



# Full wwPDB X-ray Structure Validation Report ⓘ

Mar 27, 2014 – 02:21 PM EDT

PDB ID : 4DA9  
Title : Crystal structure of putative Short-chain dehydrogenase/reductase from  
Sinorhizobium meliloti 1021  
Authors : Malashkevich, V.N.; Bhosle, R.; Toro, R.; Seidel, R.; Almo, S.C.; New York  
Structural Genomics Research Consortium (NYSGRG)  
Deposited on : 2012-01-12  
Resolution : 2.50 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>

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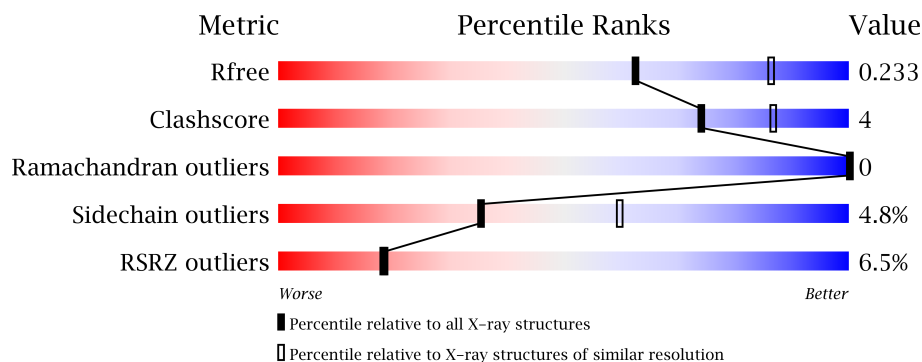
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.15 2013  
Xtriage (Phenix) : dev-1439  
EDS : stable22978  
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) : stable22978

# 1 Overall quality at a glance

The reported resolution of this entry is 2.50 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	2784 (2.50-2.50)
Clashscore	79885	3562 (2.50-2.50)
Ramachandran outliers	78287	3480 (2.50-2.50)
Sidechain outliers	78261	3482 (2.50-2.50)
RSRZ outliers	66119	2785 (2.50-2.50)

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	280	
1	B	280	
1	C	280	
1	D	280	

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 6504 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 Short-chain dehydrogenase/reductase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	219	Total	C	N	O	S	Se	0	0	0
			1587	998	283	301	2	3			
1	B	216	Total	C	N	O	S	Se	0	0	0
			1562	985	277	296	2	2			
1	C	220	Total	C	N	O	S	Se	0	0	0
			1593	1000	287	301	2	3			
1	D	219	Total	C	N	O	S	Se	0	0	0
			1593	1004	283	301	2	3			

There are 92 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-22	MSE	-	EXPRESSION TAG	UNP Q92L02
A	-21	HIS	-	EXPRESSION TAG	UNP Q92L02
A	-20	HIS	-	EXPRESSION TAG	UNP Q92L02
A	-19	HIS	-	EXPRESSION TAG	UNP Q92L02
A	-18	HIS	-	EXPRESSION TAG	UNP Q92L02
A	-17	HIS	-	EXPRESSION TAG	UNP Q92L02
A	-16	HIS	-	EXPRESSION TAG	UNP Q92L02
A	-15	SER	-	EXPRESSION TAG	UNP Q92L02
A	-14	SER	-	EXPRESSION TAG	UNP Q92L02
A	-13	GLY	-	EXPRESSION TAG	UNP Q92L02
A	-12	VAL	-	EXPRESSION TAG	UNP Q92L02
A	-11	ASP	-	EXPRESSION TAG	UNP Q92L02
A	-10	LEU	-	EXPRESSION TAG	UNP Q92L02
A	-9	GLY	-	EXPRESSION TAG	UNP Q92L02
A	-8	THR	-	EXPRESSION TAG	UNP Q92L02
A	-7	GLU	-	EXPRESSION TAG	UNP Q92L02
A	-6	ASN	-	EXPRESSION TAG	UNP Q92L02
A	-5	LEU	-	EXPRESSION TAG	UNP Q92L02
A	-4	TYR	-	EXPRESSION TAG	UNP Q92L02
A	-3	PHE	-	EXPRESSION TAG	UNP Q92L02
A	-2	GLN	-	EXPRESSION TAG	UNP Q92L02

