



wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 30, 2022 – 06:16 pm BST

PDB ID : 7ZP2
Title : Crystal Structure of truncated aspartate transcarbamoylase from Plasmodium falciparum in complex with BDA-04
Authors : Wang, C.; Zhang, B.; Groves, M.R.
Deposited on : 2022-04-26
Resolution : 2.29 Å(reported)

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

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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 : 2.30
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0267
CCP4 : 7.1.010 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.30

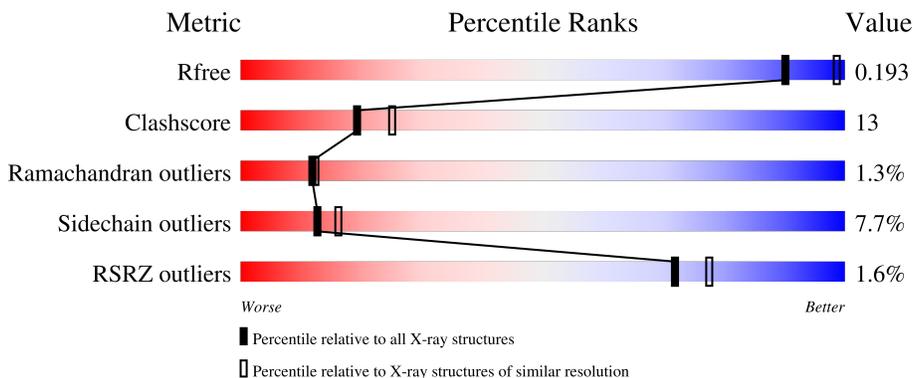
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.29 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	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

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 $\leq 5\%$. 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	349	 2% 67% 22% 6%
1	B	349	 % 72% 22% 5%
1	C	349	 2% 68% 24% 3%
1	D	349	 2% 67% 23% 6%
1	E	349	 % 70% 24% 5%

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Mol	Chain	Length	Quality of chain
1	F	349	 2% 70% 21%

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	EJG	A	401	-	-	X	-
3	SO4	D	401	-	-	X	-

2 Entry composition i

There are 5 unique types of molecules in this entry. The entry contains 33033 atoms, of which 16442 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 Aspartate carbamoyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
			Total	C	H	N	O				S
1	A	328	5330	1697	2677	437	511	8	83	0	0
1	B	346	5629	1801	2814	462	544	8	88	0	0
1	C	334	5421	1731	2717	444	521	8	85	0	0
1	D	328	5330	1697	2677	437	511	8	83	0	0
1	E	346	5629	1801	2814	462	544	8	88	0	0
1	F	334	5421	1731	2717	444	521	8	85	0	0

There are 60 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	376	SER	-	expression tag	UNP A0A5K1K910
A	377	ALA	-	expression tag	UNP A0A5K1K910
A	378	TRP	-	expression tag	UNP A0A5K1K910
A	379	SER	-	expression tag	UNP A0A5K1K910
A	380	HIS	-	expression tag	UNP A0A5K1K910
A	381	PRO	-	expression tag	UNP A0A5K1K910
A	382	GLN	-	expression tag	UNP A0A5K1K910
A	383	PHE	-	expression tag	UNP A0A5K1K910
A	384	GLU	-	expression tag	UNP A0A5K1K910
A	385	LYS	-	expression tag	UNP A0A5K1K910
B	376	SER	-	expression tag	UNP A0A5K1K910
B	377	ALA	-	expression tag	UNP A0A5K1K910
B	378	TRP	-	expression tag	UNP A0A5K1K910
B	379	SER	-	expression tag	UNP A0A5K1K910
B	380	HIS	-	expression tag	UNP A0A5K1K910
B	381	PRO	-	expression tag	UNP A0A5K1K910
B	382	GLN	-	expression tag	UNP A0A5K1K910

