



# Full wwPDB X-ray Structure Validation Report ⓘ

Sep 25, 2023 – 05:16 PM EDT

PDB ID : 5WOO  
Title : The crystal structure of the Staphylococcus aureus Fatty acid Kinase (Fak) B1 protein loaded with Myristic acid (C14:0) to 1.78 Angstrom resolution  
Authors : Cuypers, M.G.; Ericson, M.; Subramanian, C.; White, S.W.; Rock, C.O.  
Deposited on : 2017-08-02  
Resolution : 1.78 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

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.35.1  
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) : 2.35.1

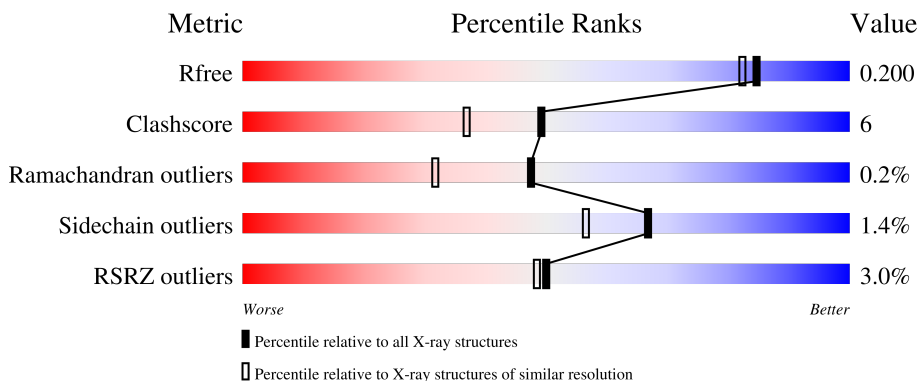
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

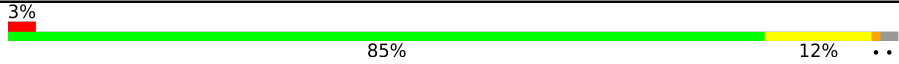

The reported resolution of this entry is 1.78 Å.

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	9185 (1.80-1.76)
Clashscore	141614	10184 (1.80-1.76)
Ramachandran outliers	138981	10051 (1.80-1.76)
Sidechain outliers	138945	10050 (1.80-1.76)
RSRZ outliers	127900	9032 (1.80-1.76)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	294	
1	B	294	

## 2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 5334 atoms, of which 8 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 EDD domain protein, DegV family.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	288	Total	C	N	O	S	0	11	0
			2332	1480	379	460	13			
1	B	287	Total	C	N	O	S	0	6	0
			2297	1456	378	451	12			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-5	VAL	-	expression tag	UNP X5EH37
A	-4	PRO	-	expression tag	UNP X5EH37
A	-3	ARG	-	expression tag	UNP X5EH37
A	-2	GLY	-	expression tag	UNP X5EH37
A	-1	SER	-	expression tag	UNP X5EH37
A	0	HIS	-	expression tag	UNP X5EH37
B	-5	VAL	-	expression tag	UNP X5EH37
B	-4	PRO	-	expression tag	UNP X5EH37
B	-3	ARG	-	expression tag	UNP X5EH37
B	-2	GLY	-	expression tag	UNP X5EH37
B	-1	SER	-	expression tag	UNP X5EH37
B	0	HIS	-	expression tag	UNP X5EH37

- Molecule 2 is MYRISTIC ACID (three-letter code: MYR) (formula: C<sub>14</sub>H<sub>28</sub>O<sub>2</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			16	14	2		
2	B	1	Total	C	O	0	0
			16	14	2		

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula:  $C_3H_8O_3$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	H	O	0	0
			14	3	8	3		

