



# wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 31, 2016 – 06:36 PM GMT

PDB ID : 1BJQ  
Title : THE DOLICHOS BIFLORUS SEED LECTIN IN COMPLEX WITH ADENINE  
Authors : Hamelryck, T.W.; Loris, R.; Bouckaert, J.; Dao-Thi, M.H.; Wyns, L.; Etzler, M.  
Deposited on : 1998-06-26  
Resolution : 2.65 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](mailto: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.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
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) : trunk26865

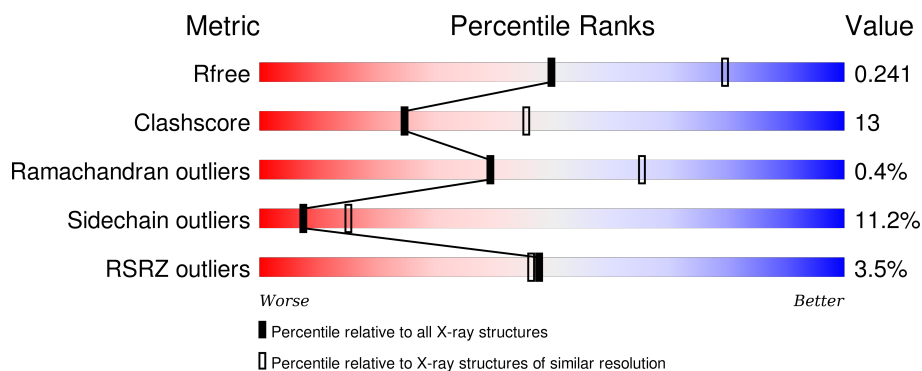
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.65 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))
$R_{free}$	91344	3152 (2.70-2.62)
Clashscore	102246	3524 (2.70-2.62)
Ramachandran outliers	100387	3469 (2.70-2.62)
Sidechain outliers	100360	3469 (2.70-2.62)
RSRZ outliers	91569	3161 (2.70-2.62)

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  $\geq 3$ , 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	253	<div> <div>2%</div> <div>66% 31% ..</div> </div>
1	B	253	<div> <div>2%</div> <div>68% 29% .</div> </div>
1	C	253	<div> <div>%</div> <div>64% 26% . 8%</div> </div>
1	D	253	<div> <div>%</div> <div>62% 28% . 8%</div> </div>
1	E	253	<div> <div>3%</div> <div>62% 28% . 8%</div> </div>

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Mol	Chain	Length	Quality of chain
1	F	253	
1	G	253	
1	H	253	

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
4	ADE	A	601	-	-	-	X
4	ADE	B	601	-	-	-	X
4	ADE	C	601	-	-	-	X
4	ADE	D	601	-	-	-	X
4	ADE	E	601	-	-	-	X
4	ADE	F	601	-	-	-	X
4	ADE	G	601	-	-	-	X
4	ADE	H	601	-	-	-	X

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 14698 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 LECTIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	251	Total	C	N	O	S	0	0	0
			1887	1198	306	382	1			
1	B	253	Total	C	N	O	S	0	0	0
			1898	1204	308	385	1			
1	C	233	Total	C	N	O	S	0	0	0
			1758	1116	287	354	1			
1	D	233	Total	C	N	O	S	0	0	0
			1758	1116	287	354	1			
1	E	233	Total	C	N	O	S	0	0	0
			1758	1116	287	354	1			
1	F	233	Total	C	N	O	S	0	0	0
			1758	1116	287	354	1			
1	G	251	Total	C	N	O	S	0	0	0
			1887	1198	306	382	1			
1	H	253	Total	C	N	O	S	0	0	0
			1898	1204	308	385	1			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	127	LEU	PHE	CONFLICT	UNP P05045
B	127	LEU	PHE	CONFLICT	UNP P05045
C	127	LEU	PHE	CONFLICT	UNP P05045
D	127	LEU	PHE	CONFLICT	UNP P05045
E	127	LEU	PHE	CONFLICT	UNP P05045
F	127	LEU	PHE	CONFLICT	UNP P05045
G	127	LEU	PHE	CONFLICT	UNP P05045
H	127	LEU	PHE	CONFLICT	UNP P05045

