



# Full wwPDB X-ray Structure Validation Report

Feb 26, 2014 – 07:43 PM GMT

PDB ID : 3K6X  
Title : M. acetivorans Molybdate-Binding Protein (ModA) in Molybdate-Bound Close Form with 2 Molecules in Asymmetric Unit Forming Beta Barrel  
Authors : Chan, S.; Chernishof, I.; Giuroiu, I.; Sawaya, M.R.; Chiang, J.; Gunsalus, R.P.; Arbing, M.A.; Perry, L.J.  
Deposited on : 2009-10-09  
Resolution : 2.25 Å(reported)

This is a full wwPDB 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/ValidationPDFNotes.html>

---

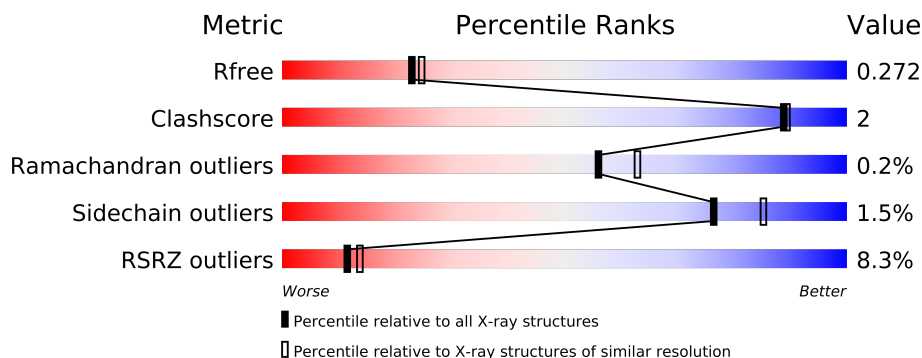
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.15 2013  
Xtriage (Phenix) : dev-1323  
EDS : stable22639  
Percentile statistics : 21963  
Refmac : 5.8.0049  
CCP4 : 6.3.0 (Settle)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : stable22683

# 1 Overall quality at a glance

The reported resolution of this entry is 2.25 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))
$R_{free}$	66092	1108 (2.28-2.24)
Clashscore	79885	1326 (2.28-2.24)
Ramachandran outliers	78287	1291 (2.28-2.24)
Sidechain outliers	78261	1291 (2.28-2.24)
RSRZ outliers	66119	1110 (2.28-2.24)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	354	
1	B	354	

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 5137 atoms, of which 0 are hydrogen and 0 are deuterium.

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 Solute-binding protein MA\_0280.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	322	Total	C	N	O	S	0	0	0
			2494	1578	395	511	10			
1	B	322	Total	C	N	O	S	0	0	0
			2498	1580	395	513	10			

There are 56 discrepancies between the modelled and reference sequences:

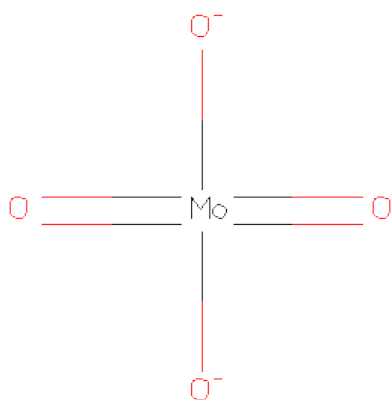
Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	MET	-	EXPRESSION TAG	UNP Q8TTZ5
A	0	LYS	-	EXPRESSION TAG	UNP Q8TTZ5
A	1	HIS	-	EXPRESSION TAG	UNP Q8TTZ5
A	2	HIS	-	EXPRESSION TAG	UNP Q8TTZ5
A	3	HIS	-	EXPRESSION TAG	UNP Q8TTZ5
A	4	HIS	-	EXPRESSION TAG	UNP Q8TTZ5
A	5	HIS	-	EXPRESSION TAG	UNP Q8TTZ5
A	6	HIS	-	EXPRESSION TAG	UNP Q8TTZ5
A	7	PRO	-	EXPRESSION TAG	UNP Q8TTZ5
A	8	MET	-	EXPRESSION TAG	UNP Q8TTZ5
A	9	SER	-	EXPRESSION TAG	UNP Q8TTZ5
A	10	ASP	-	EXPRESSION TAG	UNP Q8TTZ5
A	11	TYR	-	EXPRESSION TAG	UNP Q8TTZ5
A	12	ASP	-	EXPRESSION TAG	UNP Q8TTZ5
A	13	ILE	-	EXPRESSION TAG	UNP Q8TTZ5
A	14	PRO	-	EXPRESSION TAG	UNP Q8TTZ5
A	15	THR	-	EXPRESSION TAG	UNP Q8TTZ5
A	16	THR	-	EXPRESSION TAG	UNP Q8TTZ5
A	17	GLU	-	EXPRESSION TAG	UNP Q8TTZ5
A	18	ASN	-	EXPRESSION TAG	UNP Q8TTZ5
A	19	LEU	-	EXPRESSION TAG	UNP Q8TTZ5
A	20	TYR	-	EXPRESSION TAG	UNP Q8TTZ5
A	21	PHE	-	EXPRESSION TAG	UNP Q8TTZ5
A	22	GLN	-	EXPRESSION TAG	UNP Q8TTZ5
A	23	GLY	-	EXPRESSION TAG	UNP Q8TTZ5

