



# Full wwPDB X-ray Structure Validation Report ⓘ

Apr 20, 2016 – 01:14 PM EDT

PDB ID : 5C2G  
Title : GWS1B RubisCO: Form II RubisCO derived from uncultivated Gallionellacea species (CABP-bound).  
Authors : Arbing, M.A.; Varaljay, V.A.; Satagopan, S.; Tabita, F.R.  
Deposited on : 2015-06-15  
Resolution : 2.60 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-20027257  
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-20027257

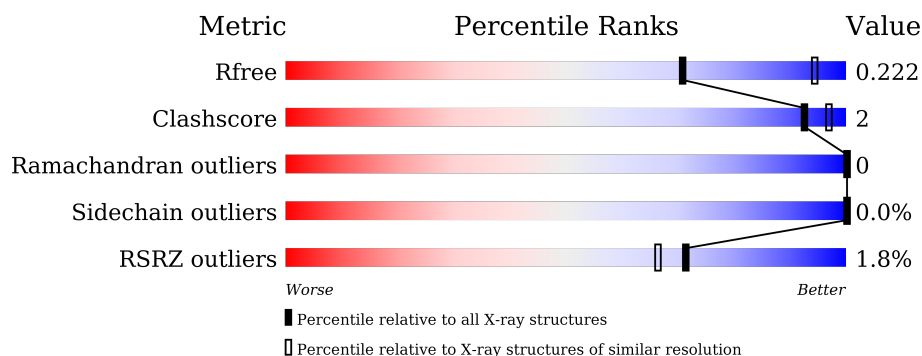
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.60 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	2328 (2.60-2.60)
Clashscore	102246	2679 (2.60-2.60)
Ramachandran outliers	100387	2635 (2.60-2.60)
Sidechain outliers	100360	2635 (2.60-2.60)
RSRZ outliers	91569	2334 (2.60-2.60)

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  $\geq 3$ , 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	479	<div> <div></div> <div>91%5% .</div> </div>
1	B	479	<div> <div>4%</div> <div>91% . 5%</div> </div>
1	C	479	<div> <div>%</div> <div>90%6% .</div> </div>
1	D	479	<div> <div>3%</div> <div>92% . .</div> </div>
1	E	479	<div> <div>2%</div> <div>92% . 5%</div> </div>
1	F	479	<div> <div>%</div> <div>91% . 5%</div> </div>

## 2 Entry composition [i](#)

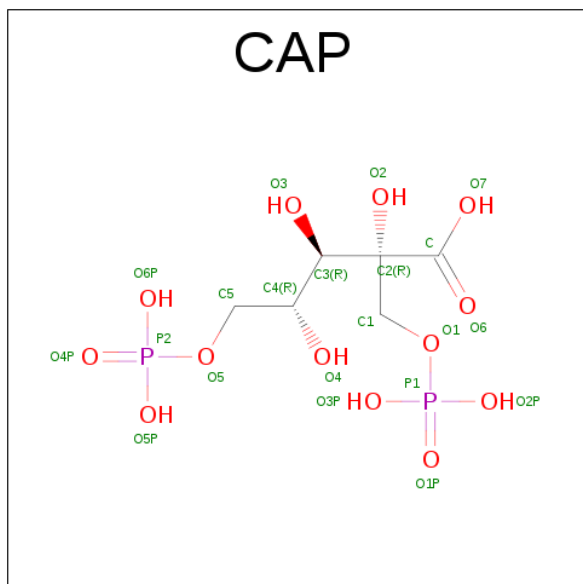
There are 4 unique types of molecules in this entry. The entry contains 41944 atoms, of which 20100 are hydrogens and 0 are deuteriums.