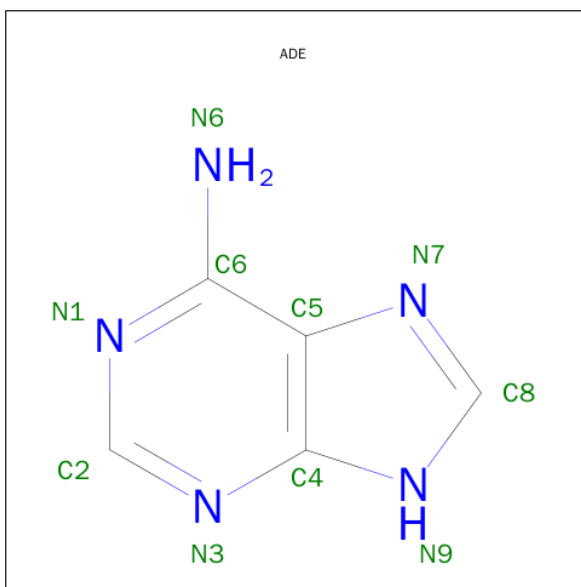
- Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	G	1	Total Ca 1 1	0	0
2	D	1	Total Ca 1 1	0	0
2	E	1	Total Ca 1 1	0	0
2	H	1	Total Ca 1 1	0	0
2	B	1	Total Ca 1 1	0	0
2	C	1	Total Ca 1 1	0	0
2	A	1	Total Ca 1 1	0	0
2	F	1	Total Ca 1 1	0	0

- Molecule 3 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	G	1	Total Mn 1 1	0	0
3	D	1	Total Mn 1 1	0	0
3	E	1	Total Mn 1 1	0	0
3	H	1	Total Mn 1 1	0	0
3	B	1	Total Mn 1 1	0	0
3	C	1	Total Mn 1 1	0	0
3	A	1	Total Mn 1 1	0	0
3	F	1	Total Mn 1 1	0	0

- Molecule 4 is ADENINE (three-letter code: ADE) (formula: C<sub>5</sub>H<sub>5</sub>N<sub>5</sub>).

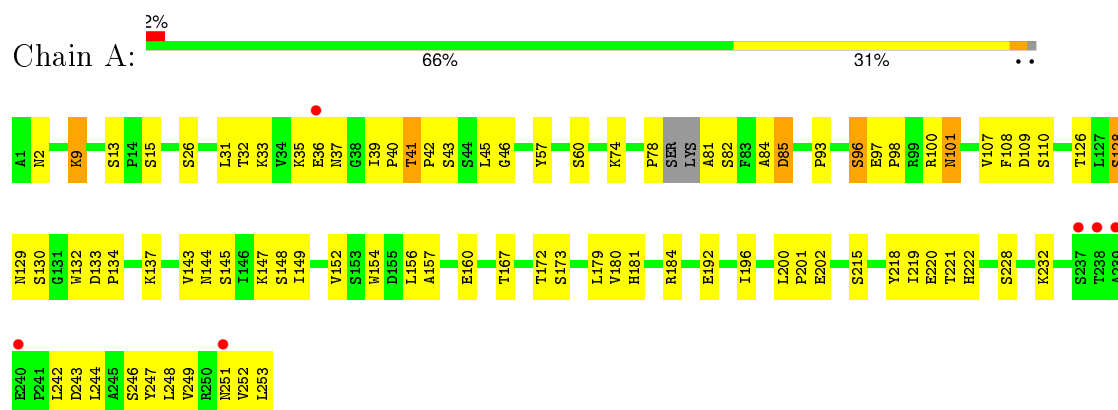


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	N	0	0
			10	5	5		
4	B	1	Total	C	N	0	0
			10	5	5		
4	C	1	Total	C	N	0	0
			10	5	5		
4	D	1	Total	C	N	0	0
			10	5	5		
4	E	1	Total	C	N	0	0
			10	5	5		
4	F	1	Total	C	N	0	0
			10	5	5		
4	G	1	Total	C	N	0	0
			10	5	5		
4	H	1	Total	C	N	0	0
			10	5	5		

