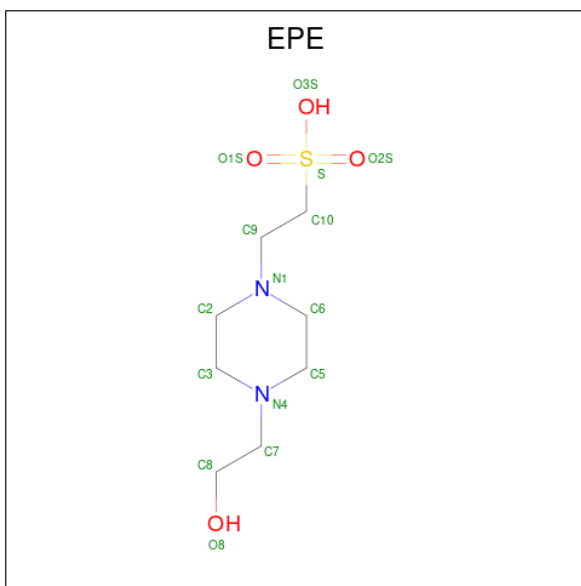
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	A	1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

- Molecule 3 is (3S)-N 1 -(2-aminoethyl)-N 3 -(4-chloro-3-fluorophenyl)piperidine-1,3-dicarboxamide (three-letter code: O51) (formula: C₁₅H₂₀ClFN₄O₂) (labeled as "Ligand of Interest" by author).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
3	A	1	Total	C	Cl	F	N	O	0	0
			23	15	1	1	4	2		

- Molecule 4 is 4-(2-HYDROXYETHYL)-1-PIPERAZINE ETHANESULFONIC ACID (three-letter code: EPE) (formula: $C_8H_{18}N_2O_4S$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	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	3	Total 3	O 3	0	0

- Molecule 1: HIV-1 LM/HS clade A/E CRF01 gp120 core



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	65.82Å 66.58Å 86.15Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	33.29 – 2.50 33.29 – 2.50	Depositor EDS
% Data completeness (in resolution range)	76.5 (33.29-2.50) 76.5 (33.29-2.50)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.19 (at 2.51Å)	Xtriage
Refinement program	PHENIX (1.15.2_3472: ???), REFMAC 5.8.0257	Depositor
R, R_{free}	0.246 , 0.301 0.246 , 0.301	Depositor DCC
R_{free} test set	506 reflections (4.85%)	wwPDB-VP
Wilson B-factor (Å ²)	63.4	Xtriage
Anisotropy	0.348	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 22.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.43$, $\langle L^2 \rangle = 0.26$	Xtriage
Estimated twinning fraction	0.054 for k,h,-l	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	2854	wwPDB-VP
Average B, all atoms (Å ²)	61.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.26% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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: O51, EPE, NAG

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	0.33	0/2730	0.55	1/3705 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	218	CYS	C-N-CA	5.12	134.49	121.70

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	2673	0	2602	96	3
2	A	140	0	130	2	2
3	A	23	0	0	0	0
4	A	15	0	17	3	0
5	A	3	0	0	2	0
All	All	2854	0	2749	97	3

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 17.