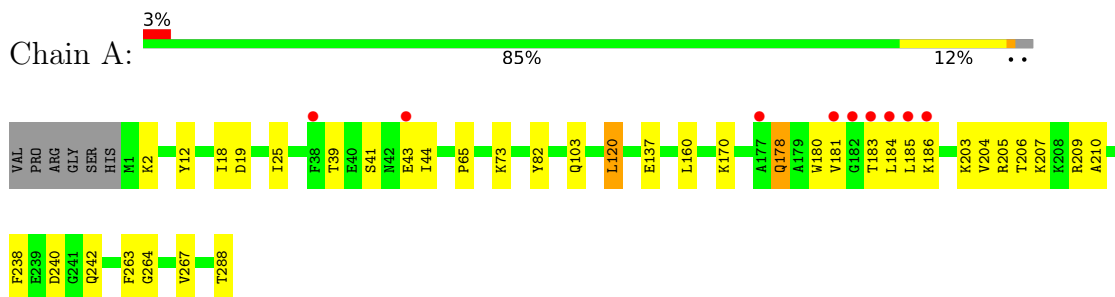
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	330	Total 337	O 337	0	7
4	B	322	Total 322	O 322	0	0

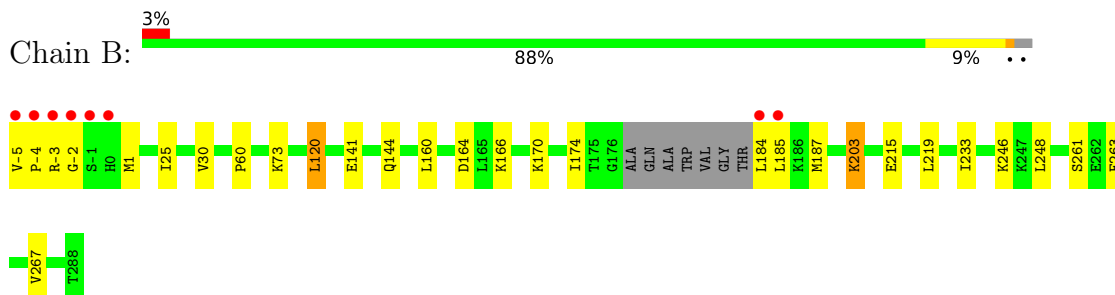
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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: EDD domain protein, DegV family



- Molecule 1: EDD domain protein, DegV family



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	33.39Å 54.45Å 84.91Å 104.89° 90.20° 107.76°	Depositor
Resolution (Å)	36.90 – 1.78 36.90 – 1.78	Depositor EDS
% Data completeness (in resolution range)	96.2 (36.90-1.78) 96.2 (36.90-1.78)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.05 (at 1.78Å)	Xtrriage
Refinement program	PHENIX (1.12_2829: ???)	Depositor
R, $R_{free}$	0.151 , 0.200 0.151 , 0.200	Depositor DCC
$R_{free}$ test set	2306 reflections (4.56%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	20.3	Xtrriage
Anisotropy	0.394	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 53.8	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	0.035 for h,-h-k,-l	Xtrriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	5334	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	27.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.59% 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: GOL, MYR

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	0.35	0/2370	0.54	1/3198 (0.0%)
1	B	0.34	0/2335	0.53	1/3146 (0.0%)
All	All	0.35	0/4705	0.54	2/6344 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	120	LEU	CA-CB-CG	-5.53	102.57	115.30
1	A	120	LEU	CA-CB-CG	-5.04	103.70	115.30

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	2332	0	2329	33	2
1	B	2297	0	2286	22	0
2	A	16	0	27	0	0
2	B	16	0	27	0	0
3	A	6	8	8	0	0
4	A	337	0	0	7	2
4	B	322	0	0	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	5326	8	4677	55	2

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.