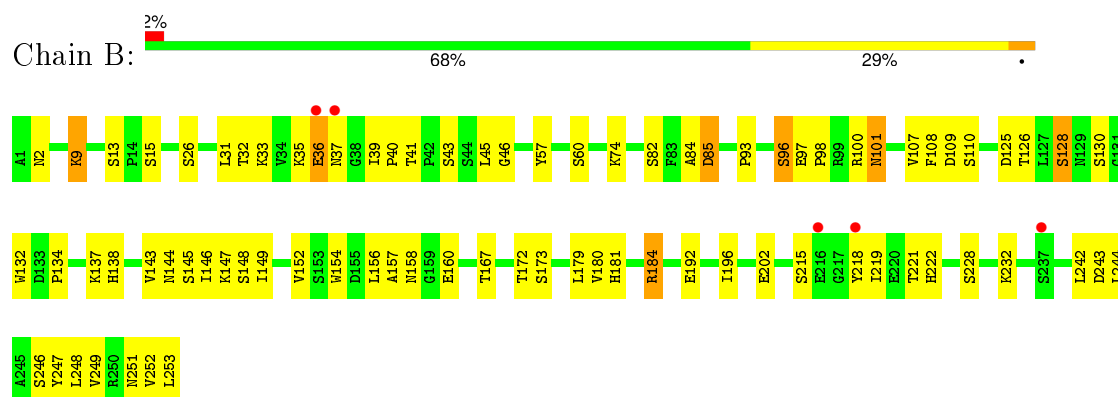
### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

