



# Full wwPDB X-ray Structure Validation Report ⓘ

Dec 28, 2016 – 05:26 AM EST

PDB ID : 5HAO  
Title : Structure function studies of R. palustris RubisCO (M331A mutant; CABP-bound)  
Authors : Arbing, M.A.; Shin, A.; Satagopan, S.; North, J.A.; Tabita, F.R.  
Deposited on : 2015-12-30  
Resolution : 2.18 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](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 : 1.7.1 (RC1), CSD as537be (2016)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20028442  
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) : rb-20028442

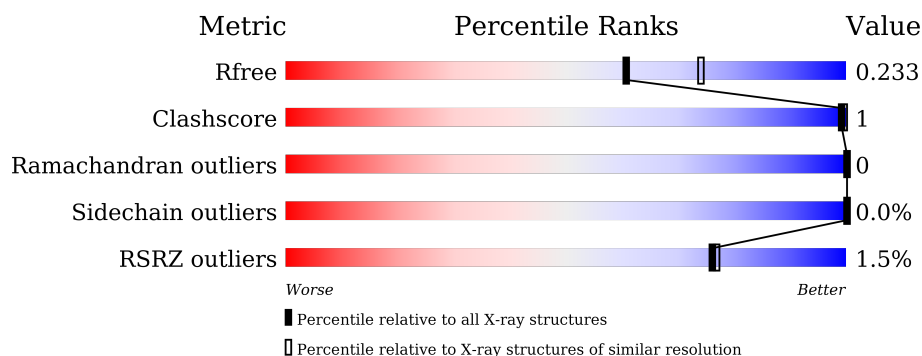
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.18 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	5130 (2.20-2.16)
Clashscore	102246	5965 (2.20-2.16)
Ramachandran outliers	100387	5863 (2.20-2.16)
Sidechain outliers	100360	5864 (2.20-2.16)
RSRZ outliers	91569	5142 (2.20-2.16)

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	481	<div> <div style="width: 92%;"></div> <div>92%</div> <div>5%</div> </div>
1	B	481	<div> <div style="width: 94%;"></div> <div>94%</div> <div>5%</div> </div>
1	C	481	<div> <div style="width: 93%;"></div> <div>93%</div> <div>5%</div> </div>
1	D	481	<div> <div style="width: 93%;"></div> <div>93%</div> <div>5%</div> </div>
1	E	481	<div> <div style="width: 92%;"></div> <div>92%</div> <div>5%</div> </div>
1	F	481	<div> <div style="width: 93%;"></div> <div>93%</div> <div>5%</div> </div>

## 2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 42545 atoms, of which 20339 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 Ribulose biphosphate carboxylase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	455	Total	C	H	N	O	S	0	0	0
			6897	2233	3381	610	655	18			
1	B	455	Total	C	H	N	O	S	0	0	0
			6895	2233	3379	610	655	18			
1	C	455	Total	C	H	N	O	S	0	0	0
			6896	2233	3380	610	655	18			
1	D	455	Total	C	H	N	O	S	0	0	0
			6898	2233	3382	610	655	18			
1	E	455	Total	C	H	N	O	S	0	0	0
			6897	2233	3381	610	655	18			
1	F	455	Total	C	H	N	O	S	0	0	0
			6898	2233	3382	610	655	18			

There are 126 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	initiating methionine	UNP Q6N0W9
A	-18	GLY	-	expression tag	UNP Q6N0W9
A	-17	SER	-	expression tag	UNP Q6N0W9
A	-16	SER	-	expression tag	UNP Q6N0W9
A	-15	HIS	-	expression tag	UNP Q6N0W9
A	-14	HIS	-	expression tag	UNP Q6N0W9
A	-13	HIS	-	expression tag	UNP Q6N0W9
A	-12	HIS	-	expression tag	UNP Q6N0W9
A	-11	HIS	-	expression tag	UNP Q6N0W9
A	-10	HIS	-	expression tag	UNP Q6N0W9
A	-9	SER	-	expression tag	UNP Q6N0W9
A	-8	SER	-	expression tag	UNP Q6N0W9
A	-7	GLY	-	expression tag	UNP Q6N0W9
A	-6	LEU	-	expression tag	UNP Q6N0W9
A	-5	VAL	-	expression tag	UNP Q6N0W9
A	-4	PRO	-	expression tag	UNP Q6N0W9
A	-3	ARG	-	expression tag	UNP Q6N0W9

