W O R L D W I D E
wwPDB
PROTEIN DATA BANK

wwPDB X-ray Structure Validation Summary Report (i)

May 23, 2020 – 10:14 pm BST

PDB ID	:	4YWL
Title	:	Pyrococcus furiosus MCM N-terminal domain F179A point mutant pentameric ring
Authors	:	Froelich, C.A.; Enemark, E.J.
Deposited on	:	2015-03-20
Resolution	:	3.20 Å(reported)

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

|		
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

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 3.20 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.
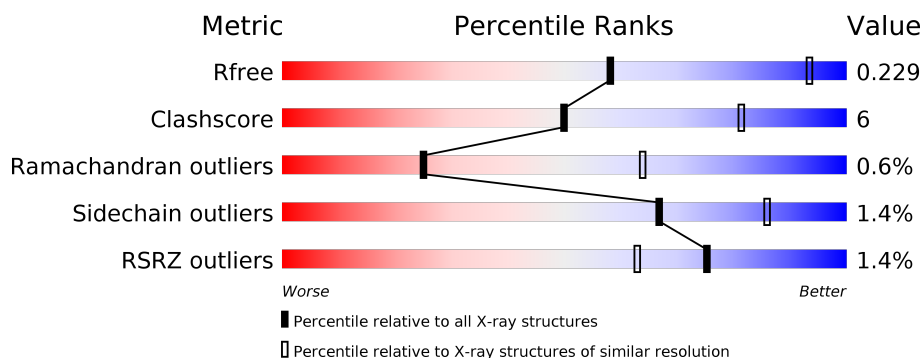
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1133 (3.20-3.20)
Clashscore	141614	1253 (3.20-3.20)
Ramachandran outliers	138981	1234 (3.20-3.20)
Sidechain outliers	138945	1233 (3.20-3.20)
RSRZ outliers	127900	1095 (3.20-3.20)

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 >=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 <=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	257	2%　81%　18%
1	B	257	2%　82%　17%
1	C	257	%　81%　17%
1	D	257	3%　81%　18%
1	E	257	%　82%　17%
1	F	257	88%　11%

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Mol	Chain	Length	Quality of chain
1	G	257	86% 13%
1	H	257	% 85% 13%
1	I	257	83% 15%
1	J	257	4% 84% 15%

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 20365 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 Cell division control protein 21.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	254	Total	C	N	O	S	0	0	0
			2031	1285	349	388	9			
1	B	254	Total	C	N	O	S	0	0	0
			2031	1285	349	388	9			
1	C	254	Total	C	N	O	S	0	0	0
			2031	1285	349	388	9			
1	D	254	Total	C	N	O	S	0	0	0
			2031	1285	349	388	9			
1	E	254	Total	C	N	O	S	0	0	0
			2031	1285	349	388	9			
1	F	254	Total	C	N	O	S	0	0	0
			2031	1285	349	388	9			
1	G	254	Total	C	N	O	S	0	0	0
			2031	1285	349	388	9			
1	H	254	Total	C	N	O	S	0	0	0
			2031	1285	349	388	9			
1	I	254	Total	C	N	O	S	0	0	0
			2031	1285	349	388	9			
1	J	254	Total	C	N	O	S	0	0	0
			2031	1285	349	388	9			

There are 30 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	SER	-	expression tag	UNP Q8U3I4
A	1	VAL	-	expression tag	UNP Q8U3I4
A	179	ALA	PHE	engineered mutation	UNP Q8U3I4
B	0	SER	-	expression tag	UNP Q8U3I4
B	1	VAL	-	expression tag	UNP Q8U3I4
B	179	ALA	PHE	engineered mutation	UNP Q8U3I4
C	0	SER	-	expression tag	UNP Q8U3I4
C	1	VAL	-	expression tag	UNP Q8U3I4
C	179	ALA	PHE	engineered mutation	UNP Q8U3I4

