Full wwPDB X-ray Structure Validation Report ⓘ

Nov 5, 2023 – 02:01 AM EST

PDB ID	:	6WV5
Title	:	Human VKOR C43S mutant with vitamin K1 epoxide
Authors	:	Liu, S.; Sukumar, N.; Li, W.
Deposited on	:	2020-05-05
Resolution	:	2.80 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 types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references ⓘ) were used in the production of this report:

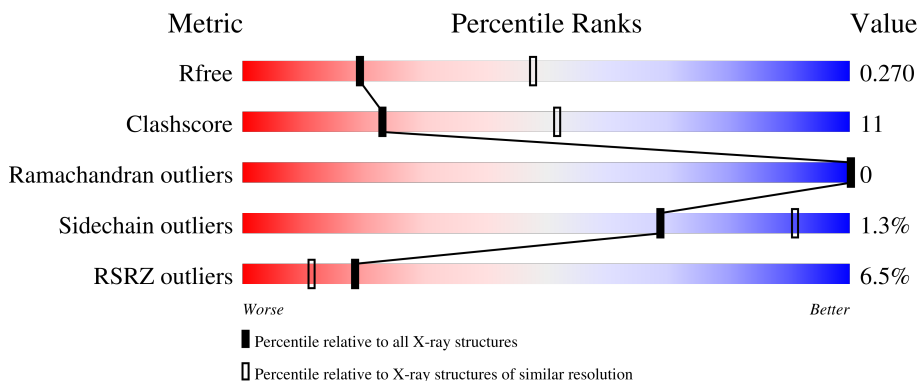|		
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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 2.80 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	Percentile Ranks	Value
Rfree		0.270
Clashscore		11
Ramachandran outliers		0
Sidechain outliers		1.3%
RSRZ outliers		6.5%

Worse   *Better*

▮ Percentile relative to all X-ray structures

▯ Percentile relative to X-ray structures of similar resolution

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	3140 (2.80-2.80)
Clashscore	141614	3569 (2.80-2.80)
Ramachandran outliers	138981	3498 (2.80-2.80)
Sidechain outliers	138945	3500 (2.80-2.80)
RSRZ outliers	127900	3078 (2.80-2.80)

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	390	6% 71% 24% • 5%

2 Entry composition ⓘ

There are 2 unique types of molecules in this entry. The entry contains 2992 atoms, of which 31 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 Vitamin K epoxide reductase Cys43Ser mutant, termini restrained by green fluorescent protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	371	2935	1880	504	538	13	22	0	0

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	2	SER	ARG	conflict	UNP A0A059PIQ0
A	30	ARG	SER	conflict	UNP A0A059PIQ0
A	66	CRO	THR	chromophore	UNP A0A059PIQ0
A	66	CRO	TYR	chromophore	UNP A0A059PIQ0
A	66	CRO	GLY	chromophore	UNP A0A059PIQ0
A	72	SER	ALA	conflict	UNP A0A059PIQ0
A	80	ARG	GLN	conflict	UNP A0A059PIQ0
A	185	SER	CYS	engineered mutation	UNP Q9BQB6
A	358	VAL	ALA	conflict	UNP A0A059PIQ0
A	384	HIS	-	expression tag	UNP A0A059PIQ0
A	385	HIS	-	expression tag	UNP A0A059PIQ0
A	386	HIS	-	expression tag	UNP A0A059PIQ0
A	387	HIS	-	expression tag	UNP A0A059PIQ0
A	388	HIS	-	expression tag	UNP A0A059PIQ0
A	389	HIS	-	expression tag	UNP A0A059PIQ0
A	390	HIS	-	expression tag	UNP A0A059PIQ0
A	391	HIS	-	expression tag	UNP A0A059PIQ0
A	392	HIS	-	expression tag	UNP A0A059PIQ0