All (55) 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:185[B]:LEU:HG	1:A:186[B]:LYS:H	1.43	0.82
1:B:166[B]:LYS:NZ	4:B:401:HOH:O	2.17	0.77
1:A:184:LEU:HB3	4:A:647:HOH:O	1.84	0.76
1:A:185[B]:LEU:HG	1:A:186[B]:LYS:HD2	1.68	0.76
1:A:65:PRO:O	4:A:401:HOH:O	2.03	0.75
1:B:-5:VAL:HB	1:B:-4:PRO:HD3	1.67	0.75
1:B:164:ASP:OD2	1:B:166[B]:LYS:HD3	1.88	0.74
1:A:178:GLN:O	1:A:181:VAL:HG22	1.88	0.73
1:A:288:THR:OG1	4:A:402:HOH:O	2.08	0.71
1:A:186[B]:LYS:HG2	1:A:205:ARG:O	1.92	0.69
1:A:184:LEU:HD12	1:A:184:LEU:O	1.93	0.69
1:A:184:LEU:HG	4:A:628:HOH:O	1.93	0.68
1:B:141:GLU:HG2	1:B:144:GLN:HG3	1.84	0.59
1:B:166[A]:LYS:HG2	4:B:404:HOH:O	2.03	0.58
1:A:185[B]:LEU:CG	1:A:186[B]:LYS:H	2.12	0.58
1:B:166[B]:LYS:HD2	1:B:166[B]:LYS:N	2.20	0.57
1:A:207:LYS:NZ	1:A:240:ASP:OD2	2.26	0.56
1:A:205:ARG:HG3	1:A:209:ARG:HD2	1.88	0.56
1:A:238:PHE:CE2	1:A:242:GLN:HG3	2.41	0.56
1:A:186[B]:LYS:NZ	1:A:205:ARG:HB2	2.21	0.56
1:A:180:TRP:CZ2	1:A:203:LYS:HG3	2.43	0.54
1:B:187:MET:HB2	1:B:203:LYS:HG2	1.92	0.51
1:A:238:PHE:CZ	1:A:242:GLN:HG3	2.46	0.50
1:B:-2:GLY:O	1:B:1:MET:HG3	2.12	0.50
1:B:30:VAL:HG12	1:B:60:PRO:HB2	1.94	0.50
1:B:164:ASP:OD2	1:B:166[A]:LYS:HD2	2.12	0.49
1:A:183:THR:HG22	1:A:183:THR:O	2.12	0.49
1:A:41:SER:OG	1:A:43:GLU:HG2	2.12	0.49
1:A:39:THR:O	1:A:44:ILE:HD11	2.14	0.48
1:A:180:TRP:CH2	1:A:203:LYS:HG3	2.50	0.47
1:A:205:ARG:CG	1:A:209:ARG:HD2	2.45	0.47
1:B:263[A]:PHE:CD1	1:B:267:VAL:HG11	2.49	0.47
1:B:170:LYS:HA	1:B:170:LYS:HD2	1.81	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:215:GLU:O	1:B:219[A]:LEU:HD13	2.16	0.46
1:B:187:MET:CB	1:B:203:LYS:HG2	2.46	0.45
1:A:2:LYS:HE2	1:A:82:TYR:CE1	2.52	0.45
1:A:18:ILE:HD13	1:A:25[B]:ILE:HD11	2.00	0.44
1:A:204:VAL:HG21	1:A:210:ALA:CA	2.48	0.44
1:A:137:GLU:OE2	4:A:403:HOH:O	2.21	0.44
1:B:261:SER:HB2	4:B:499:HOH:O	2.17	0.44
1:A:73:LYS:NZ	4:A:623[B]:HOH:O	2.25	0.44
1:B:174:ILE:HG22	4:B:554:HOH:O	2.17	0.44
1:A:185[B]:LEU:CG	1:A:186[B]:LYS:N	2.81	0.42
1:A:205:ARG:HG3	1:A:206:THR:HG23	2.01	0.42
1:B:215:GLU:HG3	1:B:248:LEU:HD21	2.01	0.41
1:A:12:TYR:CE1	1:A:264:GLY:HA3	2.55	0.41
1:A:186[A]:LYS:HB2	1:A:186[A]:LYS:HE3	1.86	0.41
1:B:25:ILE:O	1:B:73:LYS:NZ	2.53	0.41
1:B:233:ILE:HG22	1:B:263[A]:PHE:CE1	2.55	0.41
1:B:164:ASP:CG	1:B:166[B]:LYS:HD3	2.40	0.41
1:A:170:LYS:HE3	4:A:521:HOH:O	2.21	0.41
1:A:185[B]:LEU:HG	1:A:186[B]:LYS:CD	2.45	0.41
1:B:246:LYS:HE2	1:B:246:LYS:HB3	1.89	0.41
1:A:263:PHE:CD1	1:A:267:VAL:HG11	2.56	0.41
1:B:184:LEU:CB	1:B:203:LYS:HD3	2.50	0.40

