



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2026 – 08:23 PM UTC

PDB ID : 3MLP / pdb\_00003mlp  
Title : Early B-cell Factor 1 (Ebf1) bound to DNA  
Authors : Treiber, N.; Treiber, T.; Zocher, G.; Grosschedl, R.  
Deposited on : 2010-04-17  
Resolution : 2.80 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

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4-5-2 with Phenix2.0  
Mogul : 2022.3.0, CSD as543be (2022)  
Xtriage (Phenix) : 2.0  
EDS : 3.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
CCP4 : 9.0.010 (Gargrove)  
Density-Fitness : 1.0.12  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

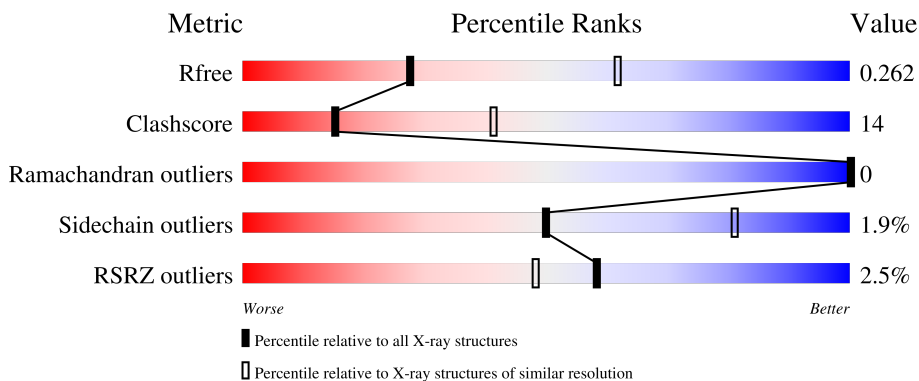
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.80 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))
$R_{free}$	180053	3866 (2.80-2.80)
Clashscore	190562	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)
RSRZ outliers	180081	3869 (2.80-2.80)

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  $\geq 3$ , 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  $\leq 5\%$ . 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	402	 3% 62% 22% 16%
1	B	402	 3% 58% 24% 17%
1	E	402	 2% 56% 18% 25%
1	F	402	 % 54% 20% 26%
2	C	22	 59% 41%

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Mol	Chain	Length	Quality of chain
2	D	22	 55% 36% 9%
2	G	22	 86% 14%
2	H	22	 64% 32% 5%

## 2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 11961 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 Transcription factor COE1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	337	2626	1653	475	482	16	0	0	0
1	B	332	2591	1637	462	477	15	0	0	0
1	E	303	2399	1511	435	438	15	0	0	0
1	F	298	2334	1475	415	429	15	0	0	0

There are 76 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	GLY	deletion	UNP Q07802
A	?	-	THR	deletion	UNP Q07802
A	?	-	PRO	deletion	UNP Q07802
A	?	-	SER	deletion	UNP Q07802
A	?	-	TYR	deletion	UNP Q07802
A	?	-	LEU	deletion	UNP Q07802
A	?	-	GLU	deletion	UNP Q07802
A	252	ALA	HIS	engineered mutation	UNP Q07802
A	415	ALA	-	expression tag	UNP Q07802
A	416	ALA	-	expression tag	UNP Q07802
A	417	VAL	-	expression tag	UNP Q07802
A	418	LEU	-	expression tag	UNP Q07802
A	419	GLU	-	expression tag	UNP Q07802
A	420	HIS	-	expression tag	UNP Q07802
A	421	HIS	-	expression tag	UNP Q07802
A	422	HIS	-	expression tag	UNP Q07802
A	423	HIS	-	expression tag	UNP Q07802
A	424	HIS	-	expression tag	UNP Q07802
A	425	HIS	-	expression tag	UNP Q07802
B	?	-	GLY	deletion	UNP Q07802
B	?	-	THR	deletion	UNP Q07802

