



wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 16, 2018 – 08:56 PM EST

PDB ID : 2CLP
Title : Crystal structure of human aflatoxin B1 aldehyde reductase member 3
Authors : Debreczeni, J.E.; Marsden, B.D.; Johansson, C.; Kavanagh, K.; Guo, K.; Smees, C.; Gileadi, O.; Turnbull, A.; Papagrigoriou, E.; von Delft, F.; Edwards, A.; Arrowsmith, C.; Weigelt, J.; Sundstrom, M.; Oppermann, U.
Deposited on : 2006-04-28
Resolution : 3.00 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

<http://wwpdb.org/validation/2016/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 : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20030736
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20030736

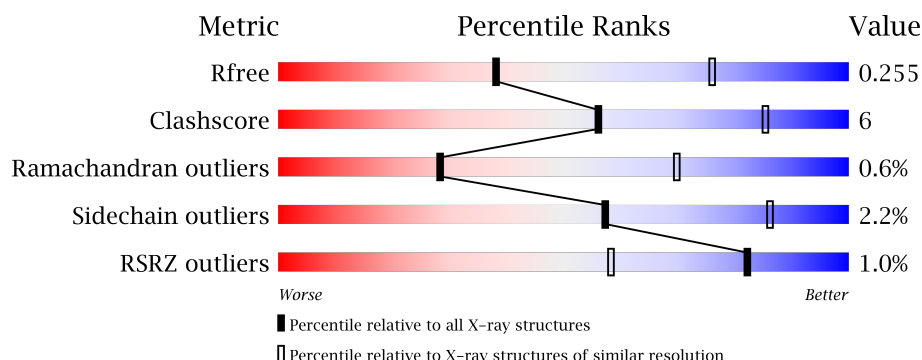
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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}	100719	1692 (3.00-3.00)
Clashscore	112137	2037 (3.00-3.00)
Ramachandran outliers	110173	1973 (3.00-3.00)
Sidechain outliers	110143	1976 (3.00-3.00)
RSRZ outliers	101464	1716 (3.00-3.00)

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	347	<div> <div>84%</div> <div>7% • 7%</div> </div>
1	B	347	<div> <div>84%</div> <div>8% • 7%</div> </div>
1	C	347	<div> <div>84%</div> <div>8% • 7%</div> </div>
1	D	347	<div> <div>85%</div> <div>7% • 7%</div> </div>
1	E	347	<div> <div>85%</div> <div>7% • 7%</div> </div>

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Mol	Chain	Length	Quality of chain
1	F	347	<div><div></div><div>85%</div><div>7% • 7%</div></div>
1	G	347	<div><div></div><div>85%</div><div>7% • 7%</div></div>
1	H	347	<div><div>%</div><div></div><div>84%</div><div>8% • 7%</div></div>
1	I	347	<div><div>5%</div><div></div><div>84%</div><div>7% • 7%</div></div>
1	J	347	<div><div>3%</div><div></div><div>86%</div><div>6% • 7%</div></div>
1	K	347	<div><div></div><div>84%</div><div>8% • 7%</div></div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 27441 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 AFLATOXIN B1 ALDEHYDE REDUCTASE MEMBER 3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	323	Total	C	N	O	S	0	0	0
			2445	1566	419	444	16			
1	B	323	Total	C	N	O	S	0	0	0
			2445	1566	418	445	16			
1	C	323	Total	C	N	O	S	0	0	0
			2443	1565	417	445	16			
1	D	323	Total	C	N	O	S	0	0	0
			2444	1568	416	444	16			
1	E	323	Total	C	N	O	S	0	0	0
			2445	1568	417	444	16			
1	F	323	Total	C	N	O	S	0	0	0
			2451	1569	420	446	16			
1	G	323	Total	C	N	O	S	0	0	0
			2455	1569	424	446	16			
1	H	323	Total	C	N	O	S	0	0	0
			2439	1564	417	442	16			
1	I	322	Total	C	N	O	S	0	0	0
			2427	1556	412	443	16			
1	J	323	Total	C	N	O	S	0	0	0
			2443	1565	417	445	16			
1	K	323	Total	C	N	O	S	0	0	0
			2460	1573	424	447	16			

