



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 1, 2019 – 09:35 PM EDT

PDB ID : 1H2B
Title : Crystal Structure of the Alcohol Dehydrogenase from the Hyperthermophilic Archaeon Aeropyrum pernix at 1.65Å Resolution
Authors : Guy, J.E.; Isupov, M.N.; Littlechild, J.A.
Deposited on : 2002-08-02
Resolution : 1.62 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.0 (224370), CSD as540be (2019)
Xtriage (Phenix) : 1.13
EDS : 2.4
buster-report : 1.1.7 (2018)
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)
Refmac : 5.8.0158
CCP4 : 7.0 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.4

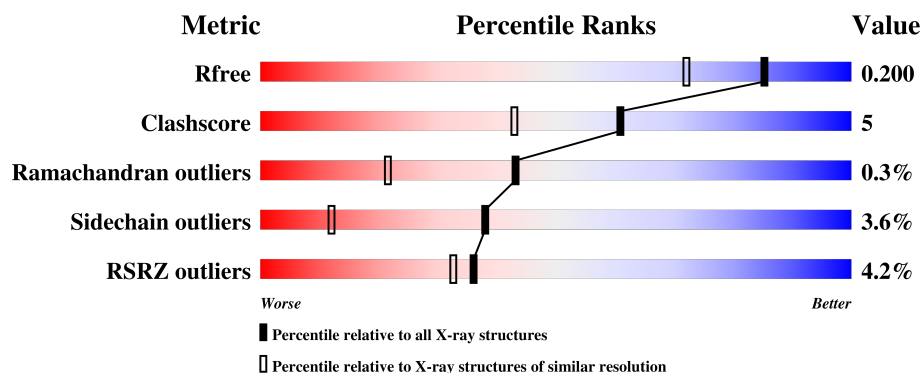
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION


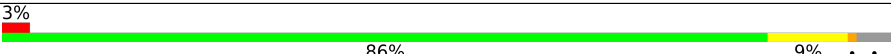
The reported resolution of this entry is 1.62 Å.

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}	111664	3975 (1.64-1.60)
Clashscore	122126	4258 (1.64-1.60)
Ramachandran outliers	120053	4162 (1.64-1.60)
Sidechain outliers	120020	4161 (1.64-1.60)
RSRZ outliers	108989	3894 (1.64-1.60)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	359	 6% 84% 11% 3% . .
1	B	359	 3% 86% 9% 2% . .

2 Entry composition [i](#)

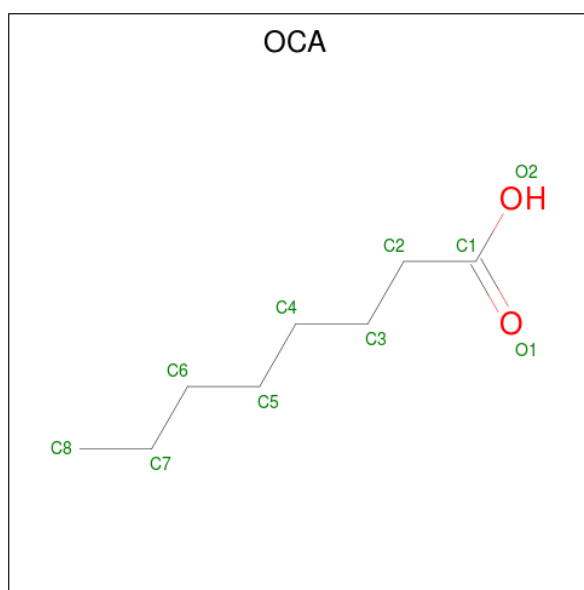
There are 5 unique types of molecules in this entry. The entry contains 6104 atoms, of which 0 are hydrogens and 0 are deuteriums.

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.