All (97) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:52:LEU:H	1:A:103:GLN:HE22	1.21	0.88
1:A:279:ASN:HB3	1:A:282:LYS:HG2	1.55	0.88
1:A:83:GLU:OE1	1:A:83:GLU:O	1.93	0.85
1:A:121:LYS:HD3	1:A:201:ILE:HD11	1.59	0.82
1:A:83:GLU:C	1:A:83:GLU:OE1	2.18	0.82
1:A:65:VAL:HB	1:A:115:SER:HB3	1.62	0.79
1:A:390:LEU:HD11	1:A:416:LEU:HD11	1.65	0.79
1:A:464:SER:OG	1:A:465:ASN:ND2	2.18	0.77
1:A:463:THR:HG22	1:A:465:ASN:H	1.54	0.73
1:A:112:TRP:CZ2	1:A:255[B]:VAL:HG21	2.27	0.70
1:A:103:GLN:NE2	4:A:512:EPE:O8	2.21	0.70
1:A:457:ASP:OD2	1:A:469:ARG:NH2	2.24	0.69
1:A:254:VAL:O	5:A:601:HOH:O	2.11	0.67
1:A:258:GLN:NE2	1:A:387:THR:HG21	2.11	0.66
1:A:118:PRO:HG2	1:A:121:LYS:HD2	1.77	0.65
1:A:112:TRP:CH2	1:A:255[B]:VAL:HG21	2.32	0.65
1:A:83:GLU:CD	1:A:83:GLU:O	2.35	0.65
1:A:231:LYS:HE2	1:A:267:GLU:HB2	1.80	0.63
1:A:370:GLU:OE1	1:A:384:TYR:OH	2.16	0.63
1:A:336:THR:OG1	1:A:411:ASN:O	2.16	0.62
1:A:232:ASN:HD21	1:A:268:GLU:HB3	1.66	0.61
1:A:258:GLN:HG2	1:A:470:PRO:HB2	1.83	0.60
1:A:327:ARG:NH2	1:A:422:GLN:OE1	2.33	0.60
1:A:256:SER:N	1:A:475:MET:HE1	2.18	0.58
1:A:44:VAL:HG13	1:A:492:GLU:HB2	1.86	0.57
1:A:93:PHE:HB2	1:A:233:PHE:CZ	2.39	0.57
1:A:86:LEU:HB2	1:A:89:VAL:HG11	1.85	0.57
1:A:286:VAL:HG22	1:A:452:ILE:HB	1.87	0.57
1:A:93:PHE:HB2	1:A:233:PHE:HZ	1.72	0.54
1:A:298:ARG:HD3	1:A:326:ILE:O	2.08	0.54
1:A:298:ARG:HG2	1:A:328:LYS:O	2.08	0.54
1:A:91:GLU:HG3	1:A:226:LEU:HD13	1.90	0.54
1:A:386:ASN:OD1	1:A:388:THR:OG1	2.21	0.53
1:A:101:VAL:HG11	1:A:480:ARG:NH2	2.23	0.53
1:A:343:LYS:O	1:A:347:GLU:HG2	2.09	0.52
1:A:390:LEU:HG	1:A:416:LEU:HD21	1.91	0.52
1:A:229:ASN:HD21	1:A:243:SER:HB3	1.74	0.52
1:A:258:GLN:HE22	1:A:387:THR:HG21	1.73	0.51
1:A:223:TYR:HA	1:A:490:GLN:HA	1.93	0.51
1:A:358:THR:HB	1:A:465:ASN:ND2	2.26	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:478:ASN:HB3	5:A:601:HOH:O	2.10	0.51
1:A:272:ILE:HD12	1:A:286:VAL:HG12	1.94	0.50
1:A:327:ARG:HH11	1:A:327:ARG:HG3	1.77	0.50
1:A:112:TRP:CE3	1:A:116:LEU:HD13	2.47	0.50
1:A:294:ILE:HD12	1:A:333:ILE:HD11	1.94	0.49
1:A:360:ILE:HG23	1:A:393:ASN:ND2	2.28	0.49
1:A:87:GLU:OE1	1:A:88:ASN:N	2.46	0.49