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	GLY	-	expression tag	UNP Q6N0W9
A	-1	SER	-	expression tag	UNP Q6N0W9
A	0	HIS	-	expression tag	UNP Q6N0W9
A	331	ALA	MET	engineered mutation	UNP Q6N0W9
B	-19	MET	-	initiating methionine	UNP Q6N0W9
B	-18	GLY	-	expression tag	UNP Q6N0W9
B	-17	SER	-	expression tag	UNP Q6N0W9
B	-16	SER	-	expression tag	UNP Q6N0W9
B	-15	HIS	-	expression tag	UNP Q6N0W9
B	-14	HIS	-	expression tag	UNP Q6N0W9
B	-13	HIS	-	expression tag	UNP Q6N0W9
B	-12	HIS	-	expression tag	UNP Q6N0W9
B	-11	HIS	-	expression tag	UNP Q6N0W9
B	-10	HIS	-	expression tag	UNP Q6N0W9
B	-9	SER	-	expression tag	UNP Q6N0W9
B	-8	SER	-	expression tag	UNP Q6N0W9
B	-7	GLY	-	expression tag	UNP Q6N0W9
B	-6	LEU	-	expression tag	UNP Q6N0W9
B	-5	VAL	-	expression tag	UNP Q6N0W9
B	-4	PRO	-	expression tag	UNP Q6N0W9
B	-3	ARG	-	expression tag	UNP Q6N0W9
B	-2	GLY	-	expression tag	UNP Q6N0W9
B	-1	SER	-	expression tag	UNP Q6N0W9
B	0	HIS	-	expression tag	UNP Q6N0W9
B	331	ALA	MET	engineered mutation	UNP Q6N0W9
C	-19	MET	-	initiating methionine	UNP Q6N0W9
C	-18	GLY	-	expression tag	UNP Q6N0W9
C	-17	SER	-	expression tag	UNP Q6N0W9
C	-16	SER	-	expression tag	UNP Q6N0W9
C	-15	HIS	-	expression tag	UNP Q6N0W9
C	-14	HIS	-	expression tag	UNP Q6N0W9
C	-13	HIS	-	expression tag	UNP Q6N0W9
C	-12	HIS	-	expression tag	UNP Q6N0W9
C	-11	HIS	-	expression tag	UNP Q6N0W9
C	-10	HIS	-	expression tag	UNP Q6N0W9
C	-9	SER	-	expression tag	UNP Q6N0W9
C	-8	SER	-	expression tag	UNP Q6N0W9
C	-7	GLY	-	expression tag	UNP Q6N0W9
C	-6	LEU	-	expression tag	UNP Q6N0W9
C	-5	VAL	-	expression tag	UNP Q6N0W9
C	-4	PRO	-	expression tag	UNP Q6N0W9
C	-3	ARG	-	expression tag	UNP Q6N0W9

