

Full wwPDB X-ray Structure Validation Report (i)

Sep 20, 2023 – 12:02 AM EDT

PDB ID	:	5KJE
Title	:	F322L horse liver alcohol dehydrogenase complexed with NAD+ and pentaflu-
		orobenzyl alcohol
Authors	:	Plapp, B.V.
Deposited on	:	2016-06-18
Resolution	:	1.26 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 (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:

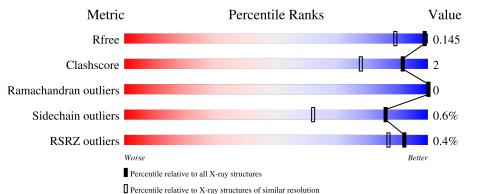
MolProbity	:	4.02b-467 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)		
EDS	:	2.35.1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35.1

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: $X\text{-}RAY \, DIFFRACTION$

The reported resolution of this entry is 1.26 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	$\begin{array}{c} \textbf{Whole archive} \\ (\#\textbf{Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
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						
1	А	374	% 96%	•				
1	В	374	97%	•				



2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 6873 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 Alcohol dehydrogenase E chain.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace	
1	Δ	374	Total C		Ν	0	\mathbf{S}	0	25	0
1	Л	574	2872	1829	482	534	27	0	20	0
1	В	374	Total	С	Ν	0	S	0	10	0
	D	574	2854	1812	479	537	26	0	10	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
А	322	LEU	PHE	engineered mutation	UNP P00327
В	322	LEU	PHE	engineered mutation	UNP P00327

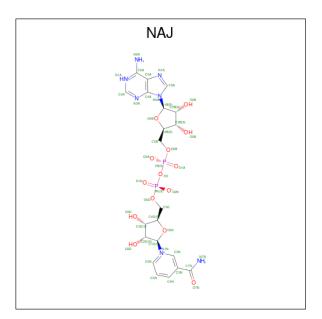
• Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	А	2	Total Zn 2 2	0	0
2	В	2	Total Zn 2 2	0	0

• Molecule 3 is NICOTINAMIDE-ADENINE-DINUCLEOTIDE (ACIDIC FORM) (three-letter code: NAJ) (formula: $C_{21}H_{27}N_7O_{14}P_2$).

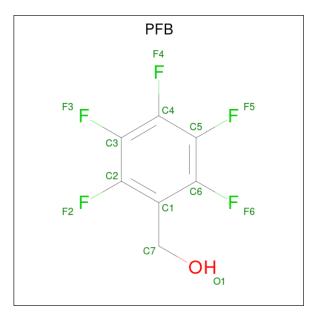






Mol	Chain	Residues		Ate	oms			ZeroOcc	AltConf
2	Δ	1	Total	С	Ν	Ο	Р	0	0
0	A	1	44	21	7	14	2	0	0
2	P	1	Total	С	Ν	Ο	Р	0	0
0	D		44	21	$\overline{7}$	14	2	U	

• Molecule 4 is 2,3,4,5,6-PENTAFLUOROBENZYL ALCOHOL (three-letter code: PFB) (formula: $C_7H_3F_5O$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	А	1	Total 13	С 7	F 5	0 1	0	0

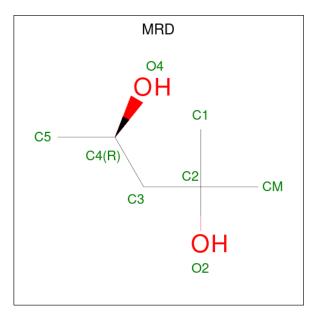
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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	В	1	Total C F O 13 7 5 1	0	0

• Molecule 5 is (4R)-2-METHYLPENTANE-2,4-DIOL (three-letter code: MRD) (formula: $C_6H_{14}O_2$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	А	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 8 & 6 & 2 \end{array}$	0	0
5	А	1	$\begin{array}{ccc} \text{Total} \text{C} \text{O} \\ 8 6 2 \end{array}$	0	0
5	А	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 8 & 6 & 2 \end{array}$	0	0
5	В	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 8 & 6 & 2 \end{array}$	0	0

• Molecule 6 is water.