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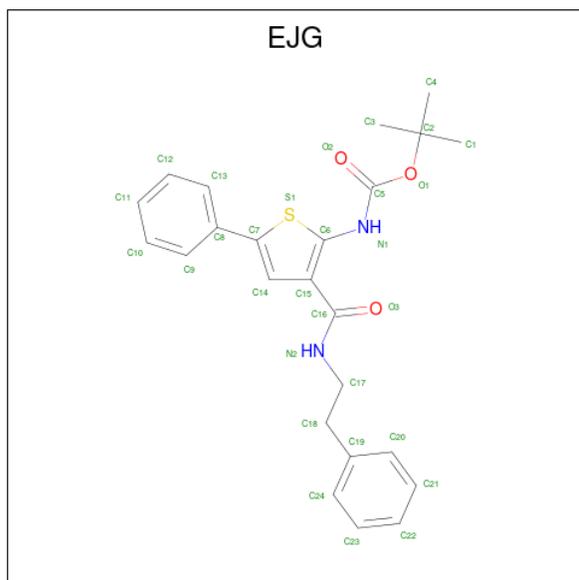
Chain	Residue	Modelled	Actual	Comment	Reference
B	383	PHE	-	expression tag	UNP A0A5K1K910
B	384	GLU	-	expression tag	UNP A0A5K1K910
B	385	LYS	-	expression tag	UNP A0A5K1K910
C	376	SER	-	expression tag	UNP A0A5K1K910
C	377	ALA	-	expression tag	UNP A0A5K1K910
C	378	TRP	-	expression tag	UNP A0A5K1K910
C	379	SER	-	expression tag	UNP A0A5K1K910
C	380	HIS	-	expression tag	UNP A0A5K1K910
C	381	PRO	-	expression tag	UNP A0A5K1K910
C	382	GLN	-	expression tag	UNP A0A5K1K910
C	383	PHE	-	expression tag	UNP A0A5K1K910
C	384	GLU	-	expression tag	UNP A0A5K1K910
C	385	LYS	-	expression tag	UNP A0A5K1K910
D	376	SER	-	expression tag	UNP A0A5K1K910
D	377	ALA	-	expression tag	UNP A0A5K1K910
D	378	TRP	-	expression tag	UNP A0A5K1K910
D	379	SER	-	expression tag	UNP A0A5K1K910
D	380	HIS	-	expression tag	UNP A0A5K1K910
D	381	PRO	-	expression tag	UNP A0A5K1K910
D	382	GLN	-	expression tag	UNP A0A5K1K910
D	383	PHE	-	expression tag	UNP A0A5K1K910
D	384	GLU	-	expression tag	UNP A0A5K1K910
D	385	LYS	-	expression tag	UNP A0A5K1K910
E	376	SER	-	expression tag	UNP A0A5K1K910
E	377	ALA	-	expression tag	UNP A0A5K1K910
E	378	TRP	-	expression tag	UNP A0A5K1K910
E	379	SER	-	expression tag	UNP A0A5K1K910
E	380	HIS	-	expression tag	UNP A0A5K1K910
E	381	PRO	-	expression tag	UNP A0A5K1K910
E	382	GLN	-	expression tag	UNP A0A5K1K910
E	383	PHE	-	expression tag	UNP A0A5K1K910
E	384	GLU	-	expression tag	UNP A0A5K1K910
E	385	LYS	-	expression tag	UNP A0A5K1K910
F	376	SER	-	expression tag	UNP A0A5K1K910
F	377	ALA	-	expression tag	UNP A0A5K1K910
F	378	TRP	-	expression tag	UNP A0A5K1K910
F	379	SER	-	expression tag	UNP A0A5K1K910
F	380	HIS	-	expression tag	UNP A0A5K1K910
F	381	PRO	-	expression tag	UNP A0A5K1K910
F	382	GLN	-	expression tag	UNP A0A5K1K910
F	383	PHE	-	expression tag	UNP A0A5K1K910
F	384	GLU	-	expression tag	UNP A0A5K1K910