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Chain	Residue	Modelled	Actual	Comment	Reference
D	0	SER	-	expression tag	UNP Q8U3I4
D	1	VAL	-	expression tag	UNP Q8U3I4
D	179	ALA	PHE	engineered mutation	UNP Q8U3I4
E	0	SER	-	expression tag	UNP Q8U3I4
E	1	VAL	-	expression tag	UNP Q8U3I4
E	179	ALA	PHE	engineered mutation	UNP Q8U3I4
F	0	SER	-	expression tag	UNP Q8U3I4
F	1	VAL	-	expression tag	UNP Q8U3I4
F	179	ALA	PHE	engineered mutation	UNP Q8U3I4
G	0	SER	-	expression tag	UNP Q8U3I4
G	1	VAL	-	expression tag	UNP Q8U3I4
G	179	ALA	PHE	engineered mutation	UNP Q8U3I4
H	0	SER	-	expression tag	UNP Q8U3I4
H	1	VAL	-	expression tag	UNP Q8U3I4
H	179	ALA	PHE	engineered mutation	UNP Q8U3I4
I	0	SER	-	expression tag	UNP Q8U3I4
I	1	VAL	-	expression tag	UNP Q8U3I4
I	179	ALA	PHE	engineered mutation	UNP Q8U3I4
J	0	SER	-	expression tag	UNP Q8U3I4
J	1	VAL	-	expression tag	UNP Q8U3I4
J	179	ALA	PHE	engineered mutation	UNP Q8U3I4

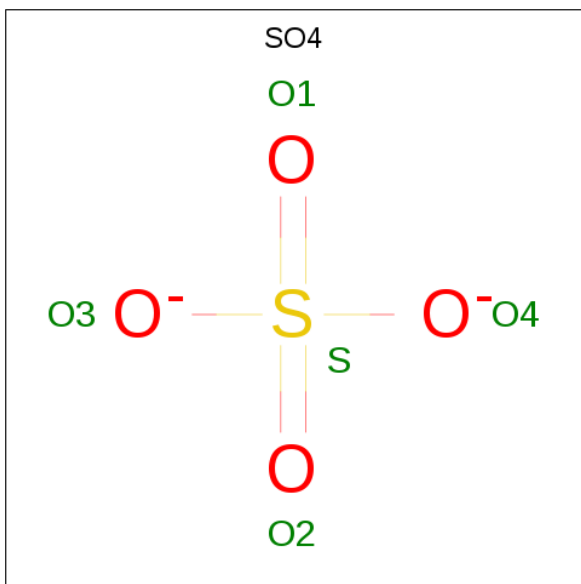- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	G	1	Total 1	Zn 1	0	0
2	J	1	Total 1	Zn 1	0	0
2	D	1	Total 1	Zn 1	0	0
2	E	1	Total 1	Zn 1	0	0
2	H	1	Total 1	Zn 1	0	0
2	B	1	Total 1	Zn 1	0	0
2	I	1	Total 1	Zn 1	0	0
2	C	1	Total 1	Zn 1	0	0
2	A	1	Total 1	Zn 1	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	F	1	Total 1	Zn 1	0	0

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O_4S).

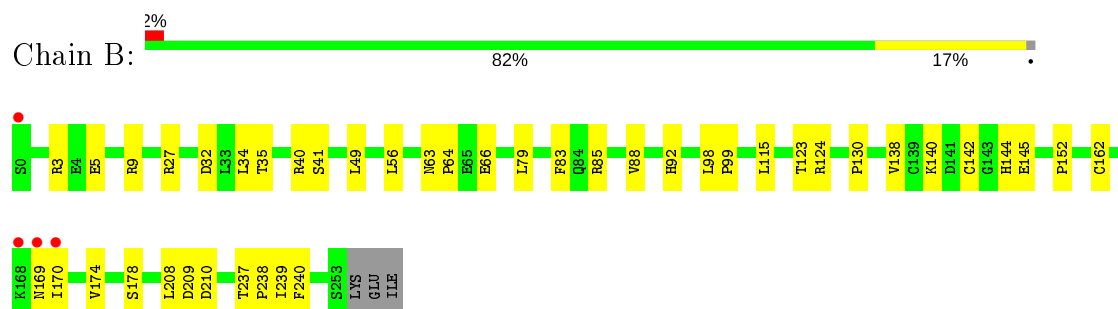| Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total 5	O 4	S 1	0	0
3	B	1	Total 5	O 4	S 1	0	0
3	B	1	Total 5	O 4	S 1	0	0
3	C	1	Total 5	O 4	S 1	0	0
3	C	1	Total 5	O 4	S 1	0	0
3	D	1	Total 5	O 4	S 1	0	0
3	D	1	Total 5	O 4	S 1	0	0
3	E	1	Total 5	O 4	S 1	0	0
3	G	1	Total 5	O 4	S 1	0	0