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 Form II RubisCO.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	461	Total	C	H	N	O	S	0	0	0
			6937	2256	3385	607	667	22			
1	B	454	Total	C	H	N	O	S	0	0	0
			6798	2214	3315	593	655	21			
1	C	459	Total	C	H	N	O	S	0	0	0
			6874	2238	3349	602	663	22			
1	D	461	Total	C	H	N	O	S	0	0	0
			6861	2238	3338	602	661	22			
1	E	457	Total	C	H	N	O	S	0	0	0
			6780	2216	3289	596	657	22			
1	F	457	Total	C	H	N	O	S	0	0	0
			6888	2237	3370	601	659	21			

- 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	141	Total	O	0	0
			141	141		
4	B	81	Total	O	0	0
			81	81		
4	C	152	Total	O	0	0
			152	152		
4	D	86	Total	O	0	0
			86	86		
4	E	82	Total	O	0	0
			82	82		
4	F	78	Total	O	0	0
			78	78		

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

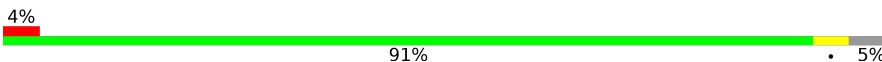
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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.

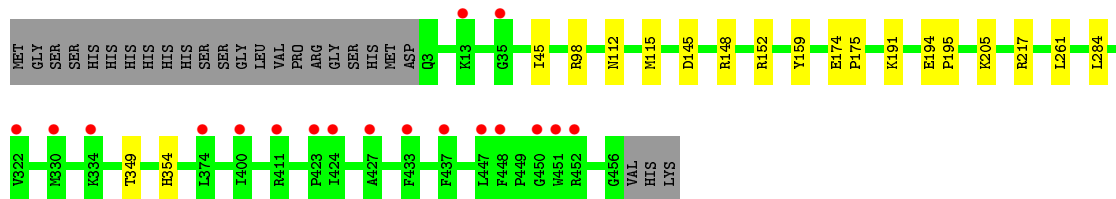
#### • Molecule 1: Form II RubisCO

Chain A: 



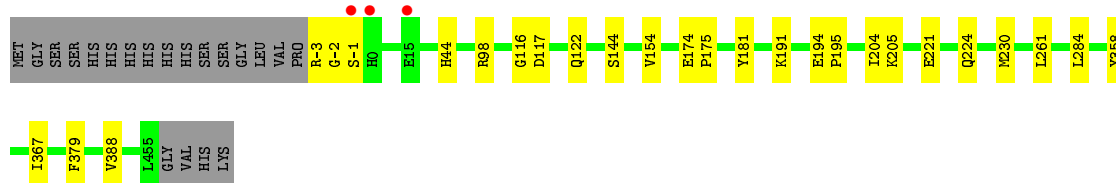
#### • Molecule 1: Form II RubisCO

Chain B: 

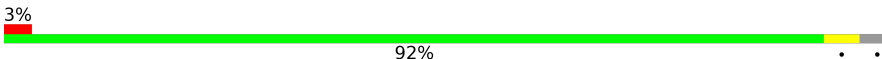


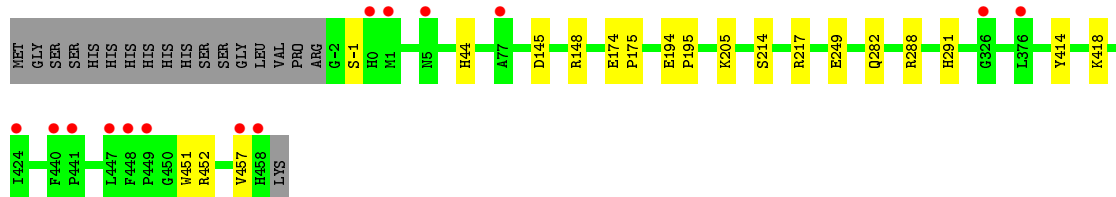
#### • Molecule 1: Form II RubisCO

Chain C: 