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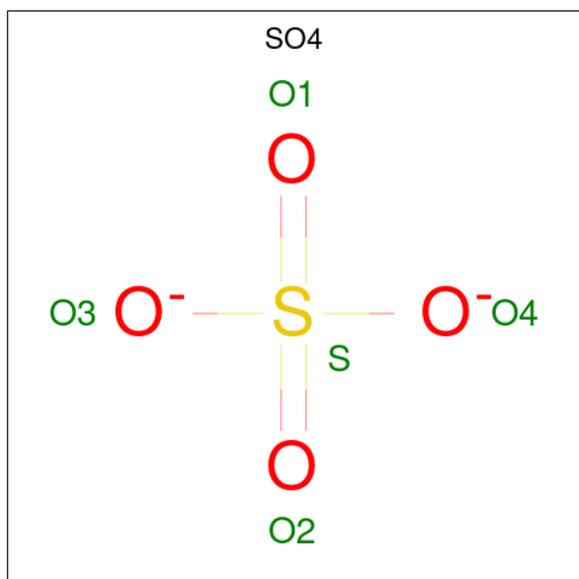
Chain	Residue	Modelled	Actual	Comment	Reference
F	385	LYS	-	expression tag	UNP A0A5K1K910

- Molecule 2 is tert-butyl N-[5-phenyl-3-(2-phenylethylcarbamoyl)thiophen-2-yl]carbamate (three-letter code: EJJ) (formula: C₂₄H₂₆N₂O₃S) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	
			Total	C	H	N	O			S
2	A	1	56	24	26	2	3	1	0	0

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	B	1	Total	O	S	0	0
			5	4	1		
3	C	1	Total	O	S	0	0
			5	4	1		
3	D	1	Total	O	S	0	0
			5	4	1		
3	D	1	Total	O	S	0	0
			5	4	1		

- Molecule 4 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	1	Total	Na	0	0
			1	1		
4	F	1	Total	Na	0	0
			1	1		

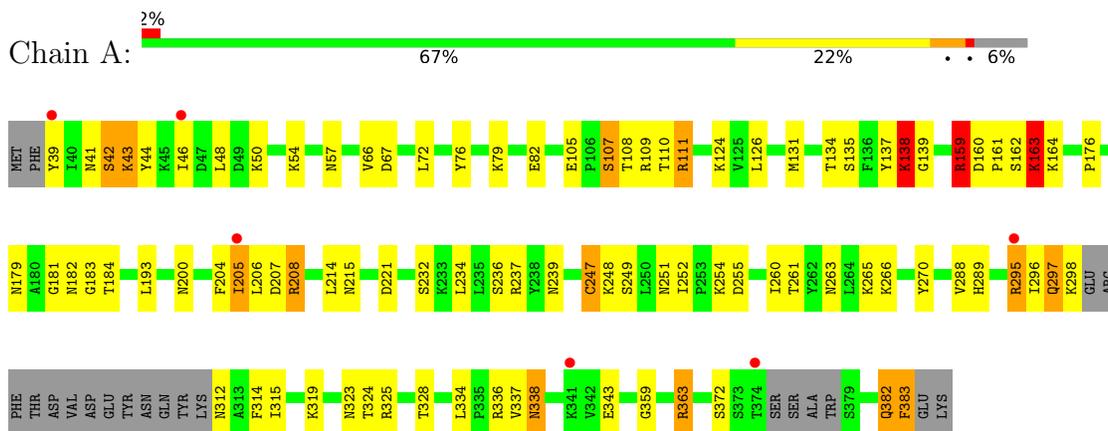
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	24	Total	O	0	0
			24	24		
5	B	30	Total	O	0	0
			30	30		
5	C	28	Total	O	0	0
			28	28		
5	D	41	Total	O	0	0
			41	41		
5	E	43	Total	O	0	0
			43	43		
5	F	29	Total	O	0	0
			29	29		