*Continued on next page...*

*Continued from previous page...*

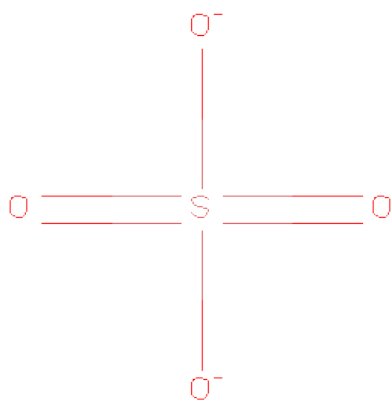
Chain	Residue	Modelled	Actual	Comment	Reference
A	24	ALA	-	EXPRESSION TAG	UNP Q8TTZ5
A	25	MET	-	EXPRESSION TAG	UNP Q8TTZ5
A	26	ALA	-	EXPRESSION TAG	UNP Q8TTZ5
B	-1	MET	-	EXPRESSION TAG	UNP Q8TTZ5
B	0	LYS	-	EXPRESSION TAG	UNP Q8TTZ5
B	1	HIS	-	EXPRESSION TAG	UNP Q8TTZ5
B	2	HIS	-	EXPRESSION TAG	UNP Q8TTZ5
B	3	HIS	-	EXPRESSION TAG	UNP Q8TTZ5
B	4	HIS	-	EXPRESSION TAG	UNP Q8TTZ5
B	5	HIS	-	EXPRESSION TAG	UNP Q8TTZ5
B	6	HIS	-	EXPRESSION TAG	UNP Q8TTZ5
B	7	PRO	-	EXPRESSION TAG	UNP Q8TTZ5
B	8	MET	-	EXPRESSION TAG	UNP Q8TTZ5
B	9	SER	-	EXPRESSION TAG	UNP Q8TTZ5
B	10	ASP	-	EXPRESSION TAG	UNP Q8TTZ5
B	11	TYR	-	EXPRESSION TAG	UNP Q8TTZ5
B	12	ASP	-	EXPRESSION TAG	UNP Q8TTZ5
B	13	ILE	-	EXPRESSION TAG	UNP Q8TTZ5
B	14	PRO	-	EXPRESSION TAG	UNP Q8TTZ5
B	15	THR	-	EXPRESSION TAG	UNP Q8TTZ5
B	16	THR	-	EXPRESSION TAG	UNP Q8TTZ5
B	17	GLU	-	EXPRESSION TAG	UNP Q8TTZ5
B	18	ASN	-	EXPRESSION TAG	UNP Q8TTZ5
B	19	LEU	-	EXPRESSION TAG	UNP Q8TTZ5
B	20	TYR	-	EXPRESSION TAG	UNP Q8TTZ5
B	21	PHE	-	EXPRESSION TAG	UNP Q8TTZ5
B	22	GLN	-	EXPRESSION TAG	UNP Q8TTZ5
B	23	GLY	-	EXPRESSION TAG	UNP Q8TTZ5
B	24	ALA	-	EXPRESSION TAG	UNP Q8TTZ5
B	25	MET	-	EXPRESSION TAG	UNP Q8TTZ5
B	26	ALA	-	EXPRESSION TAG	UNP Q8TTZ5