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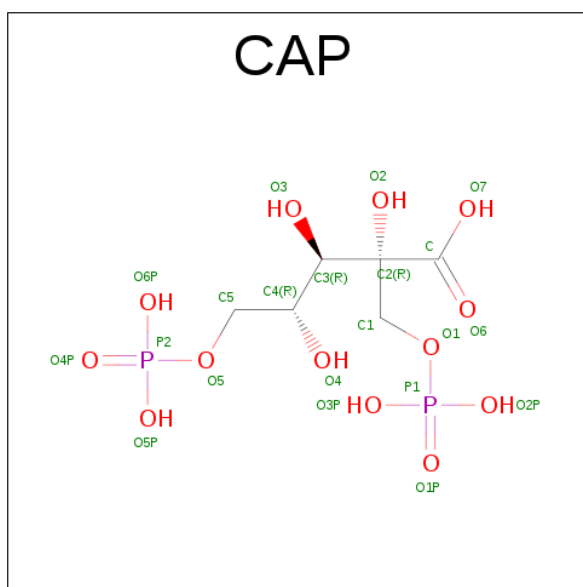
Chain	Residue	Modelled	Actual	Comment	Reference
C	-2	GLY	-	expression tag	UNP Q6N0W9
C	-1	SER	-	expression tag	UNP Q6N0W9
C	0	HIS	-	expression tag	UNP Q6N0W9
C	331	ALA	MET	engineered mutation	UNP Q6N0W9
D	-19	MET	-	initiating methionine	UNP Q6N0W9
D	-18	GLY	-	expression tag	UNP Q6N0W9
D	-17	SER	-	expression tag	UNP Q6N0W9
D	-16	SER	-	expression tag	UNP Q6N0W9
D	-15	HIS	-	expression tag	UNP Q6N0W9
D	-14	HIS	-	expression tag	UNP Q6N0W9
D	-13	HIS	-	expression tag	UNP Q6N0W9
D	-12	HIS	-	expression tag	UNP Q6N0W9
D	-11	HIS	-	expression tag	UNP Q6N0W9
D	-10	HIS	-	expression tag	UNP Q6N0W9
D	-9	SER	-	expression tag	UNP Q6N0W9
D	-8	SER	-	expression tag	UNP Q6N0W9
D	-7	GLY	-	expression tag	UNP Q6N0W9
D	-6	LEU	-	expression tag	UNP Q6N0W9
D	-5	VAL	-	expression tag	UNP Q6N0W9
D	-4	PRO	-	expression tag	UNP Q6N0W9
D	-3	ARG	-	expression tag	UNP Q6N0W9
D	-2	GLY	-	expression tag	UNP Q6N0W9
D	-1	SER	-	expression tag	UNP Q6N0W9
D	0	HIS	-	expression tag	UNP Q6N0W9
D	331	ALA	MET	engineered mutation	UNP Q6N0W9
E	-19	MET	-	initiating methionine	UNP Q6N0W9
E	-18	GLY	-	expression tag	UNP Q6N0W9
E	-17	SER	-	expression tag	UNP Q6N0W9
E	-16	SER	-	expression tag	UNP Q6N0W9
E	-15	HIS	-	expression tag	UNP Q6N0W9
E	-14	HIS	-	expression tag	UNP Q6N0W9
E	-13	HIS	-	expression tag	UNP Q6N0W9
E	-12	HIS	-	expression tag	UNP Q6N0W9
E	-11	HIS	-	expression tag	UNP Q6N0W9
E	-10	HIS	-	expression tag	UNP Q6N0W9
E	-9	SER	-	expression tag	UNP Q6N0W9
E	-8	SER	-	expression tag	UNP Q6N0W9
E	-7	GLY	-	expression tag	UNP Q6N0W9
E	-6	LEU	-	expression tag	UNP Q6N0W9
E	-5	VAL	-	expression tag	UNP Q6N0W9
E	-4	PRO	-	expression tag	UNP Q6N0W9
E	-3	ARG	-	expression tag	UNP Q6N0W9

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Chain	Residue	Modelled	Actual	Comment	Reference
E	-2	GLY	-	expression tag	UNP Q6N0W9
E	-1	SER	-	expression tag	UNP Q6N0W9
E	0	HIS	-	expression tag	UNP Q6N0W9
E	331	ALA	MET	engineered mutation	UNP Q6N0W9
F	-19	MET	-	initiating methionine	UNP Q6N0W9
F	-18	GLY	-	expression tag	UNP Q6N0W9
F	-17	SER	-	expression tag	UNP Q6N0W9
F	-16	SER	-	expression tag	UNP Q6N0W9
F	-15	HIS	-	expression tag	UNP Q6N0W9
F	-14	HIS	-	expression tag	UNP Q6N0W9
F	-13	HIS	-	expression tag	UNP Q6N0W9
F	-12	HIS	-	expression tag	UNP Q6N0W9
F	-11	HIS	-	expression tag	UNP Q6N0W9
F	-10	HIS	-	expression tag	UNP Q6N0W9
F	-9	SER	-	expression tag	UNP Q6N0W9
F	-8	SER	-	expression tag	UNP Q6N0W9
F	-7	GLY	-	expression tag	UNP Q6N0W9
F	-6	LEU	-	expression tag	UNP Q6N0W9
F	-5	VAL	-	expression tag	UNP Q6N0W9
F	-4	PRO	-	expression tag	UNP Q6N0W9
F	-3	ARG	-	expression tag	UNP Q6N0W9
F	-2	GLY	-	expression tag	UNP Q6N0W9
F	-1	SER	-	expression tag	UNP Q6N0W9
F	0	HIS	-	expression tag	UNP Q6N0W9
F	331	ALA	MET	engineered mutation	UNP Q6N0W9

