



# wwPDB X-ray Structure Validation Summary Report ⓘ

Sep 22, 2016 – 05:23 PM EDT

PDB ID : 5A8R  
Title : METHYL-COENZYME M REDUCTASE II FROM METHANOTHERMOBACTER MARBURGENSIS AT 2.15 Å RESOLUTION  
Authors : Wagner, T.; Ermler, U.  
Deposited on : 2015-07-16  
Resolution : 2.15 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 : 1.7.1 (RC1), CSD as537be (2016)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20027939  
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-20027939

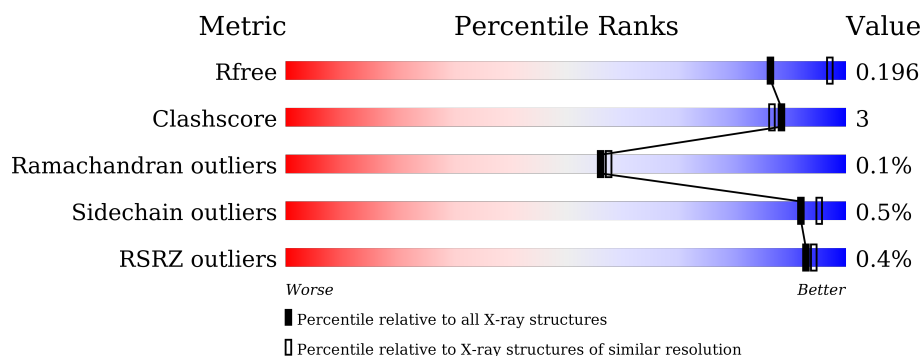
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.15 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	1045 (2.16-2.16)
Clashscore	102246	1152 (2.16-2.16)
Ramachandran outliers	100387	1131 (2.16-2.16)
Sidechain outliers	100360	1131 (2.16-2.16)
RSRZ outliers	91569	1050 (2.16-2.16)

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	553	<div> <div>93%</div> <div>5% .</div> </div>
1	D	553	<div> <div>92%</div> <div>6% .</div> </div>
1	G	553	<div> <div>91%</div> <div>8% .</div> </div>
1	J	553	<div> <div>93%</div> <div>6% .</div> </div>
2	B	443	<div> <div>%</div> <div>93%</div> <div>7%</div> </div>
2	E	443	<div> <div>94%</div> <div>5%</div> </div>

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Mol	Chain	Length	Quality of chain
2	H	443	 92% 8%
2	K	443	 95% 5%
3	C	265	 % 92% 7% .
3	F	265	 89% 9% .
3	I	265	 % 92% 7% .
3	L	265	 % 92% 7% .

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	COM	G	601	-	-	X	-
6	F43	A	603	X	-	-	-
6	F43	D	603	X	-	-	-
6	F43	G	603	X	-	-	-
6	F43	J	603	X	-	-	-

## 2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 40798 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 METHYL-COENZYME M REDUCTASE II SUBUNIT ALPHA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	548	Total	C	N	O	S	0	0	0
			4235	2676	714	822	23			
1	D	548	Total	C	N	O	S	0	0	0
			4235	2676	714	822	23			
1	G	548	Total	C	N	O	S	0	0	0
			4235	2676	714	822	23			
1	J	548	Total	C	N	O	S	0	1	0
			4238	2678	714	823	23			

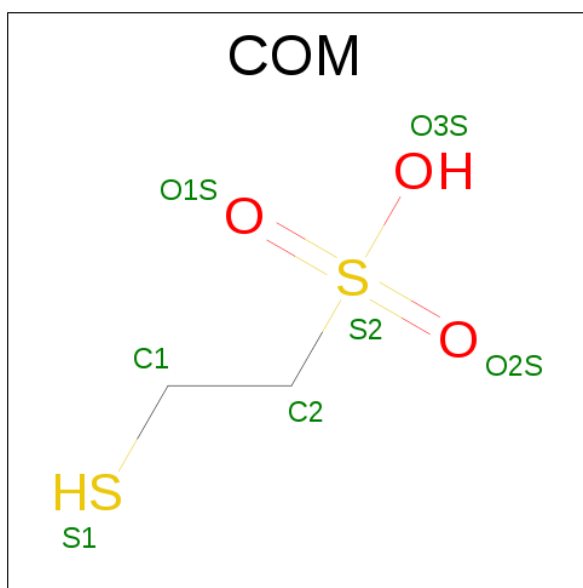
- Molecule 2 is a protein called METHYL-COENZYME M REDUCTASE II SUBUNIT GAMMA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	442	Total	C	N	O	S	0	0	0
			3296	2087	557	639	13			
2	E	442	Total	C	N	O	S	0	0	0
			3296	2087	557	639	13			
2	H	442	Total	C	N	O	S	0	0	0
			3296	2087	557	639	13			
2	K	442	Total	C	N	O	S	0	0	0
			3296	2087	557	639	13			

- Molecule 3 is a protein called METHYL-COENZYME M REDUCTASE II, SUBUNIT BETA.