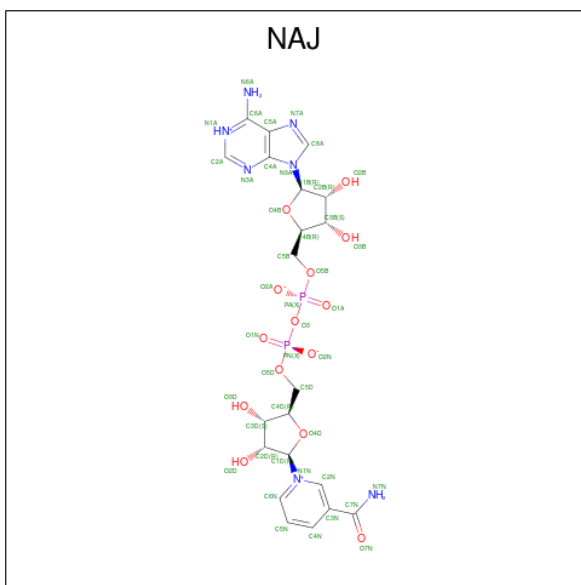
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	343	Total	C	N	O	S	0	5	0
			2668	1697	468	488	15			
1	B	344	Total	C	N	O	S	0	3	0
			2663	1693	468	488	14			

- Molecule 2 is OCTANOIC ACID (CAPRYLIC ACID) (three-letter code: OCA) (formula: $C_8H_{16}O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			10	8	2		
2	B	1	Total	C	O	0	0
			10	8	2		

- 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	Atoms					ZeroOcc	AltConf
3	A	1	Total 44	C 21	N 7	O 14	P 2	0	0
3	B	1	Total 44	C 21	N 7	O 14	P 2	0	0

- Molecule 4 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	B	2	Total Zn 2 2	0	0
4	A	3	Total Zn 3 3	0	0

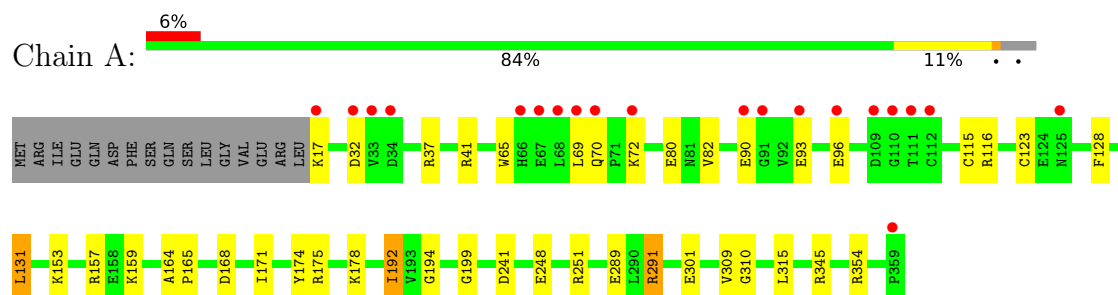
- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	311	Total O 311 311	0	0
5	B	349	Total O 349 349	0	0

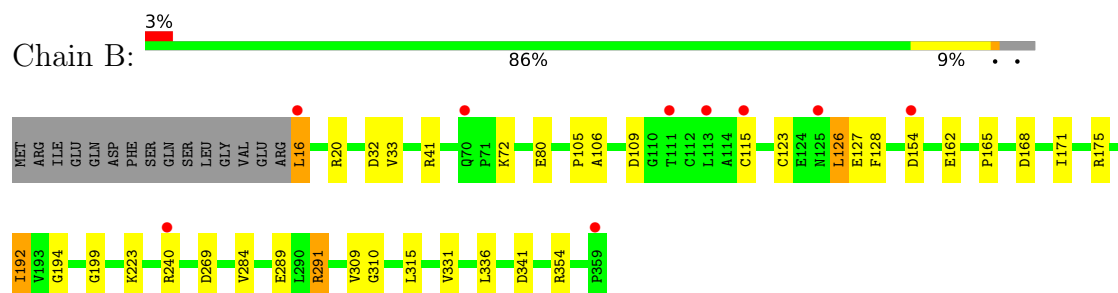
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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



• Molecule 1: ALCOHOL DEHYDROGENASE



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	100.66Å 103.19Å 67.52Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	15.00 – 1.62 13.99 – 1.62	Depositor EDS
% Data completeness (in resolution range)	99.7 (15.00-1.62) 97.8 (13.99-1.62)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.18 (at 1.62Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.168 , 0.203 0.167 , 0.200	Depositor DCC
R_{free} test set	1759 reflections (2.00%)	wwPDB-VP
Wilson B-factor (Å ²)	20.5	Xtriage
Anisotropy	0.168	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 50.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.014 for k,h,-l	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	6104	wwPDB-VP
Average B, all atoms (Å ²)	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.07% of the height of the origin peak. No significant pseudotranslation is detected.*

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.