1:A:337:LYS:HD3	2:A:507:NAG:H61	1.95	0.48
1:A:382:PHE:CE1	1:A:424:ILE:HD13	2.48	0.48
1:A:110:SER:O	1:A:114:GLN:HG3	2.14	0.48
2:A:509:NAG:O3	2:A:509:NAG:O7	2.27	0.48
1:A:232:ASN:HD21	1:A:269:GLU:H	1.62	0.47
1:A:91:GLU:HG3	1:A:226:LEU:CD1	2.44	0.47
1:A:230:ASP:OD2	1:A:239:CYS:HA	2.14	0.47
1:A:107:ASP:OD1	4:A:512:EPE:H52	2.15	0.47
1:A:62:GLU:HG3	1:A:64:GLU:H	1.79	0.47
1:A:121:LYS:HB2	1:A:201:ILE:HG13	1.96	0.47
1:A:328:LYS:HA	1:A:328:LYS:HD3	1.76	0.47
1:A:59:LYS:HD2	1:A:61:TYR:CE2	2.50	0.47
1:A:257:THR:O	1:A:259:LEU:N	2.47	0.47
1:A:59:LYS:HB3	1:A:61:TYR:CE2	2.49	0.47
1:A:66:HIS:HB3	1:A:213:ILE:HG12	1.98	0.45
1:A:452:ILE:HG22	1:A:454:LEU:HG	1.98	0.45
1:A:360:ILE:CD1	1:A:465:ASN:HB3	2.46	0.45
1:A:476:ARG:HB3	1:A:480:ARG:HH21	1.81	0.45
1:A:338:TRP:CZ2	1:A:342:LEU:HD13	2.52	0.45
1:A:59:LYS:HD2	1:A:61:TYR:HE2	1.82	0.45
1:A:65:VAL:CB	1:A:115:SER:HB3	2.42	0.45
1:A:94:ASN:ND2	1:A:97:LYS:HB2	2.32	0.44
1:A:55:ALA:HB3	1:A:216:HIS:HB2	1.99	0.44
1:A:107:ASP:OD2	4:A:512:EPE:H32	2.17	0.44
1:A:454:LEU:HD23	1:A:470:PRO:HA	2.00	0.43
1:A:286:VAL:CG2	1:A:452:ILE:HB	2.48	0.43
1:A:340:LYS:O	1:A:344:GLN:HG3	2.19	0.43
1:A:258:GLN:CG	1:A:470:PRO:HB2	2.48	0.43
1:A:298:ARG:NH2	1:A:441:GLY:O	2.44	0.43
1:A:349:LEU:O	1:A:353:PHE:HD2	2.02	0.42
1:A:101:VAL:HG11	1:A:480:ARG:HH21	1.84	0.42
1:A:423:ILE:HA	1:A:433:ALA:O	2.19	0.42
1:A:96:TRP:HA	1:A:480:ARG:HH11	1.84	0.42
1:A:121:LYS:CD	1:A:201:ILE:HD11	2.39	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:83:GLU:CD	1:A:83:GLU:C	2.77	0.42
1:A:392:ASN:OD1	1:A:394:THR:OG1	2.29	0.41
1:A:335:GLY:O	1:A:339:ASN:ND2	2.53	0.41
1:A:375:SER:HA	1:A:383:PHE:O	2.20	0.41
1:A:86:LEU:CB	1:A:89:VAL:HG11	2.48	0.41
1:A:104:MET:O	1:A:108:ILE:HG12	2.21	0.41
1:A:108:ILE:HG22	1:A:427:TRP:CH2	2.55	0.41
1:A:298:ARG:HG3	1:A:420:ILE:HD12	2.03	0.41
1:A:358:THR:HB	1:A:465:ASN:HD22	1.85	0.41
1:A:348:LYS:HB2	1:A:348:LYS:HE2	1.77	0.40
1:A:381:GLU:HG3	1:A:443:ILE:HD13	2.03	0.40
1:A:331:CYS:HB2	1:A:416:LEU:HB2	2.03	0.40
1:A:338:TRP:NE1	1:A:390:LEU:HB3	2.36	0.40
1:A:364:PRO:HD3	1:A:470:PRO:HG2	2.02	0.40