- Molecule 2 is 2-CARBOXYARABINITOL-1,5-DIPHOSPHATE (three-letter code: CAP) (formula:  $C_6H_{14}O_{13}P_2$ ).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	H	O	P	0	0
			30	6	9	13	2		
2	B	1	Total	C	H	O	P	0	0
			30	6	9	13	2		
2	C	1	Total	C	H	O	P	0	0
			30	6	9	13	2		
2	D	1	Total	C	H	O	P	0	0
			30	6	9	13	2		
2	E	1	Total	C	H	O	P	0	0
			30	6	9	13	2		
2	F	1	Total	C	H	O	P	0	0
			30	6	9	13	2		

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

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

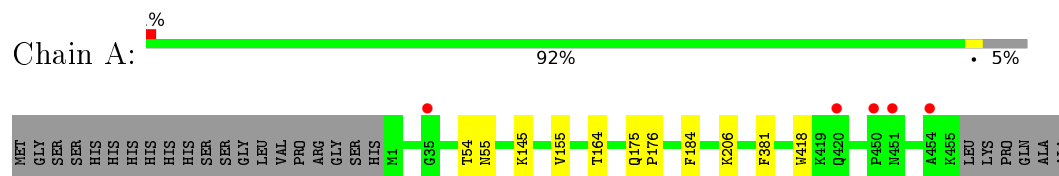
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	158	Total 158	O 158	0	0
4	B	193	Total 193	O 193	0	0
4	C	171	Total 171	O 171	0	0
4	D	142	Total 142	O 142	0	0
4	E	162	Total 162	O 162	0	0
4	F	152	Total 152	O 152	0	0

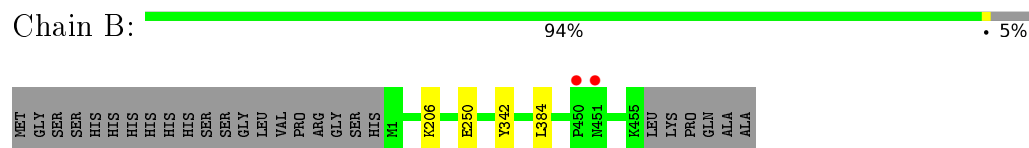
### 3 Residue-property plots [i](#)

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

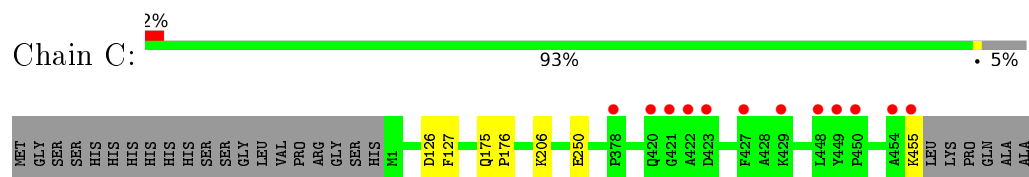
- Molecule 1: Ribulose biphosphate carboxylase



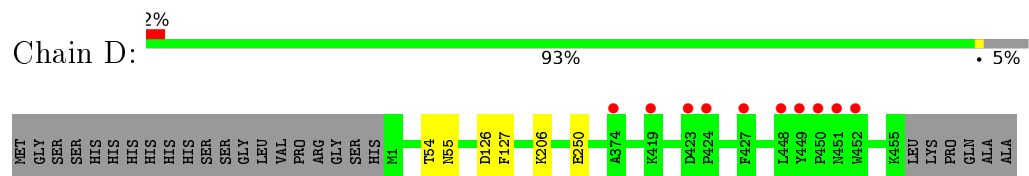
- Molecule 1: Ribulose biphosphate carboxylase



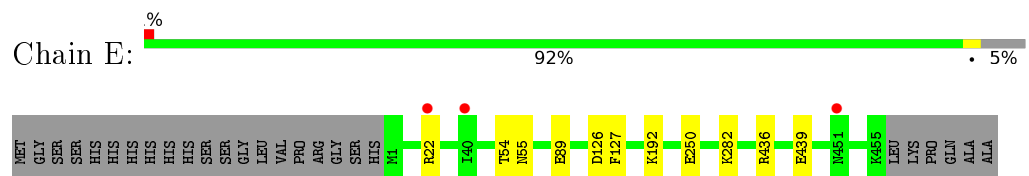
- Molecule 1: Ribulose biphosphate carboxylase