- Molecule 2 is (2R,3R)-2-hydroxy-3-methyl-2-[(2E,7S)-3,7,11,15-tetramethylhexadec-2-en-1-yl]-2,3-dihydronaphthalene-1,4-dione (three-letter code: UAV) (formula: $C_{31}H_{48}O_3$) (labeled as "Ligand of Interest" by depositor).
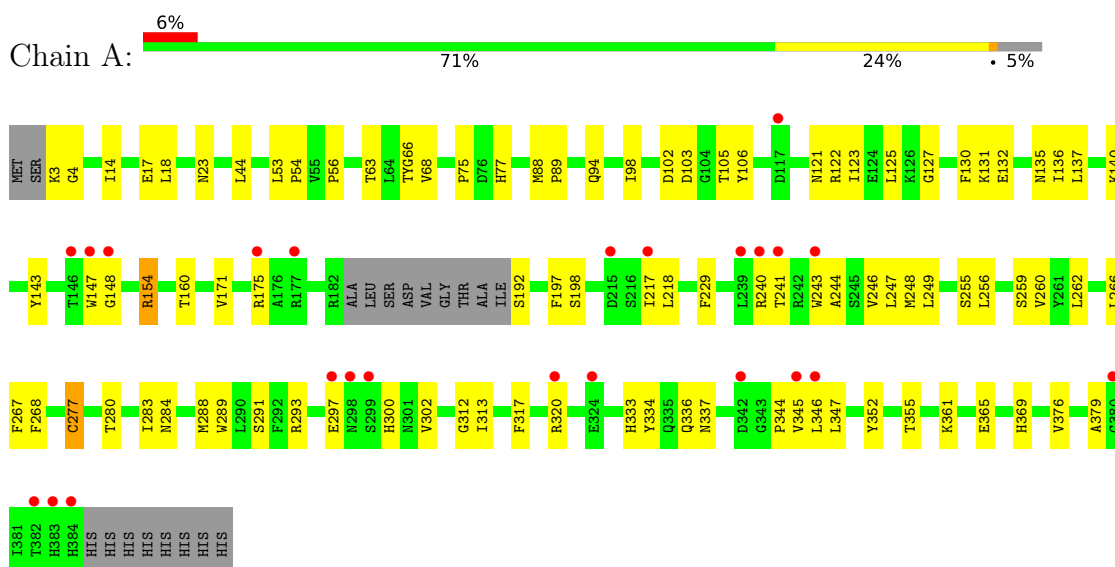
UAV
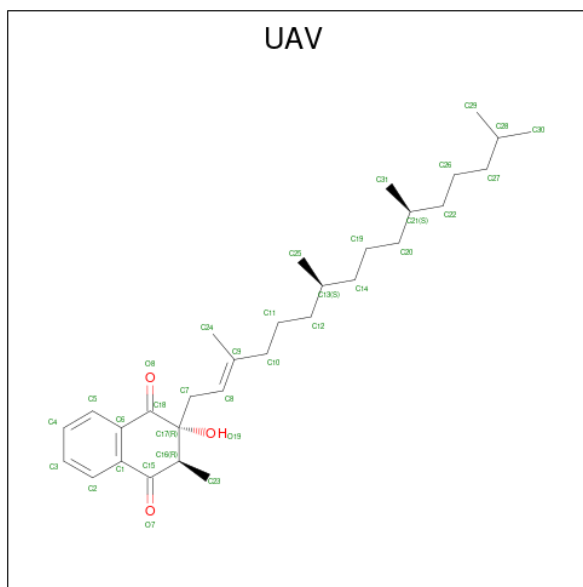
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	H	O		
2	A	1	57	23	31	3	0	0

3 Residue-property plots ⓘ

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: Vitamin K epoxide reductase Cys43Ser mutant, termini restrained by green fluorescent protein

4 Data and refinement statistics ⓘ

Property	Value	Source
Space group	H 3	Depositor
Cell constants a, b, c, α, β, γ	88.93Å 88.93Å 229.89Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	39.48 – 2.80 39.48 – 2.80	Depositor EDS
% Data completeness (in resolution range)	94.2 (39.48-2.80) 94.2 (39.48-2.80)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.26 (at 2.81Å)	Xtriage
Refinement program	PHENIX 1.11.1_2575	Depositor
R, R_{free}	0.231 , 0.270 0.231 , 0.270	Depositor DCC
R_{free} test set	793 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å^2)	58.1	Xtriage
Anisotropy	0.608	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.30 , 32.2	EDS
L-test for twinning[2]	$< |L| > = 0.49, < L^2 > = 0.32$	Xtriage
Estimated twinning fraction	0.018 for -1/3*h+1/3*k+1/3*l,-k,8/3*h+4/3*k+1/3*l 0.024 for -2/3*h-1/3*k-1/3*l,-1/3*h-2/3*k+1/3*l,-4/3*h+4/3*k+1/3*l 0.017 for -h,1/3*h-1/3*k-1/3*l,-4/3*h-8/3*k+1/3*l 0.020 for -h,2/3*h+1/3*k+1/3*l,4/3*h+8/3*k-1/3*l 0.010 for 1/3*h+2/3*k-1/3*l,-k,-8/3*h-4/3*k-1/3*l 0.020 for -1/3*h-2/3*k+1/3*l,-2/3*h-1/3*k-1/3*l,4/3*h-4/3*k-1/3*l 0.046 for -h-k,k,-l	Xtriage
F_o,F_c correlation	0.88	EDS
Total number of atoms	2992	wwPDB-VP
Average B, all atoms (Å^2)	62.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.21% of the height of the origin peak. No significant pseudotranslation is detected.*