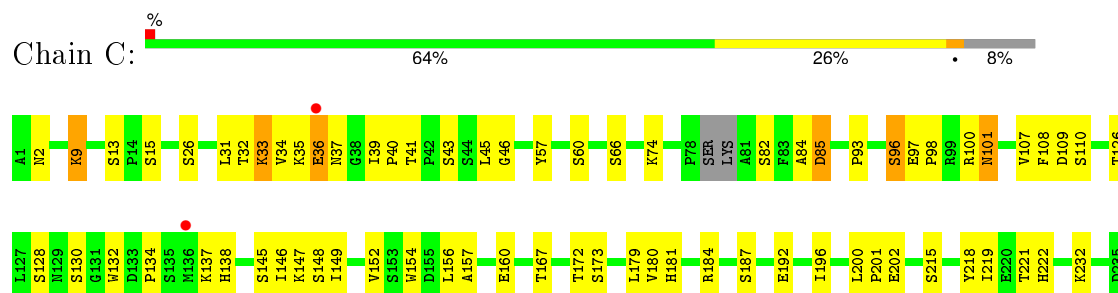
#### • Molecule 1: LECTIN



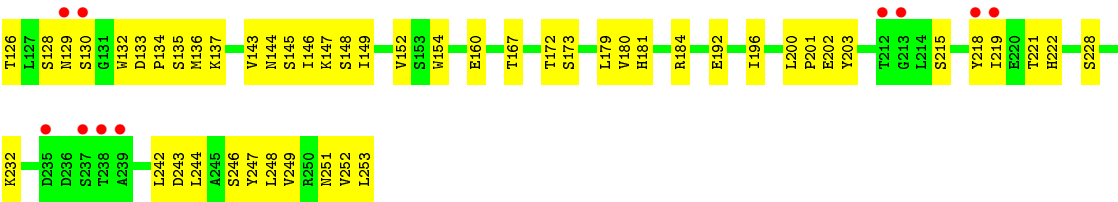
#### • Molecule 1: LECTIN



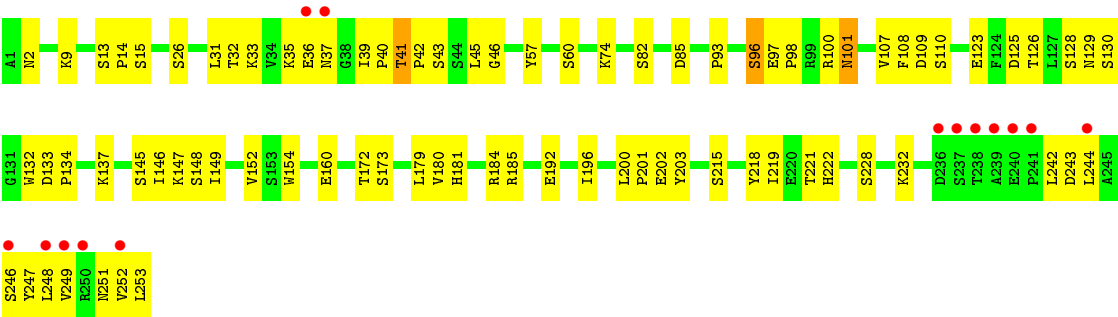
#### • Molecule 1: LECTIN



Category	Count
A1	10
K9	15
S13	10
P14	10
S15	10
S26	10
L31	10
T32	10
K33	10
V34	10
K35	10
E36	10
N37	10
G38	10
I39	10
P40	10
T41	10
P42	10
S43	10
S44	10
L45	10
G46	10
Y57	10
S60	10
K74	10
P78	10
SER	10
LYS	10
A81	10
S82	10
F83	10
A84	10
D85	10
P93	10
V94	10
G95	10
S96	10
E97	10
F98	10
R99	10
A100	10
M101	10
V107	10
F108	10
D109	10
S110	10
D111	10
S115	10



• Molecule 1: LECTIN



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	81.38Å 116.14Å 224.62Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.65 20.00 – 2.65	Depositor EDS
% Data completeness (in resolution range)	92.5 (20.00-2.65) 92.5 (20.00-2.65)	Depositor EDS
$R_{merge}$	0.12	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.98 (at 2.67Å)	Xtriage
Refinement program	X-PLOR 3.851	Depositor
R, $R_{free}$	0.219 , 0.246 0.216 , 0.241	Depositor DCC
$R_{free}$ test set	5889 reflections (10.18%)	DCC
Wilson B-factor (Å <sup>2</sup> )	28.8	Xtriage
Anisotropy	0.249	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 38.5	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	1 of 57851 reflections (0.002%)	Xtriage
$F_o, F_c$ correlation	0.91	EDS
Total number of atoms	14698	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.93% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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: CA, MN, ADE

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	0.44	0/1929	0.67	0/2634
1	B	0.44	0/1941	0.68	0/2652
1	C	0.45	0/1798	0.68	0/2453
1	D	0.45	0/1798	0.68	0/2453
1	E	0.45	0/1798	0.67	0/2453
1	F	0.46	0/1798	0.68	0/2453
1	G	0.45	0/1929	0.67	0/2634
1	H	0.44	0/1941	0.67	0/2652
All	All	0.45	0/14932	0.67	0/20384

There are no bond length outliers.

There are no bond angle outliers.