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Chain	Residue	Modelled	Actual	Comment	Reference
B	?	-	PRO	deletion	UNP Q07802
B	?	-	SER	deletion	UNP Q07802
B	?	-	TYR	deletion	UNP Q07802
B	?	-	LEU	deletion	UNP Q07802
B	?	-	GLU	deletion	UNP Q07802
B	252	ALA	HIS	engineered mutation	UNP Q07802
B	415	ALA	-	expression tag	UNP Q07802
B	416	ALA	-	expression tag	UNP Q07802
B	417	VAL	-	expression tag	UNP Q07802
B	418	LEU	-	expression tag	UNP Q07802
B	419	GLU	-	expression tag	UNP Q07802
B	420	HIS	-	expression tag	UNP Q07802
B	421	HIS	-	expression tag	UNP Q07802
B	422	HIS	-	expression tag	UNP Q07802
B	423	HIS	-	expression tag	UNP Q07802
B	424	HIS	-	expression tag	UNP Q07802
B	425	HIS	-	expression tag	UNP Q07802
E	?	-	GLY	deletion	UNP Q07802
E	?	-	THR	deletion	UNP Q07802
E	?	-	PRO	deletion	UNP Q07802
E	?	-	SER	deletion	UNP Q07802
E	?	-	TYR	deletion	UNP Q07802
E	?	-	LEU	deletion	UNP Q07802
E	?	-	GLU	deletion	UNP Q07802
E	252	ALA	HIS	engineered mutation	UNP Q07802
E	415	ALA	-	expression tag	UNP Q07802
E	416	ALA	-	expression tag	UNP Q07802
E	417	VAL	-	expression tag	UNP Q07802
E	418	LEU	-	expression tag	UNP Q07802
E	419	GLU	-	expression tag	UNP Q07802
E	420	HIS	-	expression tag	UNP Q07802
E	421	HIS	-	expression tag	UNP Q07802
E	422	HIS	-	expression tag	UNP Q07802
E	423	HIS	-	expression tag	UNP Q07802
E	424	HIS	-	expression tag	UNP Q07802
E	425	HIS	-	expression tag	UNP Q07802
F	?	-	GLY	deletion	UNP Q07802
F	?	-	THR	deletion	UNP Q07802
F	?	-	PRO	deletion	UNP Q07802
F	?	-	SER	deletion	UNP Q07802
F	?	-	TYR	deletion	UNP Q07802
F	?	-	LEU	deletion	UNP Q07802

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Chain	Residue	Modelled	Actual	Comment	Reference
F	?	-	GLU	deletion	UNP Q07802
F	252	ALA	HIS	engineered mutation	UNP Q07802
F	415	ALA	-	expression tag	UNP Q07802
F	416	ALA	-	expression tag	UNP Q07802
F	417	VAL	-	expression tag	UNP Q07802
F	418	LEU	-	expression tag	UNP Q07802
F	419	GLU	-	expression tag	UNP Q07802
F	420	HIS	-	expression tag	UNP Q07802
F	421	HIS	-	expression tag	UNP Q07802
F	422	HIS	-	expression tag	UNP Q07802
F	423	HIS	-	expression tag	UNP Q07802
F	424	HIS	-	expression tag	UNP Q07802
F	425	HIS	-	expression tag	UNP Q07802