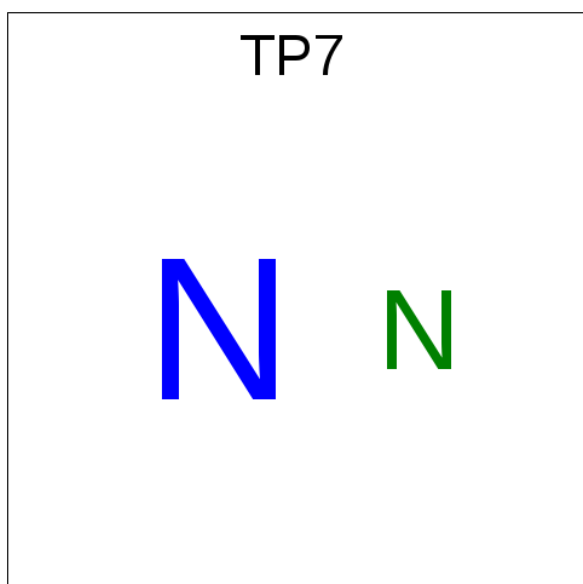
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	262	Total	C	N	O	S	0	0	0
			2122	1321	376	415	10			
3	F	261	Total	C	N	O	S	0	0	0
			2114	1317	375	412	10			
3	I	262	Total	C	N	O	S	0	0	0
			2120	1320	376	414	10			
3	L	263	Total	C	N	O	S	0	0	0
			2128	1324	377	417	10			

- Molecule 4 is 1-THIOETHANESULFONIC ACID (three-letter code: COM) (formula:  $C_2H_6O_3S_2$ ).



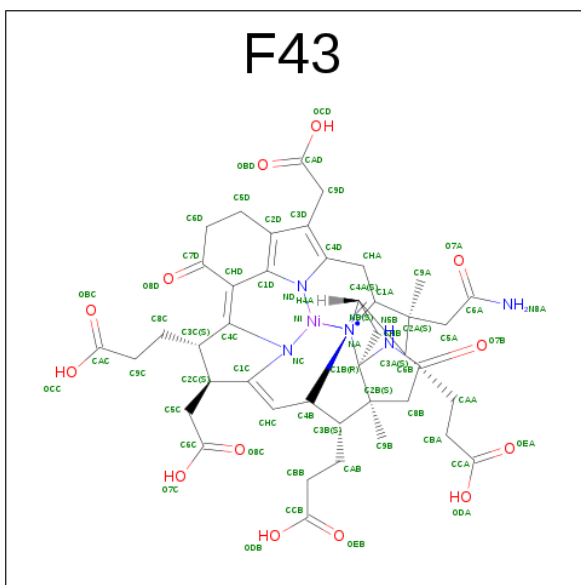
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	O	S	0	0
			7	2	3	2		
4	D	1	Total	C	O	S	0	0
			7	2	3	2		
4	G	1	Total	C	O	S	0	0
			7	2	3	2		
4	J	1	Total	C	O	S	0	0
			7	2	3	2		

- Molecule 5 is COENZYME B (three-letter code: TP7) (formula:  $C_{11}H_{22}NO_7PS$ ).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
5	A	1	Total 21	C 11	N 1	O 7	P 1	S 1	0	0
5	D	1	Total 21	C 11	N 1	O 7	P 1	S 1	0	0
5	G	1	Total 21	C 11	N 1	O 7	P 1	S 1	0	0
5	J	1	Total 21	C 11	N 1	O 7	P 1	S 1	0	0

- Molecule 6 is FACTOR 430 (three-letter code: F43) (formula:  $\text{C}_{42}\text{H}_{49}\text{N}_6\text{NiO}_{13}$ ).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
6	A	1	Total 62	C 42	N 6	Ni 1	O 13	0	0
6	D	1	Total 62	C 42	N 6	Ni 1	O 13	0	0
6	G	1	Total 62	C 42	N 6	Ni 1	O 13	0	0
6	J	1	Total 62	C 42	N 6	Ni 1	O 13	0	0

- Molecule 7 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	G	1	Total K 1 1	0	0
7	J	3	Total K 3 3	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	1	Total 1	O 1	0	0
7	D	2	Total 2	O 2	0	0

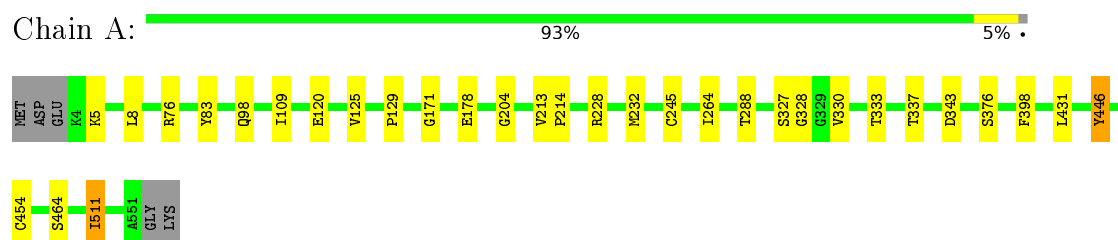
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	297	Total 297	O 297	0	0
8	B	146	Total 146	O 146	0	0
8	C	72	Total 72	O 72	0	0
8	D	208	Total 208	O 208	0	0
8	E	110	Total 110	O 110	0	0
8	F	71	Total 71	O 71	0	0
8	G	260	Total 260	O 260	0	0
8	H	158	Total 158	O 158	0	0
8	I	45	Total 45	O 45	0	0
8	J	220	Total 220	O 220	0	0
8	K	137	Total 137	O 137	0	0
8	L	96	Total 96	O 96	0	0