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[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: UAV, CRO

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	0.26	0/2979	0.43	0/4039

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	2935	0	2881	65	0
2	A	26	31	0	2	0
All	All	2961	31	2881	66	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.

All (66) 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:355:THR:HG22	1:A:376:VAL:HG22	1.54	0.90
1:A:53:LEU:HD12	1:A:54:PRO:HD2	1.60	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:154:ARG:NH2	1:A:248:MET:SD	2.57	0.78
1:A:171:VAL:HG11	1:A:197:PHE:CD2	2.28	0.68
1:A:241:THR:HG23	1:A:244:ALA:H	1.57	0.68
1:A:105:THR:O	1:A:127:GLY:HA2	1.93	0.68
1:A:267:PHE:O	1:A:268:PHE:HB2	1.96	0.66
1:A:243:TRP:HA	1:A:246:VAL:HG22	1.78	0.65
1:A:249:LEU:HA	1:A:291:SER:OG	1.97	0.64
1:A:14:ILE:CG2	1:A:44:LEU:HD21	2.27	0.64
1:A:175:ARG:HD2	1:A:198:SER:HB3	1.80	0.63
1:A:344:PRO:HG2	1:A:347:LEU:HD23	1.80	0.63
1:A:302:VAL:HG13	1:A:317:PHE:CD1	2.34	0.62
1:A:217:ILE:HD12	1:A:218:LEU:N	2.15	0.61
1:A:241:THR:HG21	1:A:243:TRP:NE1	2.15	0.61
1:A:14:ILE:HG21	1:A:44:LEU:HD21	1.82	0.61
1:A:288:MET:HE3	1:A:288:MET:HA	1.86	0.57
1:A:63:THR:CG2	1:A:123:ILE:HG21	2.35	0.57
1:A:102:ASP:O	1:A:131:LYS:NZ	2.25	0.56
1:A:56:PRO:HD3	1:A:136:ILE:O	2.06	0.55
1:A:243:TRP:HA	1:A:246:VAL:CG2	2.36	0.55
1:A:143:TYR:CE2	1:A:361:LYS:HE2	2.44	0.53
1:A:345:VAL:C	1:A:346:LEU:HD12	2.31	0.52
1:A:88:MET:HB3	1:A:89:PRO:HA	1.92	0.51
1:A:256:LEU:HD22	1:A:288:MET:HG2	1.91	0.51
1:A:289:TRP:HE1	1:A:293:ARG:HE	1.58	0.51
1:A:277:CYS:O	1:A:280:THR:HB	2.11	0.51
1:A:297:GLU:C	1:A:320:ARG:HD2	2.31	0.51
1:A:94:GLN:HB2	1:A:337:ASN:ND2	2.26	0.51
1:A:365:GLU:HB3	1:A:369:HIS:CE1	2.46	0.50
1:A:259:SER:OG	1:A:284:ASN:ND2	2.45	0.50
1:A:68:VAL:O	1:A:68:VAL:HG23	2.11	0.49
1:A:98:ILE:HB	1:A:106:TYR:HB2	1.93	0.49
1:A:317:PHE:O	1:A:333:HIS:HB2	2.13	0.49
1:A:136:ILE:HD12	1:A:136:ILE:N	2.28	0.49
1:A:262:LEU:HB3	2:A:401:UAV:O7	2.12	0.49
1:A:352:TYR:CZ	1:A:379:ALA:HB3	2.48	0.49
1:A:160:THR:CG2	1:A:283:ILE:HD11	2.43	0.48
1:A:121:ASN:ND2	1:A:123:ILE:HD11	2.28	0.48
1:A:334:TYR:OH	1:A:336:GLN:NE2	2.23	0.48
1:A:312:GLY:HA3	1:A:337:ASN:O	2.13	0.48
1:A:135:ASN:HA	1:A:140:LYS:HB2	1.95	0.48
1:A:125:LEU:C	1:A:125:LEU:HD23	2.34	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:345:VAL:O	1:A:346:LEU:HD12	2.14	0.47
1:A:267:PHE:O	1:A:268:PHE:CB	2.62	0.47
1:A:313:ILE:HG12	1:A:337:ASN:HB2	1.97	0.46
1:A:18:LEU:C	1:A:18:LEU:HD23	2.36	0.46
1:A:148:GLY:HA3	1:A:240:ARG:NH2	2.31	0.46
1:A:345:VAL:HG12	1:A:346:LEU:HD12	1.97	0.45
1:A:355:THR:HG22	1:A:376:VAL:CG2	2.38	0.45
1:A:132:GLU:HA	1:A:137:LEU:HB2	1.98	0.44
1:A:23:ASN:ND2	1:A:130:PHE:O	2.50	0.44
2:A:401:UAV:C23	2:A:401:UAV:C8	2.95	0.44
1:A:334:TYR:CE2	1:A:336:GLN:HG3	2.53	0.43
1:A:243:TRP:O	1:A:247:LEU:HB2	2.19	0.43
1:A:300:HIS:CE1	1:A:320:ARG:HG2	2.53	0.43
1:A:103:ASP:OD2	1:A:136:ILE:HD13	2.18	0.43
1:A:3:LYS:HB2	1:A:4:GLY:H	1.51	0.43
1:A:241:THR:HG21	1:A:243:TRP:CE2	2.53	0.43
1:A:302:VAL:O	1:A:352:TYR:HB2	2.19	0.42
1:A:17:GLU:OE2	1:A:122:ARG:NH1	2.47	0.42
1:A:229:PHE:CE1	1:A:255:SER:HB3	2.56	0.41
1:A:256:LEU:O	1:A:260:VAL:HG23	2.21	0.41
1:A:217:ILE:H	1:A:217:ILE:HG13	1.72	0.41
1:A:266:LEU:HD21	1:A:277:CYS:HB3	2.03	0.40
1:A:75:PRO:HB2	1:A:77:HIS:CE1	2.57	0.40