All (2) 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)
1:A:19:ASP:OD1	4:A:725:HOH:O[1_545]	2.16	0.04
1:A:103:GLN:OE1	4:A:648:HOH:O[1_445]	2.18	0.02

## 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	297/294 (101%)	292 (98%)	5 (2%)	0	100	100
1	B	289/294 (98%)	285 (99%)	3 (1%)	1 (0%)	41	25
All	All	586/588 (100%)	577 (98%)	8 (1%)	1 (0%)	47	32

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	185	LEU

### 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	257/251 (102%)	254 (99%)	3 (1%)	71	62
1	B	252/251 (100%)	247 (98%)	5 (2%)	55	40
All	All	509/502 (101%)	501 (98%)	8 (2%)	67	51

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	120	LEU
1	A	160	LEU
1	A	178	GLN
1	B	-3[A]	ARG
1	B	-3[B]	ARG
1	B	120	LEU
1	B	160	LEU
1	B	203	LYS

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

### 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 monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

3 ligands 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
2	MYR	A	301	-	15,15,15	0.71	0	15,15,15	1.11	1 (6%)
3	GOL	A	302	-	5,5,5	1.02	0	5,5,5	0.85	0
2	MYR	B	301	-	15,15,15	0.77	0	15,15,15	1.07	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	MYR	A	301	-	-	2/13/13/13	-
3	GOL	A	302	-	-	3/4/4/4	-
2	MYR	B	301	-	-	2/13/13/13	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	301	MYR	O2-C1-C2	2.12	120.83	114.03

There are no chirality outliers.

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	302	GOL	C1-C2-C3-O3
3	A	302	GOL	O2-C2-C3-O3
3	A	302	GOL	O1-C1-C2-C3
2	A	301	MYR	O2-C1-C2-C3
2	A	301	MYR	O1-C1-C2-C3
2	B	301	MYR	O2-C1-C2-C3
2	B	301	MYR	O1-C1-C2-C3

There are no ring outliers.

No monomer is involved in short contacts.

## 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	288/294 (97%)	-0.13	9 (3%) 49 47	14, 22, 43, 80	0
1	B	287/294 (97%)	-0.15	8 (2%) 53 51	14, 22, 46, 78	0
All	All	575/588 (97%)	-0.14	17 (2%) 50 48	14, 22, 46, 80	0

All (17) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	185[A]	LEU	11.3
1	B	-2	GLY	7.7
1	B	-5	VAL	7.6
1	B	-1	SER	5.6
1	A	184	LEU	5.4
1	A	183	THR	4.9
1	B	-3[A]	ARG	4.8
1	A	186[A]	LYS	4.5
1	A	182	GLY	4.2
1	B	0	HIS	4.0
1	B	-4	PRO	3.7
1	B	185	LEU	3.4
1	A	38	PHE	3.2
1	A	181	VAL	3.1
1	B	184	LEU	2.9
1	A	177	ALA	2.5
1	A	43	GLU	2.4

### 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 monosaccharides in this entry.

### 6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
2	MYR	A	301	16/16	0.91	0.15	13,17,29,31	0
3	GOL	A	302	6/6	0.91	0.15	26,56,68,76	0
2	MYR	B	301	16/16	0.93	0.11	13,16,28,29	0

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

There are no such residues in this entry.