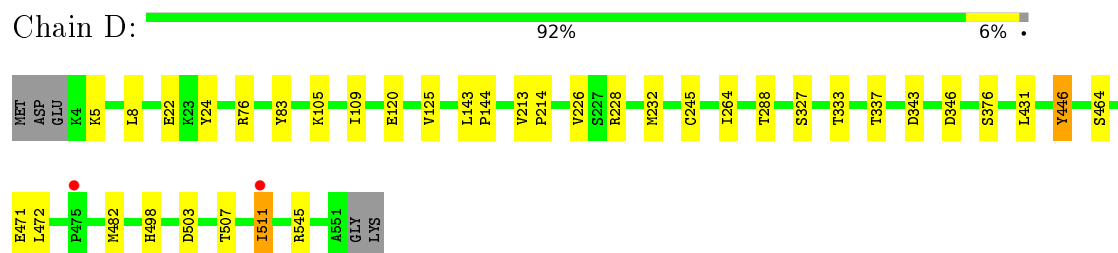
### 3 Residue-property plots

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.

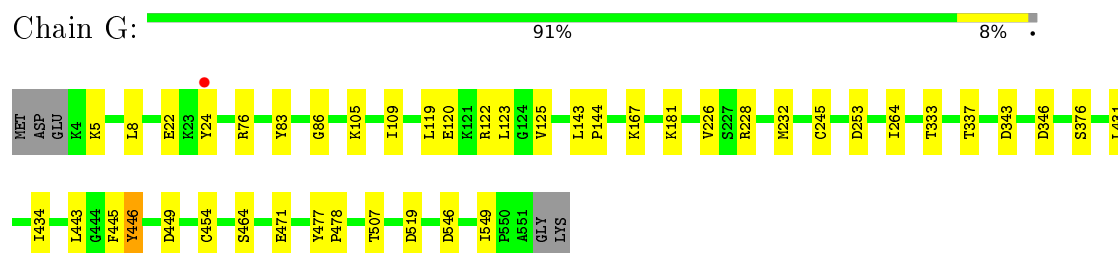
#### • Molecule 1: METHYL-COENZYME M REDUCTASE II SUBUNIT ALPHA



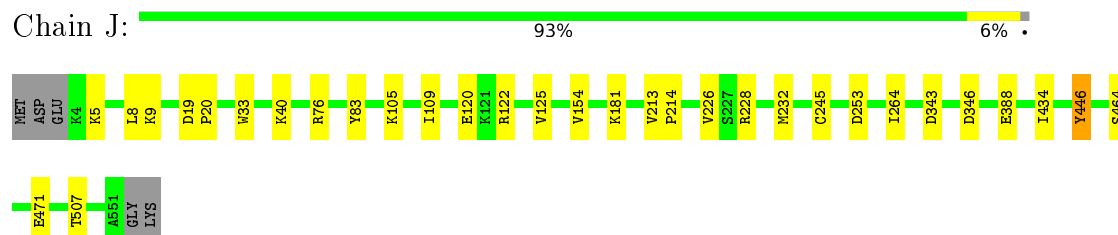
#### • Molecule 1: METHYL-COENZYME M REDUCTASE II SUBUNIT ALPHA