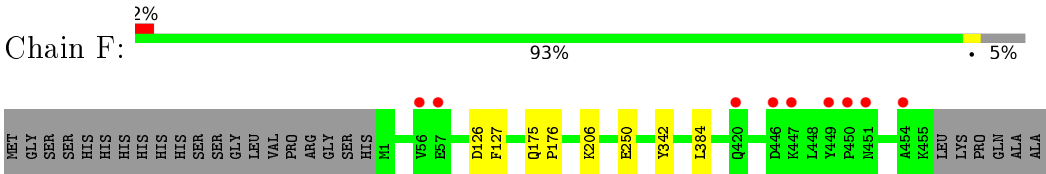
- Molecule 1: Ribulose biphosphate carboxylase



- Molecule 1: Ribulose biphosphate carboxylase



- Molecule 1: Ribulose biphosphate carboxylase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	75.75Å 100.12Å 100.31Å 112.82° 108.14° 88.76°	Depositor
Resolution (Å)	91.69 – 2.18 91.69 – 2.18	Depositor EDS
% Data completeness (in resolution range)	91.4 (91.69-2.18) 80.6 (91.69-2.18)	Depositor EDS
$R_{merge}$	0.12	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	0.96 (at 2.18Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.9_1692)	Depositor
R, $R_{free}$	0.201 , 0.233 0.202 , 0.233	Depositor DCC
$R_{free}$ test set	12198 reflections (10.00%)	DCC
Wilson B-factor (Å <sup>2</sup> )	28.6	Xtriage
Anisotropy	0.135	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.38 , 41.3	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	42545	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.72% 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: MG, CAP, KCX

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	0.24	0/3592	0.41	0/4861
1	B	0.24	0/3592	0.40	0/4861
1	C	0.24	0/3592	0.40	0/4861
1	D	0.24	0/3592	0.41	0/4861
1	E	0.23	0/3592	0.40	0/4861
1	F	0.23	0/3592	0.39	0/4861
All	All	0.24	0/21552	0.40	0/29166

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	3516	3381	3386	6	0
1	B	3516	3379	3386	3	0
1	C	3516	3380	3386	4	0
1	D	3516	3382	3386	4	0
1	E	3516	3381	3386	7	0
1	F	3516	3382	3386	5	0
2	A	21	9	8	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	21	9	7	0	0
2	C	21	9	7	0	0
2	D	21	9	7	0	0
2	E	21	9	7	1	0
2	F	21	9	7	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
4	A	158	0	0	0	0
4	B	193	0	0	0	0
4	C	171	0	0	0	0
4	D	142	0	0	0	0
4	E	162	0	0	1	0
4	F	152	0	0	0	0
All	All	22206	20339	20359	24	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 1.