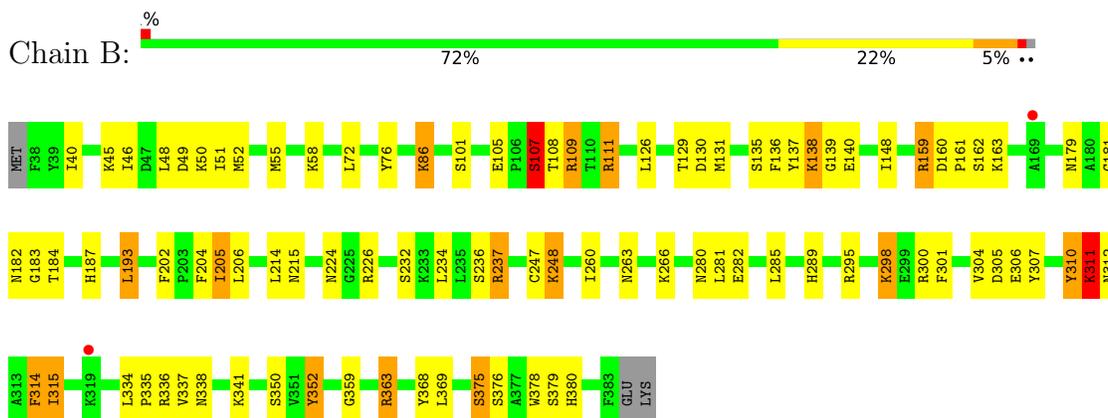
3 Residue-property plots [i](#)

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.

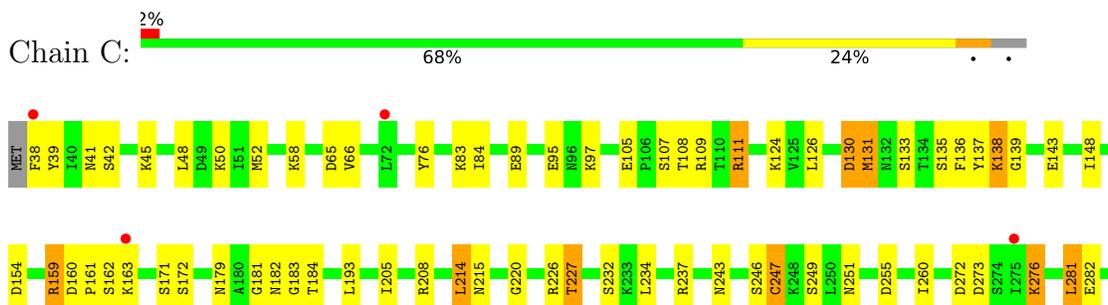
- Molecule 1: Aspartate carbamoyltransferase



- Molecule 1: Aspartate carbamoyltransferase



- Molecule 1: Aspartate carbamoyltransferase





• Molecule 1: Aspartate carbamoyltransferase



LYS

• Molecule 1: Aspartate carbamoyltransferase



• Molecule 1: Aspartate carbamoyltransferase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	87.06Å 87.36Å 104.64Å 89.98° 90.04° 117.72°	Depositor
Resolution (Å)	62.19 – 2.29 62.19 – 2.30	Depositor EDS
% Data completeness (in resolution range)	96.0 (62.19-2.29) 96.0 (62.19-2.30)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.45 (at 2.29Å)	Xtriage
Refinement program	REFMAC 5.8.0267, REFMAC 5.8.0267	Depositor
R, R_{free}	0.164 , 0.191 0.166 , 0.193	Depositor DCC
R_{free} test set	6216 reflections (5.28%)	wwPDB-VP
Wilson B-factor (Å ²)	50.0	Xtriage
Anisotropy	0.009	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	(Not available) , (Not available)	EDS
L-test for twinning ²	$\langle L \rangle = 0.41$, $\langle L^2 \rangle = 0.24$	Xtriage
Estimated twinning fraction	0.065 for -k,h+k,l 0.065 for h+k,-h,l 0.065 for -h-k,h,l 0.065 for k,-h-k,l 0.070 for h,-h-k,-l 0.069 for -h-k,k,-l 0.458 for -h,-k,l 0.240 for -k,-h,-l 0.239 for k,h,-l 0.069 for -h,h+k,-l 0.068 for h+k,-k,-l	Xtriage
Reported twinning fraction	0.400 for H, K, L 0.367 for -h,-k,l 0.081 for K, H, -L 0.152 for -K, -H, -L	Depositor
Outliers	0 of 117673 reflections	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	33033	wwPDB-VP
Average B, all atoms (Å ²)	58.0	wwPDB-VP

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.