#### • Molecule 1: METHYL-COENZYME M REDUCTASE II SUBUNIT ALPHA

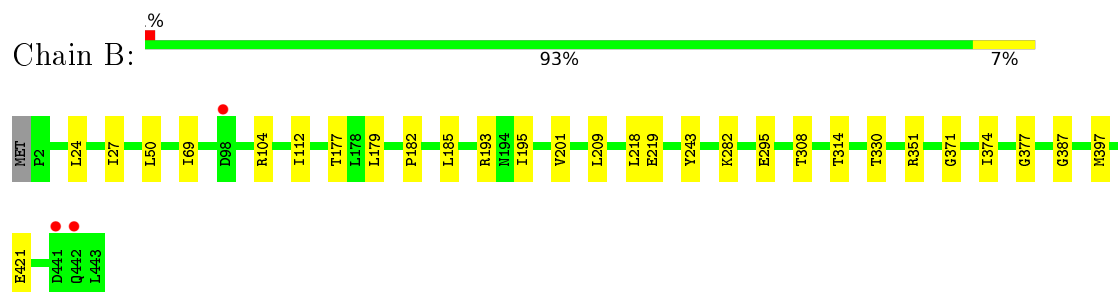


#### • Molecule 1: METHYL-COENZYME M REDUCTASE II SUBUNIT ALPHA

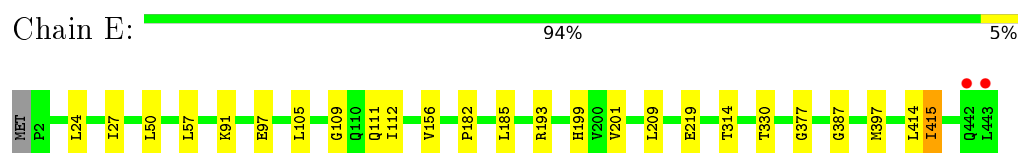




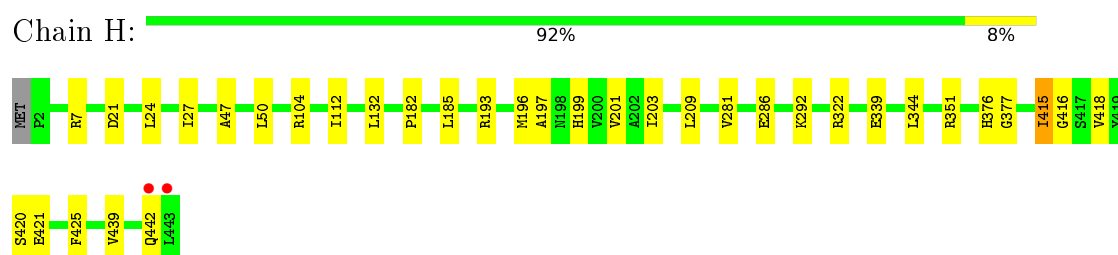
- Molecule 2: METHYL-COENZYME M REDUCTASE II SUBUNIT GAMMA



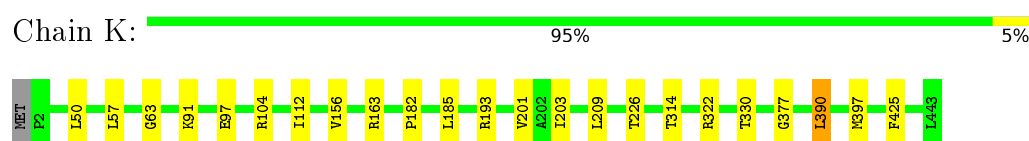
- Molecule 2: METHYL-COENZYME M REDUCTASE II SUBUNIT GAMMA



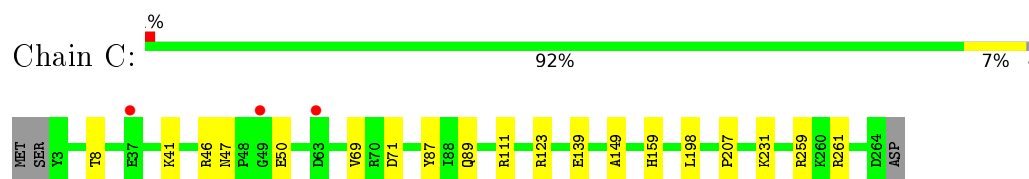
- Molecule 2: METHYL-COENZYME M REDUCTASE II SUBUNIT GAMMA



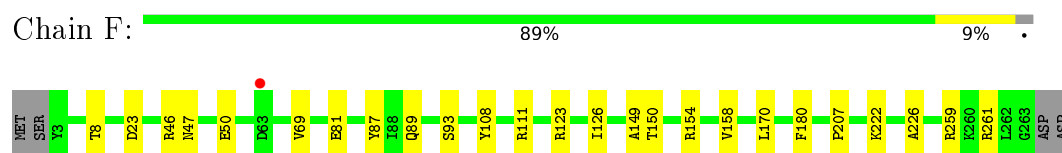
- Molecule 2: METHYL-COENZYME M REDUCTASE II SUBUNIT GAMMA



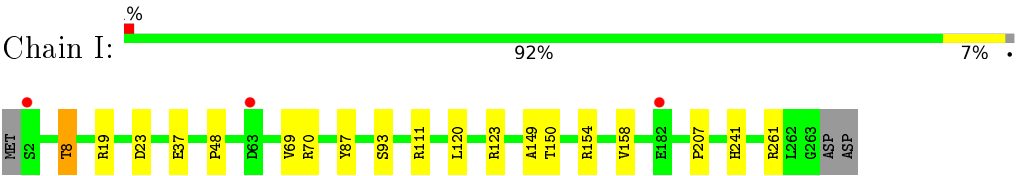
- Molecule 3: METHYL-COENZYME M REDUCTASE II, SUBUNIT BETA



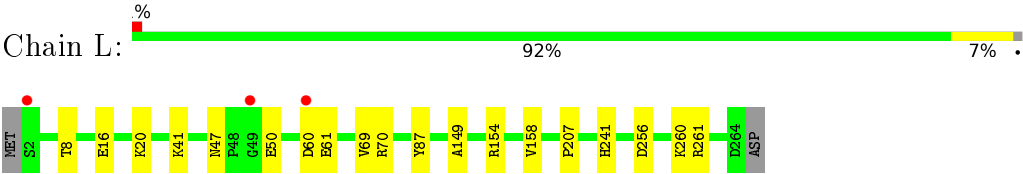
- Molecule 3: METHYL-COENZYME M REDUCTASE II, SUBUNIT BETA