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: OCA, NAJ, 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	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.67	0/2734	0.86	3/3698 (0.1%)
1	B	0.72	0/2722	0.89	5/3683 (0.1%)
All	All	0.70	0/5456	0.88	8/7381 (0.1%)

There are no bond length outliers.

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	345	ARG	NE-CZ-NH2	-5.91	117.34	120.30
1	B	341	ASP	CB-CG-OD2	5.80	123.52	118.30
1	B	269	ASP	CB-CG-OD1	5.64	123.38	118.30
1	A	241	ASP	CB-CG-OD2	5.56	123.30	118.30
1	B	168	ASP	CB-CG-OD2	5.46	123.22	118.30
1	A	168	ASP	CB-CG-OD2	5.45	123.20	118.30
1	B	154	ASP	CB-CG-OD2	5.43	123.18	118.30
1	B	109	ASP	CB-CG-OD2	5.06	122.85	118.30

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2668	0	2729	21	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	2663	0	2722	33	0
2	A	10	0	15	0	0
2	B	10	0	15	0	0
3	A	44	0	27	0	0
3	B	44	0	27	2	0
4	A	3	0	0	0	0
4	B	2	0	0	0	0
5	A	311	0	0	1	0
5	B	349	0	0	6	0
All	All	6104	0	5535	54	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 5.