There are no symmetry-related clashes.

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	364/390 (93%)	349 (96%)	15 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	317/339 (94%)	313 (99%)	4 (1%)	69 91

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	147	TRP
1	A	154	ARG
1	A	192	SER
1	A	277	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	336	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

1 non-standard protein/DNA/RNA residue is 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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	#|Z| > 2	Counts	RMSZ	#|Z| > 2
1	CRO	A	66	1	23,23,24	2.73	7 (30%)	30,32,34	2.77	8 (26%)

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
1	CRO	A	66	1	-	3/12/31/32	0/2/2/2

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	66	CRO	C1-N2	7.12	1.42	1.32
1	A	66	CRO	CA2-C2	6.15	1.54	1.48
1	A	66	CRO	C1-N3	5.22	1.46	1.37
1	A	66	CRO	C2-N3	3.89	1.49	1.39
1	A	66	CRO	CG2-CB2	3.50	1.53	1.46
1	A	66	CRO	CB2-CA2	-3.02	1.32	1.35
1	A	66	CRO	CA2-N2	2.29	1.43	1.38

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	66	CRO	O2-C2-CA2	-7.90	126.52	130.96
1	A	66	CRO	CA2-C2-N3	7.69	107.01	103.37
1	A	66	CRO	CG2-CB2-CA2	-5.17	123.61	129.94
1	A	66	CRO	CA2-N2-C1	4.89	109.38	105.77
1	A	66	CRO	C2-N3-C1	-4.81	105.53	107.97
1	A	66	CRO	C2-CA2-N2	-3.60	106.41	108.93
1	A	66	CRO	CB2-CA2-C2	2.78	125.59	122.28
1	A	66	CRO	O3-C3-CA3	-2.15	119.90	126.39

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	66	CRO	C3-CA3-N3-C2

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Mol	Chain	Res	Type	Atoms
1	A	66	CRO	N2-CA2-CB2-CG2
1	A	66	CRO	C2-CA2-CB2-CG2