- Molecule 3: METHYL-COENZYME M REDUCTASE II, SUBUNIT BETA



• Molecule 3: METHYL-COENZYME M REDUCTASE II, SUBUNIT BETA



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	216.66Å 246.61Å 103.65Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	55.36 – 2.15 65.48 – 2.15	Depositor EDS
% Data completeness (in resolution range)	99.9 (55.36-2.15) 99.9 (65.48-2.15)	Depositor EDS
$R_{merge}$	0.16	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.02 (at 2.14Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, $R_{free}$	0.156 , 0.196 0.161 , 0.196	Depositor DCC
$R_{free}$ test set	15160 reflections (5.32%)	DCC
Wilson B-factor (Å <sup>2</sup> )	25.7	Xtriage
Anisotropy	0.306	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 43.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	40798	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	26.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.19% 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: AGM, SMC, K, F43, MGN, TP7, MHS, GL3, COM, DYA

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	0.31	0/4270	0.50	0/5779
1	D	0.31	0/4270	0.49	0/5779
1	G	0.30	0/4270	0.49	0/5779
1	J	0.31	0/4276	0.49	0/5787
2	B	0.29	0/3350	0.51	0/4552
2	E	0.29	0/3350	0.51	0/4552
2	H	0.30	0/3350	0.50	0/4552
2	K	0.30	0/3350	0.51	0/4552
3	C	0.28	0/2162	0.51	0/2913
3	F	0.29	0/2154	0.51	0/2902
3	I	0.27	0/2160	0.50	0/2910
3	L	0.29	0/2168	0.50	0/2921
All	All	0.30	0/39130	0.50	0/52978

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	4235	0	4075	19	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D	4235	0	4075	21	0
1	G	4235	0	4075	26	0
1	J	4238	0	4080	22	0
2	B	3296	0	3299	17	0
2	E	3296	0	3299	14	0
2	H	3296	0	3299	23	0
2	K	3296	0	3299	15	0
3	C	2122	0	2058	12	0
3	F	2114	0	2054	15	0
3	I	2120	0	2059	12	0
3	L	2128	0	2063	11	0
4	A	7	0	6	2	0
4	D	7	0	6	3	0
4	G	7	0	6	5	0
4	J	7	0	6	3	0
5	A	21	0	19	1	0
5	D	21	0	19	0	0
5	G	21	0	19	0	0
5	J	21	0	19	0	0
6	A	62	0	43	2	0
6	D	62	0	43	2	0
6	G	62	0	43	3	0
6	J	62	0	43	3	0
7	A	1	0	0	0	0
7	D	2	0	0	0	0
7	G	1	0	0	0	0
7	J	3	0	0	0	0
8	A	297	0	0	0	0
8	B	146	0	0	0	0
8	C	72	0	0	2	0
8	D	208	0	0	0	0
8	E	110	0	0	0	0
8	F	71	0	0	1	0
8	G	260	0	0	1	0
8	H	158	0	0	1	0
8	I	45	0	0	0	0
8	J	220	0	0	3	0
8	K	137	0	0	0	1
8	L	96	0	0	1	0
All	All	40798	0	38007	194	1

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 3.

The worst 5 of 194 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)
3:F:47:ASN:N	3:F:50:GLU:OE2	2.05	0.87
2:K:91:LYS:NZ	2:K:97:GLU:OE2	2.09	0.86
3:L:256:ASP:OD1	3:L:260:LYS:NZ	2.15	0.79
3:F:46:ARG:HB2	3:F:50:GLU:OE2	1.83	0.77
2:H:281:VAL:HG21	2:H:344:LEU:HD11	1.73	0.70

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:K:2104:HOH:O	8:K:2104:HOH:O[2_555]	2.04	0.16

## 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	540/553 (98%)	521 (96%)	18 (3%)	1 (0%)	52	51
1	D	540/553 (98%)	521 (96%)	17 (3%)	2 (0%)	39	34
1	G	540/553 (98%)	521 (96%)	18 (3%)	1 (0%)	52	51
1	J	541/553 (98%)	522 (96%)	18 (3%)	1 (0%)	52	51
2	B	440/443 (99%)	433 (98%)	7 (2%)	0	100	100
2	E	440/443 (99%)	432 (98%)	8 (2%)	0	100	100
2	H	440/443 (99%)	432 (98%)	8 (2%)	0	100	100
2	K	440/443 (99%)	431 (98%)	9 (2%)	0	100	100
3	C	260/265 (98%)	253 (97%)	7 (3%)	0	100	100
3	F	259/265 (98%)	252 (97%)	7 (3%)	0	100	100
3	I	260/265 (98%)	253 (97%)	7 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	L	261/265 (98%)	254 (97%)	7 (3%)	0	100	100
All	All	4961/5044 (98%)	4825 (97%)	131 (3%)	5 (0%)	56	57

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	464	SER
1	D	464	SER
1	G	464	SER
1	J	464	SER
1	D	327	SER