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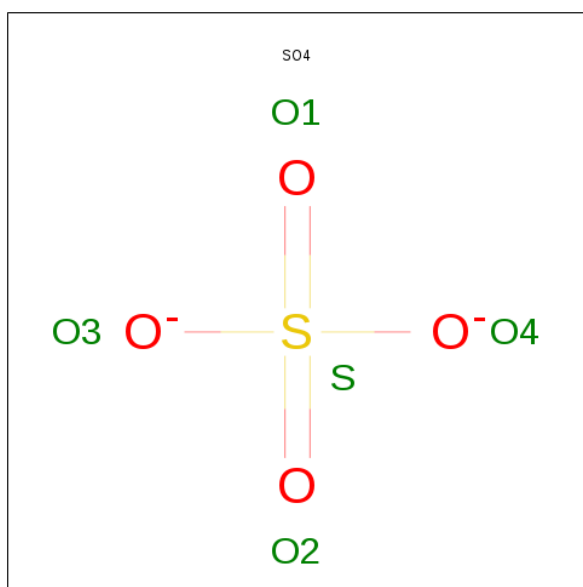
Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	SER	-	EXPRESSION TAG	UNP Q92L02
A	0	MSE	-	EXPRESSION TAG	UNP Q92L02
B	-22	MSE	-	EXPRESSION TAG	UNP Q92L02
B	-21	HIS	-	EXPRESSION TAG	UNP Q92L02
B	-20	HIS	-	EXPRESSION TAG	UNP Q92L02
B	-19	HIS	-	EXPRESSION TAG	UNP Q92L02
B	-18	HIS	-	EXPRESSION TAG	UNP Q92L02
B	-17	HIS	-	EXPRESSION TAG	UNP Q92L02
B	-16	HIS	-	EXPRESSION TAG	UNP Q92L02
B	-15	SER	-	EXPRESSION TAG	UNP Q92L02
B	-14	SER	-	EXPRESSION TAG	UNP Q92L02
B	-13	GLY	-	EXPRESSION TAG	UNP Q92L02
B	-12	VAL	-	EXPRESSION TAG	UNP Q92L02
B	-11	ASP	-	EXPRESSION TAG	UNP Q92L02
B	-10	LEU	-	EXPRESSION TAG	UNP Q92L02
B	-9	GLY	-	EXPRESSION TAG	UNP Q92L02
B	-8	THR	-	EXPRESSION TAG	UNP Q92L02
B	-7	GLU	-	EXPRESSION TAG	UNP Q92L02
B	-6	ASN	-	EXPRESSION TAG	UNP Q92L02
B	-5	LEU	-	EXPRESSION TAG	UNP Q92L02
B	-4	TYR	-	EXPRESSION TAG	UNP Q92L02
B	-3	PHE	-	EXPRESSION TAG	UNP Q92L02
B	-2	GLN	-	EXPRESSION TAG	UNP Q92L02
B	-1	SER	-	EXPRESSION TAG	UNP Q92L02
B	0	MSE	-	EXPRESSION TAG	UNP Q92L02
C	-22	MSE	-	EXPRESSION TAG	UNP Q92L02
C	-21	HIS	-	EXPRESSION TAG	UNP Q92L02
C	-20	HIS	-	EXPRESSION TAG	UNP Q92L02
C	-19	HIS	-	EXPRESSION TAG	UNP Q92L02
C	-18	HIS	-	EXPRESSION TAG	UNP Q92L02
C	-17	HIS	-	EXPRESSION TAG	UNP Q92L02
C	-16	HIS	-	EXPRESSION TAG	UNP Q92L02
C	-15	SER	-	EXPRESSION TAG	UNP Q92L02
C	-14	SER	-	EXPRESSION TAG	UNP Q92L02
C	-13	GLY	-	EXPRESSION TAG	UNP Q92L02
C	-12	VAL	-	EXPRESSION TAG	UNP Q92L02
C	-11	ASP	-	EXPRESSION TAG	UNP Q92L02
C	-10	LEU	-	EXPRESSION TAG	UNP Q92L02
C	-9	GLY	-	EXPRESSION TAG	UNP Q92L02
C	-8	THR	-	EXPRESSION TAG	UNP Q92L02
C	-7	GLU	-	EXPRESSION TAG	UNP Q92L02
C	-6	ASN	-	EXPRESSION TAG	UNP Q92L02