All (54) 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:289:GLU:HG2	1:A:291:ARG:NH2	1.89	0.87
1:B:289:GLU:HG2	1:B:291:ARG:NH2	1.97	0.79
1:A:289:GLU:CG	1:A:291:ARG:NH2	2.50	0.73
1:B:336:LEU:HG	5:B:2324:HOH:O	1.90	0.72
1:A:289:GLU:HG2	1:A:291:ARG:CZ	2.24	0.66
1:B:20:ARG:HD2	1:B:33:VAL:HG11	1.80	0.63
1:B:126:LEU:HD12	1:B:127:GLU:N	2.13	0.63
1:B:115:CYS:SG	1:B:123[B]:CYS:HB2	2.41	0.60
1:B:240:ARG:HB2	1:B:240:ARG:NH1	2.16	0.60
1:A:171:ILE:HD12	1:A:315:LEU:HB2	1.83	0.60
1:B:20:ARG:HD2	1:B:33:VAL:CG1	2.35	0.57
1:A:115:CYS:SG	1:A:123[B]:CYS:HB2	2.44	0.56
1:B:289:GLU:CG	1:B:291:ARG:NH2	2.68	0.56
1:B:223:LYS:HD3	3:B:1361:NAJ:O3B	2.08	0.53
1:B:106:ALA:HB1	1:B:126:LEU:HD11	1.92	0.51
1:B:240:ARG:NH1	5:B:2245:HOH:O	2.44	0.50
1:A:289:GLU:HG2	1:A:291:ARG:HH21	1.69	0.50
1:A:289:GLU:HB3	1:A:291:ARG:CZ	2.42	0.49
1:A:128:PHE:CE2	1:A:131:LEU:HD13	2.47	0.49
1:B:194:GLY:O	1:B:199:GLY:HA3	2.12	0.49
1:A:175:ARG:HD2	1:A:310:GLY:HA2	1.95	0.48
1:A:248:GLU:HG3	5:A:2211:HOH:O	2.12	0.48
1:A:194:GLY:O	1:A:199:GLY:HA3	2.13	0.48
1:B:240:ARG:CB	1:B:240:ARG:CZ	2.92	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:41:ARG:NH1	1:B:127:GLU:HG3	2.29	0.47
1:B:171:ILE:HD12	1:B:315:LEU:HB2	1.98	0.46
1:B:72:LYS:HE2	5:B:2075:HOH:O	2.15	0.46
1:B:16:LEU:HB3	1:B:33:VAL:O	2.16	0.46
1:B:16:LEU:O	1:B:32:ASP:HA	2.15	0.45
1:B:105:PRO:HB2	1:B:128:PHE:CZ	2.51	0.45
1:B:80:GLU:CD	1:B:165:PRO:HA	2.37	0.45
1:A:65:TRP:HB3	1:A:69:LEU:HD22	1.98	0.45
1:A:80:GLU:CD	1:A:165:PRO:HA	2.38	0.44
1:B:240:ARG:NH2	5:B:2246:HOH:O	2.36	0.44
1:B:240:ARG:NH1	1:B:240:ARG:CB	2.81	0.44
1:B:240:ARG:HH11	1:B:240:ARG:HB2	1.81	0.44
1:A:65:TRP:O	1:A:69:LEU:HB2	2.18	0.43
1:B:289:GLU:HG2	1:B:291:ARG:CZ	2.46	0.43
1:A:116:ARG:HA	1:A:116:ARG:HD2	1.85	0.43
1:B:175:ARG:HD2	1:B:310:GLY:HA2	1.99	0.43
1:A:174:TYR:CZ	1:A:178[B]:LYS:HE3	2.54	0.43
1:B:240:ARG:NH2	5:B:2244:HOH:O	2.53	0.42
1:A:192:ILE:C	1:A:192:ILE:HD13	2.40	0.42
1:B:162:GLU:HG2	1:B:331:VAL:HG21	2.02	0.42
1:B:240:ARG:HB3	1:B:240:ARG:CZ	2.50	0.41
1:B:284:VAL:O	3:B:1361:NAJ:H2N	2.20	0.41
1:A:289:GLU:CD	1:A:291:ARG:NH2	2.74	0.41
1:B:165:PRO:HB3	1:B:354:ARG:HG2	2.03	0.41
1:A:165:PRO:HB3	1:A:354:ARG:HG2	2.03	0.41
1:B:240:ARG:NE	5:B:2246:HOH:O	2.53	0.41
1:B:192:ILE:HD13	1:B:192:ILE:C	2.42	0.40
1:A:82:VAL:HG22	1:A:164:ALA:HB2	2.03	0.40
1:B:126:LEU:HD12	1:B:127:GLU:O	2.20	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	346/359 (96%)	338 (98%)	7 (2%)	1 (0%)	43	21
1	B	345/359 (96%)	339 (98%)	5 (1%)	1 (0%)	43	21
All	All	691/718 (96%)	677 (98%)	12 (2%)	2 (0%)	43	21

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	309	VAL
1	B	309	VAL

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	286/296 (97%)	270 (94%)	16 (6%)	23	5
1	B	284/296 (96%)	280 (99%)	4 (1%)	69	48
All	All	570/592 (96%)	550 (96%)	20 (4%)	38	13

All (20) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	17	LYS
1	A	32	ASP
1	A	37	ARG
1	A	41	ARG
1	A	70	GLN
1	A	72	LYS
1	A	90	GLU
1	A	93	GLU
1	A	96	GLU
1	A	131	LEU
1	A	153	LYS
1	A	157	ARG
1	A	159	LYS
1	A	192	ILE

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Mol	Chain	Res	Type
1	A	251	ARG
1	A	291	ARG
1	B	16	LEU
1	B	126	LEU
1	B	192	ILE
1	B	291	ARG

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

Mol	Chain	Res	Type
1	A	316	HIS

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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 9 ligands modelled in this entry, 5 are monoatomic - leaving 4 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	OCA	A	1360	4	6,9,9	0.31	0	5,9,9	0.63	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	NAJ	A	1361	-	39,48,48	1.27	3 (7%)	44,73,73	1.65	8 (18%)
2	OCA	B	1360	4	6,9,9	0.30	0	5,9,9	0.60	0
3	NAJ	B	1361	-	39,48,48	1.30	4 (10%)	44,73,73	2.05	9 (20%)