There are 11 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	244	ASP	ASN	variant	UNP O95154
B	244	ASP	ASN	variant	UNP O95154
C	244	ASP	ASN	variant	UNP O95154
D	244	ASP	ASN	variant	UNP O95154
E	244	ASP	ASN	variant	UNP O95154
F	244	ASP	ASN	variant	UNP O95154
G	244	ASP	ASN	variant	UNP O95154

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Chain	Residue	Modelled	Actual	Comment	Reference
H	244	ASP	ASN	variant	UNP O95154
I	244	ASP	ASN	variant	UNP O95154
J	244	ASP	ASN	variant	UNP O95154
K	244	ASP	ASN	variant	UNP O95154

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- The chemical structure of NDP (Nucleoside Diphosphate) is shown. It consists of a sugar moiety (ribose or deoxyribose) linked to a phosphate group, which is further linked to a nucleobase. The sugar is a five-membered ring with an oxygen atom at the top. The phosphate group is a central phosphorus atom (P) bonded to four oxygen atoms. The nucleobase is a six-membered ring with a nitrogen atom at the bottom. The structure is labeled with various atoms and bonds, including NH₂, NH, N, O, P, and C. The sugar is labeled with C1, C2, C3, C4, and C5. The phosphate group is labeled with P1, P2, and P3. The nucleobase is labeled with N1, N2, N3, N4, N5, and N6. The structure is shown in a 3D representation with wedges and dashes indicating stereochemistry.

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	J	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
2	K	1	Total	C	N	O	P	0	0
			48	21	7	17	3		

- Molecule 3 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	G	1	Total	Ca	0	0
			1	1		
3	A	1	Total	Ca	0	0
			1	1		
3	C	1	Total	Ca	0	0
			1	1		
3	E	1	Total	Ca	0	0
			1	1		

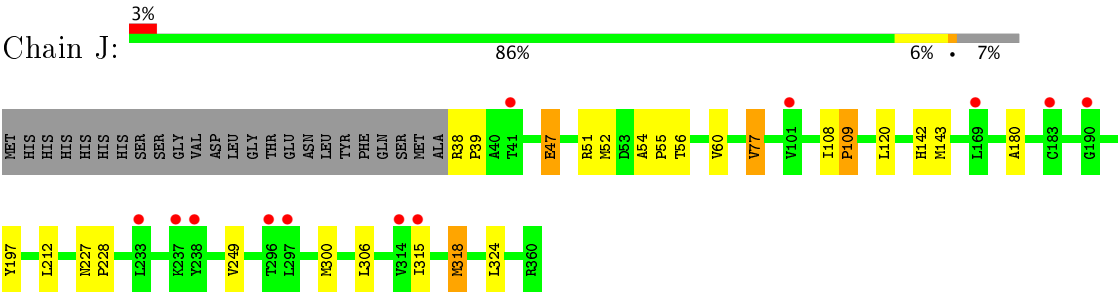
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	2	Total	O	0	0
			2	2		
4	B	2	Total	O	0	0
			2	2		
4	D	1	Total	O	0	0
			1	1		
4	E	2	Total	O	0	0
			2	2		
4	F	2	Total	O	0	0
			2	2		
4	G	1	Total	O	0	0
			1	1		
4	H	1	Total	O	0	0
			1	1		
4	K	1	Total	O	0	0
			1	1		

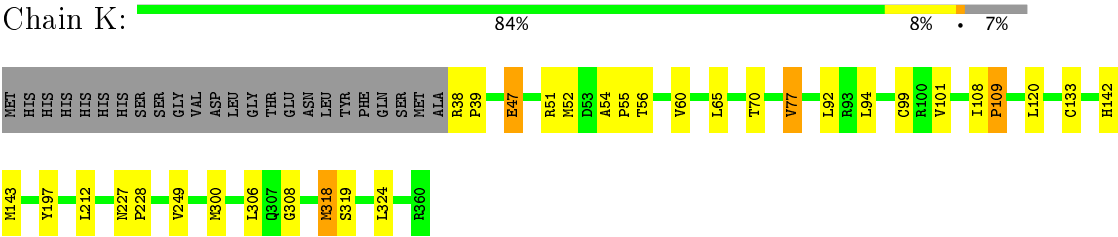
- Molecule 1: AFLATOXIN B1 ALDEHYDE REDUCTASE MEMBER 3