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.59% of the height of the origin peak. No significant pseudotranslation is detected.*

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: NA, SO4, EJG

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	0.95	1/2701 (0.0%)	1.11	12/3646 (0.3%)
1	B	0.92	2/2871 (0.1%)	1.09	9/3880 (0.2%)
1	C	0.90	3/2756 (0.1%)	1.10	6/3723 (0.2%)
1	D	0.90	3/2701 (0.1%)	1.09	6/3646 (0.2%)
1	E	0.95	4/2871 (0.1%)	1.12	14/3880 (0.4%)
1	F	0.88	0/2756	1.10	9/3723 (0.2%)
All	All	0.92	13/16656 (0.1%)	1.10	56/22498 (0.2%)

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	B	0	3
1	D	0	2
1	E	0	3
1	F	0	1
All	All	0	9

The worst 5 of 13 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	101	SER	CA-CB	-7.08	1.42	1.52
1	B	363	ARG	CD-NE	-6.70	1.35	1.46
1	A	82	GLU	CD-OE2	-6.45	1.18	1.25
1	E	293	MET	C-O	5.57	1.33	1.23
1	D	163	LYS	C-O	5.50	1.33	1.23

The worst 5 of 56 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	363	ARG	NE-CZ-NH1	-12.55	114.02	120.30
1	D	363	ARG	NE-CZ-NH1	-12.02	114.29	120.30
1	A	363	ARG	NE-CZ-NH2	11.75	126.17	120.30
1	E	363	ARG	NE-CZ-NH1	-11.73	114.43	120.30
1	C	363	ARG	NE-CZ-NH1	-10.96	114.82	120.30

There are no chirality outliers.

5 of 9 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	310	TYR	Peptide
1	B	314	PHE	Mainchain
1	B	375	SER	Peptide
1	D	372	SER	Peptide
1	D	373	SER	Peptide

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	2653	2677	2668	69	0
1	B	2815	2814	2807	86	0
1	C	2704	2717	2709	71	0
1	D	2653	2677	2668	72	0
1	E	2815	2814	2807	84	0
1	F	2704	2717	2709	63	0
2	A	30	26	0	10	0
3	B	5	0	0	1	0
3	C	5	0	0	1	0
3	D	10	0	0	3	0
4	B	1	0	0	0	0
4	F	1	0	0	0	0
5	A	24	0	0	2	0
5	B	30	0	0	2	0
5	C	28	0	0	4	0
5	D	41	0	0	6	0
5	E	43	0	0	3	0
5	F	29	0	0	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	16591	16442	16368	424	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 13.

The worst 5 of 424 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:E:237:ARG:HD2	5:E:414:HOH:O	1.53	1.09
1:A:163:LYS:HB3	1:A:184:THR:HG23	1.39	1.04
1:C:372:SER:HB3	1:C:374:THR:HG23	1.39	1.04
1:A:110:THR:OG1	2:A:401:EJG:C3	2.06	1.04
1:D:163:LYS:CD	1:D:163:LYS:H	1.65	1.02

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	322/349 (92%)	306 (95%)	11 (3%)	5 (2%)	9 9
1	B	344/349 (99%)	324 (94%)	16 (5%)	4 (1%)	13 14
1	C	330/349 (95%)	312 (94%)	14 (4%)	4 (1%)	13 14
1	D	322/349 (92%)	308 (96%)	11 (3%)	3 (1%)	17 20
1	E	344/349 (99%)	324 (94%)	15 (4%)	5 (2%)	10 10
1	F	330/349 (95%)	310 (94%)	15 (4%)	5 (2%)	10 10
All	All	1992/2094 (95%)	1884 (95%)	82 (4%)	26 (1%)	12 12