All (3) 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:83:GLU:OE1	2:A:507:NAG:O4[3_444]	2.10	0.10
1:A:83:GLU:OE2	2:A:507:NAG:C6[3_444]	2.12	0.08
1:A:62:GLU:OE2	1:A:92:ASN:ND2[2_454]	2.16	0.04

5.3 Torsion angles

5.3.1 Protein backbone

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	335/355 (94%)	318 (95%)	17 (5%)	0	100 100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	305/313 (97%)	298 (98%)	7 (2%)	50 76

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	83	GLU
1	A	116	LEU
1	A	207	LYS
1	A	340	LYS
1	A	411	ASN
1	A	464	SER
1	A	469	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	103	GLN
1	A	114	GLN
1	A	203	GLN
1	A	229	ASN
1	A	232	ASN
1	A	258	GLN
1	A	465	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

12 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	510	1	14,14,15	0.24	0	17,19,21	0.70	1 (5%)
2	NAG	A	508	1	14,14,15	0.45	0	17,19,21	0.56	0
2	NAG	A	503	1	14,14,15	0.26	0	17,19,21	0.53	0
4	EPE	A	512	-	15,15,15	0.82	1 (6%)	18,20,20	1.91	6 (33%)
2	NAG	A	504	1	14,14,15	0.38	0	17,19,21	0.54	0
2	NAG	A	509	1	14,14,15	0.44	0	17,19,21	1.13	1 (5%)
2	NAG	A	501	1	14,14,15	0.26	0	17,19,21	0.42	0
2	NAG	A	507	1	14,14,15	2.45	2 (14%)	17,19,21	1.40	2 (11%)
2	NAG	A	506	1	14,14,15	0.26	0	17,19,21	0.42	0
2	NAG	A	502	1	14,14,15	0.72	0	17,19,21	0.71	1 (5%)
2	NAG	A	505	1	14,14,15	0.33	0	17,19,21	0.54	0
3	O51	A	511	-	24,24,24	2.82	9 (37%)	31,32,32	3.00	8 (25%)

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	510	1	-	2/6/23/26	0/1/1/1
2	NAG	A	508	1	-	0/6/23/26	0/1/1/1
2	NAG	A	503	1	-	0/6/23/26	0/1/1/1
4	EPE	A	512	-	-	5/9/19/19	0/1/1/1
2	NAG	A	504	1	-	3/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	A	509	1	-	2/6/23/26	0/1/1/1
2	NAG	A	501	1	-	0/6/23/26	0/1/1/1
2	NAG	A	507	1	-	2/6/23/26	0/1/1/1
2	NAG	A	506	1	-	2/6/23/26	0/1/1/1
2	NAG	A	502	1	-	0/6/23/26	0/1/1/1
2	NAG	A	505	1	-	0/6/23/26	0/1/1/1
3	O51	A	511	-	-	1/16/26/26	0/2/2/2

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	507	NAG	O5-C1	-8.61	1.30	1.43
3	A	511	O51	C05-N06	6.35	1.48	1.36
3	A	511	O51	C16-C14	5.87	1.47	1.38
3	A	511	O51	C09-N11	5.22	1.47	1.35
3	A	511	O51	C08-C09	4.88	1.60	1.51
3	A	511	O51	C13-C14	3.82	1.44	1.37
3	A	511	O51	C07-C08	3.56	1.58	1.53
3	A	511	O51	C05-N04	2.97	1.47	1.34
2	A	507	NAG	C1-C2	-2.71	1.48	1.52
3	A	511	O51	C12-N11	2.69	1.47	1.41
4	A	512	EPE	C10-S	2.68	1.81	1.77
3	A	511	O51	C21-C22	2.00	1.58	1.51