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	OCA	A	1360	4	-	1/5/7/7	-
3	NAJ	A	1361	-	-	1/22/62/62	0/5/5/5
2	OCA	B	1360	4	-	0/5/7/7	-
3	NAJ	B	1361	-	-	3/22/62/62	0/5/5/5

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	1361	NAJ	O7N-C7N	5.50	1.34	1.24
3	A	1361	NAJ	O7N-C7N	4.42	1.32	1.24
3	A	1361	NAJ	C2A-N1A	3.45	1.40	1.33
3	B	1361	NAJ	C4N-C3N	2.64	1.43	1.39
3	B	1361	NAJ	C2A-N1A	2.61	1.38	1.33
3	A	1361	NAJ	C4N-C3N	2.23	1.43	1.39
3	B	1361	NAJ	C2A-N3A	2.06	1.35	1.32

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	1361	NAJ	C3N-C7N-N7N	6.87	125.56	117.75
3	B	1361	NAJ	N3A-C2A-N1A	-6.23	118.64	128.68
3	A	1361	NAJ	C3N-C7N-N7N	4.75	123.15	117.75
3	B	1361	NAJ	C5N-C4N-C3N	-4.65	114.77	120.34
3	A	1361	NAJ	N3A-C2A-N1A	-3.91	122.37	128.68
3	B	1361	NAJ	O7N-C7N-C3N	-3.89	114.91	119.62
3	A	1361	NAJ	C2N-C3N-C4N	3.87	122.71	118.26
3	A	1361	NAJ	O7N-C7N-C3N	-3.84	114.97	119.62
3	B	1361	NAJ	C2N-C3N-C4N	3.39	122.16	118.26
3	A	1361	NAJ	C5N-C4N-C3N	-3.14	116.57	120.34
3	A	1361	NAJ	C1B-N9A-C4A	-3.02	121.41	126.64
3	B	1361	NAJ	C4B-O4B-C1B	-2.36	107.37	109.83

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1361	NAJ	C4A-C5A-N7A	-2.35	106.95	109.40
3	B	1361	NAJ	O7N-C7N-N7N	-2.23	119.42	122.60
3	A	1361	NAJ	O2N-PN-O1N	2.16	123.04	112.21
3	B	1361	NAJ	O4B-C4B-C3B	2.10	109.29	105.14
3	B	1361	NAJ	C2A-N1A-C6A	2.01	122.25	118.77

There are no chirality outliers.

All (5) torsion outliers are listed below:

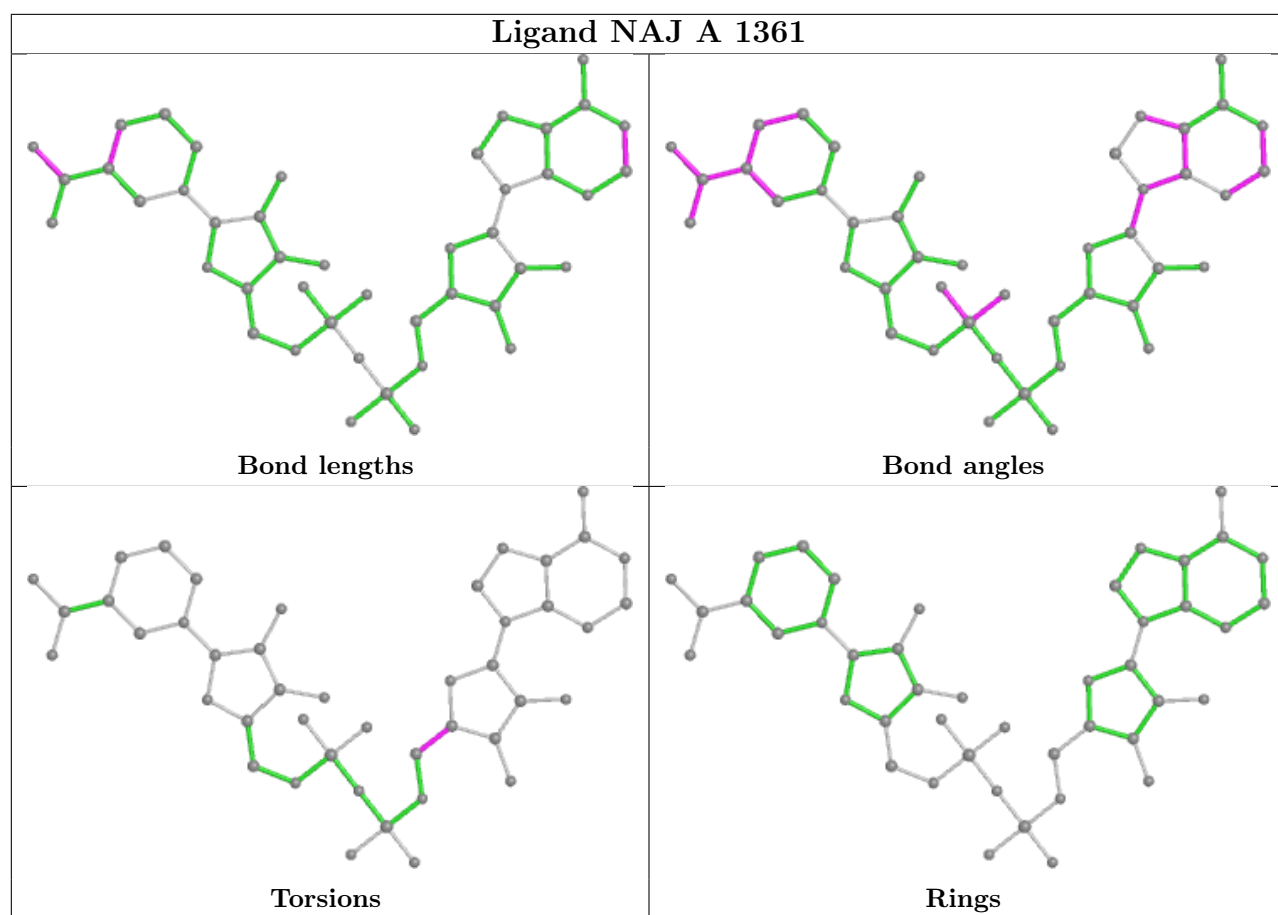
Mol	Chain	Res	Type	Atoms
3	B	1361	NAJ	PN-O3-PA-O1A
3	A	1361	NAJ	O4B-C4B-C5B-O5B
2	A	1360	OCA	C3-C4-C5-C6
3	B	1361	NAJ	O4B-C4B-C5B-O5B
3	B	1361	NAJ	PN-O3-PA-O2A

