

wwPDB X-ray Structure Validation Summary Report (i)

Dec 26, 2024 – 12:22 PM JST

PDB ID : 9JT7

Title: SFX reaction state structure (0-60min) of alanine racemase

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Deposited on : 2024-10-02

Resolution : 2.30 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) 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 (1)) were used in the production of this report:

MolProbity: 4.02b-467

Mogul : 1.8.5 (274361), CSD as541be (2020)

Xtriage (Phenix) : 1.21

EDS : 3.0

buster-report : 1.1.7 (2018)

Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)

CCP4 : 9.0.004 (Gargrove)

Density-Fitness : 1.0.11

Ideal geometry (proteins) : Engh & Huber (2001) Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

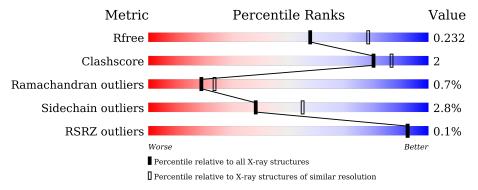
Validation Pipeline (wwPDB-VP) : 2.40

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 2.30 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 $(\# \mathrm{Entries})$	$\begin{array}{c} {\rm Similar\ resolution} \\ (\#{\rm Entries},{\rm resolution\ range}(\mathring{\rm A})) \end{array}$
R_{free}	164625	5963 (2.30-2.30)
Clashscore	180529	6698 (2.30-2.30)
Ramachandran outliers	177936	6640 (2.30-2.30)
Sidechain outliers	177891	6640 (2.30-2.30)
RSRZ outliers	164620	5963 (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 <=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	398	88%	8% •
1	В	398	88%	8% • •
1	С	398	89%	7% • •
1	D	398	88%	8% • •

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



ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	ALA	В	601	_	X	-	-



2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 12294 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 Alanine racemase 2.

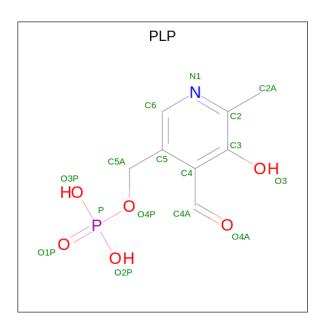
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace	
1	1 Λ	386	Total	С	N	О	S	0	0	0
1	A	300	3009	1924	527	544	14	0	U	0
1	1 B	386	Total	С	N	О	S	0	0	0
1	Ъ	300	3009	1924	527	544	14	0		0
1	C	C 386	Total	С	N	О	S	0	0	0
1			3009	1924	527	544	14	0	U	0
1 D	296	Total	С	N	О	S	0	0	0	
	386	3009	1924	527	544	14		0	U	

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-3	GLY	-	expression tag	UNP P94494
A	-2	SER	-	expression tag	UNP P94494
A	-1	HIS	-	expression tag	UNP P94494
A	0	MET	-	expression tag	UNP P94494
В	-3	GLY	-	expression tag	UNP P94494
В	-2	SER	-	expression tag	UNP P94494
В	-1	HIS	-	expression tag	UNP P94494
В	0	MET	-	expression tag	UNP P94494
С	-3	GLY	-	expression tag	UNP P94494
С	-2	SER	-	expression tag	UNP P94494
С	-1	HIS	-	expression tag	UNP P94494
С	0	MET	-	expression tag	UNP P94494
D	-3	GLY	-	expression tag	UNP P94494
D	-2	SER	-	expression tag	UNP P94494
D	-1	HIS	-	expression tag	UNP P94494
D	0	MET	_	expression tag	UNP P94494

• Molecule 2 is PYRIDOXAL-5'-PHOSPHATE (three-letter code: PLP) (formula: C₈H₁₀NO₆P).