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

5.6 Ligand geometry ⓘ

1 ligand is 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	UAV	A	401	-	26,27,35	0.59	0	31,38,48	1.42	6 (19%)

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	UAV	A	401	-	-	3/15/39/48	0/2/2/2

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	401	UAV	C1-C6-C18	-3.44	117.42	120.98
2	A	401	UAV	C7-C8-C9	-3.05	121.23	127.97

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	401	UAV	O7-C15-C1	-2.31	118.28	121.98
2	A	401	UAV	C5-C6-C18	2.21	122.23	119.39
2	A	401	UAV	C24-C9-C10	2.21	118.98	115.27
2	A	401	UAV	C1-C15-C16	2.05	121.84	117.95

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	401	UAV	C10-C11-C12-C13
2	A	401	UAV	C11-C10-C9-C24
2	A	401	UAV	C11-C10-C9-C8

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	401	UAV	2	0

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

Ligand UAV A 401

Bond lengths

Bond angles

Torsions

Rings
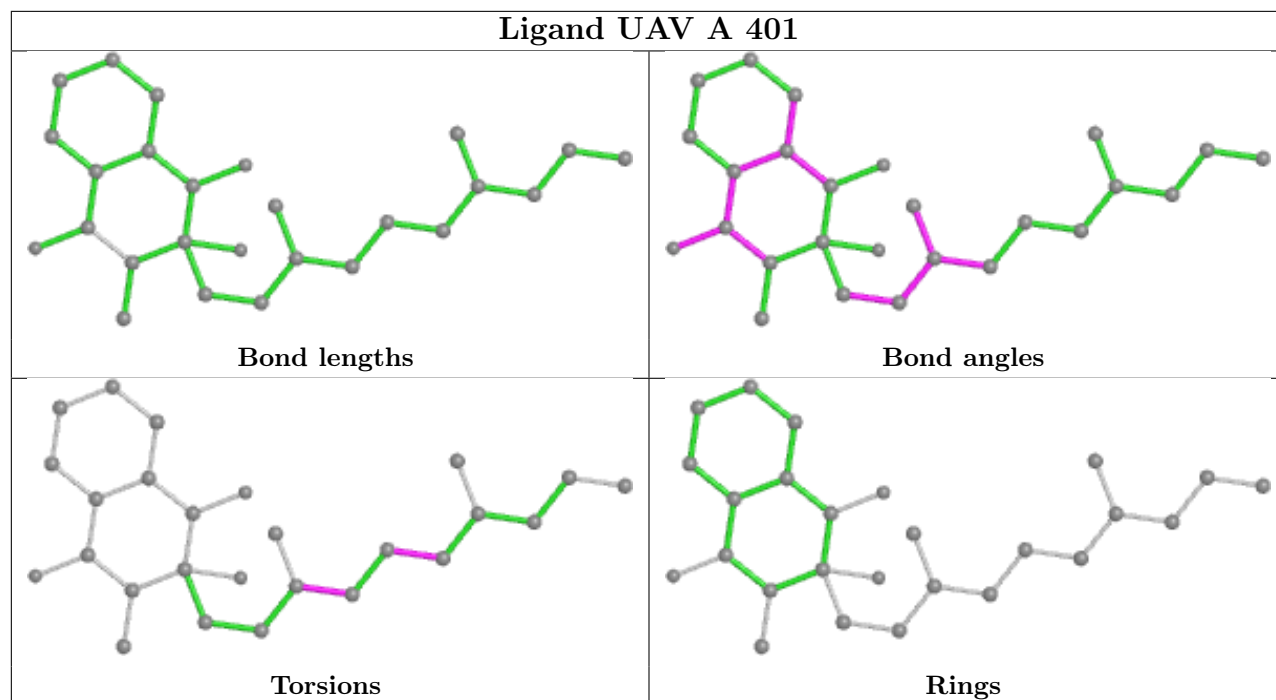
5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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	370/390 (94%)	0.05	24 (6%)	18	11	37, 57, 96, 139	0

All (24) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	384	HIS	7.2
1	A	383	HIS	6.9
1	A	345	VAL	6.4
1	A	382	THR	4.7
1	A	346	LEU	4.5
1	A	342	ASP	4.4
1	A	147	TRP	4.2
1	A	177	ARG	4.0
1	A	215	ASP	3.6
1	A	241	THR	3.1
1	A	380	GLY	2.9
1	A	299	SER	2.8
1	A	175	ARG	2.7
1	A	217	ILE	2.7
1	A	297	GLU	2.6
1	A	239	LEU	2.5
1	A	243	TRP	2.5
1	A	298	ASN	2.4
1	A	148	GLY	2.3
1	A	240	ARG	2.3
1	A	117	ASP	2.2
1	A	320	ARG	2.1
1	A	324	GLU	2.0
1	A	146	THR	2.0

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

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.

