Full wwPDB X-ray Structure Validation Report ⓘ

Nov 29, 2023 – 12:24 pm GMT

PDB ID	:	8Q77
Title	:	STRUCTURE OF PROTEIN KINASE CK2 CATALYTIC SUBUNIT (ISOFORM CK2ALPHA'; CSNK2A2 GENE PRODUCT) IN COMPLEX WITH THE BISUBSTRATE INHIBITOR ARC-780
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Deposited on	:	2023-08-15
Resolution	:	1.25 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:

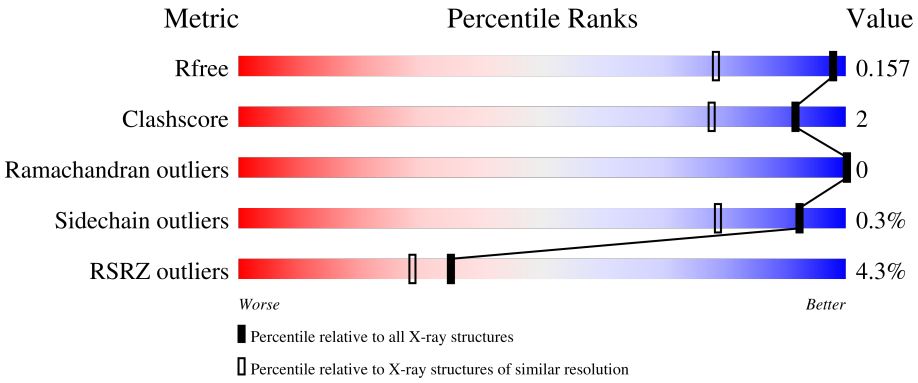
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 1.25 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	1023 (1.28-1.24)
Clashscore	141614	1060 (1.28-1.24)
Ramachandran outliers	138981	1029 (1.28-1.24)
Sidechain outliers	138945	1028 (1.28-1.24)
RSRZ outliers	127900	1004 (1.28-1.24)

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	364	4% 81% 8% · 10%

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 6158 atoms, of which 2898 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.

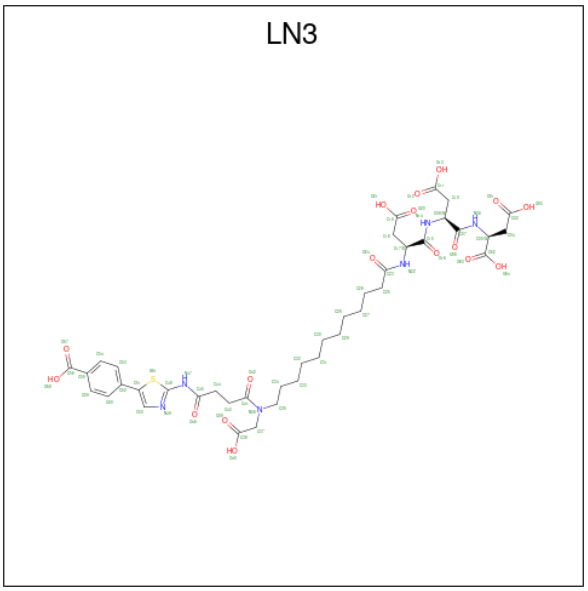
- Molecule 1 is a protein called Casein kinase II subunit alpha'.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	328	Total	C	H	N	O	S	0	6	0
			5563	1796	2770	489	497	11			

There are 15 discrepancies between the modelled and reference sequences:

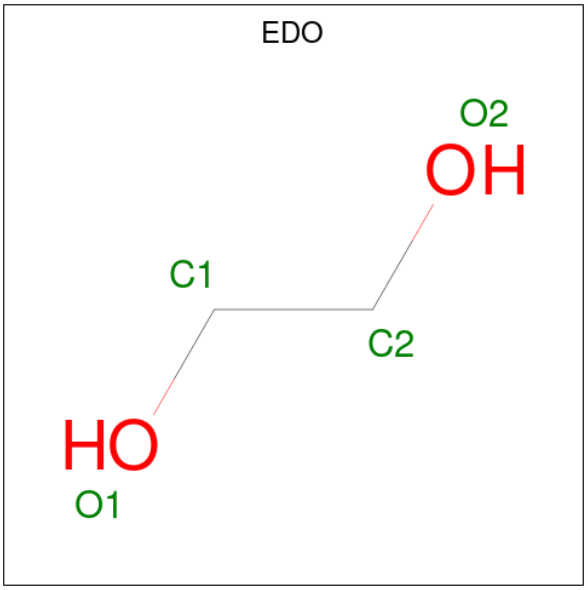
Chain	Residue	Modelled	Actual	Comment	Reference
A	-13	MET	-	initiating methionine	UNP P19784
A	-12	GLY	-	expression tag	UNP P19784
A	-11	SER	-	expression tag	UNP P19784
A	-10	SER	-	expression tag	UNP P19784
A	-9	HIS	-	expression tag	UNP P19784
A	-8	HIS	-	expression tag	UNP P19784
A	-7	HIS	-	expression tag	UNP P19784
A	-6	HIS	-	expression tag	UNP P19784
A	-5	HIS	-	expression tag	UNP P19784
A	-4	HIS	-	expression tag	UNP P19784
A	-3	SER	-	expression tag	UNP P19784
A	-2	GLN	-	expression tag	UNP P19784
A	-1	ASP	-	expression tag	UNP P19784
A	0	PRO	-	expression tag	UNP P19784
A	336	SER	CYS	engineered mutation	UNP P19784

- Molecule 2 is (2 {S})-2-[[(2 {S})-2-[[(2 {S})-2-[12-[[4-[[5-(4-carboxyphenyl)-1,3-thiazol-2-yl]amino]-4-oxidanylidene-butanoyl]-(2-hydroxy-2-oxoethyl)amino]dodecanoylamino]-4-oxidanyl-4-oxidanylidene-butanoyl]amino]-4-oxidanyl-4-oxidanylidene-butanoyl]amino]butanedioic acid (three-letter code: LN3) (formula: $C_{40}H_{52}N_6O_{17}S$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	A	1	Total	C	H	N	O	S	0	0
			110	40	46	6	17	1		
2	A	1	Total	C	H	N	O	S	0	0
			110	40	46	6	17	1		

- Molecule 3 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	H	O	0	0
			10	2	6	2		
3	A	1	Total	C	H	O	0	0
			10	2	6	2		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	H	O	0	0
			10	2	6	2		
3	A	1	Total	C	H	O	0	0
			10	2	6	2		
3	A	1	Total	C	H	O	0	0
			10	2	6	2		
3	A	1	Total	C	H	O	0	0
			10	2	6	2		

- Molecule 4 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Cl	0	0
			1	1		

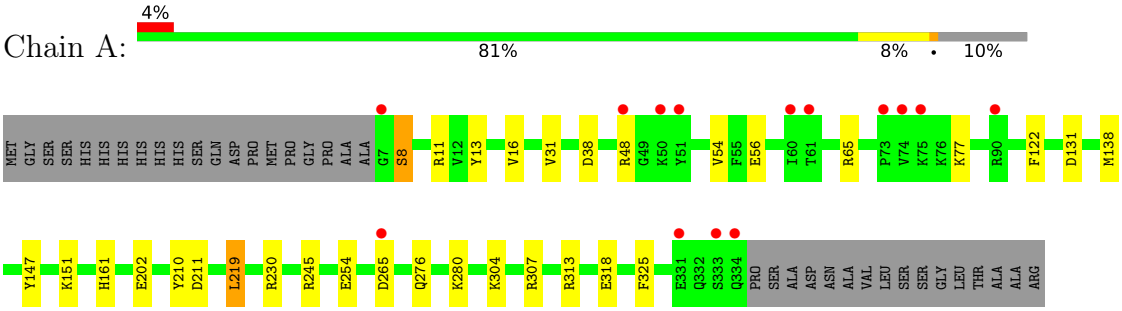
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	311	Total	O	0	3
			314	314		