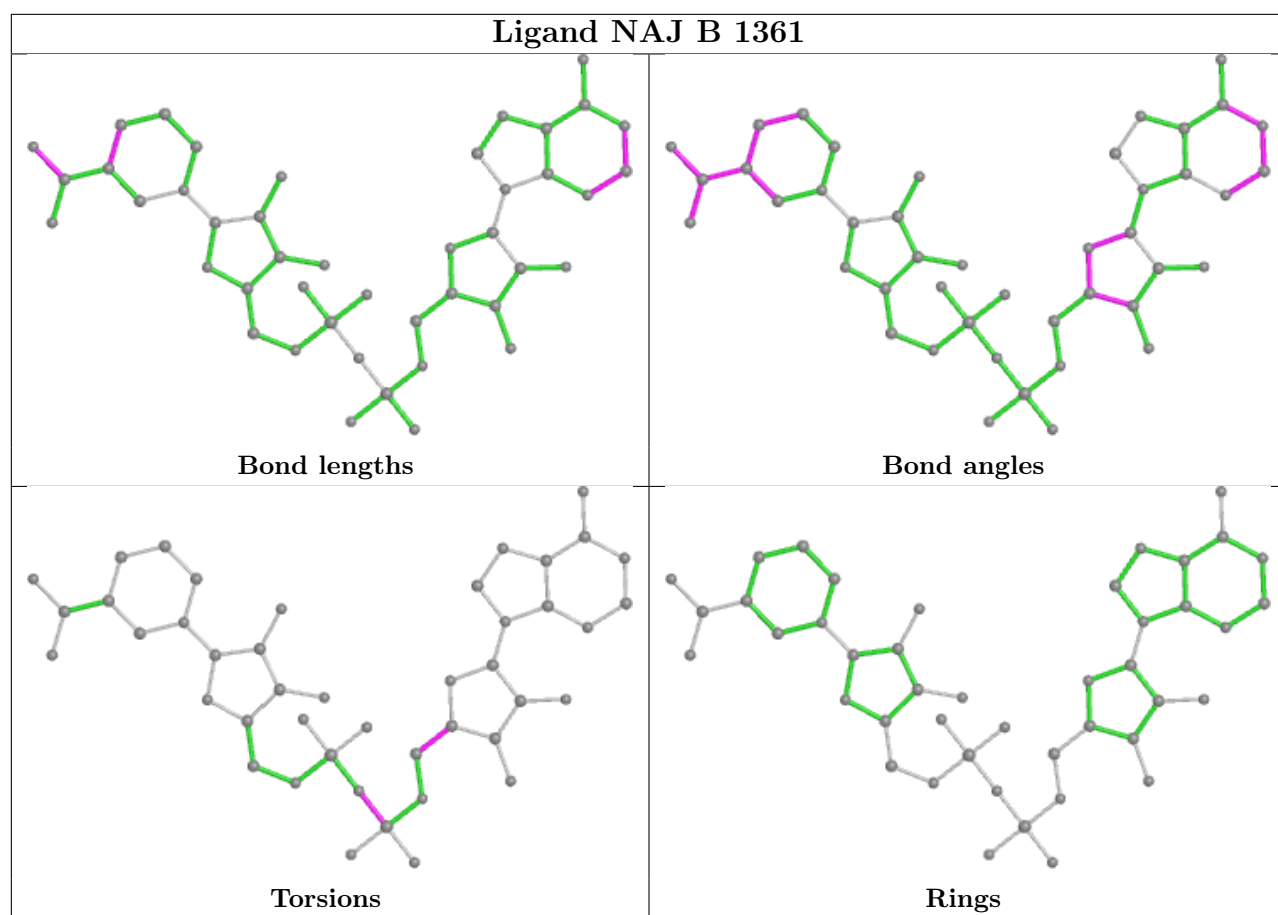
There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	1361	NAJ	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 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

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	343/359 (95%)	-0.08	20 (5%) 23 20	14, 22, 45, 72	0
1	B	344/359 (95%)	-0.25	9 (2%) 56 54	13, 20, 41, 53	0
All	All	687/718 (95%)	-0.16	29 (4%) 36 32	13, 21, 43, 72	0

All (29) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	16	LEU	8.3
1	A	70	GLN	4.3
1	A	72	LYS	4.3
1	A	91	GLY	4.0
1	A	68	LEU	3.9
1	A	359	PRO	3.9
1	A	93	GLU	3.8
1	B	113	LEU	3.7
1	A	66	HIS	3.7
1	A	111	THR	3.6
1	A	125	ASN	3.5
1	A	90	GLU	3.2
1	B	240	ARG	3.1
1	A	67	GLU	3.0
1	A	69	LEU	2.9
1	B	125	ASN	2.8
1	B	111	THR	2.8
1	A	32	ASP	2.6
1	B	70	GLN	2.5
1	A	33	VAL	2.4
1	B	359	PRO	2.4
1	A	112	CYS	2.3
1	A	17	LYS	2.3
1	A	34	ASP	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	110	GLY	2.2
1	B	115	CYS	2.1
1	B	154	ASP	2.0
1	A	96	GLU	2.0
1	A	109	ASP	2.0

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 carbohydrates in this entry.