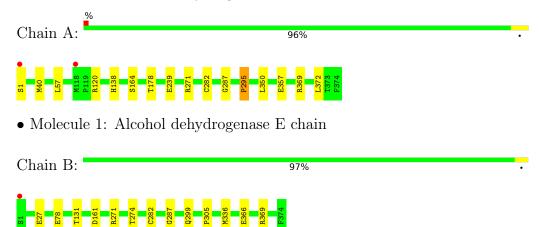
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	А	519	Total O 533 533	0	21
6	В	453	Total O 464 464	0	16



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: Alcohol dehydrogenase E chain





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1	Depositor
Cell constants	44.37Å 51.28Å 92.50Å	Depositor
a, b, c, α , β , γ	92.02° 102.94° 110.01°	Depositor
Resolution (Å)	20.00 - 1.26	Depositor
Resolution (A)	19.88 - 1.26	EDS
% Data completeness	82.7 (20.00-1.26)	Depositor
(in resolution range)	82.7 (19.88-1.26)	EDS
R _{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	3.74 (at 1.26\AA)	Xtriage
Refinement program	REFMAC 5.8.0131	Depositor
D D.	0.124 , 0.144	Depositor
R, R_{free}	0.124 , 0.145	DCC
R_{free} test set	1589 reflections (0.96%)	wwPDB-VP
Wilson B-factor $(Å^2)$	12.8	Xtriage
Anisotropy	0.435	Xtriage
Bulk solvent $k_{sol}(e/Å^3), B_{sol}(Å^2)$	0.34, 51.3	EDS
L-test for twinning ²	$ < L >=0.51, < L^2>=0.35$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.98	EDS
Total number of atoms	6873	wwPDB-VP
Average B, all atoms $(Å^2)$	19.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 6.05% of the height of the origin peak. No significant pseudotranslation is detected.

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.



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: MRD, NAJ, PFB, ZN

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	Bo	Bond lengths		nd angles
	RMSZ		# Z > 5	RMSZ	# Z > 5
1	А	0.79	2/3035~(0.1%)	0.90	3/4095~(0.1%)
1	В	0.76	1/2978~(0.0%)	0.87	3/4018~(0.1%)
All	All	0.77	3/6013~(0.0%)	0.89	6/8113~(0.1%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	А	164	SER	CA-CB	10.00	1.68	1.52
1	В	78	GLU	CD-OE1	-7.55	1.17	1.25
1	А	164	SER	CB-OG	-7.17	1.32	1.42

All (6)	bond ang	gle out	liers are	listed below:		
Mol	Chain	Res	Type	Atoms	Z	O
1	D	161	ACD	CD CC OD1	6.00	

Mol	Chain	\mathbf{Res}	Type	Atoms		$\mathbf{Observed}(^{o})$	$Ideal(^{o})$
1	В	161	ASP	CB-CG-OD1	6.89	124.50	118.30
1	А	369	ARG	NE-CZ-NH2	-6.71	116.94	120.30
1	В	369	ARG	NE-CZ-NH2	-6.13	117.23	120.30
1	А	271	ARG	NE-CZ-NH2	-5.97	117.31	120.30
1	В	161	ASP	CB-CG-OD2	-5.46	113.39	118.30
1	A	369	ARG	NE-CZ-NH1	5.43	123.02	120.30

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



Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	А	2872	0	2945	10	0
1	В	2854	0	2920	9	0
2	А	2	0	0	0	0
2	В	2	0	0	0	0
3	А	44	0	27	1	0
3	В	44	0	27	0	0
4	А	13	0	2	1	0
4	В	13	0	2	0	0
5	А	24	0	42	0	0
5	В	8	0	14	0	0
6	А	533	0	0	6	0
6	В	464	0	0	3	0
All	All	6873	0	5979	19	0

the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

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 (19) 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:138[B]:HIS:HE1	6:A:914:HOH:O	1.70	0.75	
1:B:299[A]:GLN:NE2	6:B:702:HOH:O	2.31	0.63	
1:A:57[B]:LEU:HD21	4:A:378:PFB:F5	1.91	0.59	
1:A:357:GLU:HG3	6:A:631:HOH:O	2.03	0.58	
1:B:336[B]:MET:HE1	6:B:667:HOH:O	2.06	0.55	
1:A:138[B]:HIS:CE1	6:A:914:HOH:O	2.52	0.54	
1:B:366[A]:GLU:O	1:B:366[A]:GLU:CG	2.55	0.53	
1:B:282[B]:CYS:HB3	1:B:287:GLY:HA3	1.97	0.46	
1:A:178:THR:HG21	3:A:377:NAJ:C4N	2.47	0.45	
1:A:120:ARG:NH2	6:A:915[B]:HOH:O	2.37	0.43	
1:B:27[A]:GLU:HB2	1:B:131:THR:OG1	2.18	0.43	
1:B:27[B]:GLU:HB2	1:B:131:THR:OG1	2.18	0.42	
1:A:295:PRO:HG3	1:B:305:PRO:HG2	1.99	0.42	
1:B:131:THR:HG23	6:B:426:HOH:O	2.20	0.41	
1:A:350:LEU:O	1:A:372:LEU:HA	2.21	0.41	
1:B:271:ARG:HB2	1:B:274:THR:OG1	2.21	0.41	
1:A:282[B]:CYS:HB3	1:A:287:GLY:HA3	2.03	0.41	
1:A:120:ARG:HB2	6:A:723:HOH:O	2.20	0.40	