- Molecule 2 is MOLYBDATE ION (three-letter code: MOO) (formula: MoO<sub>4</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	Mo	O	0	0
			5	1	4		
2	B	1	Total	Mo	O	0	0
			5	1	4		

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	S	0	0
			5	4	1		
3	A	1	Total	O	S	0	0
			5	4	1		

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	S	0	0
			5	4	1		
3	A	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		

- Molecule 4 is water.

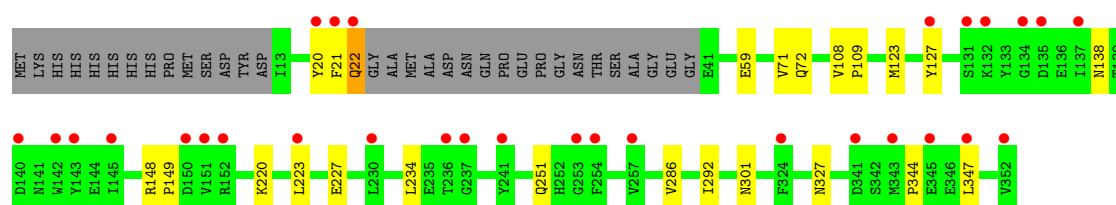
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	47	Total	O	0	0
			47	47		
4	B	48	Total	O	0	0
			48	48		

### 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.

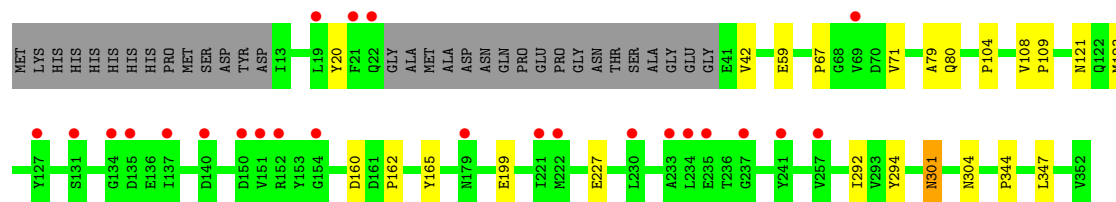
#### • Molecule 1: Solute-binding protein MA\_0280

Chain A: 



#### • Molecule 1: Solute-binding protein MA\_0280

Chain B: 



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	147.19Å 65.59Å 94.77Å 90.00° 123.95° 90.00°	Depositor
Resolution (Å)	57.74 – 2.25 57.78 – 2.25	Depositor EDS
% Data completeness (in resolution range)	87.5 (57.74-2.25) 87.6 (57.78-2.25)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	0.04	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.05 (at 2.25Å)	Xtriage
Refinement program	REFMAC 5.5.0072	Depositor
R, $R_{free}$	0.237 , 0.273 0.241 , 0.272	Depositor DCC
$R_{free}$ test set	1592 reflections (5.36%)	DCC
Wilson B-factor (Å <sup>2</sup> )	44.7	Xtriage
Anisotropy	0.150	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , 29.8	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	2 of 31302 reflections (0.006%)	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	5137	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 86.07 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 1.0488e-07. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<sup>1</sup>Intensities estimated from amplitudes.



## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MOO, 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	0.43	0/2546	0.70	1/3474 (0.0%)
1	B	0.43	0/2550	0.69	0/3479
All	All	0.43	0/5096	0.69	1/6953 (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	A	223	LEU	CA-CB-CG	5.03	126.87	115.30

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Close contacts

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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2494	0	2375	11	0
1	B	2498	0	2379	12	0
2	A	5	0	0	0	0
2	B	5	0	0	0	0
3	A	20	0	0	0	0
3	B	20	0	0	0	0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	47	0	0	0	0
4	B	48	0	0	0	0
All	All	5137	0	4754	22	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 2.