6.4 Ligands [i](#)

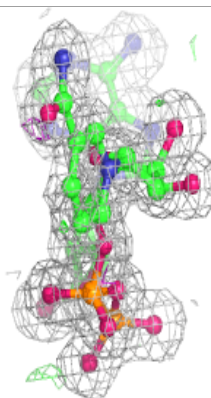
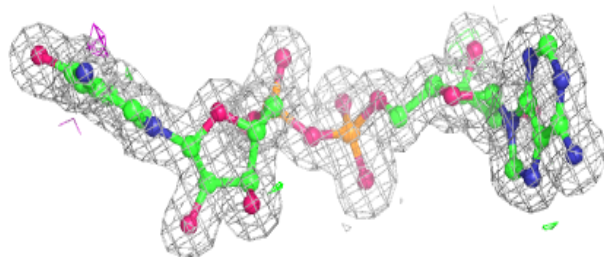
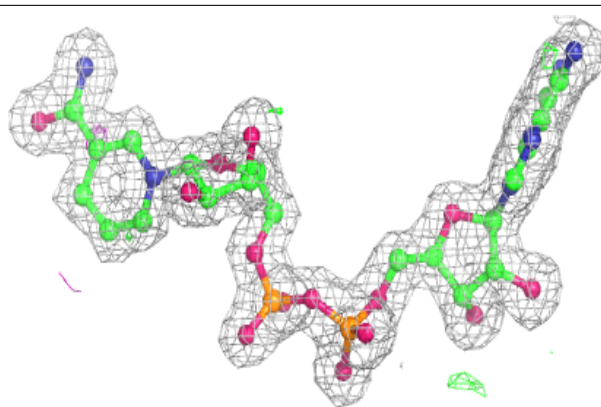
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	OCA	A	1360	10/10	0.92	0.09	19,30,33,40	0
2	OCA	B	1360	10/10	0.93	0.08	19,25,31,35	0
4	ZN	B	1363	1/1	0.98	0.12	32,32,32,32	1
3	NAJ	B	1361	44/44	0.98	0.05	13,15,18,19	0
3	NAJ	A	1361	44/44	0.98	0.05	12,15,17,19	0
4	ZN	A	1364	1/1	0.99	0.11	30,30,30,30	1
4	ZN	A	1363	1/1	0.99	0.04	22,22,22,22	0
4	ZN	B	1362	1/1	1.00	0.02	17,17,17,17	0
4	ZN	A	1362	1/1	1.00	0.02	19,19,19,19	0

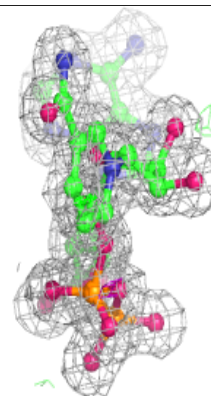
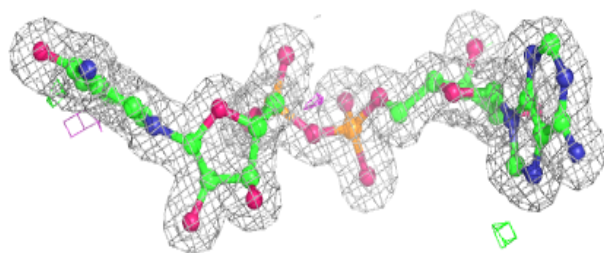
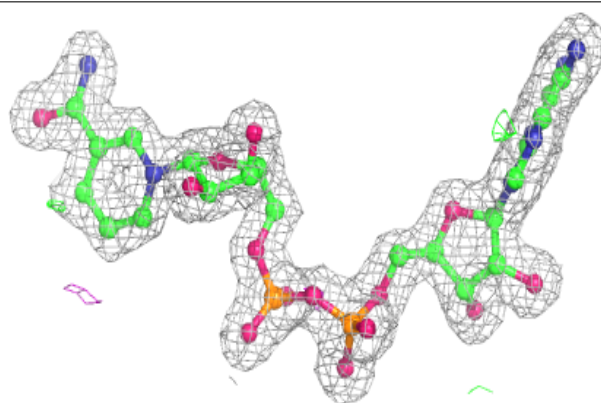
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around NAJ B 1361:

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

**Electron density around NAJ A 1361:**

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



6.5 Other polymers [i](#)

There are no such residues in this entry.