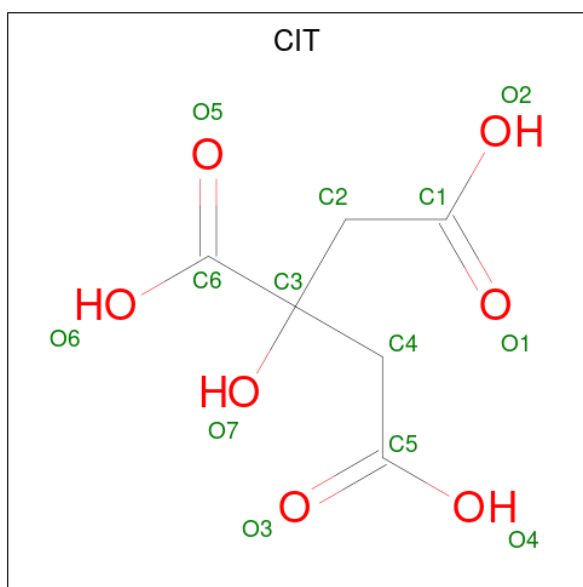
- Molecule 2 is a DNA chain called DNA (5'-D(\*CP\*TP\*TP\*TP\*AP\*TP\*TP\*CP\*CP\*CP\*AP\*TP\*GP\*GP\*GP\*AP\*AP\*TP\*AP\*AP\*AP\*G)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
2	C	22	448	216	81	130	21	0	0	0
2	D	22	448	216	81	130	21	0	0	0
2	G	22	448	216	81	130	21	0	0	0
2	H	22	448	216	81	130	21	0	0	0

- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Zn	0	0
			1	1		
3	B	1	Total	Zn	0	0
			1	1		
3	E	1	Total	Zn	0	0
			1	1		
3	F	1	Total	Zn	0	0
			1	1		

- Molecule 4 is CITRIC ACID (CCD ID: CIT) (formula: C<sub>6</sub>H<sub>8</sub>O<sub>7</sub>).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O 13 6 7	0	0
4	A	1	Total C O 13 6 7	0	0
4	B	1	Total C O 13 6 7	0	0
4	E	1	Total C O 13 6 7	0	0
4	F	1	Total C O 13 6 7	0	0

- Molecule 5 is water.

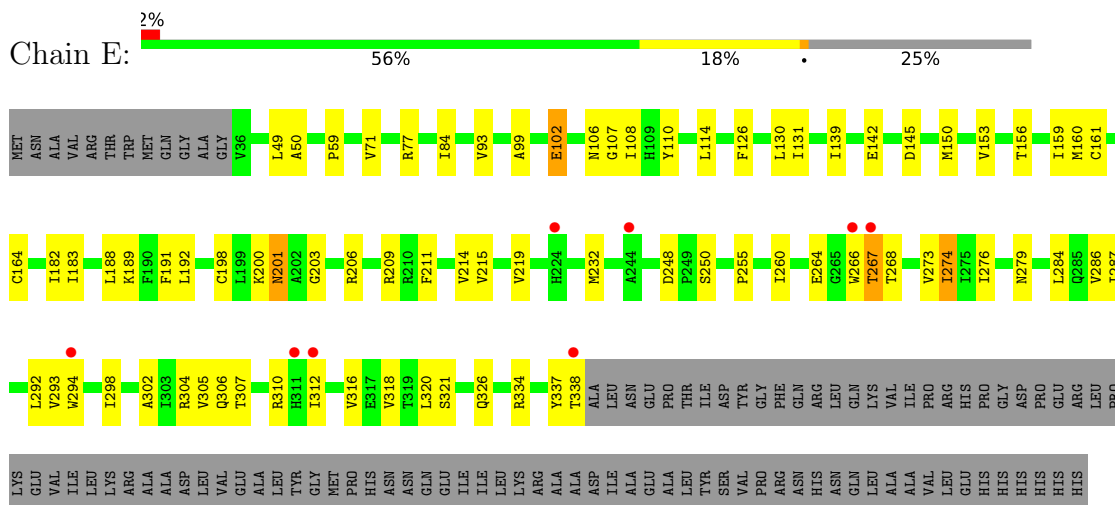
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	36	Total O 36 36	0	0
5	B	24	Total O 24 24	0	0
5	C	3	Total O 3 3	0	0
5	D	4	Total O 4 4	0	0
5	E	34	Total O 34 34	0	0
5	F	35	Total O 35 35	0	0
5	G	8	Total O 8 8	0	0