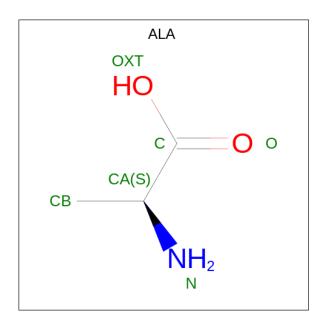
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf			
2	2 1	1	Total	С	N	О	Р	0	0	
2	A	1	15	8	1	5	1	0	U	
2	D	B 1	Total	С	N	О	Р	0	0	
2	Б		15	8	1	5	1	0		
2	С	C 1	Total	С	N	О	Р	0	0	
2	$\frac{2}{2}$ C		15	8	1	5	1	0	U	
2	2 D	1	Total	С	N	О	Р	0	0	
		1	15	8	1	5	1			

• Molecule 3 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total Cl 1 1	0	0
3	В	1	Total Cl 1 1	0	0
3	С	1	Total Cl 1 1	0	0
3	D	1	Total Cl 1 1	0	0

• Molecule 4 is ALANINE (three-letter code: ALA) (formula: C₃H₇NO₂) (labeled as "Ligand of Interest" by depositor).





Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	В	1	Total C N O 6 3 1 2	0	0
4	С	1	Total C N O 6 3 1 2	0	0
4	D	1	Total C N O 6 3 1 2	0	0

• Molecule 5 is water.

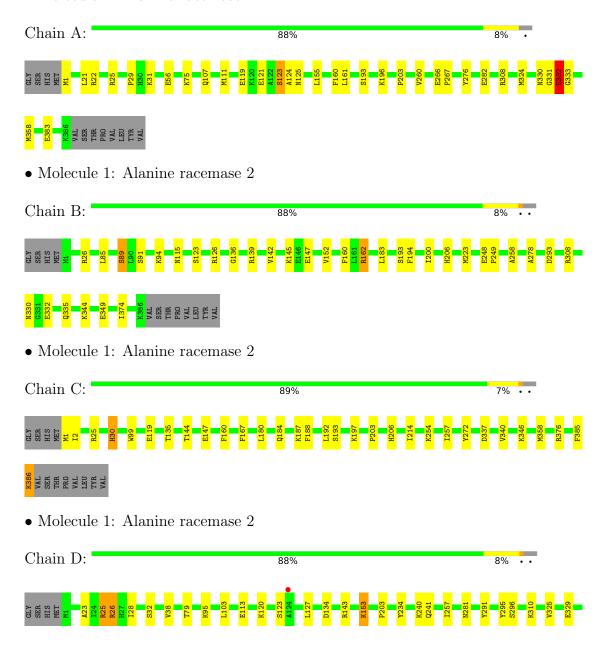
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	53	Total O 53 53	0	0
5	В	46	Total O 46 46	0	0
5	С	42	Total O 42 42	0	0
5	D	35	Total O 35 35	0	0



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: Alanine racemase 2









4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants	90.20Å 112.90Å 91.80Å	Domositon
a, b, c, α , β , γ	90.00° 114.00° 90.00°	Depositor
Resolution (Å)	67.32 - 2.30	Depositor
Resolution (A)	67.32 - 2.30	EDS
% Data completeness	100.0 (67.32-2.30)	Depositor
(in resolution range)	99.9 (67.32-2.30)	EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	1.50 (at 2.29Å)	Xtriage
Refinement program	PHENIX (1.19.2_4158: ???)	Depositor
D D	0.185 , 0.233	Depositor
R, R_{free}	0.185 , 0.232	DCC
R_{free} test set	74149 reflections (0.68%)	wwPDB-VP
Wilson B-factor (Å ²)	51.1	Xtriage
Anisotropy	0.164	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.28 , 44.8	EDS
L-test for twinning ²	$< L >=0.44, < L^2>=0.26$	Xtriage
Estimated twinning fraction	0.085 for l,-k,h	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	12294	wwPDB-VP
Average B, all atoms (Å ²)	53.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 3.93% of the height of the origin peak. No significant pseudotranslation is detected.

²Theoretical 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.



¹Intensities estimated from amplitudes.

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: CL, PLP

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 C	Chain	Bond	lengths	Bond angles		
IVIOI	Chain	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	A	0.48	0/3063	0.65	0/4135	
1	В	0.46	0/3063	0.64	1/4135~(0.0%)	
1	С	0.44	0/3063	0.63	0/4135	
1	D	0.48	0/3063	0.64	0/4135	
All	All	0.47	0/12252	0.64	$1/16540 \; (0.0\%)$	

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 maintain group or atoms of a sidechain that are expected to be planar.