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 the various outlier classes 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.
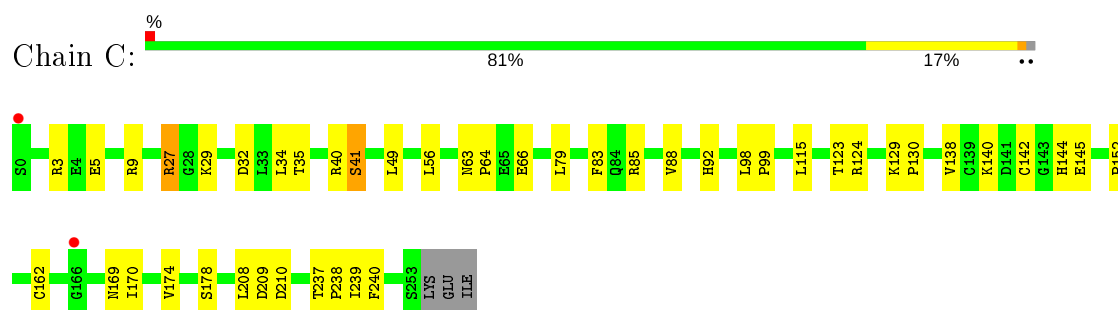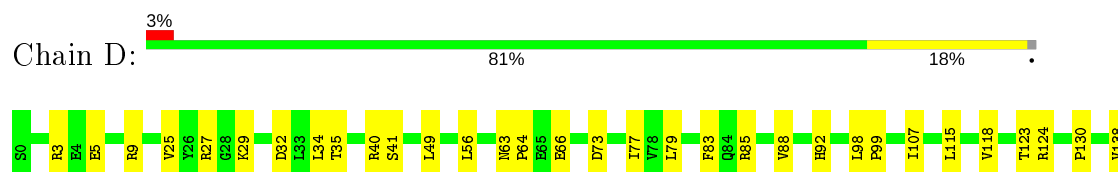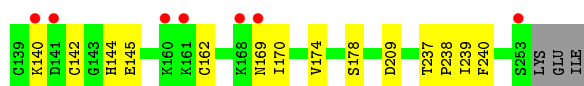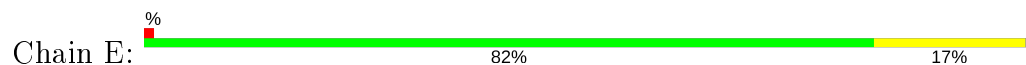
- Molecule 1: Cell division control protein 21

- Molecule 1: Cell division control protein 21

- Molecule 1: Cell division control protein 21

- Molecule 1: Cell division control protein 21

C139 K140 D141 C142 G143 H144 E145 K160 K161 C162 K168 N169 I170 V174 S178 D209 T237 P238 I239 F240 S253 LYS GLU ILE

• Molecule 1: Cell division control protein 21

Chain E:

S0 R3 R27 D32 L33 L34 T35 I36 R40 S41 L49 L56 N63 P64 E65 E66 L79 F83 Q84 R85 V88 H92 A93 R94 L98 P99 L115 T123 R124 K129 P130 V138 C139 K140 D141 C142 G143 H144 E145 P152 K161 C162