All (22) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:123:MET:HG2	1:B:292:ILE:HD11	1.85	0.57
1:B:80:GLN:HB2	1:B:160:ASP:HB2	1.88	0.56
1:A:127:TYR:HA	1:A:234:LEU:HD11	1.90	0.54
1:A:123:MET:HG2	1:A:292:ILE:HD11	1.91	0.53
1:A:59:GLU:HG3	1:A:71:VAL:HB	1.91	0.51
1:B:301:ASN:HD22	1:B:301:ASN:H	1.60	0.50
1:B:42:VAL:O	1:B:304:ASN:ND2	2.45	0.48
1:B:121:ASN:HB2	1:B:294:TYR:HE2	1.79	0.48
1:B:59:GLU:HG3	1:B:71:VAL:HB	1.96	0.47
1:B:162:PRO:HA	1:B:165:TYR:CZ	2.50	0.46
1:A:344:PRO:HD2	1:A:347:LEU:HD12	1.97	0.46
1:A:21:PHE:CD1	1:A:72:GLN:HB3	2.51	0.46
1:B:344:PRO:HD2	1:B:347:LEU:HD12	1.98	0.45
1:B:104:PRO:HA	1:B:108:VAL:HB	1.98	0.44
1:A:22:GLN:HA	1:A:22:GLN:HE21	1.85	0.42
1:B:108:VAL:HA	1:B:109:PRO:HA	1.75	0.42
1:A:251:GLN:HE21	1:A:327:ASN:HB3	1.86	0.41
1:A:108:VAL:HA	1:A:109:PRO:HA	1.83	0.41
1:A:148:ARG:O	1:A:220:LYS:NZ	2.52	0.41
1:A:148:ARG:HA	1:A:149:PRO:HD3	1.90	0.41
1:A:286:VAL:HB	1:B:199:GLU:HG2	2.03	0.40
1:B:79:ALA:HB3	1:B:160:ASP:HA	2.02	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	318/354 (90%)	308 (97%)	10 (3%)	0	100	100
1	B	318/354 (90%)	309 (97%)	8 (2%)	1 (0%)	50	54
All	All	636/708 (90%)	617 (97%)	18 (3%)	1 (0%)	56	63

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	67	PRO

### 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	269/298 (90%)	264 (98%)	5 (2%)	69	78
1	B	270/298 (91%)	267 (99%)	3 (1%)	84	90
All	All	539/596 (90%)	531 (98%)	8 (2%)	76	85

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

Mol	Chain	Res	Type
1	A	20	TYR
1	A	22	GLN
1	A	138	ASN
1	A	227	GLU
1	A	301	ASN
1	B	20	TYR
1	B	227	GLU
1	B	301	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	22	GLN

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	A	138	ASN
1	A	301	ASN
1	A	329	GLN
1	B	22	GLN
1	B	65	GLN
1	B	301	ASN
1	B	329	GLN

### 5.3.3 RNA ⓘ

There are no RNA chains in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

### 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

### 5.6 Ligand geometry ⓘ

10 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	MOO	A	500	-	2,4,4	6.60	2 (100%)	0,6,6	0.00	-
3	SO4	A	501	-	4,4,4	0.20	0	6,6,6	0.07	0
3	SO4	A	502	-	4,4,4	0.19	0	6,6,6	0.09	0
3	SO4	A	503	-	4,4,4	0.20	0	6,6,6	0.07	0
3	SO4	A	504	-	4,4,4	0.20	0	6,6,6	0.07	0
2	MOO	B	500	-	2,4,4	6.68	2 (100%)	0,6,6	0.00	-