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

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$\operatorname{Observed}(^{o})$	$ \operatorname{Ideal}(^o) $
1	В	278	ALA	C-N-CA	5.24	134.80	121.70

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	D	25	ARG	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	3009	0	3113	17	0
1	В	3009	0	3113	17	0
1	С	3009	0	3113	16	0
1	D	3009	0	3113	14	0
2	A	15	0	7	0	0
2	В	15	0	7	0	0
2	С	15	0	7	0	0
2	D	15	0	7	0	0
3	A	1	0	0	0	0
3	В	1	0	0	0	0
3	С	1	0	0	0	0
3	D	1	0	0	0	0
4	В	6	0	4	0	0
4	С	6	0	4	1	0
4	D	6	0	4	0	0
5	A	53	0	0	0	0
5	В	46	0	0	0	0
5	С	42	0	0	0	0
5	D	35	0	0	0	0
All	All	12294	0	12492	61	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.

The worst 5 of 61 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$\begin{array}{c} {\rm Interatomic} \\ {\rm distance} \ ({\rm \AA}) \end{array}$	$egin{aligned} ext{Clash} \ ext{overlap } (ext{Å}) \end{aligned}$
1:D:281:ASN:HB3	1:D:329:GLU:HG2	1.78	0.66
1:B:293:ASP:HB3	1:B:374:ILE:HD11	1.78	0.64
1:A:111:MET:HE1	1:A:155:LEU:HD13	1.81	0.61
1:B:258:ALA:O	1:B:335:GLN:NE2	2.34	0.58
1:A:193:SER:HA	1:A:196:LYS:HE3	1.85	0.57

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	384/398 (96%)	366 (95%)	13 (3%)	5 (1%)	10	11	
1	В	384/398 (96%)	362 (94%)	20 (5%)	2 (0%)	25	32	
1	С	384/398 (96%)	371 (97%)	12 (3%)	1 (0%)	37	47	
1	D	384/398~(96%)	364 (95%)	18 (5%)	2 (0%)	25	32	
All	All	$1536/1592 \ (96\%)$	1463 (95%)	63 (4%)	10 (1%)	19	23	

5 of 10 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	124	ALA
1	В	123	SER
1	D	26	ARG
1	A	123	SER
1	A	330	ASN

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	320/331 (97%)	311 (97%)	9 (3%)	38 55		
1	В	320/331 (97%)	314 (98%)	6 (2%)	52 69		
1	С	320/331 (97%)	312 (98%)	8 (2%)	42 60		
1	D	320/331 (97%)	307 (96%)	13 (4%)	26 39		
All	All	1280/1324 (97%)	1244 (97%)	36 (3%)	38 55		



5 of 36 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	241	GLN
1	D	384	ILE
1	D	296	SER
1	D	334	LYS
1	В	183	LEU

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

Mol	Chain	Res	Type
1	В	115	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 oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 11 ligands modelled in this entry, 4 are monoatomic - leaving 7 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).

Mo	J Twn	Type Chain		Link	Bond lengths			Bond angles		
1010	n ryp	e Chan	Res	Lilik	Counts	RMSZ	# Z > 2	Counts	$RMSZ \mid \# Z >$	# Z > 2
2	PLI	В	602	-	15,15,16	1.14	1 (6%)	20,22,23	1.46	3 (15%)
2	PLI	D	402	4	15,15,16	1.29	2 (13%)	20,22,23	1.57	4 (20%)



Mol	Tuno	Chain	Res	Link	Bond lengths			Bond angles			
MIOI	Type		nes	Lilik	Counts	RMSZ	# Z > 2	Counts	$\mid \text{RMSZ} \mid \# Z > 2$		
2	PLP	A	401	-	15,15,16	1.19	2 (13%)	20,22,23	1.80	4 (20%)	
4	ALA	В	601	-	5,5,5	2.14	2 (40%)	6,6,6	1.61	2 (33%)	
4	ALA	D	401	-	5,5,5	1.11	1 (20%)	6,6,6	1.34	1 (16%)	
4	ALA	С	402	2	5,5,5	1.14	1 (20%)	6,6,6	1.06	0	
2	PLP	С	401	-	15,15,16	1.28	1 (6%)	20,22,23	1.70	6 (30%)	