- Molecule 1: AFLATOXIN B1 ALDEHYDE REDUCTASE MEMBER 3



● Molecule 1: AFLATOXIN B1 ALDEHYDE REDUCTASE MEMBER 3



4 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α , β , γ	126.96Å 126.96Å 490.50Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	164.40 – 3.00 59.18 – 3.00	Depositor EDS
% Data completeness (in resolution range)	99.8 (164.40-3.00) 99.7 (59.18-3.00)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.34 (at 3.01Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.239 , 0.253 0.243 , 0.255	Depositor DCC
R_{free} test set	4628 reflections (5.25%)	DCC
Wilson B-factor (Å ²)	54.2	Xtriage
Anisotropy	0.047	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.25 , 19.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.39$, $\langle L^2 \rangle = 0.22$	Xtriage
Estimated twinning fraction	0.097 for -h,-k,l	Xtriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	27441	wwPDB-VP
Average B, all atoms (Å ²)	55.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.08% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: NDP, CA

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	0.46	0/2512	0.56	0/3420
1	B	0.44	0/2512	0.55	0/3420
1	C	0.45	0/2510	0.54	0/3417
1	D	0.46	0/2511	0.55	0/3416
1	E	0.45	0/2512	0.55	0/3419
1	F	0.46	0/2518	0.57	0/3427
1	G	0.46	0/2522	0.57	0/3434
1	H	0.41	0/2506	0.54	0/3412
1	I	0.36	0/2494	0.52	0/3397
1	J	0.36	0/2510	0.51	0/3417
1	K	0.49	0/2527	0.57	0/3438
All	All	0.44	0/27634	0.55	0/37617

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	F	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	F	269	HIS	Sidechain

5.2 Too-close contacts ⓘ

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	2445	0	2278	32	0
1	B	2445	0	2279	29	0
1	C	2443	0	2276	26	0
1	D	2444	0	2271	27	0
1	E	2445	0	2281	29	0
1	F	2451	0	2289	25	0
1	G	2455	0	2296	29	0
1	H	2439	0	2274	34	0
1	I	2427	0	2255	33	0
1	J	2443	0	2276	25	0
1	K	2460	0	2303	27	0
2	A	48	0	26	6	0
2	B	48	0	26	3	0
2	C	48	0	26	2	0
2	D	48	0	26	2	0
2	E	48	0	26	2	0
2	F	48	0	26	2	0
2	G	48	0	26	0	0
2	H	48	0	26	2	0
2	I	48	0	26	5	0
2	J	48	0	26	1	0
2	K	48	0	26	1	0
3	A	1	0	0	0	0
3	C	1	0	0	0	0
3	E	1	0	0	0	0
3	G	1	0	0	0	0
4	A	2	0	0	1	0
4	B	2	0	0	0	0
4	D	1	0	0	0	0
4	E	2	0	0	0	0
4	F	2	0	0	0	0
4	G	1	0	0	0	0
4	H	1	0	0	2	0
4	K	1	0	0	0	0
All	All	27441	0	25364	308	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 6.

The worst 5 of 308 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:J:60:VAL:HG13	1:J:324:LEU:HD22	1.42	1.00
1:E:60:VAL:HG13	1:E:324:LEU:HD22	1.44	0.99
1:H:60:VAL:HG13	1:H:324:LEU:HD22	1.45	0.99
1:K:60:VAL:HG13	1:K:324:LEU:HD22	1.42	0.99
1:G:60:VAL:HG13	1:G:324:LEU:HD22	1.45	0.98