G166 N169 I170 V174 S178 L208 D209 D210 T237 P238 I239 F240 S253 LYS GLU ILE

• Molecule 1: Cell division control protein 21

Chain F:

S0 R3 I7 T18 N23 P24 V25 T37 L49 L56 L79 R80 F83 Q84 B85 B86 D87 V88 L98 P99 H111 I116 K129 P130 C162 I170 V174 S178 F185 G197 G205 R220 V252 S253 LYS GLU ILE

• Molecule 1: Cell division control protein 21

Chain G:

S0 R3 I7 T18 N23 P24 V25 T31 D32 L33 I36 L49 L56 L79 R80 F83 Q84 R85 B86 D87 V88 H92 A93 R94 L98 P99 K129 P130 C139 N169 I170 E171 V174 S178 F185 G196 G205 R220

V252 S253 LYS GLU ILE

• Molecule 1: Cell division control protein 21

Chain H:

S0 R3 I7 A11 P24 V25 Y26 R27 T31 D32 L33 L34 T35 I36 T37 P38 L49 L56 L79 R80 F83 Q84 R85 B86 D87 V88 L98 P99 H111 I116 K129 P130 K151 P152 Y153 C162 I170 V174 S178 G196

L208 R220 V252 S253 LYS GLU ILE

• Molecule 1: Cell division control protein 21

Chain I:

S0 R3 I7 T18 N23 P24 V25 D32 L33 L49 L56 L79 R80 F83 Q84 R85 E86 D87 V88 H92 A93 R94 L98 P99 H111 I116 K129 P130 C139 K151 P152 Y153 C162 N169 I170 E171 V174 S178 F182

F185 R186 G196 F202 G205 R220 V252 S253 LYS GLU ILE

• Molecule 1: Cell division control protein 21

Chain J:

4%

84% 15%

S0 R3 I7 F10 A11 N12 E16 Y17 T18 N23 P24 V25 T35 I36 T37 P38 K39 L49 L56 N63 E66 L79 R80 F83 Q84 R85 E86 D87 V88 R94 L98 P99 H111 I116 K129 P130 P152 C162 N169 I170

V174 S178 G196 L208 D209 D210 V214 R220 E235 K236 T237 V252 S253 LYS GLU ILE

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α, β, γ	213.02Å 213.02Å 213.98Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	50.00 – 3.20 49.86 – 3.20	Depositor EDS
% Data completeness (in resolution range)	99.8 (50.00-3.20) 99.7 (49.86-3.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.19	Depositor
$< I/\sigma(I) >$ [1]	2.48 (at 3.19Å)	Xtriage
Refinement program	REFMAC 5.8.0049	Depositor
R, R_{free}	0.202 , 0.230 0.202 , 0.229	Depositor DCC
R_{free} test set	4642 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å^2)	62.0	Xtriage
Anisotropy	0.025	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.31 , 59.6	EDS
L-test for twinning[2]	$< \|L\| > = 0.50, < L^2 > = 0.33$	Xtriage
Estimated twinning fraction	0.012 for -h,-k,l	Xtriage
F_o,F_c correlation	0.92	EDS
Total number of atoms	20365	wwPDB-VP
Average B, all atoms (Å^2)	66.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.43% of the height of the origin peak. No significant pseudotranslation is detected.*

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[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< \|L\| >$, $< L^2 >$ 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, SO4

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	0.38	0/2065	0.59	0/2789
1	B	0.38	0/2065	0.59	0/2789
1	C	0.39	0/2065	0.60	0/2789
1	D	0.39	0/2065	0.60	0/2789
1	E	0.39	0/2065	0.61	0/2789
1	F	0.37	0/2065	0.56	0/2789
1	G	0.41	0/2065	0.59	0/2789
1	H	0.38	0/2065	0.57	0/2789
1	I	0.40	0/2065	0.59	0/2789
1	J	0.37	0/2065	0.57	0/2789
All	All	0.39	0/20650	0.59	0/27890