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	PLP	В	602	-	-	0/6/6/8	0/1/1/1
2	PLP	D	402	4	-	0/6/6/8	0/1/1/1
2	PLP	A	401	-	-	0/6/6/8	0/1/1/1
4	ALA	В	601	-	-	3/4/4/4	-
4	ALA	D	401	-	-	1/4/4/4	-
4	ALA	С	402	2	-	2/4/4/4	-
2	PLP	С	401	-	-	0/6/6/8	0/1/1/1

The worst 5 of 10 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$\operatorname{Observed}(\text{\AA})$	Ideal(Å)
4	В	601	ALA	CA-C	-3.93	1.50	1.54
2	D	402	PLP	C2A-C2	3.20	1.55	1.50
2	С	401	PLP	C2A-C2	2.91	1.55	1.50
2	A	401	PLP	C2A-C2	2.88	1.55	1.50
4	В	601	ALA	OXT-C	-2.53	1.22	1.30

The worst 5 of 20 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$\mathbf{Observed}(^{o})$	$\operatorname{Ideal}({}^{o})$
2	A	401	PLP	O4P-C5A-C5	-4.64	100.50	109.35
2	D	402	PLP	O4P-C5A-C5	-4.23	101.29	109.35
2	В	602	PLP	O4P-C5A-C5	-3.68	102.35	109.35
2	A	401	PLP	C5-C6-N1	-3.32	118.29	123.82
4	В	601	ALA	OXT-C-O	-3.11	117.02	124.09

There are no chirality outliers.

5 of 6 torsion outliers are listed below:



Mol	Chain	Res	Type	Atoms
4	В	601	ALA	OXT-C-CA-N
4	В	601	ALA	O-C-CA-CB
4	В	601	ALA	OXT-C-CA-CB
4	С	402	ALA	O-C-CA-CB
4	С	402	ALA	OXT-C-CA-CB

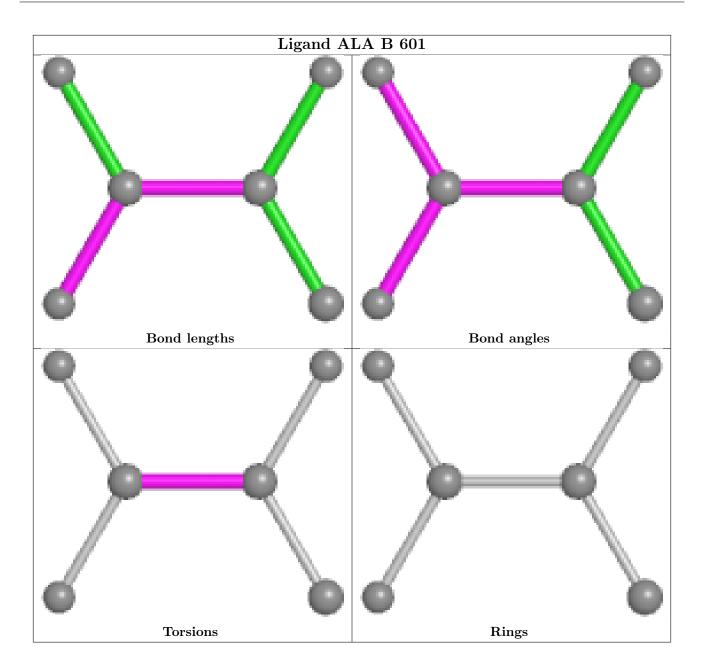
There are no ring outliers.

1 monomer is involved in 1 short contact:

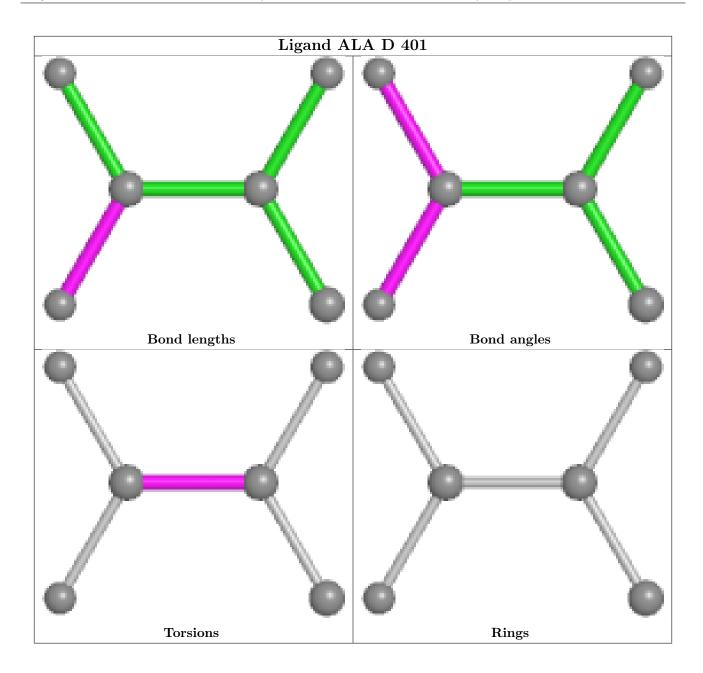
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	С	402	ALA	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less 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.

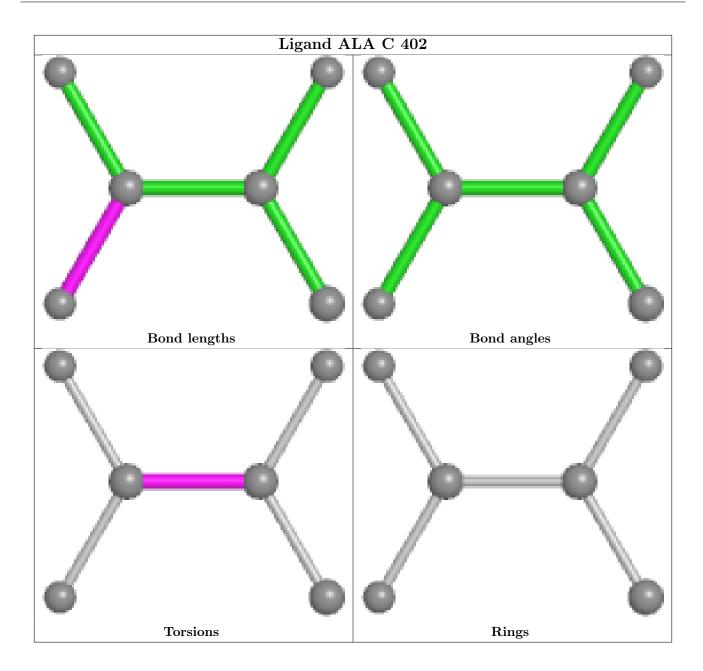












5.7 Other polymers (i)

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 (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, 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 $>$	#RSI	RZ>2	$\mathbf{OWAB}(\mathbf{\mathring{A}}^2)$	Q<0.9
1	A	386/398 (96%)	-0.44	0 100	100	37, 49, 74, 90	0
1	В	386/398 (96%)	-0.37	0 100	100	36, 51, 70, 88	0
1	С	386/398 (96%)	-0.25	0 100	100	39, 55, 73, 92	0
1	D	386/398 (96%)	-0.40	1 (0%)	90 90	38, 50, 71, 87	0
All	All	1544/1592 (96%)	-0.36	1 (0%)	92 92	36, 51, 72, 92	0

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	124	ALA	3.1

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, 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	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q < 0.9
4	ALA	В	601	6/6	0.85	0.12	46,47,57,61	0

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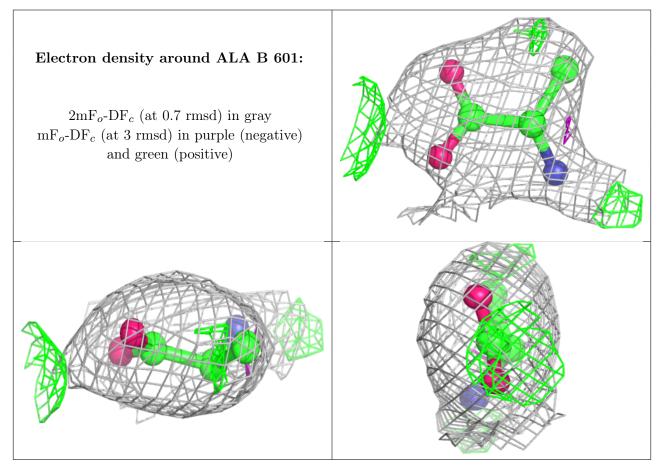