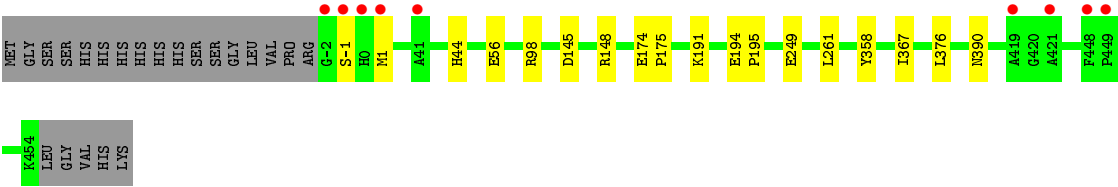
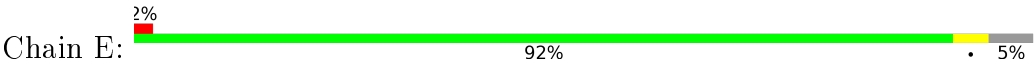


#### • Molecule 1: Form II RubisCO

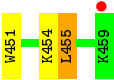
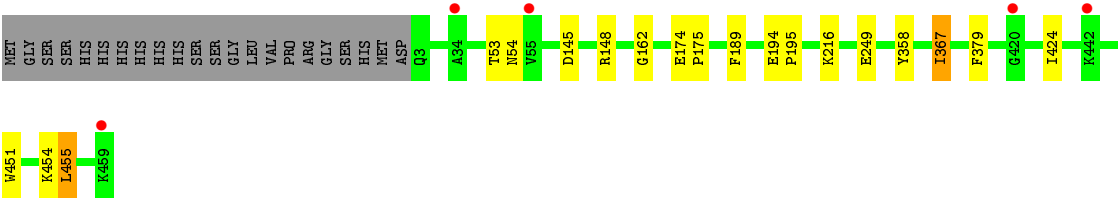
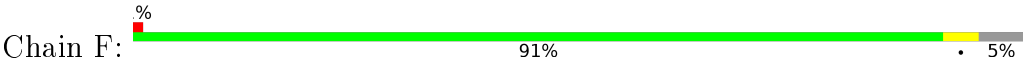
Chain D: 



#### • Molecule 1: Form II RubisCO



● Molecule 1: Form II RubisCO



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	74.38 Å 120.93 Å 161.44 Å 90.00° 90.54° 90.00°	Depositor
Resolution (Å)	40.36 – 2.60 80.72 – 2.60	Depositor EDS
% Data completeness (in resolution range)	98.3 (40.36-2.60) 98.3 (80.72-2.60)	Depositor EDS
$R_{merge}$	0.24	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.03 (at 2.58 Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.9_1692)	Depositor
R, $R_{free}$	0.181 , 0.222 0.181 , 0.222	Depositor DCC
$R_{free}$ test set	4335 reflections (5.00%)	DCC
Wilson B-factor (Å <sup>2</sup> )	22.7	Xtriage
Anisotropy	0.157	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.43 , 53.3	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	0.036 for h,-k,-l	Xtriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	41944	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.66% 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: 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	0.28	0/3630	0.51	0/4912
1	B	0.27	0/3559	0.49	0/4821
1	C	0.29	0/3602	0.52	0/4876
1	D	0.28	0/3600	0.50	0/4877
1	E	0.28	0/3568	0.50	0/4836
1	F	0.27	0/3595	0.49	1/4865 (0.0%)
All	All	0.28	0/21554	0.50	1/29187 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	367	ILE	CG1-CB-CG2	-5.68	98.89	111.40

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	3552	3385	3422	16	0
1	B	3483	3315	3338	14	0
1	C	3525	3349	3381	20	0
1	D	3523	3338	3372	17	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	E	3491	3289	3325	14	0
1	F	3518	3370	3389	12	0
2	A	21	9	8	0	0
2	B	21	9	7	0	0
2	C	21	9	9	0	0
2	D	21	9	8	0	0
2	E	21	9	9	0	0
2	F	21	9	9	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	141	0	0	0	0
4	B	81	0	0	1	0
4	C	152	0	0	2	0
4	D	86	0	0	1	0
4	E	82	0	0	0	0
4	F	78	0	0	1	0
All	All	21844	20100	20277	84	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 2.