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	1887	0	1826	54	0
1	B	1898	0	1834	57	0
1	C	1758	0	1703	44	0
1	D	1758	0	1703	45	0
1	E	1758	0	1703	45	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	F	1758	0	1703	44	0
1	G	1887	0	1826	61	0
1	H	1898	0	1834	51	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
2	E	1	0	0	0	0
2	F	1	0	0	0	0
2	G	1	0	0	0	0
2	H	1	0	0	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
3	E	1	0	0	0	0
3	F	1	0	0	0	0
3	G	1	0	0	0	0
3	H	1	0	0	0	0
4	A	10	0	4	1	0
4	B	10	0	4	1	0
4	C	10	0	4	1	0
4	D	10	0	4	0	0
4	E	10	0	4	1	0
4	F	10	0	4	1	0
4	G	10	0	4	1	0
4	H	10	0	4	0	0
All	All	14698	0	14164	368	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 368 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:B:158:ASN:H	1:G:136:MET:HE1	1.01	1.12
1:B:158:ASN:N	1:G:136:MET:HE1	1.83	0.92
1:G:37:ASN:HD21	1:G:39:ILE:HG12	1.39	0.86
1:D:37:ASN:HD21	1:D:39:ILE:HG12	1.41	0.85
1:F:37:ASN:HD21	1:F:39:ILE:HG12	1.41	0.85

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	247/253 (98%)	231 (94%)	15 (6%)	1 (0%)	39	65
1	B	251/253 (99%)	237 (94%)	13 (5%)	1 (0%)	39	65
1	C	229/253 (90%)	217 (95%)	11 (5%)	1 (0%)	39	65
1	D	229/253 (90%)	218 (95%)	10 (4%)	1 (0%)	39	65
1	E	229/253 (90%)	217 (95%)	11 (5%)	1 (0%)	39	65
1	F	229/253 (90%)	217 (95%)	11 (5%)	1 (0%)	39	65
1	G	247/253 (98%)	230 (93%)	16 (6%)	1 (0%)	39	65
1	H	251/253 (99%)	234 (93%)	16 (6%)	1 (0%)	39	65
All	All	1912/2024 (94%)	1801 (94%)	103 (5%)	8 (0%)	39	65

5 of 8 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	96	SER
1	B	96	SER
1	C	96	SER
1	D	96	SER
1	E	96	SER

### 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	209/214 (98%)	185 (88%)	24 (12%)	7	14
1	B	210/214 (98%)	186 (89%)	24 (11%)	7	14
1	C	195/214 (91%)	173 (89%)	22 (11%)	7	15
1	D	195/214 (91%)	174 (89%)	21 (11%)	8	16
1	E	195/214 (91%)	173 (89%)	22 (11%)	7	15
1	F	195/214 (91%)	173 (89%)	22 (11%)	7	15
1	G	209/214 (98%)	186 (89%)	23 (11%)	8	16
1	H	210/214 (98%)	187 (89%)	23 (11%)	8	16
All	All	1618/1712 (94%)	1437 (89%)	181 (11%)	7	15

5 of 181 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	101	ASN
1	E	82	SER
1	H	74	LYS
1	D	145	SER
1	E	9	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 65 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	55	GLN
1	E	37	ASN
1	H	101	ASN
1	D	101	ASN
1	D	222	HIS

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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 24 ligands modelled in this entry, 16 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	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
4	ADE	A	601	-	8,11,11	0.95	0	4,15,15	0.75	0
4	ADE	B	601	-	8,11,11	0.92	0	4,15,15	0.74	0
4	ADE	C	601	-	8,11,11	0.92	0	4,15,15	0.96	0
4	ADE	D	601	-	8,11,11	0.94	0	4,15,15	0.99	0
4	ADE	E	601	-	8,11,11	0.90	0	4,15,15	0.90	0
4	ADE	F	601	-	8,11,11	0.86	0	4,15,15	0.91	0
4	ADE	G	601	-	8,11,11	0.89	0	4,15,15	0.91	0
4	ADE	H	601	-	8,11,11	0.89	0	4,15,15	0.88	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
4	ADE	A	601	-	-	0/0/0/0	0/2/2/2
4	ADE	B	601	-	-	0/0/0/0	0/2/2/2
4	ADE	C	601	-	-	0/0/0/0	0/2/2/2
4	ADE	D	601	-	-	0/0/0/0	0/2/2/2
4	ADE	E	601	-	-	0/0/0/0	0/2/2/2
4	ADE	F	601	-	-	0/0/0/0	0/2/2/2
4	ADE	G	601	-	-	0/0/0/0	0/2/2/2
4	ADE	H	601	-	-	0/0/0/0	0/2/2/2