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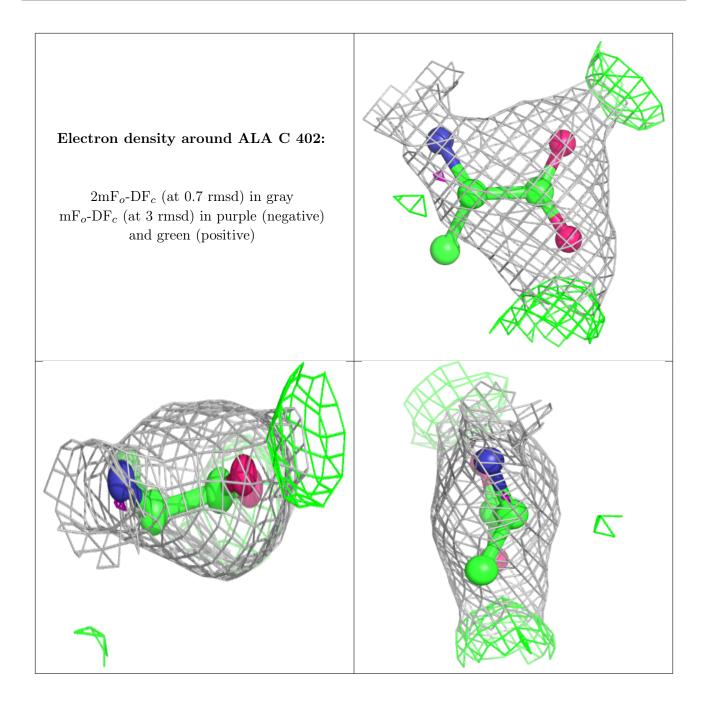
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q < 0.9
4	ALA	С	402	6/6	0.88	0.12	49,52,60,62	0
4	ALA	D	401	6/6	0.91	0.10	55,56,61,61	0
2	PLP	D	402	15/16	0.92	0.09	46,52,59,62	0
2	PLP	В	602	15/16	0.93	0.09	46,56,62,63	0
2	PLP	С	401	15/16	0.93	0.09	51,56,63,66	0
2	PLP	A	401	15/16	0.94	0.10	41,49,58,61	0
3	CL	A	402	1/1	0.96	0.09	52,52,52,52	0
3	CL	D	403	1/1	0.97	0.06	48,48,48,48	0
3	CL	С	403	1/1	0.97	0.07	52,52,52,52	0
3	CL	В	603	1/1	0.98	0.08	51,51,51,51	0

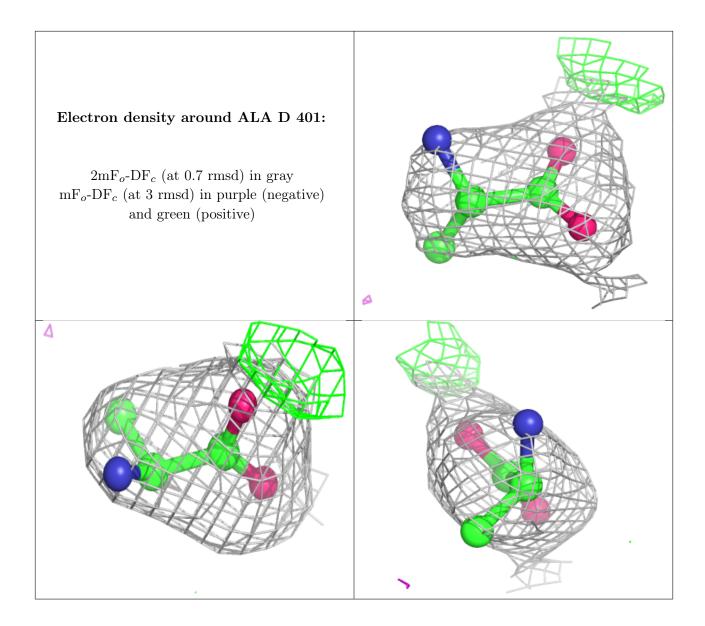
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.











6.5 Other polymers (i)

There are no such residues in this entry.