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-5	LEU	-	EXPRESSION TAG	UNP Q92L02
C	-4	TYR	-	EXPRESSION TAG	UNP Q92L02
C	-3	PHE	-	EXPRESSION TAG	UNP Q92L02
C	-2	GLN	-	EXPRESSION TAG	UNP Q92L02
C	-1	SER	-	EXPRESSION TAG	UNP Q92L02
C	0	MSE	-	EXPRESSION TAG	UNP Q92L02
D	-22	MSE	-	EXPRESSION TAG	UNP Q92L02
D	-21	HIS	-	EXPRESSION TAG	UNP Q92L02
D	-20	HIS	-	EXPRESSION TAG	UNP Q92L02
D	-19	HIS	-	EXPRESSION TAG	UNP Q92L02
D	-18	HIS	-	EXPRESSION TAG	UNP Q92L02
D	-17	HIS	-	EXPRESSION TAG	UNP Q92L02
D	-16	HIS	-	EXPRESSION TAG	UNP Q92L02
D	-15	SER	-	EXPRESSION TAG	UNP Q92L02
D	-14	SER	-	EXPRESSION TAG	UNP Q92L02
D	-13	GLY	-	EXPRESSION TAG	UNP Q92L02
D	-12	VAL	-	EXPRESSION TAG	UNP Q92L02
D	-11	ASP	-	EXPRESSION TAG	UNP Q92L02
D	-10	LEU	-	EXPRESSION TAG	UNP Q92L02
D	-9	GLY	-	EXPRESSION TAG	UNP Q92L02
D	-8	THR	-	EXPRESSION TAG	UNP Q92L02
D	-7	GLU	-	EXPRESSION TAG	UNP Q92L02
D	-6	ASN	-	EXPRESSION TAG	UNP Q92L02
D	-5	LEU	-	EXPRESSION TAG	UNP Q92L02
D	-4	TYR	-	EXPRESSION TAG	UNP Q92L02
D	-3	PHE	-	EXPRESSION TAG	UNP Q92L02
D	-2	GLN	-	EXPRESSION TAG	UNP Q92L02
D	-1	SER	-	EXPRESSION TAG	UNP Q92L02
D	0	MSE	-	EXPRESSION TAG	UNP Q92L02

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	D	1	Total	O	S	0	0
			5	4	1		

- Molecule 3 is water.

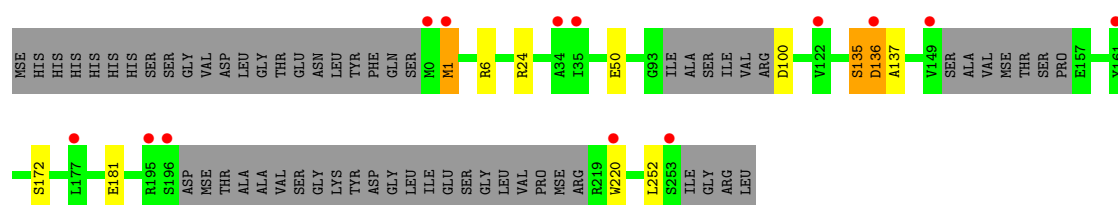
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	51	Total	O	0	0
			51	51		
3	B	29	Total	O	0	0
			29	29		
3	C	44	Total	O	0	0
			44	44		
3	D	25	Total	O	0	0
			25	25		