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: Casein kinase II subunit alpha'



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α, β, γ	46.60Å 47.92Å 51.03Å 66.59° 89.67° 88.16°	Depositor
Resolution (Å)	41.25 – 1.25 46.58 – 1.25	Depositor EDS
% Data completeness (in resolution range)	72.5 (41.25-1.25) 70.4 (46.58-1.25)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	0.05	Depositor
$< I/\sigma(I) >$ [1]	1.62 (at 1.26Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, R_{free}	0.120 , 0.157 0.121 , 0.157	Depositor DCC
R_{free} test set	1216 reflections (1.51%)	wwPDB-VP
Wilson B-factor (Å^2)	9.4	Xtriage
Anisotropy	0.010	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.45 , 59.5	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	0.023 for h,-k,-l	Xtriage
F_o,F_c correlation	0.98	EDS
Total number of atoms	6158	wwPDB-VP
Average B, all atoms (Å^2)	17.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.50% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: EDO, LN3, CL

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	1.07	11/2894 (0.4%)	1.05	15/3907 (0.4%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	280	LYS	CE-NZ	7.24	1.67	1.49
1	A	276	GLN	CG-CD	6.90	1.67	1.51
1	A	318	GLU	CD-OE1	-6.72	1.18	1.25
1	A	54	VAL	CB-CG1	-6.67	1.38	1.52
1	A	147	TYR	CE1-CZ	-6.46	1.30	1.38
1	A	77	LYS	CB-CG	-6.37	1.35	1.52
1	A	280	LYS	CD-CE	5.97	1.66	1.51
1	A	8	SER	CB-OG	5.88	1.49	1.42
1	A	151	LYS	CD-CE	-5.46	1.37	1.51
1	A	254	GLU	CB-CG	5.44	1.62	1.52
1	A	276	GLN	CD-OE1	5.42	1.35	1.24

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	219	LEU	CB-CG-CD1	9.53	127.20	111.00
1	A	138	MET	CG-SD-CE	-7.64	87.98	100.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	38	ASP	CB-CG-OD1	7.39	124.96	118.30
1	A	325	PHE	CB-CG-CD2	6.95	125.66	120.80
1	A	211	ASP	CB-CG-OD2	6.88	124.49	118.30
1	A	265	ASP	CB-CG-OD2	-6.77	112.20	118.30
1	A	147	TYR	CB-CG-CD2	6.73	125.04	121.00
1	A	313	ARG	NE-CZ-NH1	5.92	123.26	120.30
1	A	265	ASP	CB-CG-OD1	5.75	123.47	118.30
1	A	230	ARG	NE-CZ-NH2	-5.34	117.63	120.30
1	A	131	ASP	CB-CG-OD2	-5.24	113.59	118.30
1	A	210[A]	TYR	CB-CG-CD1	-5.18	117.89	121.00
1	A	210[B]	TYR	CB-CG-CD1	-5.18	117.89	121.00
1	A	280	LYS	CD-CE-NZ	5.17	123.60	111.70
1	A	202	GLU	OE1-CD-OE2	-5.07	117.22	123.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	245	ARG	Sidechain

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	2793	2770	2745	8	0
2	A	128	92	0	2	0
3	A	24	36	36	0	0
4	A	1	0	0	0	0
5	A	314	0	0	1	0
All	All	3260	2898	2781	9	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 2.

All (9) 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:122:PHE:HE1	1:A:161[B]:HIS:CD2	2.13	0.66
1:A:304:LYS:HA	1:A:307:ARG:HE	1.78	0.48
2:A:402:LN3:S61	2:A:402:LN3:O46	2.72	0.47
1:A:13:TYR:O	1:A:16[B]:VAL:HG22	2.15	0.47
1:A:48:ARG:HD3	2:A:402:LN3:O21	2.17	0.46
1:A:31:VAL:HG12	5:A:744:HOH:O	2.16	0.45
1:A:122:PHE:HE1	1:A:161[B]:HIS:NE2	2.15	0.44
1:A:56:GLU:OE2	1:A:65:ARG:NH1	2.48	0.43
1:A:8:SER:O	1:A:11:ARG:HD2	2.21	0.41

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	332/364 (91%)	322 (97%)	10 (3%)	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	306/327 (94%)	305 (100%)	1 (0%)	92 79

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	219	LEU

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)

Of 9 ligands modelled in this entry, 1 is monoatomic - leaving 8 for Mogul analysis.