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	2031	0	2046	31	0
1	B	2031	0	2046	24	0
1	C	2031	0	2046	30	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D	2031	0	2046	27	0
1	E	2031	0	2046	31	0
1	F	2031	0	2046	20	0
1	G	2031	0	2046	22	0
1	H	2031	0	2046	22	0
1	I	2031	0	2046	27	0
1	J	2031	0	2046	28	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
2	E	1	0	0	0	0
2	F	1	0	0	0	0
2	G	1	0	0	0	0
2	H	1	0	0	0	0
2	I	1	0	0	0	0
2	J	1	0	0	0	0
3	A	5	0	0	1	0
3	B	10	0	0	0	0
3	C	10	0	0	1	0
3	D	10	0	0	1	0
3	E	5	0	0	0	0
3	G	5	0	0	0	0
All	All	20365	0	20460	236	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 6.

The worst 5 of 236 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:E:83:PHE:HA	1:I:174:VAL:HG21	1.40	1.04
1:C:83:PHE:HA	1:G:174:VAL:HG21	1.41	1.02
1:A:83:PHE:HA	1:J:174:VAL:HG21	1.50	0.91
1:J:3:ARG:HG3	1:J:3:ARG:HH21	1.37	0.90
1:F:3:ARG:HG3	1:F:3:ARG:HH21	1.37	0.87

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	252/257 (98%)	239 (95%)	12 (5%)	1 (0%)	34	69
1	B	252/257 (98%)	239 (95%)	13 (5%)	0	100	100
1	C	252/257 (98%)	239 (95%)	13 (5%)	0	100	100
1	D	252/257 (98%)	240 (95%)	11 (4%)	1 (0%)	34	69
1	E	252/257 (98%)	239 (95%)	13 (5%)	0	100	100
1	F	252/257 (98%)	234 (93%)	17 (7%)	1 (0%)	34	69
1	G	252/257 (98%)	233 (92%)	16 (6%)	3 (1%)	13	49
1	H	252/257 (98%)	233 (92%)	16 (6%)	3 (1%)	13	49
1	I	252/257 (98%)	236 (94%)	13 (5%)	3 (1%)	13	49
1	J	252/257 (98%)	235 (93%)	14 (6%)	3 (1%)	13	49
All	All	2520/2570 (98%)	2367 (94%)	138 (6%)	15 (1%)	25	64

5 of 15 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	J	35	THR
1	G	32	ASP
1	I	25	VAL
1	H	36	ILE
1	H	25	VAL

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	229/232 (99%)	226 (99%)	3 (1%)	69	87
1	B	229/232 (99%)	226 (99%)	3 (1%)	69	87
1	C	229/232 (99%)	224 (98%)	5 (2%)	52	79
1	D	229/232 (99%)	226 (99%)	3 (1%)	69	87
1	E	229/232 (99%)	225 (98%)	4 (2%)	60	83
1	F	229/232 (99%)	226 (99%)	3 (1%)	69	87
1	G	229/232 (99%)	225 (98%)	4 (2%)	60	83
1	H	229/232 (99%)	227 (99%)	2 (1%)	78	91
1	I	229/232 (99%)	225 (98%)	4 (2%)	60	83
1	J	229/232 (99%)	227 (99%)	2 (1%)	78	91
All	All	2290/2320 (99%)	2257 (99%)	33 (1%)	67	86

5 of 33 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	3	ARG
1	F	3	ARG
1	I	178	SER
1	E	174	VAL
1	E	178	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 17 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	84	GLN
1	C	169	ASN
1	E	12	ASN
1	C	12	ASN
1	E	169	ASN

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 carbohydrates in this entry.