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	511	O51	N04-C05-N06	12.08	123.48	117.67
3	A	511	O51	C13-C14-C16	-5.68	116.23	121.72
3	A	511	O51	C12-C13-C14	5.39	123.17	118.76
3	A	511	O51	C08-C09-N11	4.17	121.14	115.02
2	A	509	NAG	C2-N2-C7	3.77	128.28	122.90
4	A	512	EPE	C5-N4-C3	3.73	117.23	108.83
2	A	507	NAG	C4-C3-C2	3.66	116.39	111.02
3	A	511	O51	O10-C09-C08	-3.53	117.53	122.12
4	A	512	EPE	C7-N4-C5	3.51	120.22	111.23
3	A	511	O51	F15-C14-C13	3.06	124.70	118.61
2	A	507	NAG	C3-C4-C5	2.71	115.08	110.24
4	A	512	EPE	O1S-S-C10	2.64	110.09	106.92
2	A	510	NAG	C1-O5-C5	2.47	115.53	112.19
4	A	512	EPE	C9-N1-C6	-2.22	105.56	111.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	511	O51	O23-C05-N04	-2.21	117.62	123.53
4	A	512	EPE	C7-N4-C3	2.20	116.87	111.23
4	A	512	EPE	C5-C6-N1	2.16	115.08	110.64
2	A	502	NAG	C4-C3-C2	2.06	114.04	111.02
3	A	511	O51	O23-C05-N06	-2.05	118.90	121.78

There are no chirality outliers.

All (17) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	509	NAG	C3-C2-N2-C7
4	A	512	EPE	C8-C7-N4-C5
4	A	512	EPE	C9-C10-S-O2S
4	A	512	EPE	C9-C10-S-O3S
3	A	511	O51	N01-C02-C03-N04
2	A	506	NAG	O5-C5-C6-O6
2	A	506	NAG	C4-C5-C6-O6
2	A	507	NAG	C4-C5-C6-O6
2	A	510	NAG	O5-C5-C6-O6
2	A	509	NAG	O5-C5-C6-O6
2	A	504	NAG	C3-C2-N2-C7
2	A	507	NAG	O5-C5-C6-O6
2	A	504	NAG	C4-C5-C6-O6
4	A	512	EPE	C9-C10-S-O1S
2	A	504	NAG	O5-C5-C6-O6
4	A	512	EPE	C8-C7-N4-C3
2	A	510	NAG	C4-C5-C6-O6

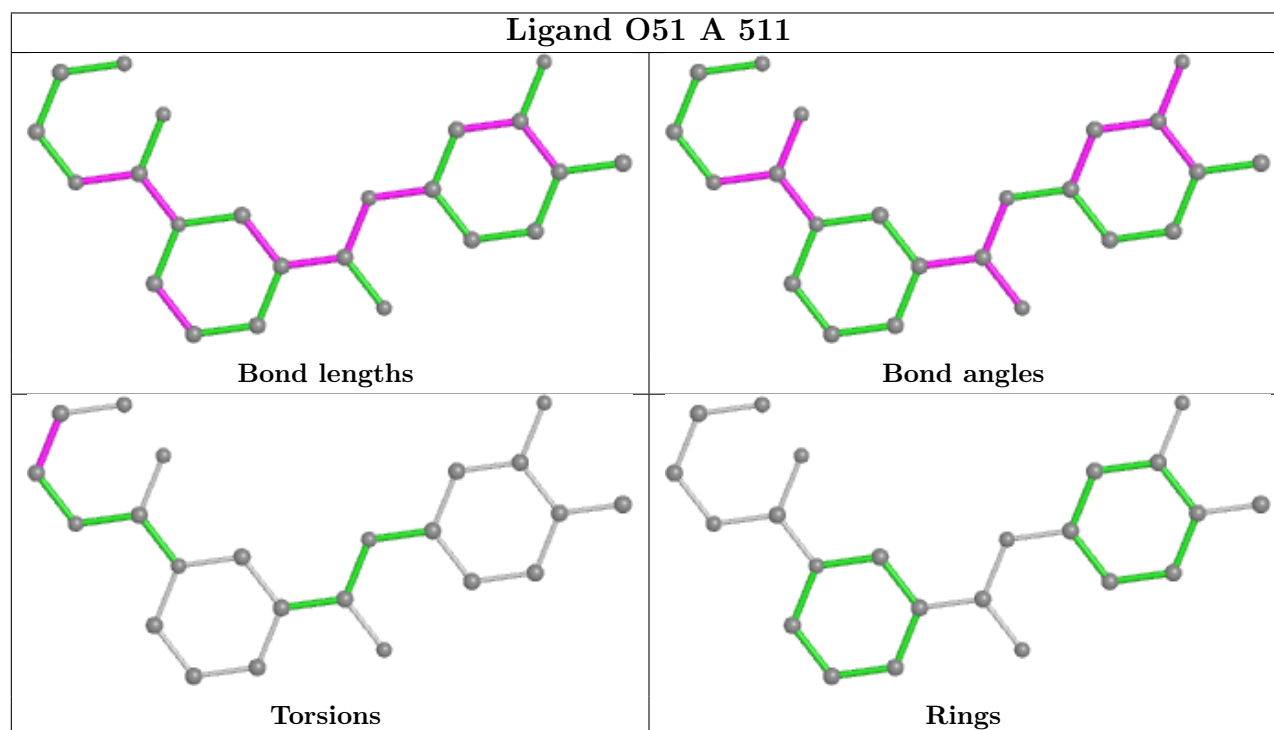
There are no ring outliers.