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	LN3	A	402	-	61,65,65	2.28	14 (22%)	77,85,85	1.76	19 (24%)
3	EDO	A	406	-	3,3,3	0.38	0	2,2,2	0.36	0
2	LN3	A	401	-	61,65,65	1.90	9 (14%)	77,85,85	1.58	15 (19%)
3	EDO	A	403	-	3,3,3	0.29	0	2,2,2	0.38	0
3	EDO	A	405	-	3,3,3	0.91	0	2,2,2	0.35	0
3	EDO	A	404	-	3,3,3	0.62	0	2,2,2	0.33	0
3	EDO	A	407	-	3,3,3	0.65	0	2,2,2	0.22	0
3	EDO	A	408	-	3,3,3	0.55	0	2,2,2	0.30	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	LN3	A	402	-	-	16/73/75/75	0/2/2/2
3	EDO	A	406	-	-	0/1/1/1	-
2	LN3	A	401	-	-	5/73/75/75	0/2/2/2
3	EDO	A	403	-	-	0/1/1/1	-
3	EDO	A	405	-	-	0/1/1/1	-
3	EDO	A	404	-	-	0/1/1/1	-
3	EDO	A	407	-	-	0/1/1/1	-
3	EDO	A	408	-	-	0/1/1/1	-

All (23) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	402	LN3	C07-N06	8.04	1.51	1.34
2	A	401	LN3	C48-N47	7.37	1.49	1.36
2	A	402	LN3	C23-N22	7.29	1.49	1.34
2	A	402	LN3	C15-N14	7.22	1.49	1.34
2	A	401	LN3	C45-N47	7.01	1.51	1.35
2	A	401	LN3	C41-N36	4.31	1.44	1.35
2	A	402	LN3	C41-N36	4.29	1.43	1.35
2	A	401	LN3	C23-N22	3.71	1.41	1.34
2	A	401	LN3	C15-N14	3.64	1.42	1.34
2	A	402	LN3	C10-C11	2.95	1.59	1.51
2	A	402	LN3	C37-N36	2.95	1.49	1.45
2	A	401	LN3	C07-N06	2.94	1.40	1.34
2	A	402	LN3	C48-N47	2.73	1.41	1.36
2	A	401	LN3	C05-N06	2.70	1.51	1.45
2	A	402	LN3	O39-C38	2.67	1.31	1.22
2	A	401	LN3	C50-N49	-2.56	1.32	1.36
2	A	401	LN3	O63-C62	2.52	1.29	1.22
2	A	402	LN3	O63-C62	2.49	1.29	1.22
2	A	402	LN3	O57-C56	2.46	1.30	1.22
2	A	402	LN3	C05-N06	2.43	1.51	1.45
2	A	402	LN3	C45-N47	2.23	1.40	1.35
2	A	402	LN3	C04-C02	2.10	1.56	1.51
2	A	402	LN3	O46-C45	-2.07	1.19	1.23