### 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.

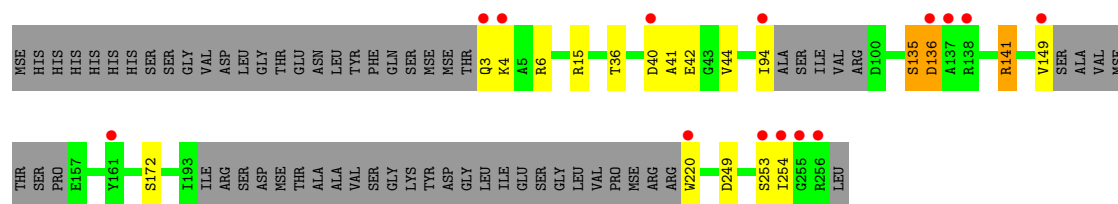
- Molecule 1: Short-chain dehydrogenase/reductase

Chain A: 



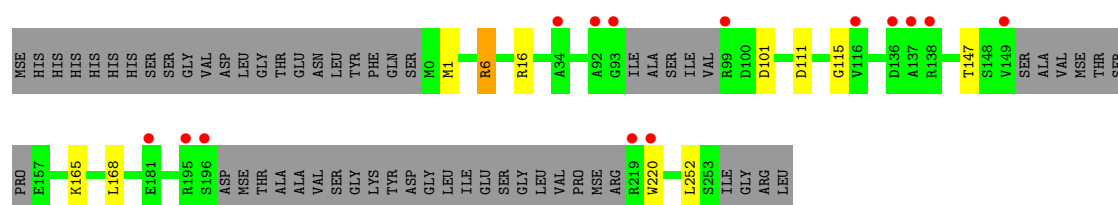
- Molecule 1: Short-chain dehydrogenase/reductase

Chain B: 



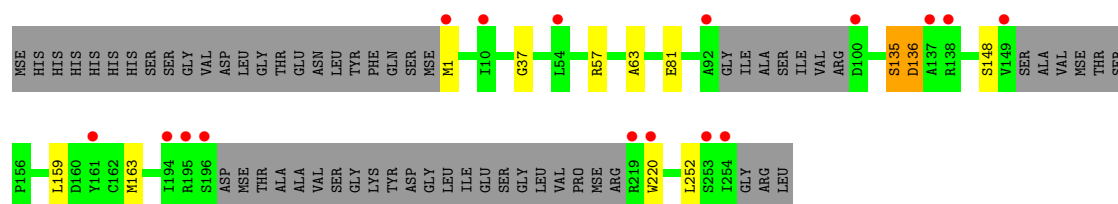
- Molecule 1: Short-chain dehydrogenase/reductase

Chain C: 



- Molecule 1: Short-chain dehydrogenase/reductase

Chain D: 



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	71.33Å 126.59Å 127.09Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.98 – 2.50 19.98 – 2.50	Depositor EDS
% Data completeness (in resolution range)	99.7 (19.98-2.50) 100.0 (19.98-2.50)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.86 (at 2.50Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
R, $R_{free}$	0.177 , 0.231 0.181 , 0.233	Depositor DCC
$R_{free}$ test set	2034 reflections (5.29%)	DCC
Wilson B-factor (Å <sup>2</sup> )	64.5	Xtriage
Anisotropy	0.076	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.29 , 43.5	EDS
Estimated twinning fraction	0.005 for -h,l,k	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.34$	Xtriage
Outliers	1 of 40461 reflections (0.002%)	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	6504	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	74.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.51% of the height of the origin peak. No significant pseudotranslation is detected.*

<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: 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	0.51	1/1600 (0.1%)	0.64	0/2155
1	B	0.50	1/1576 (0.1%)	0.67	0/2125
1	C	0.52	1/1605 (0.1%)	0.68	0/2160
1	D	0.47	1/1608 (0.1%)	0.61	0/2168
All	All	0.50	4/6389 (0.1%)	0.65	0/8608

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	220	TRP	CD2-CE2	5.26	1.47	1.41
1	B	220	TRP	CD2-CE2	5.24	1.47	1.41
1	D	220	TRP	CD2-CE2	5.11	1.47	1.41
1	C	220	TRP	CD2-CE2	5.11	1.47	1.41

There are no bond angle outliers.