All (84) 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:205:LYS:NZ	1:D:249:GLU:OE2	2.19	0.76
1:C:224:GLN:OE1	4:C:901:HOH:O	2.06	0.74
1:A:-1:SER:HB2	1:A:44:HIS:CE1	2.25	0.71
1:D:217:ARG:NH1	4:D:901:HOH:O	2.22	0.70
1:D:214:SER:OG	1:D:217:ARG:NH2	2.26	0.68
1:C:98:ARG:NH2	1:D:282:GLN:OE1	2.27	0.67
1:C:-1:SER:HB2	1:C:44:HIS:CE1	2.31	0.66
1:E:-1:SER:HB2	1:E:44:HIS:CE1	2.31	0.66
1:C:181:TYR:OH	1:C:221:GLU:OE1	2.10	0.65
1:D:214:SER:HA	1:D:217:ARG:HE	1.64	0.63
1:A:282:GLN:OE1	1:B:98:ARG:NH2	2.32	0.62
1:D:-1:SER:HB2	1:D:44:HIS:CE1	2.36	0.61
1:F:145:ASP:OD1	1:F:148:ARG:NH2	2.35	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:148:ARG:NH1	1:F:358:TYR:O	2.34	0.59
1:C:122:GLN:OE1	4:C:902:HOH:O	2.17	0.58
1:E:1:MET:HE1	1:E:56:GLU:H	1.68	0.58
1:B:191:KCX:HE3	1:B:261:LEU:CD1	2.35	0.57
1:D:451:TRP:CZ3	1:D:457:VAL:HG21	2.40	0.57
1:F:367:ILE:HG12	1:F:379:PHE:CZ	2.39	0.57
1:B:205:LYS:NZ	1:E:249:GLU:OE2	2.30	0.57
1:E:358:TYR:O	1:F:148:ARG:NH1	2.38	0.57
1:C:191:KCX:HE3	1:C:261:LEU:CD1	2.36	0.56
1:A:45:ILE:HA	1:A:115:MET:HE1	1.88	0.55
1:D:145:ASP:OD1	1:D:148:ARG:NH2	2.40	0.54
1:D:288:ARG:HG2	1:D:291:HIS:HB3	1.90	0.53
1:F:216:LYS:NZ	4:F:906:HOH:O	2.41	0.53
1:B:145:ASP:OD1	1:B:148:ARG:NH2	2.43	0.52
1:C:-3:ARG:HA	1:C:116:GLY:HA3	1.92	0.51
1:C:174:GLU:HB2	1:C:175:PRO:HD3	1.94	0.50
1:C:367:ILE:HD12	1:C:367:ILE:N	2.26	0.50
1:B:217:ARG:NH2	4:B:909:HOH:O	2.45	0.49
1:F:424:ILE:HG21	1:F:454:LYS:HD3	1.92	0.49
1:A:164:ILE:HG13	1:A:191:KCX:HD2	1.94	0.49
1:F:174:GLU:HB2	1:F:175:PRO:HD3	1.95	0.49
1:A:112:ASN:HA	1:A:115:MET:HE2	1.94	0.48
1:E:1:MET:HE1	1:E:56:GLU:N	2.29	0.48
1:C:204:ILE:HD11	1:C:230:MET:CE	2.42	0.48
1:D:174:GLU:HB2	1:D:175:PRO:HD3	1.96	0.48
1:F:451:TRP:O	1:F:455:LEU:HD22	2.13	0.48
1:C:367:ILE:CD1	1:C:388:VAL:HB	2.44	0.48
1:C:367:ILE:HG12	1:C:379:PHE:CZ	2.50	0.47
1:E:174:GLU:HB2	1:E:175:PRO:HD3	1.96	0.47
1:A:112:ASN:HA	1:A:115:MET:CE	2.45	0.47
1:B:45:ILE:HA	1:B:115:MET:HE1	1.96	0.47
1:C:358:TYR:O	1:D:148:ARG:NH1	2.47	0.47
1:A:191:KCX:HD3	1:A:391:THR:HG21	1.96	0.46