### 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	430/434 (99%)	428 (100%)	2 (0%)	92	95
1	D	430/434 (99%)	427 (99%)	3 (1%)	88	93
1	G	430/434 (99%)	428 (100%)	2 (0%)	92	95
1	J	431/434 (99%)	429 (100%)	2 (0%)	92	95
2	B	344/345 (100%)	344 (100%)	0	100	100
2	E	344/345 (100%)	343 (100%)	1 (0%)	94	97
2	H	344/345 (100%)	343 (100%)	1 (0%)	94	97
2	K	344/345 (100%)	343 (100%)	1 (0%)	94	97
3	C	228/231 (99%)	225 (99%)	3 (1%)	76	82
3	F	227/231 (98%)	225 (99%)	2 (1%)	84	89
3	I	228/231 (99%)	226 (99%)	2 (1%)	84	89
3	L	229/231 (99%)	227 (99%)	2 (1%)	84	89
All	All	4009/4040 (99%)	3988 (100%)	21 (0%)	92	95

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

Mol	Chain	Res	Type
3	F	8	THR
1	G	346	ASP
1	J	446	TYR
2	E	415	ILE
2	K	390	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 ⓘ

24 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	MHS	A	260	1	7,11,12	1.31	1 (14%)	7,14,16	1.18	1 (14%)
1	AGM	A	274	1	6,11,12	0.69	0	5,13,15	0.84	0
1	MGN	A	402	1	7,9,10	0.78	0	4,12,14	0.59	0
1	GL3	A	447	1	3,3,4	4.55	1 (33%)	2,2,4	1.58	1 (50%)
1	DYA	A	452	1	4,7,8	1.64	1 (25%)	1,8,10	3.04	1 (100%)
1	SMC	A	454	1	4,6,7	1.97	1 (25%)	2,6,8	0.56	0
1	MHS	D	260	1	7,11,12	1.30	1 (14%)	7,14,16	1.13	1 (14%)
1	AGM	D	274	1	6,11,12	0.67	0	5,13,15	0.83	0
1	MGN	D	402	1	7,9,10	0.82	0	4,12,14	0.47	0
1	GL3	D	447	1	3,3,4	4.10	1 (33%)	2,2,4	1.61	1 (50%)
1	DYA	D	452	1	4,7,8	1.74	1 (25%)	1,8,10	3.90	1 (100%)
1	SMC	D	454	1	4,6,7	1.77	1 (25%)	2,6,8	0.39	0
1	MHS	G	260	1	7,11,12	1.27	0	7,14,16	1.00	1 (14%)
1	AGM	G	274	1	6,11,12	0.72	0	5,13,15	0.96	0



Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
1	MGN	G	402	1	7,9,10	0.78	0	4,12,14	0.51	0
1	GL3	G	447	1	3,3,4	4.77	1 (33%)	2,2,4	1.70	1 (50%)
1	DYA	G	452	1	4,7,8	1.70	1 (25%)	1,8,10	3.72	1 (100%)
1	SMC	G	454	1	4,6,7	1.55	1 (25%)	2,6,8	0.59	0
1	MHS	J	260	1	7,11,12	1.31	0	7,14,16	1.09	1 (14%)
1	AGM	J	274	1	6,11,12	0.63	0	5,13,15	0.90	0
1	MGN	J	402	1	7,9,10	0.78	0	4,12,14	0.64	0
1	GL3	J	447	1	3,3,4	3.95	1 (33%)	2,2,4	1.53	1 (50%)
1	DYA	J	452	1	4,7,8	1.70	1 (25%)	1,8,10	3.28	1 (100%)
1	SMC	J	454	1	4,6,7	1.40	1 (25%)	2,6,8	0.62	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	MHS	A	260	1	-	0/4/6/8	0/1/1/1
1	AGM	A	274	1	-	0/7/11/13	0/0/0/0
1	MGN	A	402	1	-	0/7/9/12	0/0/0/0
1	GL3	A	447	1	-	0/1/1/2	0/0/0/0
1	DYA	A	452	1	-	0/1/6/8	0/0/0/0
1	SMC	A	454	1	-	0/3/5/7	0/0/0/0
1	MHS	D	260	1	-	0/4/6/8	0/1/1/1
1	AGM	D	274	1	-	0/7/11/13	0/0/0/0
1	MGN	D	402	1	-	0/7/9/12	0/0/0/0
1	GL3	D	447	1	-	0/1/1/2	0/0/0/0
1	DYA	D	452	1	-	0/1/6/8	0/0/0/0
1	SMC	D	454	1	-	0/3/5/7	0/0/0/0
1	MHS	G	260	1	-	0/4/6/8	0/1/1/1
1	AGM	G	274	1	-	0/7/11/13	0/0/0/0
1	MGN	G	402	1	-	0/7/9/12	0/0/0/0
1	GL3	G	447	1	-	0/1/1/2	0/0/0/0
1	DYA	G	452	1	-	0/1/6/8	0/0/0/0
1	SMC	G	454	1	-	0/3/5/7	0/0/0/0
1	MHS	J	260	1	-	0/4/6/8	0/1/1/1
1	AGM	J	274	1	-	0/7/11/13	0/0/0/0
1	MGN	J	402	1	-	0/7/9/12	0/0/0/0
1	GL3	J	447	1	-	0/1/1/2	0/0/0/0
1	DYA	J	452	1	-	0/1/6/8	0/0/0/0
1	SMC	J	454	1	-	0/3/5/7	0/0/0/0