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	Percent	iles
1	А	397/374~(106%)	386~(97%)	11 (3%)	0	100 1	.00
1	В	390/374~(104%)	378~(97%)	12 (3%)	0	100 1	.00
All	All	787/748~(105%)	764 (97%)	23 (3%)	0	100 1	.00

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	Perce	ntiles
1	А	333/308~(108%)	327~(98%)	6(2%)	59	21
1	В	326/308~(106%)	326 (100%)	0	100	100
All	All	659/616~(107%)	653~(99%)	6 (1%)	86	47

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	А	1	SER
1	А	40[A]	MET
1	А	40[B]	MET
1	А	239[A]	GLU
1	А	239[B]	GLU
1	А	295	PRO

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 12 ligands modelled in this entry, 4 are 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	Turne	Chain	Res	Link	Bo	ond leng	ths	В	ond ang	les
1VIOI	Type	Chain	nes	LIIIK	Counts	RMSZ	# Z >2	Counts	RMSZ	# Z > 2
4	PFB	А	378	2	13,13,13	1.07	0	19,19,19	1.07	3 (15%)
5	MRD	А	381	-	7,7,7	0.39	0	9,10,10	1.23	1 (11%)
4	PFB	В	378	2	13,13,13	0.91	0	19,19,19	1.00	1 (5%)
5	MRD	А	380	-	7,7,7	0.36	0	9,10,10	0.96	0
3	NAJ	А	377	-	42,48,48	1.50	5 (11%)	50,73,73	1.58	7 (14%)
3	NAJ	В	377	-	42,48,48	1.13	2 (4%)	50,73,73	1.56	8 (16%)
5	MRD	В	379	-	7,7,7	0.46	0	9,10,10	0.68	0
5	MRD	А	379	-	7, 7, 7	0.54	0	$9,\!10,\!10$	1.21	1 (11%)

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.



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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	PFB	А	378	2	-	0/2/2/2	0/1/1/1
5	MRD	А	381	-	-	3/5/5/5	-
4	PFB	В	378	2	-	0/2/2/2	0/1/1/1
5	MRD	А	380	-	-	0/5/5/5	-
3	NAJ	А	377	-	-	4/26/62/62	0/5/5/5
3	NAJ	В	377	-	-	4/26/62/62	0/5/5/5
5	MRD	В	379	-	-	2/5/5/5	-
5	MRD	А	379	-	-	2/5/5/5	_

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	А	377	NAJ	C4N-C3N	4.98	1.47	1.39
3	А	377	NAJ	C2N-N1N	4.21	1.40	1.35
3	В	377	NAJ	C2A-N3A	3.88	1.38	1.32
3	А	377	NAJ	C2A-N3A	3.16	1.37	1.32
3	А	377	NAJ	C5N-C4N	2.96	1.45	1.38
3	В	377	NAJ	C6N-N1N	2.66	1.41	1.35
3	А	377	NAJ	C8A-N7A	-2.38	1.30	1.34