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	1587	0	0	9	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	1562	0	0	8	0
1	C	1593	0	0	2	0
1	D	1593	0	0	7	0
2	A	5	0	0	0	0
2	B	5	0	0	0	0
2	C	5	0	0	0	0
2	D	5	0	0	0	0
3	A	51	0	0	1	0
3	B	29	0	0	1	0
3	C	44	0	0	1	0
3	D	25	0	0	1	0
All	All	6504	0	0	26	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 4.

All (26) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:141:ARG:CG	1:B:141:ARG:NH1	2.47	0.77
1:B:136:ASP:C	1:B:136:ASP:OD1	2.30	0.68
1:A:135:SER:O	1:A:136:ASP:CB	2.45	0.61
1:B:6:ARG:NH2	3:B:419:HOH:O	2.36	0.59
1:D:136:ASP:OD1	1:D:136:ASP:C	2.41	0.59
1:C:6:ARG:NH2	3:C:431:HOH:O	2.36	0.58
1:D:135:SER:O	1:D:136:ASP:CB	2.53	0.55
1:A:1:MSE:SE	1:A:1:MSE:O	2.76	0.53
1:B:135:SER:O	1:B:136:ASP:CB	2.56	0.51
1:D:136:ASP:OD1	1:D:136:ASP:O	2.29	0.51
1:A:136:ASP:OD2	1:A:136:ASP:C	2.50	0.50
1:B:135:SER:O	1:B:136:ASP:OD1	2.29	0.50
1:B:41:ALA:O	1:B:44:VAL:CG1	2.59	0.50
1:A:136:ASP:CG	1:A:136:ASP:O	2.50	0.49
1:A:1:MSE:SE	1:A:1:MSE:C	3.00	0.49
1:A:136:ASP:OD2	1:A:136:ASP:O	2.30	0.49
1:B:249:ASP:OD2	1:B:253:SER:N	2.47	0.48
1:D:1:MSE:N	3:D:408:HOH:O	2.47	0.47
1:D:37:GLY:O	1:D:63:ALA:N	2.48	0.46
1:A:136:ASP:O	1:A:137:ALA:C	2.55	0.45
1:A:24:ARG:NE	1:A:50:GLU:OE2	2.52	0.43
1:C:111:ASP:O	1:C:115:GLY:CA	2.68	0.42
1:D:57:ARG:NH1	1:D:81:GLU:OE2	2.53	0.41
1:A:6:ARG:NH2	3:A:432:HOH:O	2.54	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:D:159:LEU:O	1:D:163:MSE:CG	2.68	0.40
1:B:15:ARG:NH2	1:B:40:ASP:O	2.54	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	211/280 (75%)	203 (96%)	8 (4%)	0	100	100
1	B	208/280 (74%)	201 (97%)	7 (3%)	0	100	100
1	C	212/280 (76%)	207 (98%)	5 (2%)	0	100	100
1	D	211/280 (75%)	202 (96%)	9 (4%)	0	100	100
All	All	842/1120 (75%)	813 (97%)	29 (3%)	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	158/202 (78%)	151 (96%)	7 (4%)	39	64
1	B	155/202 (77%)	144 (93%)	11 (7%)	21	37
1	C	158/202 (78%)	150 (95%)	8 (5%)	33	57
1	D	160/202 (79%)	156 (98%)	4 (2%)	60	85
All	All	631/808 (78%)	601 (95%)	30 (5%)	35	60