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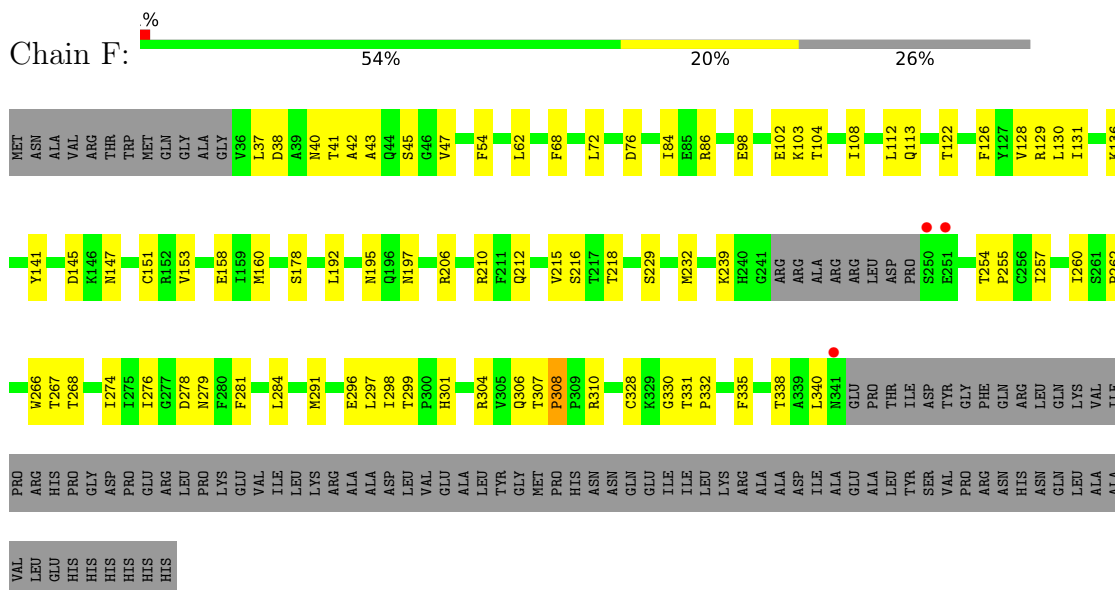
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<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>		<b>ZeroOcc</b>	<b>AltConf</b>
5	H	6	Total	O	0	0
			6	6		





● Molecule 1: Transcription factor COE1




● Molecule 2: DNA (5'-D(\*CP\*TP\*TP\*TP\*AP\*TP\*TP\*CP\*CP\*CP\*AP\*TP\*GP\*GP\*GP\*AP\*AP\*TP\*AP\*AP\*AP\*G)-3')



● Molecule 2: DNA (5'-D(\*CP\*TP\*TP\*TP\*AP\*TP\*TP\*CP\*CP\*CP\*AP\*TP\*GP\*GP\*GP\*AP\*AP\*TP\*AP\*AP\*AP\*G)-3')



- Molecule 2: DNA (5'-D(\*CP\*TP\*TP\*TP\*AP\*TP\*TP\*CP\*CP\*CP\*AP\*TP\*GP\*GP\*GP\*AP\*AP\*TP\*AP\*AP\*AP\*G)-3')

Chain G:  86% 14%



- Molecule 2: DNA (5'-D(\*CP\*TP\*TP\*TP\*AP\*TP\*TP\*CP\*CP\*CP\*AP\*TP\*GP\*GP\*GP\*AP\*AP\*TP\*AP\*AP\*AP\*G)-3')