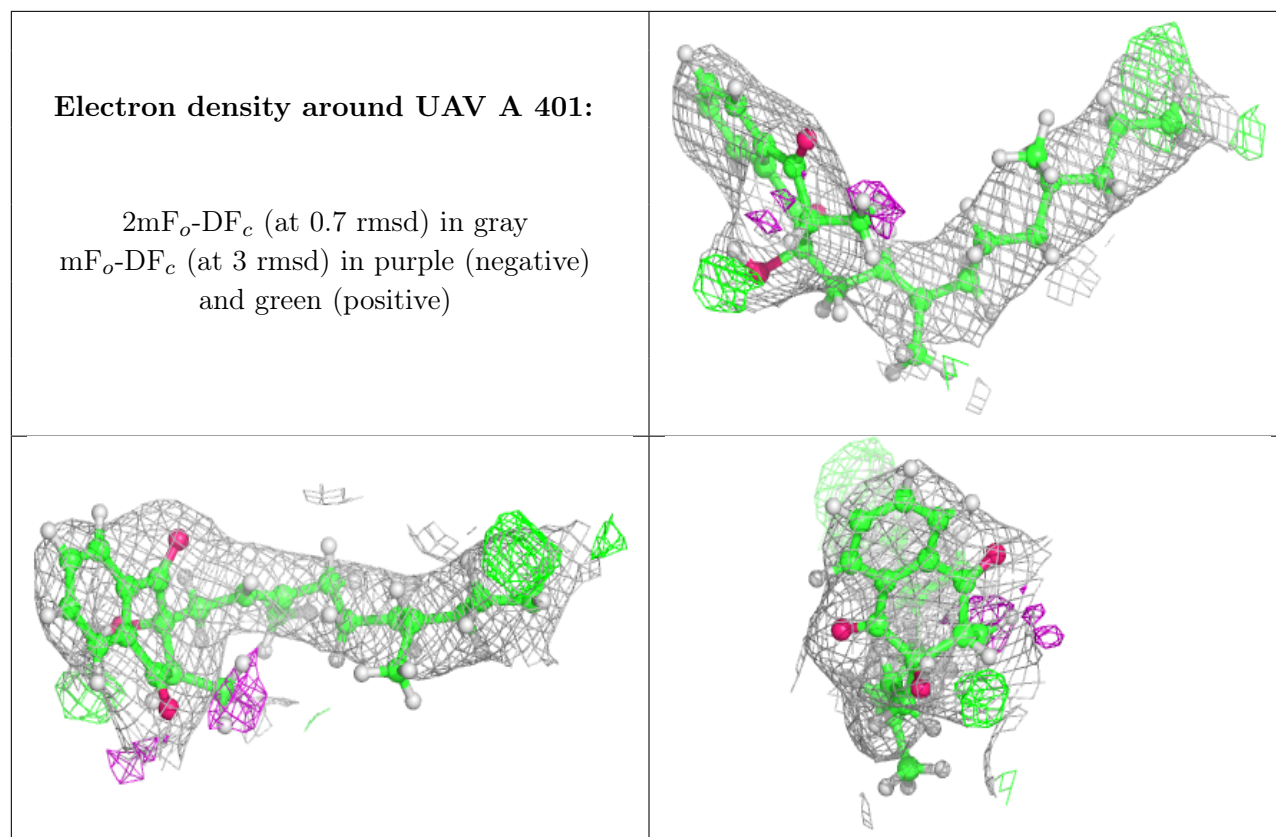| Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
1	CRO	A	66	22/23	-	-	40,52,55,56	22

6.3 Carbohydrates ⓘ

There are no monosaccharides in this entry.

6.4 Ligands ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 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	UAV	A	401	26/34	0.91	0.20	50,66,89,94	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 UAV A 401:

$2mF_o$-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.