1:B:112:ASN:HA	1:B:115:MET:CE	2.45	0.46
1:B:112:ASN:HA	1:B:115:MET:HE2	1.98	0.46
1:A:174:GLU:HB2	1:A:175:PRO:HD3	1.97	0.46
1:D:214:SER:CA	1:D:217:ARG:HH21	2.28	0.46
1:D:457:VAL:O	1:D:457:VAL:HG23	2.15	0.46
1:E:145:ASP:OD1	1:E:148:ARG:NH2	2.48	0.46
1:E:376:LEU:HD21	1:E:390:ASN:ND2	2.31	0.46
1:C:-2:GLY:HA2	1:C:117:ASP:HB3	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:94:VAL:HG21	1:C:204:ILE:HG21	1.99	0.45
1:E:191:KCX:HE3	1:E:261:LEU:CD1	2.48	0.44
1:B:174:GLU:HB2	1:B:175:PRO:HD3	1.99	0.44
1:B:194:GLU:N	1:B:195:PRO:CD	2.81	0.43
1:D:452:ARG:HA	1:D:457:VAL:HG22	1.99	0.43
1:E:194:GLU:N	1:E:195:PRO:CD	2.82	0.43
1:C:204:ILE:HD11	1:C:230:MET:HE3	2.01	0.42
1:F:194:GLU:N	1:F:195:PRO:CD	2.82	0.42
1:C:284:LEU:C	1:C:284:LEU:HD23	2.40	0.42
1:D:205:LYS:NZ	1:F:249:GLU:OE2	2.48	0.42
1:B:152:ARG:NH1	1:B:159:TYR:O	2.54	0.41
1:A:-1:SER:HA	1:A:54:ASN:HB2	2.02	0.41
1:D:194:GLU:N	1:D:195:PRO:CD	2.83	0.41
1:E:367:ILE:HD12	1:E:367:ILE:N	2.35	0.41
1:A:125:ASP:OD1	1:A:126:PHE:N	2.53	0.41
1:A:194:GLU:N	1:A:195:PRO:CD	2.83	0.41
1:A:1:MET:HE1	1:A:56:GLU:H	1.84	0.41
1:E:-1:SER:HB2	1:E:44:HIS:ND1	2.36	0.41
1:E:98:ARG:HH11	1:E:98:ARG:HG3	1.86	0.41
1:F:162:GLY:HA2	1:F:189:PHE:O	2.21	0.41
1:A:457:VAL:HG23	1:A:458:HIS:N	2.36	0.41
1:B:284:LEU:C	1:B:284:LEU:HD23	2.41	0.41
1:C:194:GLU:N	1:C:195:PRO:CD	2.83	0.41
1:B:349:THR:HA	1:B:354:HIS:HA	2.02	0.40
1:D:414:TYR:CE2	1:D:418:LYS:HE3	2.55	0.40
1:F:53:THR:OG1	1:F:54:ASN:N	2.53	0.40
1:C:204:ILE:HG23	1:C:205:LYS:N	2.36	0.40
1:A:367:ILE:HD12	1:A:367:ILE:HG23	1.91	0.40
1:B:191:KCX:HE3	1:B:261:LEU:HD11	2.03	0.40
1:C:144:SER:HB2	1:C:154:VAL:HG13	2.03	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	458/479 (96%)	440 (96%)	18 (4%)	0	100	100
1	B	451/479 (94%)	434 (96%)	17 (4%)	0	100	100
1	C	456/479 (95%)	438 (96%)	18 (4%)	0	100	100
1	D	458/479 (96%)	442 (96%)	16 (4%)	0	100	100
1	E	454/479 (95%)	437 (96%)	17 (4%)	0	100	100
1	F	454/479 (95%)	435 (96%)	19 (4%)	0	100	100
All	All	2731/2874 (95%)	2626 (96%)	105 (4%)	0	100	100