The worst 5 of 14 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	G	447	GL3	C-S	-8.26	1.52	1.80
1	A	447	GL3	C-S	-7.88	1.53	1.80
1	D	447	GL3	C-S	-7.11	1.56	1.80
1	J	447	GL3	C-S	-6.84	1.57	1.80
1	A	454	SMC	CB-SG	-3.78	1.76	1.80

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	452	DYA	O-C-CA	-3.90	120.15	125.59
1	G	452	DYA	O-C-CA	-3.72	120.39	125.59
1	J	452	DYA	O-C-CA	-3.28	121.01	125.59
1	A	452	DYA	O-C-CA	-3.04	121.34	125.59
1	G	260	MHS	CM-ND1-CG	2.11	127.25	124.44

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	454	SMC	1	0
1	G	454	SMC	1	0

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 19 ligands modelled in this entry, 7 are monoatomic - leaving 12 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	COM	A	601	-	6,6,6	1.43	2 (33%)	6,8,8	4.19	4 (66%)
5	TP7	A	602	-	15,20,20	0.45	0	19,26,26	1.10	1 (5%)
6	F43	A	603	1	42,71,71	3.22	6 (14%)	39,118,118	2.79	11 (28%)
4	COM	D	601	-	6,6,6	1.42	2 (33%)	6,8,8	4.41	3 (50%)
5	TP7	D	602	-	15,20,20	0.46	0	19,26,26	1.05	1 (5%)
6	F43	D	603	1	42,71,71	3.23	7 (16%)	39,118,118	2.83	11 (28%)
4	COM	G	601	-	6,6,6	1.39	2 (33%)	6,8,8	4.86	4 (66%)
5	TP7	G	602	-	15,20,20	0.44	0	19,26,26	1.13	1 (5%)
6	F43	G	603	1	42,71,71	3.24	7 (16%)	39,118,118	2.77	11 (28%)
4	COM	J	601	-	6,6,6	1.37	2 (33%)	6,8,8	3.51	4 (66%)
5	TP7	J	602	-	15,20,20	0.44	0	19,26,26	1.11	1 (5%)
6	F43	J	603	1	42,71,71	3.15	5 (11%)	39,118,118	2.90	11 (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
4	COM	A	601	-	-	0/4/4/4	0/0/0/0
5	TP7	A	602	-	-	0/20/24/24	0/0/0/0
6	F43	A	603	1	1/1/25/27	0/18/165/165	0/0/10/10
4	COM	D	601	-	-	0/4/4/4	0/0/0/0
5	TP7	D	602	-	-	0/20/24/24	0/0/0/0
6	F43	D	603	1	1/1/25/27	0/18/165/165	0/0/10/10
4	COM	G	601	-	-	0/4/4/4	0/0/0/0
5	TP7	G	602	-	-	0/20/24/24	0/0/0/0
6	F43	G	603	1	1/1/25/27	0/18/165/165	0/0/10/10
4	COM	J	601	-	-	0/4/4/4	0/0/0/0
5	TP7	J	602	-	-	0/20/24/24	0/0/0/0
6	F43	J	603	1	1/1/25/27	0/18/165/165	0/0/10/10

The worst 5 of 33 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	G	603	F43	C4B-NB	-14.99	1.26	1.49
6	A	603	F43	C4B-NB	-14.92	1.26	1.49
6	D	603	F43	C4B-NB	-14.86	1.26	1.49
6	J	603	F43	C4B-NB	-14.74	1.26	1.49
6	D	603	F43	C1B-NB	-2.16	1.46	1.49

The worst 5 of 63 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	J	603	F43	CHA-C4D-C3D	-13.56	113.32	129.68
6	D	603	F43	CHA-C4D-C3D	-12.21	114.95	129.68
6	A	603	F43	CHA-C4D-C3D	-12.19	114.97	129.68
6	G	603	F43	CHA-C4D-C3D	-12.16	115.01	129.68
6	D	603	F43	C9D-C3D-C4D	-9.18	109.92	127.13

All (4) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
6	A	603	F43	C4B
6	G	603	F43	C4B
6	D	603	F43	C4B
6	J	603	F43	C4B

There are no torsion outliers.

There are no ring outliers.