5 of 26 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	138	LYS
1	A	248	LYS
1	B	138	LYS
1	B	248	LYS
1	C	138	LYS

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	308/328 (94%)	284 (92%)	24 (8%)	12	16
1	B	325/328 (99%)	300 (92%)	25 (8%)	13	16
1	C	313/328 (95%)	287 (92%)	26 (8%)	11	14
1	D	308/328 (94%)	280 (91%)	28 (9%)	9	11
1	E	325/328 (99%)	302 (93%)	23 (7%)	14	19
1	F	313/328 (95%)	293 (94%)	20 (6%)	17	23
All	All	1892/1968 (96%)	1746 (92%)	146 (8%)	13	16

5 of 146 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	281	LEU
1	F	373	SER
1	E	311	LYS
1	F	171	SER
1	B	352	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 60 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	96	ASN
1	F	251	ASN
1	D	280	ASN
1	F	243	ASN

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Mol	Chain	Res	Type
1	F	338	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](#)

Of 7 ligands modelled in this entry, 2 are monoatomic - leaving 5 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	$\# Z > 2$
3	SO4	B	401	-	4,4,4	0.19	0	6,6,6	0.32	0
3	SO4	D	401	-	4,4,4	0.35	0	6,6,6	0.41	0
3	SO4	C	401	-	4,4,4	0.26	0	6,6,6	0.25	0
2	EJG	A	401	-	29,32,32	0.72	0	34,44,44	1.15	5 (14%)
3	SO4	D	402	-	4,4,4	0.22	0	6,6,6	0.16	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	EJG	A	401	-	-	9/19/23/23	0/3/3/3

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	401	EJG	C6-N1-C5	-3.44	116.09	123.67
2	A	401	EJG	O1-C2-C3	-2.94	95.59	107.20
2	A	401	EJG	O1-C2-C4	2.47	116.99	107.20
2	A	401	EJG	C17-C18-C19	-2.22	107.71	112.87
2	A	401	EJG	C1-C2-C3	2.10	116.68	111.16

There are no chirality outliers.

5 of 9 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	401	EJG	O1-C5-N1-C6
2	A	401	EJG	O2-C5-N1-C6
2	A	401	EJG	C15-C16-N2-C17
2	A	401	EJG	O3-C16-N2-C17
2	A	401	EJG	N2-C17-C18-C19