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	321/347 (92%)	310 (97%)	9 (3%)	2 (1%)	28	70
1	B	321/347 (92%)	310 (97%)	9 (3%)	2 (1%)	28	70
1	C	321/347 (92%)	310 (97%)	9 (3%)	2 (1%)	28	70
1	D	321/347 (92%)	311 (97%)	8 (2%)	2 (1%)	28	70
1	E	321/347 (92%)	310 (97%)	9 (3%)	2 (1%)	28	70
1	F	321/347 (92%)	310 (97%)	10 (3%)	1 (0%)	44	81
1	G	321/347 (92%)	310 (97%)	9 (3%)	2 (1%)	28	70
1	H	321/347 (92%)	310 (97%)	9 (3%)	2 (1%)	28	70
1	I	320/347 (92%)	309 (97%)	9 (3%)	2 (1%)	28	70
1	J	321/347 (92%)	310 (97%)	9 (3%)	2 (1%)	28	70
1	K	321/347 (92%)	311 (97%)	8 (2%)	2 (1%)	28	70
All	All	3530/3817 (92%)	3411 (97%)	98 (3%)	21 (1%)	28	70

5 of 21 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	F	249	VAL
1	I	249	VAL
1	A	109	PRO
1	B	249	VAL
1	C	249	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	233/285 (82%)	228 (98%)	5 (2%)	59	87
1	B	234/285 (82%)	229 (98%)	5 (2%)	59	87
1	C	233/285 (82%)	227 (97%)	6 (3%)	51	83
1	D	230/285 (81%)	225 (98%)	5 (2%)	57	86
1	E	233/285 (82%)	228 (98%)	5 (2%)	59	87
1	F	235/285 (82%)	229 (97%)	6 (3%)	51	83
1	G	237/285 (83%)	233 (98%)	4 (2%)	66	89
1	H	232/285 (81%)	226 (97%)	6 (3%)	51	83
1	I	232/285 (81%)	227 (98%)	5 (2%)	57	86
1	J	233/285 (82%)	229 (98%)	4 (2%)	66	89
1	K	237/285 (83%)	231 (98%)	6 (2%)	53	84
All	All	2569/3135 (82%)	2512 (98%)	57 (2%)	57	86

5 of 57 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	318	MET
1	F	318	MET
1	K	77	VAL
1	F	47	GLU
1	F	97	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	269	HIS
1	C	269	HIS
1	F	269	HIS
1	G	349	HIS
1	H	269	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 15 ligands modelled in this entry, 4 are monoatomic - leaving 11 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	NDP	A	1361	-	43,52,52	1.55	4 (9%)	49,80,80	1.52	3 (6%)
2	NDP	B	1361	-	43,52,52	1.60	4 (9%)	49,80,80	1.68	6 (12%)
2	NDP	C	1361	-	43,52,52	1.46	4 (9%)	49,80,80	1.73	5 (10%)
2	NDP	D	1361	-	43,52,52	1.56	4 (9%)	49,80,80	1.60	2 (4%)
2	NDP	E	1361	-	43,52,52	1.56	4 (9%)	49,80,80	1.68	2 (4%)
2	NDP	F	1361	-	43,52,52	1.49	4 (9%)	49,80,80	1.79	4 (8%)
2	NDP	G	1361	-	43,52,52	1.50	4 (9%)	49,80,80	1.74	3 (6%)
2	NDP	H	1361	-	43,52,52	1.57	5 (11%)	49,80,80	1.73	5 (10%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	NDP	I	1361	-	43,52,52	1.56	4 (9%)	49,80,80	1.80	2 (4%)
2	NDP	J	1361	-	43,52,52	1.56	4 (9%)	49,80,80	1.76	4 (8%)
2	NDP	K	1361	-	43,52,52	1.59	4 (9%)	49,80,80	1.72	3 (6%)

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	NDP	A	1361	-	-	0/30/77/77	0/5/5/5
2	NDP	B	1361	-	-	0/30/77/77	0/5/5/5
2	NDP	C	1361	-	-	0/30/77/77	0/5/5/5
2	NDP	D	1361	-	-	0/30/77/77	0/5/5/5
2	NDP	E	1361	-	-	0/30/77/77	0/5/5/5
2	NDP	F	1361	-	-	0/30/77/77	0/5/5/5
2	NDP	G	1361	-	-	1/30/77/77	0/5/5/5
2	NDP	H	1361	-	-	0/30/77/77	0/5/5/5
2	NDP	I	1361	-	-	0/30/77/77	0/5/5/5
2	NDP	J	1361	-	-	0/30/77/77	0/5/5/5
2	NDP	K	1361	-	-	0/30/77/77	0/5/5/5