5.6 Ligand geometry (i)

Of 19 ligands modelled in this entry, 10 are monoatomic - leaving 9 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	#$|Z| > 2$
3	SO4	E	302	-	4,4,4	0.38	0	6,6,6	0.24	0
3	SO4	D	302	-	4,4,4	0.35	0	6,6,6	0.25	0
3	SO4	B	302	-	4,4,4	0.31	0	6,6,6	0.26	0
3	SO4	C	303	-	4,4,4	0.35	0	6,6,6	0.19	0
3	SO4	B	303	-	4,4,4	0.33	0	6,6,6	0.19	0
3	SO4	A	302	-	4,4,4	0.37	0	6,6,6	0.20	0
3	SO4	G	302	-	4,4,4	0.42	0	6,6,6	0.42	0
3	SO4	D	303	-	4,4,4	0.35	0	6,6,6	0.26	0
3	SO4	C	302	-	4,4,4	0.30	0	6,6,6	0.26	0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	303	SO4	1	0
3	A	302	SO4	1	0
3	D	303	SO4	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 (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, 95th 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^2)	Q<0.9
1	A	254/257 (98%)	-0.17	4 (1%)	72	59	33, 58, 120, 151	0
1	B	254/257 (98%)	-0.19	4 (1%)	72	59	28, 56, 119, 142	0
1	C	254/257 (98%)	-0.30	2 (0%)	86	78	27, 49, 102, 143	0
1	D	254/257 (98%)	-0.14	7 (2%)	53	37	32, 54, 118, 142	0
1	E	254/257 (98%)	-0.24	3 (1%)	79	67	33, 50, 103, 149	0
1	F	254/257 (98%)	-0.08	1 (0%)	92	89	35, 70, 137, 182	0
1	G	254/257 (98%)	-0.20	0	100	100	25, 52, 109, 185	0
1	H	254/257 (98%)	-0.10	3 (1%)	79	67	28, 65, 136, 180	0
1	I	254/257 (98%)	-0.22	1 (0%)	92	89	27, 52, 109, 196	0
1	J	254/257 (98%)	0.12	10 (3%)	39	25	37, 80, 155, 262	0
All	All	2540/2570 (98%)	-0.15	35 (1%)	75	63	25, 58, 126, 262	0

The worst 5 of 35 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	0	SER	5.2
1	D	168	LYS	4.0
1	H	0	SER	3.8
1	J	88	VAL	3.5
1	J	0	SER	3.4

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 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. The B-factors column lists the minimum, median, 95th 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^2)	Q<0.9
3	SO4	D	302	5/5	0.78	0.24	118,118,118,118	0
3	SO4	E	302	5/5	0.81	0.17	131,131,131,131	0
3	SO4	B	302	5/5	0.82	0.19	121,121,121,121	0
3	SO4	G	302	5/5	0.83	0.28	108,108,108,108	0
3	SO4	C	302	5/5	0.83	0.21	126,126,126,126	0
2	ZN	A	301	1/1	0.84	0.04	145,145,145,145	0
3	SO4	B	303	5/5	0.89	0.24	119,119,119,119	0
3	SO4	D	303	5/5	0.93	0.19	109,109,109,109	0
3	SO4	A	302	5/5	0.93	0.21	117,117,117,117	0
3	SO4	C	303	5/5	0.94	0.17	110,110,110,110	0
2	ZN	D	301	1/1	0.94	0.07	157,157,157,157	0
2	ZN	F	301	1/1	0.95	0.10	84,84,84,84	0
2	ZN	B	301	1/1	0.97	0.05	153,153,153,153	0
2	ZN	H	301	1/1	0.97	0.09	73,73,73,73	0
2	ZN	J	301	1/1	0.98	0.07	94,94,94,94	0
2	ZN	G	301	1/1	0.98	0.08	59,59,59,59	0
2	ZN	E	301	1/1	0.98	0.07	89,89,89,89	0
2	ZN	C	301	1/1	0.98	0.07	87,87,87,87	0
2	ZN	I	301	1/1	0.99	0.08	71,71,71,71	0

6.5 Other polymers (i)

There are no such residues in this entry.