All (34) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	402	LN3	C25-C23-N22	4.90	124.32	115.83
2	A	402	LN3	C51-C50-N49	4.70	118.54	109.09
2	A	402	LN3	C60-C59-C55	-4.45	115.60	120.78
2	A	401	LN3	O24-C23-C25	3.83	129.02	122.02
2	A	401	LN3	C48-N47-C45	-3.53	120.02	129.54
2	A	401	LN3	O24-C23-N22	-3.42	117.18	122.95
2	A	402	LN3	C59-C60-C52	3.32	125.91	121.13
2	A	401	LN3	C38-C37-N36	3.25	116.55	113.05
2	A	401	LN3	C18-C17-N22	-3.12	104.48	110.60
2	A	401	LN3	C51-C50-N49	3.09	115.30	109.09
2	A	402	LN3	O46-C45-C44	3.02	127.54	122.02
2	A	402	LN3	C37-N36-C35	2.96	121.10	117.36
2	A	402	LN3	O24-C23-C25	-2.94	116.64	122.02
2	A	402	LN3	O58-C56-C55	2.91	122.41	114.85
2	A	402	LN3	O13-C11-C10	2.91	123.39	114.07
2	A	402	LN3	C48-N47-C45	-2.83	121.90	129.54
2	A	402	LN3	O13-C11-O12	-2.69	116.59	123.30
2	A	401	LN3	O03-C02-O01	-2.60	116.81	123.30
2	A	402	LN3	C53-C52-C51	2.60	124.48	120.21
2	A	402	LN3	C15-C17-N22	2.52	118.02	111.16
2	A	401	LN3	C60-C52-C51	-2.52	116.07	120.21
2	A	401	LN3	C04-C05-C62	2.50	115.67	110.83
2	A	401	LN3	C60-C52-C53	2.49	122.56	117.59
2	A	401	LN3	C15-C17-N22	-2.41	104.61	111.16
2	A	402	LN3	O57-C56-C55	-2.40	115.05	121.45
2	A	402	LN3	O03-C02-O01	-2.38	117.37	123.30
2	A	401	LN3	O46-C45-C44	-2.37	117.69	122.02
2	A	402	LN3	O24-C23-N22	-2.32	119.03	122.95
2	A	402	LN3	C07-C09-N14	-2.32	104.85	111.16
2	A	401	LN3	C26-C25-C23	-2.19	107.12	113.26
2	A	402	LN3	C17-N22-C23	-2.14	116.15	121.65
2	A	401	LN3	C59-C55-C54	2.13	121.62	118.59
2	A	402	LN3	C53-C54-C55	2.11	123.24	120.78
2	A	401	LN3	O21-C19-O20	-2.01	118.28	123.30

There are no chirality outliers.

All (21) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	402	LN3	C02-C04-C05-C62
2	A	402	LN3	C07-C09-C10-C11
2	A	402	LN3	C15-C17-C18-C19
2	A	402	LN3	C29-C30-C31-C32