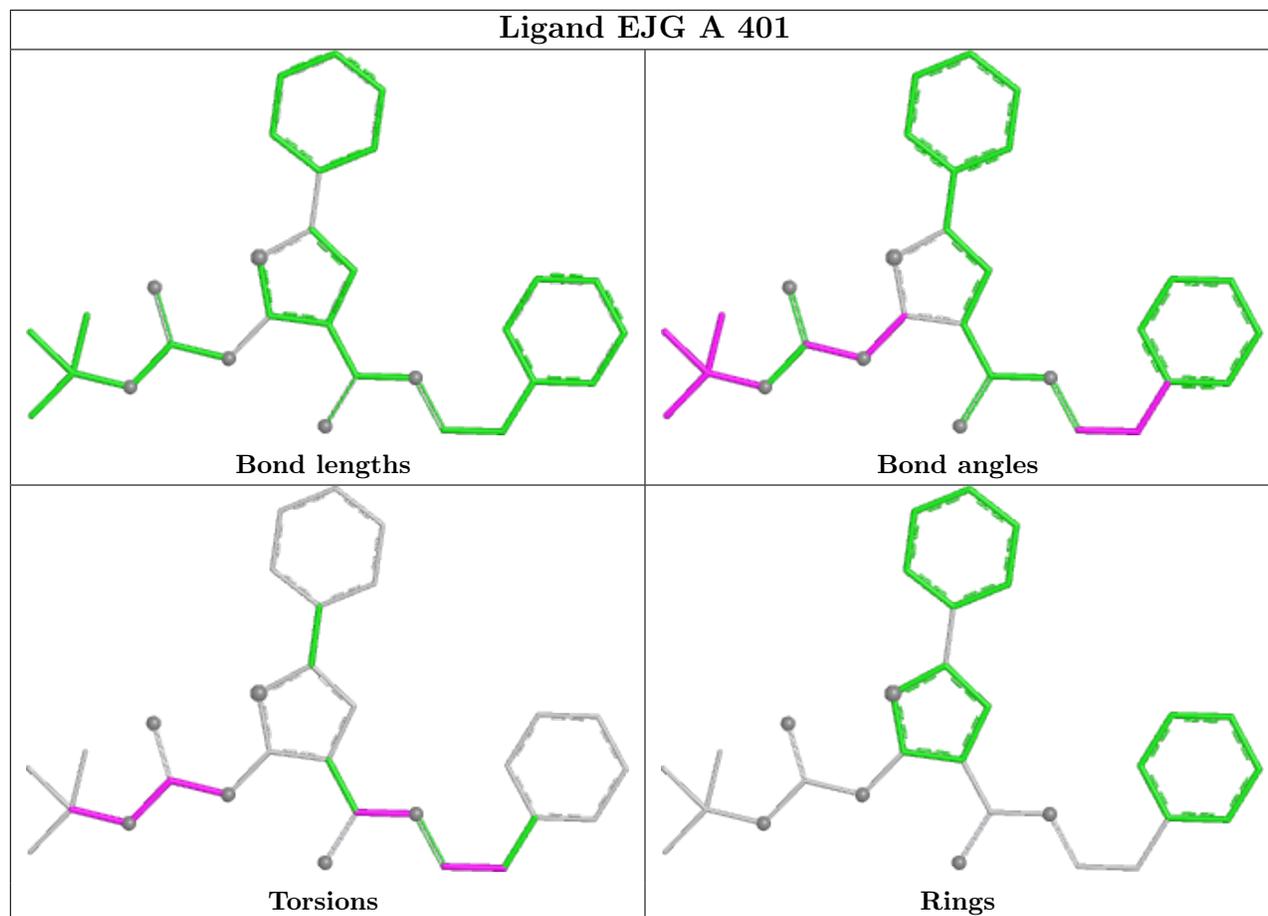
There are no ring outliers.

4 monomers are involved in 15 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	401	SO4	1	0
3	D	401	SO4	3	0
3	C	401	SO4	1	0
2	A	401	EJG	10	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.



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	328/349 (93%)	0.21	6 (1%) 68 74	37, 54, 83, 97	0
1	B	346/349 (99%)	0.18	2 (0%) 89 92	34, 52, 83, 98	0
1	C	334/349 (95%)	0.22	7 (2%) 63 70	37, 62, 87, 108	0
1	D	328/349 (93%)	0.19	7 (2%) 63 70	36, 57, 86, 103	0
1	E	346/349 (99%)	0.19	4 (1%) 79 83	34, 52, 81, 102	0
1	F	334/349 (95%)	0.19	7 (2%) 63 70	37, 60, 85, 95	0
All	All	2016/2094 (96%)	0.20	33 (1%) 72 77	34, 56, 85, 108	0

The worst 5 of 33 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	41	ASN	4.6
1	A	39	TYR	4.4
1	C	285	LEU	4.3
1	E	44	TYR	3.9
1	B	319	LYS	3.8

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](#)