The worst 5 of 45 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	H	1361	NDP	O4D-C4D	-2.16	1.40	1.45
2	G	1361	NDP	C2A-N1A	2.49	1.38	1.33
2	H	1361	NDP	C2A-N1A	2.49	1.38	1.33
2	C	1361	NDP	C2A-N1A	2.52	1.38	1.33
2	B	1361	NDP	C2A-N1A	2.53	1.38	1.33

The worst 5 of 39 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	I	1361	NDP	N3A-C2A-N1A	-11.09	119.20	128.86
2	J	1361	NDP	N3A-C2A-N1A	-10.31	119.88	128.86
2	E	1361	NDP	N3A-C2A-N1A	-10.13	120.04	128.86
2	C	1361	NDP	N3A-C2A-N1A	-10.03	120.13	128.86
2	F	1361	NDP	N3A-C2A-N1A	-10.02	120.13	128.86

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	G	1361	NDP	P2B-O2B-C2B-C1B

There are no ring outliers.

10 monomers are involved in 26 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1361	NDP	6	0
2	B	1361	NDP	3	0
2	C	1361	NDP	2	0
2	D	1361	NDP	2	0
2	E	1361	NDP	2	0
2	F	1361	NDP	2	0
2	H	1361	NDP	2	0
2	I	1361	NDP	5	0
2	J	1361	NDP	1	0
2	K	1361	NDP	1	0

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	323/347 (93%)	-0.29	0 100 100	50, 56, 61, 66	0
1	B	323/347 (93%)	-0.17	1 (0%) 93 82	47, 56, 61, 64	0
1	C	323/347 (93%)	-0.26	1 (0%) 93 82	48, 56, 61, 65	0
1	D	323/347 (93%)	-0.27	0 100 100	47, 55, 61, 66	0
1	E	323/347 (93%)	-0.31	0 100 100	48, 55, 61, 66	0
1	F	323/347 (93%)	-0.28	0 100 100	47, 56, 60, 63	0
1	G	323/347 (93%)	-0.22	0 100 100	48, 56, 60, 69	0
1	H	323/347 (93%)	-0.06	3 (0%) 84 61	48, 56, 61, 63	0
1	I	322/347 (92%)	0.30	19 (5%) 23 9	51, 56, 59, 61	0
1	J	323/347 (93%)	0.22	12 (3%) 42 18	51, 56, 60, 61	0
1	K	323/347 (93%)	-0.25	0 100 100	47, 56, 62, 66	0
All	All	3552/3817 (93%)	-0.14	36 (1%) 82 58	47, 56, 61, 69	0

The worst 5 of 36 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	I	284	ALA	3.9
1	I	316	LEU	3.7
1	J	190	GLY	3.4
1	I	300	MET	3.4
1	B	97	SER	3.4

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 [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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
2	NDP	E	1361	48/48	0.97	0.21	0.09	33,41,50,50	0
2	NDP	I	1361	48/48	0.91	0.28	-0.08	63,71,88,88	0
2	NDP	J	1361	48/48	0.94	0.23	-0.61	67,70,82,83	0
2	NDP	A	1361	48/48	0.96	0.15	-1.12	24,31,56,57	0
2	NDP	C	1361	48/48	0.96	0.14	-1.14	27,40,55,57	0
2	NDP	H	1361	48/48	0.94	0.15	-1.17	52,57,67,68	0
2	NDP	D	1361	48/48	0.97	0.14	-1.22	28,40,54,55	0
2	NDP	K	1361	48/48	0.97	0.14	-1.25	30,38,44,45	0
2	NDP	B	1361	48/48	0.96	0.15	-1.39	35,45,56,57	0
2	NDP	F	1361	48/48	0.97	0.12	-1.73	27,35,44,45	0
2	NDP	G	1361	48/48	0.97	0.12	-1.87	26,34,44,44	0
3	CA	A	1362	1/1	0.97	0.19	-	37,37,37,37	0
3	CA	G	1362	1/1	0.97	0.18	-	30,30,30,30	0
3	CA	E	1362	1/1	0.97	0.13	-	35,35,35,35	0
3	CA	C	1362	1/1	0.92	0.19	-	41,41,41,41	0

6.5 Other polymers [i](#)

There are no such residues in this entry.