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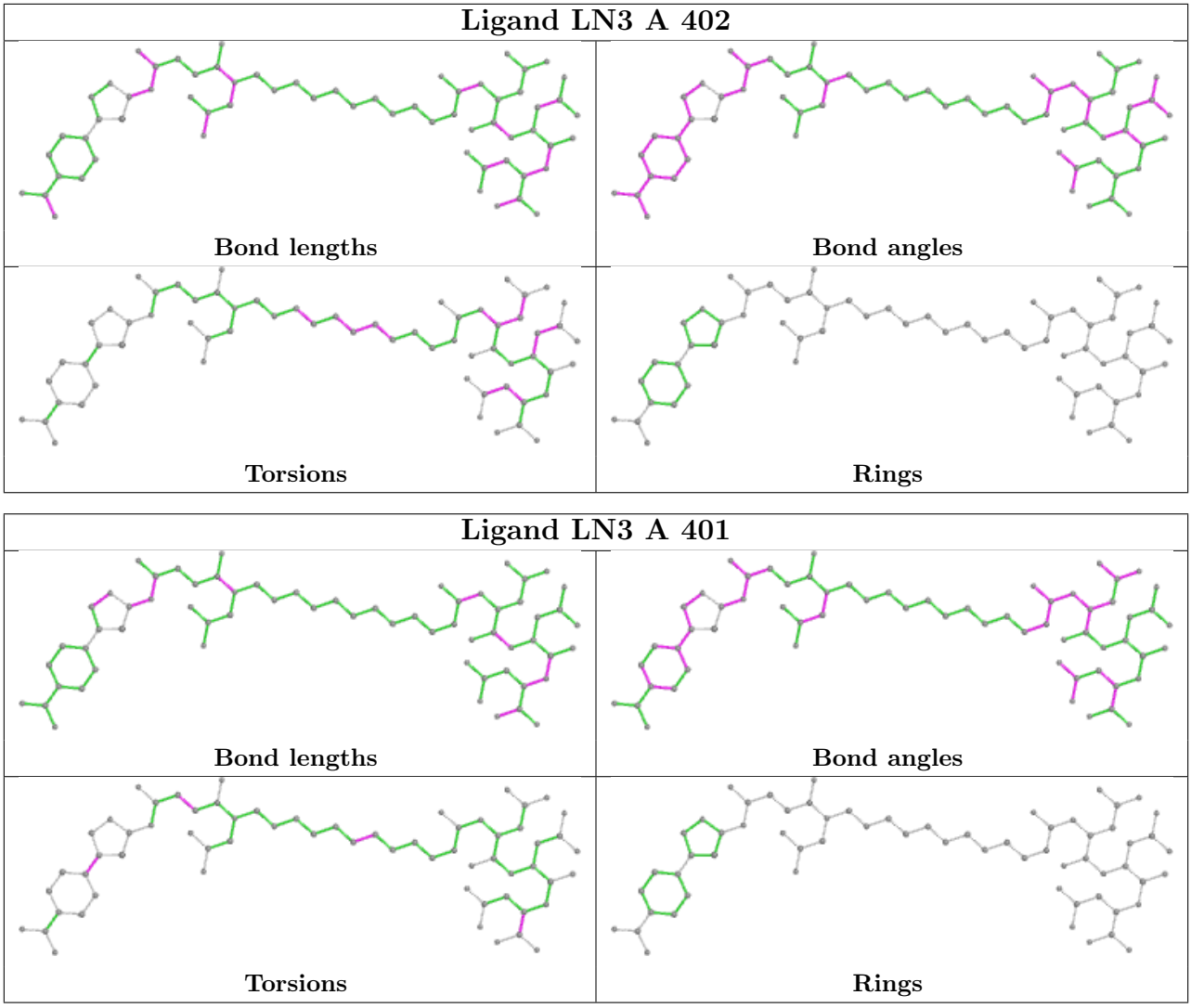
Mol	Chain	Res	Type	Atoms
2	A	402	LN3	C28-C29-C30-C31
2	A	402	LN3	C31-C32-C33-C34
2	A	402	LN3	C02-C04-C05-N06
2	A	402	LN3	N22-C17-C18-C19
2	A	401	LN3	C41-C43-C44-C45
2	A	402	LN3	O01-C02-C04-C05
2	A	402	LN3	O03-C02-C04-C05
2	A	402	LN3	C09-C10-C11-O13
2	A	402	LN3	C17-C18-C19-O20
2	A	402	LN3	C15-C17-N22-C23
2	A	402	LN3	C09-C10-C11-O12
2	A	402	LN3	C27-C28-C29-C30
2	A	402	LN3	C17-C18-C19-O21
2	A	401	LN3	C04-C05-C62-O63
2	A	401	LN3	C04-C05-C62-O64
2	A	401	LN3	C28-C29-C30-C31
2	A	401	LN3	C50-C51-C52-C60

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	402	LN3	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.



5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95^{th} percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å^2)	Q<0.9
1	A	328/364 (90%)	0.22	14 (4%)	35	28	6, 12, 27, 51	0

All (14) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	334	GLN	7.9
1	A	51	TYR	6.1
1	A	50	LYS	5.7
1	A	73	PRO	5.7
1	A	74	VAL	4.8
1	A	333	SER	4.7
1	A	7	GLY	4.1
1	A	75	LYS	3.5
1	A	60	ILE	3.3
1	A	48	ARG	2.8
1	A	61	THR	2.5
1	A	331	GLU	2.2
1	A	265	ASP	2.2
1	A	90	ARG	2.0

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

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

6.3 Carbohydrates

There are no monosaccharides in this entry.