There are no Ramachandran outliers to report.

### 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	362/381 (95%)	362 (100%)	0	100	100
1	B	352/381 (92%)	352 (100%)	0	100	100
1	C	357/381 (94%)	357 (100%)	0	100	100
1	D	355/381 (93%)	355 (100%)	0	100	100
1	E	351/381 (92%)	351 (100%)	0	100	100
1	F	357/381 (94%)	356 (100%)	1 (0%)	94	99
All	All	2134/2286 (93%)	2133 (100%)	1 (0%)	100	100

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

Mol	Chain	Res	Type
1	F	455	LEU

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	191	1,3	6,11,12	1.16	0	7,12,14	1.72	2 (28%)
1	KCX	B	191	1,3	6,11,12	1.26	1 (16%)	7,12,14	1.45	1 (14%)
1	KCX	C	191	1,3	6,11,12	1.18	1 (16%)	7,12,14	1.38	1 (14%)
1	KCX	D	191	1,3	6,11,12	1.19	1 (16%)	7,12,14	1.68	2 (28%)
1	KCX	E	191	1,3	6,11,12	1.31	1 (16%)	7,12,14	1.48	2 (28%)
1	KCX	F	191	1,3	6,11,12	1.17	0	7,12,14	1.44	2 (28%)

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	191	1,3	-	0/6/10/12	0/0/0/0
1	KCX	B	191	1,3	-	0/6/10/12	0/0/0/0
1	KCX	C	191	1,3	-	0/6/10/12	0/0/0/0
1	KCX	D	191	1,3	-	0/6/10/12	0/0/0/0
1	KCX	E	191	1,3	-	0/6/10/12	0/0/0/0
1	KCX	F	191	1,3	-	0/6/10/12	0/0/0/0

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	191	KCX	CB-CA	-2.37	1.50	1.53
1	B	191	KCX	CB-CA	-2.27	1.50	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	191	KCX	CB-CA	-2.07	1.50	1.53
1	C	191	KCX	CB-CA	-2.04	1.50	1.53

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	191	KCX	CE-NZ-CX	-3.29	120.07	123.53
1	A	191	KCX	CE-NZ-CX	-3.16	120.21	123.53
1	B	191	KCX	CE-NZ-CX	-2.90	120.48	123.53
1	E	191	KCX	CE-NZ-CX	-2.85	120.53	123.53
1	C	191	KCX	CE-NZ-CX	-2.59	120.81	123.53
1	A	191	KCX	CB-CA-N	-2.58	103.29	110.54
1	F	191	KCX	O-C-CA	-2.31	119.53	125.72
1	F	191	KCX	CE-NZ-CX	-2.28	121.13	123.53
1	D	191	KCX	CB-CA-N	-2.23	104.27	110.54
1	E	191	KCX	O-C-CA	-2.09	120.11	125.72

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	191	KCX	2	0
1	B	191	KCX	2	0
1	C	191	KCX	1	0
1	E	191	KCX	1	0

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

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	800	3	14,20,20	0.79	0	16,31,31	0.73	0
2	CAP	B	800	3	14,20,20	0.79	0	16,31,31	0.77	0
2	CAP	C	800	3	14,20,20	0.76	0	16,31,31	0.80	0
2	CAP	D	800	3	14,20,20	0.79	0	16,31,31	0.97	1 (6%)
2	CAP	E	800	3	14,20,20	0.81	0	16,31,31	0.84	0
2	CAP	F	800	3	14,20,20	0.78	0	16,31,31	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
2	CAP	A	800	3	-	0/23/29/29	0/0/0/0
2	CAP	B	800	3	-	0/23/29/29	0/0/0/0
2	CAP	C	800	3	-	0/23/29/29	0/0/0/0
2	CAP	D	800	3	-	0/23/29/29	0/0/0/0
2	CAP	E	800	3	-	0/23/29/29	0/0/0/0
2	CAP	F	800	3	-	0/23/29/29	0/0/0/0

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	800	CAP	O3-C3-C4	2.43	113.99	109.07

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.7 Other polymers ⓘ

There are no such residues in this entry.