9 monomers are involved in 16 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	601	COM	2	0
5	A	602	TP7	1	0
6	A	603	F43	2	0
4	D	601	COM	3	0
6	D	603	F43	2	0
4	G	601	COM	5	0
6	G	603	F43	3	0
4	J	601	COM	3	0
6	J	603	F43	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	542/553 (98%)	-0.64	0 <span>100</span> <span>100</span>	9, 19, 40, 64	0
1	D	542/553 (98%)	-0.26	2 (0%) <span>93</span> <span>94</span>	9, 19, 40, 65	0
1	G	542/553 (98%)	-0.63	1 (0%) <span>95</span> <span>96</span>	12, 23, 45, 78	0
1	J	542/553 (98%)	-0.45	0 <span>100</span> <span>100</span>	9, 19, 42, 73	0
2	B	442/443 (99%)	-0.28	3 (0%) <span>89</span> <span>91</span>	12, 26, 48, 82	0
2	E	442/443 (99%)	-0.46	2 (0%) <span>91</span> <span>93</span>	11, 24, 48, 70	0
2	H	442/443 (99%)	-0.31	2 (0%) <span>91</span> <span>93</span>	11, 27, 47, 76	0
2	K	442/443 (99%)	-0.58	0 <span>100</span> <span>100</span>	11, 22, 43, 66	0
3	C	262/265 (98%)	-0.37	3 (1%) <span>82</span> <span>86</span>	17, 30, 59, 92	0
3	F	261/265 (98%)	-0.35	1 (0%) <span>93</span> <span>94</span>	14, 27, 54, 75	0
3	I	262/265 (98%)	-0.30	3 (1%) <span>82</span> <span>86</span>	22, 38, 62, 79	0
3	L	263/265 (99%)	-0.39	3 (1%) <span>82</span> <span>86</span>	11, 26, 54, 83	0
All	All	4984/5044 (98%)	-0.43	20 (0%) <span>93</span> <span>94</span>	9, 24, 49, 92	0

The worst 5 of 20 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	I	63	ASP	3.8
3	L	2	SER	3.6
3	C	63	ASP	3.5
2	H	443	LEU	3.4
3	L	49	GLY	3.4

### 6.2 Non-standard residues in protein, DNA, RNA chains [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
1	SMC	D	454	7/8	0.99	0.09	-	9,13,16,18	0
1	MGN	A	402	10/11	0.98	0.09	-	11,12,17,18	0
1	MGN	J	402	10/11	0.98	0.11	-	8,10,18,21	0
1	MGN	G	402	10/11	0.98	0.08	-	15,18,24,28	0
1	GL3	G	447	4/5	0.98	0.07	-	18,18,19,20	0
1	AGM	A	274	12/13	0.97	0.16	-	10,15,22,22	0
1	GL3	D	447	4/5	0.99	0.07	-	13,18,19,22	0
1	DYA	G	452	8/9	0.98	0.07	-	17,22,28,29	0
1	AGM	J	274	12/13	0.97	0.15	-	8,16,18,20	0
1	AGM	D	274	12/13	0.98	0.16	-	7,14,16,20	0
1	MHS	G	260	11/12	0.96	0.13	-	21,26,32,34	0
1	DYA	A	452	8/9	0.98	0.08	-	12,16,20,23	0
1	GL3	A	447	4/5	0.99	0.07	-	15,16,17,20	0
1	MHS	A	260	11/12	0.97	0.07	-	19,21,28,29	0
1	MGN	D	402	10/11	0.98	0.08	-	9,14,18,19	0
1	SMC	A	454	7/8	0.99	0.08	-	11,11,22,23	0
1	SMC	J	454	7/8	0.99	0.11	-	6,12,15,19	0
1	GL3	J	447	4/5	0.99	0.09	-	12,12,14,14	0
1	MHS	D	260	11/12	0.97	0.12	-	15,26,38,38	0
1	AGM	G	274	12/13	0.97	0.12	-	12,18,20,21	0
1	MHS	J	260	11/12	0.95	0.10	-	18,31,39,39	0
1	DYA	D	452	8/9	0.98	0.09	-	12,15,19,20	0
1	SMC	G	454	7/8	0.98	0.07	-	17,18,23,27	0
1	DYA	J	452	8/9	0.98	0.13	-	7,12,16,27	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
4	COM	A	601	7/7	0.96	0.10	1.38	19,25,28,29	0
6	F43	J	603	62/62	0.98	0.11	0.87	3,14,23,30	0
4	COM	G	601	7/7	0.98	0.10	0.39	25,31,34,34	0
5	TP7	G	602	21/21	0.97	0.09	0.32	19,31,39,44	0
6	F43	G	603	62/62	0.98	0.08	0.01	9,22,31,35	0
6	F43	A	603	62/62	0.98	0.08	-0.12	5,13,20,25	0
6	F43	D	603	62/62	0.98	0.08	-0.29	1,15,25,29	0
4	COM	D	601	7/7	0.97	0.09	-0.53	20,25,26,28	0
5	TP7	J	602	21/21	0.97	0.10	-0.75	17,29,38,43	0
7	K	J	605	1/1	0.99	0.07	-0.90	26,26,26,26	0
4	COM	J	601	7/7	0.98	0.08	-1.05	17,25,34,37	0
7	K	J	604	1/1	0.99	0.07	-1.05	19,19,19,19	0
5	TP7	A	602	21/21	0.98	0.09	-1.09	10,25,36,39	0
7	K	D	605	1/1	1.00	0.08	-1.13	15,15,15,15	0
5	TP7	D	602	21/21	0.97	0.08	-1.20	10,24,30,33	0
7	K	J	606	1/1	0.98	0.05	-1.51	25,25,25,25	0
7	K	A	604	1/1	0.99	0.04	-2.15	24,24,24,24	0
7	K	G	604	1/1	0.99	0.03	-2.30	30,30,30,30	0
7	K	D	604	1/1	1.00	0.03	-2.67	22,22,22,22	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.