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

6 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	601	ADE	1	0
4	B	601	ADE	1	0
4	C	601	ADE	1	0
4	E	601	ADE	1	0
4	F	601	ADE	1	0
4	G	601	ADE	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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	251/253 (99%)	-0.30	6 (2%) 62 60	3, 18, 49, 68	0
1	B	253/253 (100%)	-0.25	5 (1%) 68 67	4, 19, 51, 70	0
1	C	233/253 (92%)	-0.30	2 (0%) 85 86	3, 19, 37, 67	0
1	D	233/253 (92%)	-0.44	2 (0%) 85 86	3, 17, 37, 68	0
1	E	233/253 (92%)	-0.12	7 (3%) 54 52	14, 27, 46, 69	0
1	F	233/253 (92%)	0.30	11 (4%) 35 33	12, 32, 50, 76	0
1	G	251/253 (99%)	0.47	21 (8%) 14 11	12, 37, 57, 78	0
1	H	253/253 (100%)	-0.00	14 (5%) 29 26	12, 26, 56, 72	0
All	All	1940/2024 (95%)	-0.08	68 (3%) 48 46	3, 24, 51, 78	0

The worst 5 of 68 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	H	249	VAL	5.6
1	F	136	MET	5.4
1	F	36	GLU	5.3
1	G	218	TYR	5.2
1	H	238	THR	4.7

### 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 ⓘ

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
4	ADE	A	601	10/10	0.94	0.39	6.94	2,2,2,2	10
4	ADE	G	601	10/10	0.94	0.33	6.49	2,2,2,2	10
4	ADE	E	601	10/10	0.90	0.33	5.94	6,7,8,9	10
4	ADE	C	601	10/10	0.89	0.30	5.65	2,2,3,5	10
4	ADE	H	601	10/10	0.88	0.42	3.77	2,2,2,2	10
4	ADE	B	601	10/10	0.93	0.34	3.75	2,2,2,2	10
4	ADE	D	601	10/10	0.91	0.32	3.37	2,2,2,2	10
4	ADE	F	601	10/10	0.84	0.34	2.83	6,7,7,8	10
2	CA	A	301	1/1	0.95	0.15	1.05	12,12,12,12	0
2	CA	B	301	1/1	0.95	0.12	-0.94	19,19,19,19	0
2	CA	H	301	1/1	0.88	0.10	-1.05	29,29,29,29	0
3	MN	D	302	1/1	0.81	0.08	-1.21	46,46,46,46	0
2	CA	F	301	1/1	0.77	0.15	-1.34	36,36,36,36	0
3	MN	H	302	1/1	0.94	0.09	-1.52	45,45,45,45	0
2	CA	E	301	1/1	0.95	0.10	-1.53	28,28,28,28	0
3	MN	A	302	1/1	0.94	0.08	-1.71	45,45,45,45	0
2	CA	D	301	1/1	0.94	0.08	-1.78	11,11,11,11	0
3	MN	F	302	1/1	0.91	0.10	-1.95	63,63,63,63	0
2	CA	C	301	1/1	0.92	0.11	-2.02	19,19,19,19	0
3	MN	B	302	1/1	0.96	0.07	-2.08	46,46,46,46	0
2	CA	G	301	1/1	0.89	0.08	-2.61	59,59,59,59	0
3	MN	G	302	1/1	0.78	0.11	-2.65	67,67,67,67	0
3	MN	E	302	1/1	0.92	0.07	-2.80	52,52,52,52	0
3	MN	C	302	1/1	0.96	0.07	-3.08	41,41,41,41	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.