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
3	В	377	NAJ	C6N-N1N-C2N	-5.36	117.09	121.97
3	А	377	NAJ	N3A-C2A-N1A	-4.89	121.04	128.68
3	В	377	NAJ	N3A-C2A-N1A	-4.72	121.30	128.68
3	А	377	NAJ	C5N-C4N-C3N	-4.22	115.35	120.34
3	А	377	NAJ	C4A-C5A-N7A	-3.84	105.40	109.40
3	В	377	NAJ	C2A-N1A-C6A	3.13	124.11	118.75
3	А	377	NAJ	N6A-C6A-N1A	2.89	124.57	118.57
3	В	377	NAJ	C4A-C5A-N7A	-2.88	106.39	109.40
3	А	377	NAJ	C2A-N1A-C6A	2.88	123.67	118.75
5	А	379	MRD	CM-C2-C1	-2.74	104.87	110.57
3	В	377	NAJ	C2N-C3N-C4N	2.37	120.94	118.26
3	В	377	NAJ	O7N-C7N-N7N	-2.34	119.25	122.58
4	В	378	PFB	O1-C7-C1	2.32	117.96	111.66
3	А	377	NAJ	O4B-C1B-C2B	-2.32	103.54	106.93
4	А	378	PFB	O1-C7-C1	2.31	117.92	111.66
5	А	381	MRD	O4-C4-C5	-2.28	99.51	109.38
4	А	378	PFB	C1-C6-C5	-2.20	119.77	122.37
3	В	377	NAJ	C1B-N9A-C4A	-2.16	122.85	126.64
3	В	377	NAJ	O4B-C1B-C2B	-2.15	103.78	106.93

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	Chain	1	1 0		Z	$Observed(^{o})$	$Ideal(^{o})$
3	А	377	NAJ	O7N-C7N-N7N	2.14	125.62	122.58
4	А	378	PFB	C6-C5-C4	2.06	121.82	119.53

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There are no chirality outliers.

All (15) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	А	377	NAJ	O4D-C1D-N1N-C2N
3	А	377	NAJ	O4D-C1D-N1N-C6N
3	А	377	NAJ	C2D-C1D-N1N-C2N
3	В	377	NAJ	O4D-C1D-N1N-C2N
3	В	377	NAJ	O4D-C1D-N1N-C6N
3	В	377	NAJ	C2D-C1D-N1N-C2N
5	А	379	MRD	C2-C3-C4-O4
5	А	379	MRD	C2-C3-C4-C5
5	А	381	MRD	O2-C2-C3-C4
5	А	381	MRD	CM-C2-C3-C4
5	В	379	MRD	C2-C3-C4-O4
5	В	379	MRD	C2-C3-C4-C5
5	А	381	MRD	C1-C2-C3-C4
3	В	377	NAJ	O4B-C4B-C5B-O5B
3	А	377	NAJ	O4B-C4B-C5B-O5B

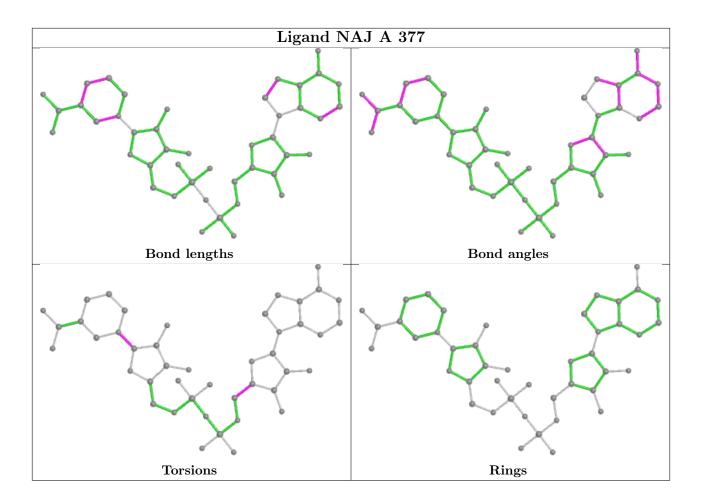
There are no ring outliers.

2 monomers are involved in 2 short contacts:

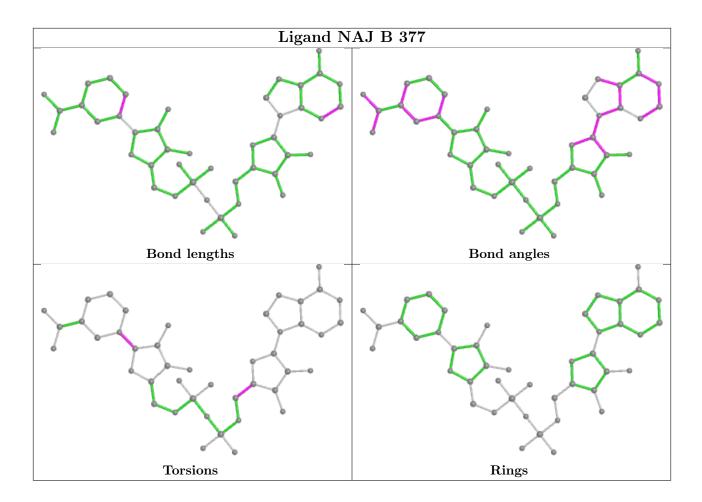
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	А	378	PFB	1	0
3	А	377	NAJ	1	0