All (24) 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:206:LYS:NZ	1:F:250:GLU:OE2	2.20	0.72
1:D:250:GLU:OE1	1:F:206:LYS:NZ	2.22	0.72
1:A:206:LYS:NZ	1:C:250:GLU:OE2	2.17	0.72
1:C:206:LYS:NZ	1:E:250:GLU:OE2	2.30	0.52
1:B:250:GLU:OE1	1:D:206:LYS:NZ	2.24	0.51
1:F:342:TYR:OH	1:F:384:LEU:O	2.25	0.49
1:E:436:ARG:NH1	1:E:439:GLU:OE1	2.46	0.48
1:E:192:KCX:OQ1	2:E:500:CAP:O3	2.32	0.47
1:E:54:THR:OG1	1:E:55:ASN:N	2.46	0.45
1:E:22:ARG:NH2	1:E:89:GLU:OE2	2.49	0.44
1:D:126:ASP:OD1	1:D:127:PHE:N	2.51	0.43
1:E:126:ASP:OD1	1:E:127:PHE:N	2.51	0.43
1:A:381:PHE:HB3	1:A:418:TRP:CE2	2.53	0.43
1:A:175:GLN:HB3	1:A:176:PRO:HD3	2.01	0.42
1:A:54:THR:OG1	1:A:55:ASN:N	2.52	0.42
1:C:126:ASP:OD1	1:C:127:PHE:N	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:54:THR:OG1	1:D:55:ASN:N	2.50	0.41
1:A:145:LYS:HG3	1:A:155:VAL:HB	2.03	0.41
1:E:282:LYS:NZ	4:E:627:HOH:O	2.53	0.41
1:C:175:GLN:HB3	1:C:176:PRO:HD3	2.02	0.41
1:F:126:ASP:OD1	1:F:127:PHE:N	2.54	0.41
1:A:164:THR:HB	1:A:184:PHE:CE1	2.55	0.41
1:F:175:GLN:HB3	1:F:176:PRO:HD3	2.03	0.41
1:B:342:TYR:OH	1:B:384:LEU:O	2.26	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	Percentiles	
1	A	452/481 (94%)	436 (96%)	16 (4%)	0	100	100
1	B	452/481 (94%)	435 (96%)	17 (4%)	0	100	100
1	C	452/481 (94%)	436 (96%)	16 (4%)	0	100	100
1	D	452/481 (94%)	435 (96%)	17 (4%)	0	100	100
1	E	452/481 (94%)	437 (97%)	15 (3%)	0	100	100
1	F	452/481 (94%)	437 (97%)	15 (3%)	0	100	100
All	All	2712/2886 (94%)	2616 (96%)	96 (4%)	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	350/371 (94%)	350 (100%)	0	100	100
1	B	350/371 (94%)	350 (100%)	0	100	100
1	C	350/371 (94%)	349 (100%)	1 (0%)	94	98
1	D	350/371 (94%)	350 (100%)	0	100	100
1	E	350/371 (94%)	350 (100%)	0	100	100
1	F	350/371 (94%)	350 (100%)	0	100	100
All	All	2100/2226 (94%)	2099 (100%)	1 (0%)	100	100

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	455	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

6 non-standard protein/DNA/RNA residues are modelled in this entry.

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	$\# Z  > 2$
1	KCX	A	192	1,3	6,11,12	0.58	0	7,12,14	0.95	1 (14%)
1	KCX	B	192	1,3	6,11,12	0.56	0	7,12,14	0.88	1 (14%)
1	KCX	C	192	1,3	6,11,12	0.57	0	7,12,14	0.92	1 (14%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
1	KCX	D	192	1,3	6,11,12	0.60	0	7,12,14	0.92	1 (14%)
1	KCX	E	192	1,3	6,11,12	0.58	0	7,12,14	0.85	1 (14%)
1	KCX	F	192	1,3	6,11,12	0.58	0	7,12,14	0.75	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
1	KCX	A	192	1,3	-	0/6/10/12	0/0/0/0
1	KCX	B	192	1,3	-	0/6/10/12	0/0/0/0
1	KCX	C	192	1,3	-	0/6/10/12	0/0/0/0
1	KCX	D	192	1,3	-	0/6/10/12	0/0/0/0
1	KCX	E	192	1,3	-	0/6/10/12	0/0/0/0
1	KCX	F	192	1,3	-	0/6/10/12	0/0/0/0

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	192	KCX	O-C-CA	-2.22	119.77	125.72
1	A	192	KCX	O-C-CA	-2.15	119.95	125.72
1	B	192	KCX	O-C-CA	-2.15	119.97	125.72
1	C	192	KCX	O-C-CA	-2.12	120.02	125.72
1	E	192	KCX	O-C-CA	-2.01	120.33	125.72

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	E	192	KCX	1	0

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry

Of 12 ligands modelled in this entry, 6 are monoatomic - leaving 6 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	CAP	A	500	3	14,20,20	0.77	0	16,31,31	0.82	1 (6%)
2	CAP	B	500	3	14,20,20	0.78	0	16,31,31	0.82	0
2	CAP	C	500	3	14,20,20	0.79	0	16,31,31	0.82	0
2	CAP	D	500	3	14,20,20	0.79	0	16,31,31	0.93	1 (6%)
2	CAP	E	500	3	14,20,20	0.79	0	16,31,31	0.80	0
2	CAP	F	500	3	14,20,20	0.80	0	16,31,31	0.85	1 (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	CAP	A	500	3	-	0/23/29/29	0/0/0/0
2	CAP	B	500	3	-	0/23/29/29	0/0/0/0
2	CAP	C	500	3	-	0/23/29/29	0/0/0/0
2	CAP	D	500	3	-	0/23/29/29	0/0/0/0
2	CAP	E	500	3	-	0/23/29/29	0/0/0/0
2	CAP	F	500	3	-	0/23/29/29	0/0/0/0