6.4 Ligands (i)

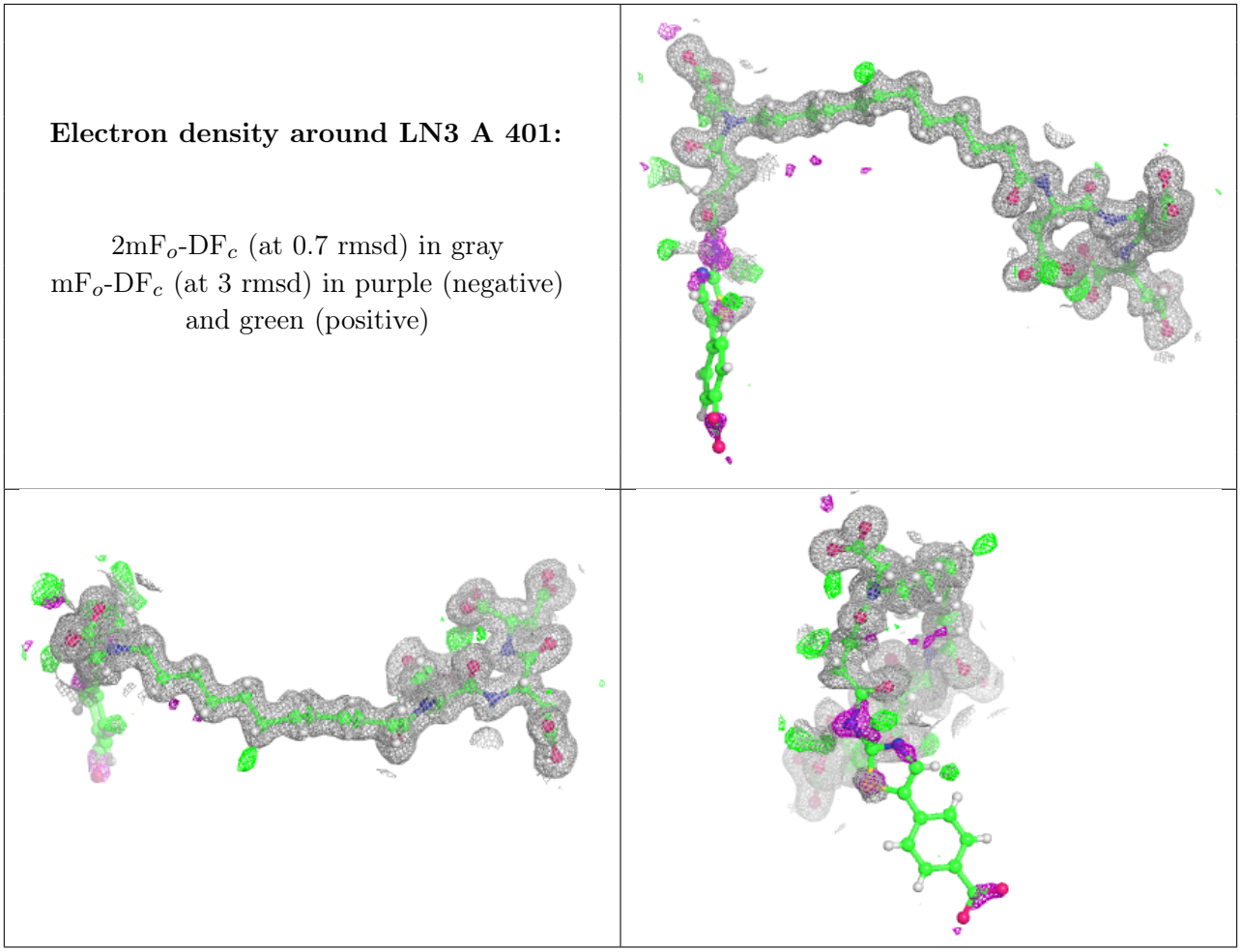
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9'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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	EDO	A	408	4/4	0.94	0.14	17,21,25,30	0
3	EDO	A	405	4/4	0.95	0.12	16,21,22,25	0
2	LN3	A	401	64/64	0.95	0.17	10,18,58,67	0
2	LN3	A	402	64/64	0.97	0.21	8,48,70,73	0
3	EDO	A	406	4/4	0.97	0.12	15,23,27,28	0
3	EDO	A	404	4/4	0.97	0.09	14,19,20,22	0
3	EDO	A	407	4/4	0.98	0.15	14,22,32,38	0
3	EDO	A	403	4/4	0.99	0.07	13,18,22,22	0
4	CL	A	409	1/1	1.00	0.09	12,12,12,12	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.