Chain H:  64% 32% 5%



## 4 Data and refinement statistics i

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	70.49Å 78.69Å 103.57Å 88.99° 90.00° 77.81°	Depositor
Resolution (Å)	38.75 – 2.80 38.75 – 2.80	Depositor EDS
% Data completeness (in resolution range)	100.0 (38.75-2.80) 96.8 (38.75-2.80)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.09	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.01 (at 2.81Å)	Xtrriage
Refinement program	REFMAC 5.5.0109	Depositor
R, $R_{free}$	0.204 , 0.264 0.204 , 0.262	Depositor DCC
$R_{free}$ test set	2592 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	47.2	Xtrriage
Anisotropy	0.386	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.30 , 46.4	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.46$ , $\langle L^2 \rangle = 0.28$	Xtrriage
Estimated twinning fraction	0.036 for -h,-k,l	Xtrriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	11961	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	50.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.77% 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, 0.333 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: ZN, CIT

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	0.63	0/2681	0.82	1/3626 (0.0%)
1	B	0.61	0/2646	0.85	0/3583
1	E	0.66	0/2451	0.84	1/3314 (0.0%)
1	F	0.66	0/2384	0.85	2/3226 (0.1%)
2	C	0.48	0/502	1.11	0/773
2	D	0.57	0/502	1.23	2/773 (0.3%)
2	G	0.46	0/502	1.11	1/773 (0.1%)
2	H	0.47	0/502	1.13	2/773 (0.3%)
All	All	0.62	0/12170	0.90	9/16841 (0.1%)

There are no bond length outliers.

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	10	DC	O3'-P-O5'	-6.40	94.40	104.00
1	F	308	PRO	CA-C-N	-6.11	114.47	120.52
1	F	308	PRO	C-N-CA	-6.11	114.47	120.52
2	D	17	DA	P-O3'-C3'	-5.62	111.76	120.20
1	A	348	GLY	N-CA-C	-5.60	107.38	114.16

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	2626	0	2563	79	0
1	B	2591	0	2527	79	0
1	E	2399	0	2378	73	0
1	F	2334	0	2296	62	0
2	C	448	0	251	8	0
2	D	448	0	251	7	0
2	G	448	0	251	2	0
2	H	448	0	251	8	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	E	1	0	0	0	0
3	F	1	0	0	0	0
4	A	26	0	10	5	0
4	B	13	0	5	3	0
4	E	13	0	5	0	0
4	F	13	0	5	1	0
5	A	36	0	0	1	0
5	B	24	0	0	1	0
5	C	3	0	0	0	0
5	D	4	0	0	1	0
5	E	34	0	0	0	0
5	F	35	0	0	0	0
5	G	8	0	0	0	0
5	H	6	0	0	1	0
All	All	11961	0	10793	306	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 14.

The worst 5 of 306 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:64:LYS:NZ	1:B:197:ASN:OD1	1.87	1.08
1:E:287:ILE:CD1	1:E:292:LEU:HD23	1.94	0.97
1:A:260:ILE:HG22	1:A:260:ILE:O	1.64	0.95
1:B:64:LYS:HZ1	1:B:197:ASN:CG	1.80	0.89
1:E:287:ILE:HD12	1:E:292:LEU:HD23	1.58	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	331/402 (82%)	306 (92%)	25 (8%)	0	100	100
1	B	326/402 (81%)	305 (94%)	21 (6%)	0	100	100
1	E	301/402 (75%)	284 (94%)	17 (6%)	0	100	100
1	F	294/402 (73%)	278 (95%)	16 (5%)	0	100	100
All	All	1252/1608 (78%)	1173 (94%)	79 (6%)	0	100	100

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	Percentiles	
1	A	282/348 (81%)	280 (99%)	2 (1%)	76	91
1	B	279/348 (80%)	273 (98%)	6 (2%)	45	78
1	E	265/348 (76%)	257 (97%)	8 (3%)	36	72
1	F	256/348 (74%)	251 (98%)	5 (2%)	48	80
All	All	1082/1392 (78%)	1061 (98%)	21 (2%)	50	81

5 of 21 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	316	VAL
1	F	206	ARG
1	F	340	LEU

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Mol	Chain	Res	Type
1	F	210	ARG
1	F	84	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 15 such sidechains are listed below:

Mol	Chain	Res	Type
1	E	100	ASN
1	F	118	ASN
1	E	174	ASN
1	F	237	ASN
1	E	326	GLN

### 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 9 ligands modelled in this entry, 4 are monoatomic - leaving 5 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	CIT	E	2	-	12,12,12	1.18	0	17,17,17	1.67	4 (23%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
4	CIT	B	4	-	12,12,12	1.24	0	17,17,17	1.70	4 (23%)
4	CIT	A	1	-	12,12,12	1.23	0	17,17,17	1.77	4 (23%)
4	CIT	F	6	-	12,12,12	1.42	1 (8%)	17,17,17	2.12	6 (35%)
4	CIT	A	3	-	12,12,12	1.03	0	17,17,17	1.70	4 (23%)

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	CIT	E	2	-	-	4/16/16/16	-
4	CIT	B	4	-	-	7/16/16/16	-
4	CIT	A	1	-	-	8/16/16/16	-
4	CIT	F	6	-	-	9/16/16/16	-
4	CIT	A	3	-	-	8/16/16/16	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	F	6	CIT	C4-C3	2.13	1.56	1.54

The worst 5 of 22 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	4	CIT	O6-C6-C3	4.50	121.77	113.14
4	A	1	CIT	O6-C6-C3	4.31	121.41	113.14
4	F	6	CIT	O6-C6-C3	3.90	120.62	113.14
4	F	6	CIT	C4-C3-C2	3.86	119.20	109.31
4	E	2	CIT	O6-C6-C3	3.79	120.41	113.14

There are no chirality outliers.

5 of 36 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	3	CIT	C2-C3-C6-O5
4	A	3	CIT	C2-C3-C6-O6
4	A	3	CIT	O7-C3-C6-O5
4	A	3	CIT	O7-C3-C6-O6

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Mol	Chain	Res	Type	Atoms
4	B	4	CIT	O7-C3-C6-O5

There are no ring outliers.

4 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	4	CIT	3	0
4	A	1	CIT	2	0
4	F	6	CIT	1	0
4	A	3	CIT	3	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 [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<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	337/402 (83%)	-0.09	12 (3%) 46 37	22, 49, 117, 155	0
1	B	332/402 (82%)	0.02	11 (3%) 49 39	29, 48, 111, 158	0
1	E	303/402 (75%)	-0.24	8 (2%) 57 47	23, 44, 94, 140	0
1	F	298/402 (74%)	-0.30	3 (1%) 79 72	22, 44, 83, 127	0
2	C	22/22 (100%)	-0.84	0 100 100	26, 34, 59, 71	0
2	D	22/22 (100%)	-0.80	0 100 100	24, 38, 60, 88	0
2	G	22/22 (100%)	-0.98	0 100 100	24, 30, 58, 67	0
2	H	22/22 (100%)	-1.01	0 100 100	22, 33, 53, 76	0
All	All	1358/1696 (80%)	-0.20	34 (2%) 58 48	22, 46, 106, 158	0

The worst 5 of 34 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	342	GLU	3.9
1	A	244	ALA	3.7
1	A	378	LEU	3.5
1	F	251	GLU	3.3
1	B	339	ALA	3.2

### 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 oligosaccharides 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<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	B-factors(Å <sup>2</sup> )	Q<0.9
4	CIT	F	6	13/13	0.73	0.14	52,59,62,63	0
4	CIT	B	4	13/13	0.79	0.10	61,68,71,71	0
4	CIT	A	3	13/13	0.83	0.09	56,63,66,68	0
4	CIT	E	2	13/13	0.89	0.09	53,56,60,60	0
4	CIT	A	1	13/13	0.91	0.07	42,46,50,51	0
3	ZN	B	501	1/1	1.00	0.02	38,38,38,38	0
3	ZN	E	501	1/1	1.00	0.01	38,38,38,38	0
3	ZN	F	501	1/1	1.00	0.02	32,32,32,32	0
3	ZN	A	501	1/1	1.00	0.02	43,43,43,43	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.