All (30) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	MSE
1	A	100	ASP
1	A	135	SER
1	A	136	ASP
1	A	172	SER
1	A	181	GLU
1	A	252	LEU
1	B	3	GLN
1	B	4	LYS
1	B	36	THR
1	B	42	GLU
1	B	94	ILE
1	B	135	SER
1	B	136	ASP
1	B	141	ARG
1	B	149	VAL
1	B	172	SER
1	B	254	ILE
1	C	1	MSE
1	C	6	ARG
1	C	16	ARG
1	C	101	ASP
1	C	147	THR
1	C	165	LYS
1	C	168	LEU
1	C	252	LEU
1	D	135	SER
1	D	136	ASP
1	D	148	SER
1	D	252	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 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 ⓘ

4 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	SO4	A	301	-	4,4,4	0.32	0	6,6,6	0.21	0
2	SO4	B	301	-	4,4,4	0.47	0	6,6,6	0.17	0
2	SO4	C	301	-	4,4,4	0.57	0	6,6,6	0.17	0
2	SO4	D	301	-	4,4,4	0.47	0	6,6,6	0.27	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	SO4	A	301	-	-	0/0/0/0	0/0/0/0
2	SO4	B	301	-	-	0/0/0/0	0/0/0/0
2	SO4	C	301	-	-	0/0/0/0	0/0/0/0
2	SO4	D	301	-	-	0/0/0/0	0/0/0/0

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.

## 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	219/280 (78%)	-0.11	13 (5%)	22 22	43, 58, 118, 159	0
1	B	216/280 (77%)	0.03	14 (6%)	18 18	49, 68, 129, 173	0
1	C	220/280 (78%)	-0.04	14 (6%)	19 19	43, 63, 118, 154	0
1	D	219/280 (78%)	0.00	16 (7%)	15 14	53, 73, 130, 160	0
All	All	874/1120 (78%)	-0.03	57 (6%)	18 18	43, 66, 124, 173	0

All (57) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	254	ILE	6.2
1	A	195	ARG	6.0
1	B	254	ILE	5.5
1	B	3	GLN	5.0
1	D	1	MSE	4.9
1	B	94	ILE	4.8
1	C	220	TRP	4.6
1	D	196	SER	4.6
1	B	149	VAL	4.4
1	C	149	VAL	4.1
1	D	195	ARG	4.0
1	B	4	LYS	4.0
1	C	99	ARG	3.9
1	B	256	ARG	3.9
1	B	255	GLY	3.9
1	B	137	ALA	3.8
1	D	149	VAL	3.7
1	D	220	TRP	3.7
1	A	220	TRP	3.6
1	B	138	ARG	3.6
1	C	137	ALA	3.6

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Mol	Chain	Res	Type	RSRZ
1	A	1	MSE	3.6
1	D	194	ILE	3.6
1	B	220	TRP	3.6
1	A	177	LEU	3.3
1	B	40	ASP	3.3
1	D	219	ARG	3.3
1	C	219	ARG	3.3
1	D	161	TYR	3.2
1	A	34	ALA	3.1
1	B	253	SER	3.1
1	C	92	ALA	3.1
1	A	196	SER	2.9
1	A	136	ASP	2.8
1	C	195	ARG	2.7
1	A	149	VAL	2.7
1	C	181	GLU	2.6
1	B	136	ASP	2.6
1	B	161	TYR	2.6
1	D	54	LEU	2.6
1	C	196	SER	2.5
1	C	136	ASP	2.4
1	A	253	SER	2.4
1	A	122	VAL	2.4
1	D	138	ARG	2.4
1	D	100	ASP	2.4
1	A	35	ILE	2.4
1	A	161	TYR	2.4
1	D	253	SER	2.3
1	C	93	GLY	2.3
1	D	92	ALA	2.3
1	C	138	ARG	2.2
1	C	34	ALA	2.2
1	C	116	VAL	2.1
1	A	0	MSE	2.1
1	D	10	ILE	2.1
1	D	137	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
2	SO4	C	301	5/5	0.17	0.98	90,113,142,156	0
2	SO4	D	301	5/5	0.16	0.27	108,111,117,136	0
2	SO4	A	301	5/5	0.07	-1.52	66,69,78,79	0
2	SO4	B	301	5/5	0.09	-1.55	90,102,114,117	0

### 6.5 Other polymers

There are no such residues in this entry.