3 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	512	EPE	3	0
2	A	509	NAG	1	0
2	A	507	NAG	1	2

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.



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	340/355 (95%)	-0.25	3 (0%) 84 86	49, 60, 76, 91	0

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	396	ILE	3.4
1	A	462	ASN	3.3
1	A	43	PRO	2.3

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(Å ²)	Q<0.9
2	NAG	A	504	14/15	0.84	0.22	69,72,76,78	0
2	NAG	A	509	14/15	0.86	0.17	77,82,89,91	0
2	NAG	A	510	14/15	0.87	0.16	61,71,74,82	0
2	NAG	A	507	14/15	0.89	0.18	72,76,83,87	0

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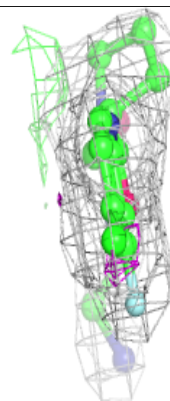
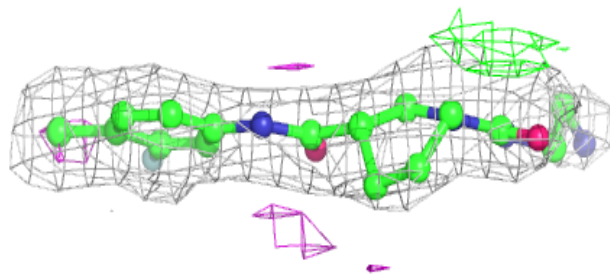
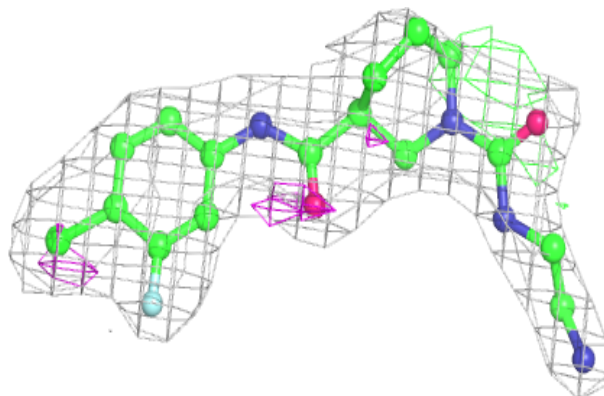
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	NAG	A	502	14/15	0.90	0.18	77,80,87,89	0
3	O51	A	511	23/23	0.91	0.16	53,55,58,61	0
2	NAG	A	508	14/15	0.92	0.18	61,65,67,70	0
2	NAG	A	505	14/15	0.94	0.10	57,61,61,61	0
2	NAG	A	501	14/15	0.94	0.12	53,55,56,58	0
2	NAG	A	506	14/15	0.95	0.13	65,68,72,74	0
4	EPE	A	512	15/15	0.96	0.15	53,54,57,57	0
2	NAG	A	503	14/15	0.96	0.12	54,58,59,60	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 O51 A 511:

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 ⓘ

There are no such residues in this entry.