## 5.8 Polymer linkage issues ⓘ

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	460/479 (96%)	-0.07	0 100 100	15, 22, 38, 68	0
1	B	453/479 (94%)	0.34	18 (3%) 42 34	17, 30, 52, 69	0
1	C	458/479 (95%)	-0.03	3 (0%) 89 87	15, 23, 41, 77	0
1	D	460/479 (96%)	0.25	14 (3%) 54 47	16, 31, 50, 81	0
1	E	456/479 (95%)	0.23	9 (1%) 68 63	21, 33, 54, 76	0
1	F	456/479 (95%)	0.17	5 (1%) 82 79	20, 31, 47, 66	0
All	All	2743/2874 (95%)	0.15	49 (1%) 71 66	15, 29, 48, 81	0

All (49) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	-2	GLY	4.6
1	E	448	PHE	4.1
1	D	447	LEU	4.1
1	B	424	ILE	3.7
1	D	457	VAL	3.7
1	E	0	HIS	3.6
1	B	450	GLY	3.6
1	C	0	HIS	3.6
1	D	326	GLY	3.6
1	D	1	MET	3.5
1	E	-1	SER	3.5
1	E	449	PRO	3.2
1	D	424	ILE	3.2
1	F	34	ALA	3.0
1	E	419	ALA	3.0
1	D	5	ASN	3.0
1	E	1	MET	2.9
1	B	423	PRO	2.9
1	D	448	PHE	2.9

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Mol	Chain	Res	Type	RSRZ
1	C	15	GLU	2.8
1	B	451	TRP	2.8
1	D	0	HIS	2.6
1	D	458	HIS	2.6
1	D	77	ALA	2.6
1	D	449	PRO	2.5
1	B	433	PHE	2.5
1	B	452	ARG	2.5
1	B	447	LEU	2.5
1	B	448	PHE	2.5
1	C	-1	SER	2.4
1	E	421	ALA	2.4
1	B	427	ALA	2.4
1	E	41	ALA	2.4
1	F	459	LYS	2.3
1	B	437	PHE	2.3
1	B	411	ARG	2.2
1	D	440	PHE	2.2
1	B	374	LEU	2.2
1	F	442	LYS	2.2
1	D	441	PRO	2.2
1	F	420	GLY	2.2
1	B	330	MET	2.2
1	B	322	VAL	2.2
1	B	400	ILE	2.1
1	B	35	GLY	2.1
1	F	55	VAL	2.0
1	B	13	LYS	2.0
1	D	376	LEU	2.0
1	B	334	LYS	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	F	191	12/13	0.95	0.16	-	22,22,23,24	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
1	KCX	E	191	12/13	0.97	0.18	-	24,25,25,25	0
1	KCX	B	191	12/13	0.96	0.14	-	24,27,30,31	0
1	KCX	D	191	12/13	0.97	0.14	-	22,24,25,25	0
1	KCX	A	191	12/13	0.93	0.17	-	15,15,18,18	0
1	KCX	C	191	12/13	0.95	0.17	-	17,20,24,26	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( $\text{\AA}^2$ )	Q<0.9
2	CAP	A	800	21/21	0.98	0.14	-0.82	20,28,34,35	0
2	CAP	B	800	21/21	0.97	0.15	-0.90	35,39,47,48	0
2	CAP	D	800	21/21	0.98	0.14	-1.01	27,32,38,39	0
2	CAP	E	800	21/21	0.97	0.14	-1.05	28,36,42,44	0
2	CAP	F	800	21/21	0.97	0.14	-1.20	34,37,42,43	0
2	CAP	C	800	21/21	0.98	0.12	-1.60	18,20,24,28	0
3	MG	C	801	1/1	0.97	0.12	-2.05	14,14,14,14	0
3	MG	B	801	1/1	0.97	0.07	-2.64	22,22,22,22	0
3	MG	E	801	1/1	0.88	0.11	-2.65	31,31,31,31	0
3	MG	F	801	1/1	0.93	0.08	-2.73	32,32,32,32	0
3	MG	D	801	1/1	0.96	0.08	-3.28	22,22,22,22	0
3	MG	A	801	1/1	0.98	0.07	-3.85	18,18,18,18	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.