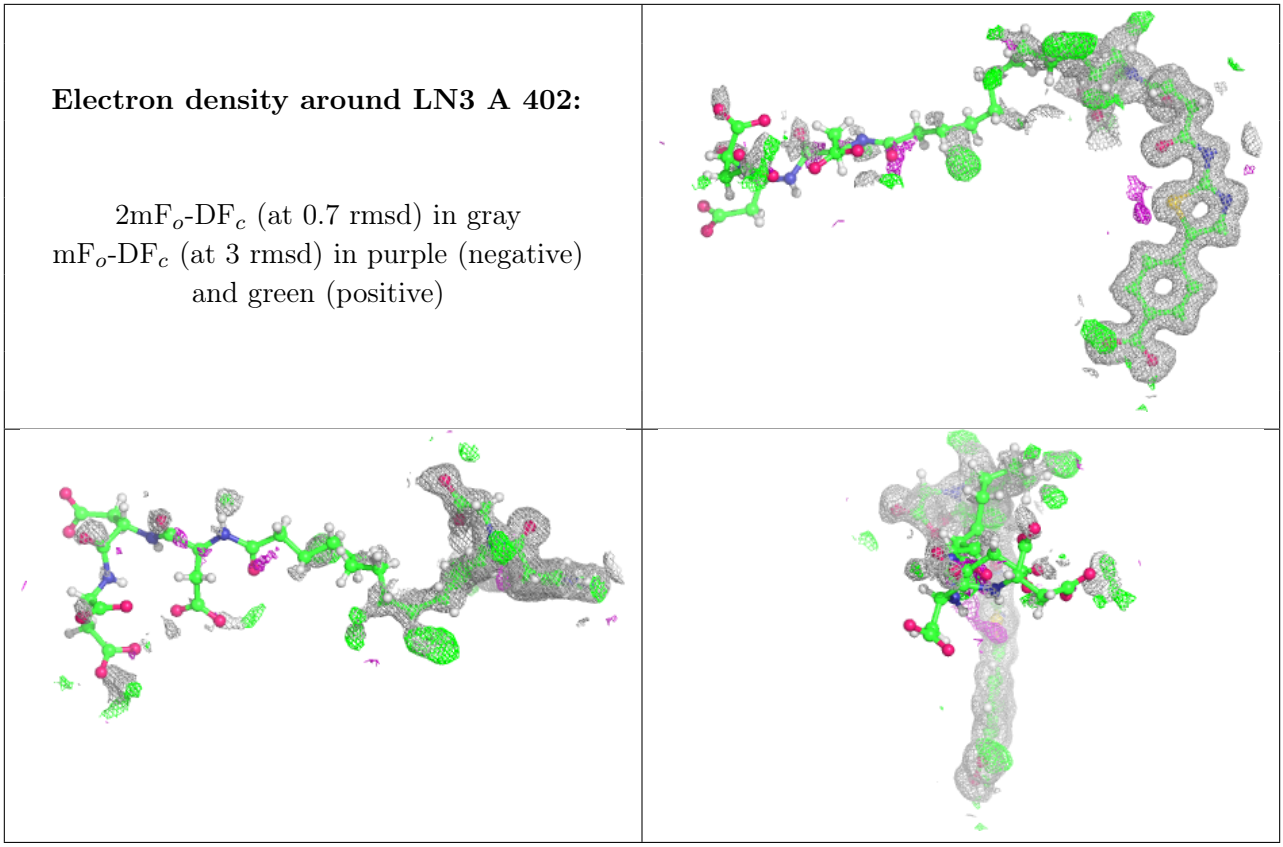
Electron density around LN3 A 401:

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



Electron density around LN3 A 402:

$2mF_o$-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.