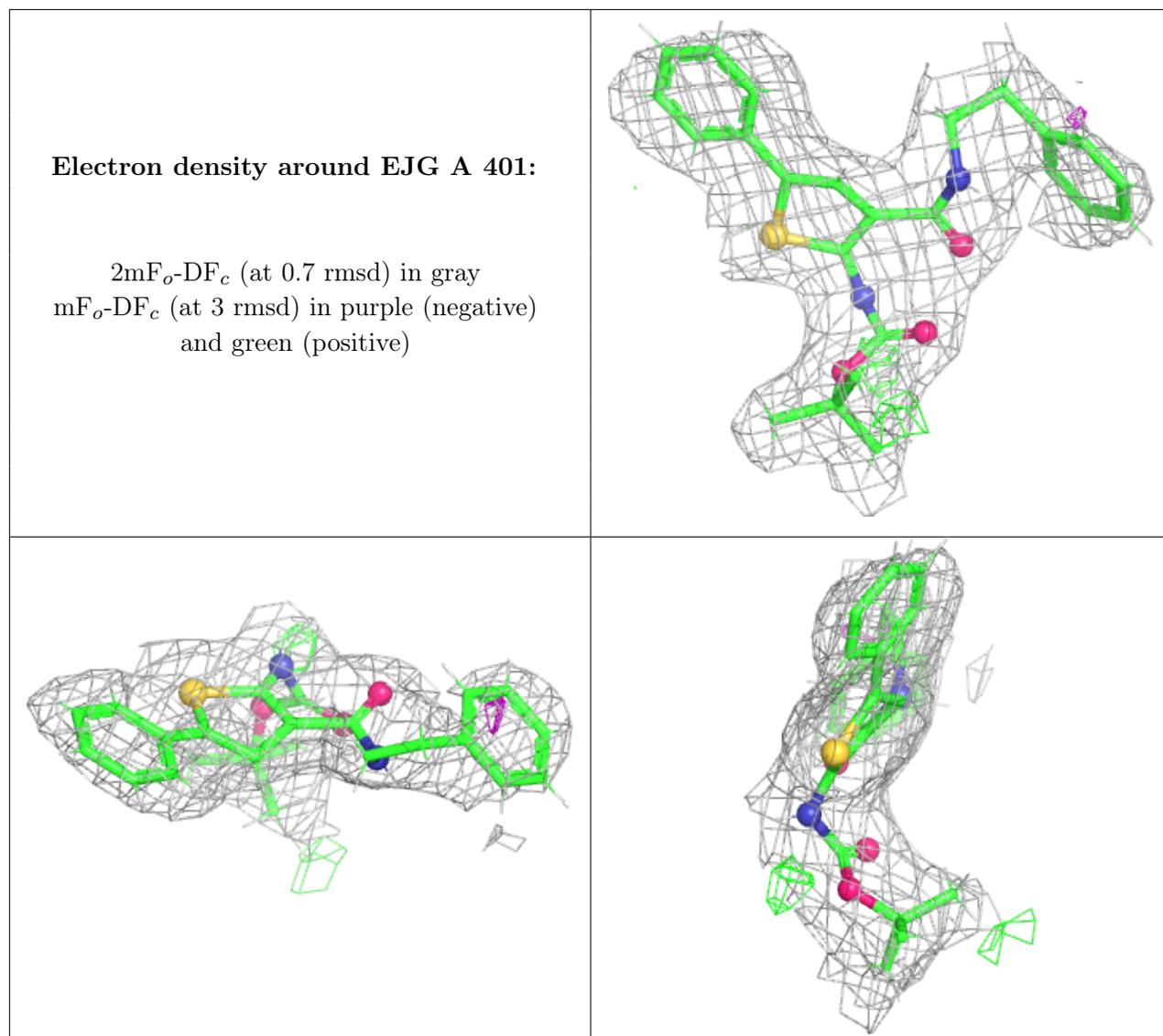
There are no monosaccharides in this entry.

6.4 Ligands

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	EJG	A	401	30/30	0.92	0.15	45,70,93,96	0
4	NA	B	402	1/1	0.97	0.14	36,36,36,36	0
3	SO4	D	402	5/5	0.98	0.08	50,52,64,72	0
3	SO4	B	401	5/5	0.98	0.11	47,49,67,69	0
4	NA	F	401	1/1	0.98	0.08	43,43,43,43	0
3	SO4	D	401	5/5	0.99	0.13	41,44,55,71	0
3	SO4	C	401	5/5	0.99	0.12	41,42,53,61	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.



6.5 Other polymers [\(i\)](#)

There are no such residues in this entry.