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 sufficient must be 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	$\langle RSRZ \rangle$	#RSRZ>2	$OWAB(Å^2)$	Q<0.9
1	А	374/374~(100%)	-0.25	2 (0%) 91 85	10, 14, 25, 59	0
1	В	374/374~(100%)	-0.21	1 (0%) 94 91	10, 16, 27, 39	0
All	All	748/748~(100%)	-0.23	3 (0%) 92 87	10, 15, 26, 59	0

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	В	1	SER	4.0
1	А	1	SER	3.9
1	А	118	MET	2.4

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	$\mathbf{B} ext{-factors}(\mathrm{\AA}^2)$	Q<0.9
5	MRD	А	379	8/8	0.85	0.18	$31,\!35,\!49,\!55$	0
5	MRD	А	381	8/8	0.85	0.18	33,43,47,49	0

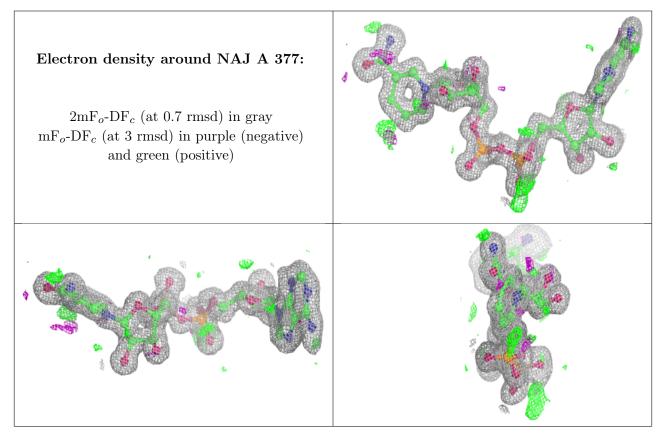
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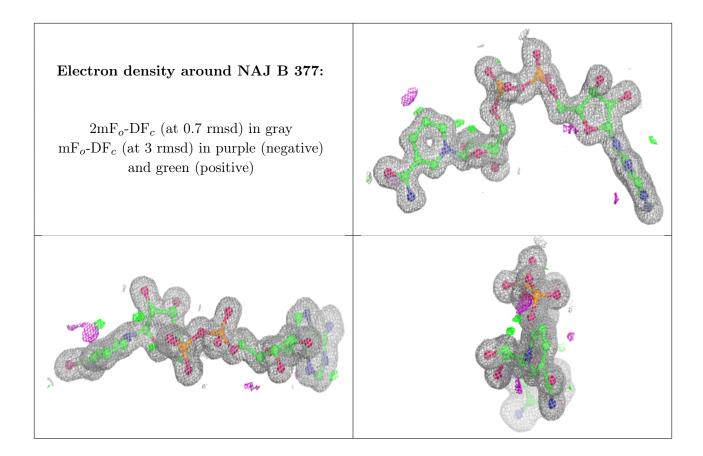
Mol	Type	Chain	Res	Atoms	RSCC	RSR	$\operatorname{B-factors}(\operatorname{\AA}^2)$	Q < 0.9
5	MRD	А	380	8/8	0.91	0.13	30,34,39,41	0
5	MRD	В	379	8/8	0.93	0.20	$36,\!44,\!52,\!59$	0
4	PFB	А	378	13/13	0.95	0.11	14,18,20,23	0
4	PFB	В	378	13/13	0.95	0.11	16,19,21,22	0
3	NAJ	А	377	44/44	0.99	0.05	$9,\!12,\!17,\!23$	0
3	NAJ	В	377	44/44	0.99	0.05	$11,\!14,\!18,\!24$	0
2	ZN	А	375	1/1	1.00	0.06	$14,\!14,\!14,\!14$	0
2	ZN	А	376	1/1	1.00	0.03	$12,\!12,\!12,\!12$	0
2	ZN	В	375	1/1	1.00	0.04	$15,\!15,\!15,\!15$	0
2	ZN	В	376	1/1	1.00	0.03	$15,\!15,\!15,\!15$	0

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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.