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	500	CAP	O3-C3-C4	2.05	113.23	109.07
2	D	500	CAP	O3-C3-C4	2.09	113.30	109.07
2	F	500	CAP	O3-C3-C4	2.12	113.38	109.07

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	E	500	CAP	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	454/481 (94%)	0.18	5 (1%) 82 83	18, 37, 66, 89	0
1	B	454/481 (94%)	0.07	2 (0%) 93 93	16, 35, 57, 69	0
1	C	454/481 (94%)	0.20	12 (2%) 59 61	20, 41, 73, 103	0
1	D	454/481 (94%)	0.19	10 (2%) 65 66	18, 39, 69, 94	0
1	E	454/481 (94%)	0.18	3 (0%) 89 89	18, 38, 63, 73	0
1	F	454/481 (94%)	0.24	9 (1%) 68 69	19, 40, 73, 100	0
All	All	2724/2886 (94%)	0.17	41 (1%) 76 77	16, 39, 66, 103	0

All (41) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	449	TYR	5.2
1	F	450	PRO	4.5
1	D	449	TYR	4.0
1	C	422	ALA	3.9
1	C	449	TYR	3.7
1	C	427	PHE	3.3
1	C	450	PRO	3.2
1	D	451	ASN	3.2
1	F	451	ASN	3.0
1	C	448	LEU	2.9
1	D	448	LEU	2.8
1	A	454	ALA	2.7
1	D	450	PRO	2.6
1	E	40	ILE	2.6
1	E	451	ASN	2.6
1	A	451	ASN	2.5
1	C	421	GLY	2.5
1	F	56	VAL	2.5
1	F	420	GLN	2.4

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Mol	Chain	Res	Type	RSRZ
1	F	447	LYS	2.4
1	C	454	ALA	2.4
1	C	455	LYS	2.4
1	D	427	PHE	2.3
1	D	374	ALA	2.3
1	F	454	ALA	2.3
1	D	452	TRP	2.2
1	A	35	GLY	2.2
1	B	450	PRO	2.2
1	C	378	PRO	2.2
1	F	446	ASP	2.2
1	C	420	GLN	2.1
1	D	419	LYS	2.1
1	A	420	GLN	2.1
1	D	424	PRO	2.1
1	C	423	ASP	2.1
1	B	451	ASN	2.1
1	C	429	LYS	2.1
1	F	57	GLU	2.0
1	D	423	ASP	2.0
1	A	450	PRO	2.0
1	E	22	ARG	2.0

## 6.2 Non-standard residues in protein, DNA, RNA chains

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
1	KCX	B	192	12/13	0.96	0.13	-	23,27,30,30	0
1	KCX	D	192	12/13	0.95	0.11	-	26,29,34,35	0
1	KCX	F	192	12/13	0.93	0.12	-	30,36,38,39	0
1	KCX	C	192	12/13	0.93	0.12	-	30,33,38,38	0
1	KCX	A	192	12/13	0.95	0.12	-	29,32,36,37	0
1	KCX	E	192	12/13	0.93	0.14	-	27,30,37,37	0

### 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, 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
2	CAP	D	500	21/21	0.97	0.14	1.03	34,40,48,48	0
2	CAP	A	500	21/21	0.97	0.14	0.29	30,37,45,50	0
2	CAP	E	500	21/21	0.96	0.12	-0.16	27,31,45,48	0
2	CAP	C	500	21/21	0.97	0.11	-0.26	37,42,49,51	0
2	CAP	F	500	21/21	0.97	0.12	-0.57	35,41,50,54	0
3	MG	D	501	1/1	0.97	0.12	-0.84	31,31,31,31	0
2	CAP	B	500	21/21	0.98	0.09	-1.85	24,30,37,38	0
3	MG	B	501	1/1	0.96	0.06	-2.75	29,29,29,29	0
3	MG	F	501	1/1	0.99	0.06	-2.84	33,33,33,33	0
3	MG	E	501	1/1	0.85	0.07	-3.41	30,30,30,30	0
3	MG	C	501	1/1	0.94	0.07	-5.14	43,43,43,43	0
3	MG	A	501	1/1	0.96	0.05	-5.62	28,28,28,28	0

### 6.5 Other polymers [i](#)

There are no such residues in this entry.