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	SO4	B	501	-	4,4,4	0.23	0	6,6,6	0.07	0
3	SO4	B	502	-	4,4,4	0.20	0	6,6,6	0.09	0
3	SO4	B	503	-	4,4,4	0.20	0	6,6,6	0.08	0
3	SO4	B	504	-	4,4,4	0.19	0	6,6,6	0.06	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	MOO	A	500	-	-	0/0/0/0	0/0/0/0
3	SO4	A	501	-	-	0/0/0/0	0/0/0/0
3	SO4	A	502	-	-	0/0/0/0	0/0/0/0
3	SO4	A	503	-	-	0/0/0/0	0/0/0/0
3	SO4	A	504	-	-	0/0/0/0	0/0/0/0
2	MOO	B	500	-	-	0/0/0/0	0/0/0/0
3	SO4	B	501	-	-	0/0/0/0	0/0/0/0
3	SO4	B	502	-	-	0/0/0/0	0/0/0/0
3	SO4	B	503	-	-	0/0/0/0	0/0/0/0
3	SO4	B	504	-	-	0/0/0/0	0/0/0/0

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	500	MOO	O2-MO	6.76	1.87	1.74
2	A	500	MOO	O2-MO	6.66	1.87	1.74
2	B	500	MOO	O1-MO	6.59	1.87	1.74
2	A	500	MOO	O1-MO	6.54	1.87	1.74

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

## 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	322/354 (90%)	0.80	30 (9%) 9 11	15, 33, 48, 74	0
1	B	322/354 (90%)	0.77	24 (7%) 14 17	13, 34, 48, 97	1 (0%)
All	All	644/708 (90%)	0.79	54 (8%) 11 13	13, 34, 48, 97	1 (0%)

All (54) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	151	VAL	5.9
1	A	21	PHE	4.7
1	B	135	ASP	4.2
1	A	145	ILE	4.1
1	B	230	LEU	3.9
1	A	131	SER	3.9
1	B	21	PHE	3.8
1	A	257	VAL	3.8
1	A	140	ASP	3.7
1	A	254	PHE	3.7
1	A	137	ILE	3.5
1	B	19	LEU	3.4
1	B	234	LEU	3.4
1	B	69	VAL	3.4
1	B	22	GLN	3.3
1	A	135	ASP	3.2
1	A	347	LEU	2.9
1	B	134	GLY	2.8
1	A	142	TRP	2.8
1	B	140	ASP	2.8
1	A	127	TYR	2.8
1	A	230	LEU	2.8
1	B	241	TYR	2.8
1	B	127	TYR	2.7

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	RSRZ
1	A	345	GLU	2.7
1	B	235	GLU	2.6
1	A	132	LYS	2.6
1	A	237	GLY	2.6
1	B	179	ASN	2.6
1	A	223	LEU	2.6
1	A	152	ARG	2.5
1	B	152	ARG	2.5
1	B	131	SER	2.5
1	B	237	GLY	2.4
1	A	241	TYR	2.4
1	B	150	ASP	2.4
1	A	236	THR	2.3
1	A	151	VAL	2.3
1	A	352	VAL	2.2
1	B	221	ILE	2.2
1	A	343	MET	2.2
1	A	22	GLN	2.2
1	A	143	TYR	2.2
1	A	253	GLY	2.1
1	B	137	ILE	2.1
1	B	222	MET	2.1
1	A	324	PHE	2.1
1	A	134	GLY	2.1
1	A	20	TYR	2.1
1	A	341	ASP	2.1
1	B	154	GLY	2.0
1	A	150	ASP	2.0
1	B	257	VAL	2.0
1	B	233	ALA	2.0

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

There are no non-standard protein/DNA/RNA residues in this entry.

## 6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.



## 6.4 Ligands

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	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
3	SO4	B	504	5/5	0.26	0.65	99,99,99,99	0
2	MOO	A	500	5/5	0.18	0.58	25,26,28,31	0
3	SO4	A	504	5/5	0.21	0.35	104,104,104,104	0
2	MOO	B	500	5/5	0.16	0.29	28,30,30,33	0
3	SO4	A	501	5/5	0.16	-0.83	82,82,82,82	0
3	SO4	B	501	5/5	0.16	-0.92	91,91,91,92	0
3	SO4	B	502	5/5	0.15	-1.66	66,67,67,68	0
3	SO4	A	502	5/5	0.14	-3.23	77,77,78,78	0
3	SO4	B	503	5/5	0.14	-	116,116,116,116	0
3	SO4	A	503	5/5	0.10	-	105,106,106,106	0

## 6.5 Other polymers

There are no such residues in this entry.