



# wwPDB X-ray Structure Validation Summary Report

May 29, 2024 – 04:45 PM EDT

PDB ID : 8SFG  
Title : Crystal Structure of the Open Unbound Catalytically Inactive Makes Caterpillars Floppy-like (MCF) Effector from *Vibrio vulnificus* CMCP6  
Authors : Minasov, G.; Shuvalova, L.; Rosas-Lemus, M.; Herrera, A.; Satchell, K.J.F.; Center for Structural Biology of Infectious Diseases (CSBID)  
Deposited on : 2023-04-11  
Resolution : 2.80 Å(reported)

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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 : 2.36.2  
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) : 2.36.2

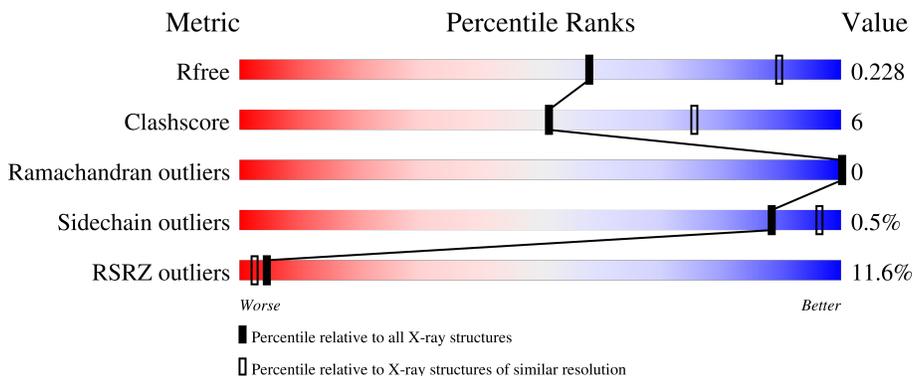
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.80 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	3140 (2.80-2.80)
Clashscore	141614	3569 (2.80-2.80)
Ramachandran outliers	138981	3498 (2.80-2.80)
Sidechain outliers	138945	3500 (2.80-2.80)
RSRZ outliers	127900	3078 (2.80-2.80)

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	365	
1	B	365	
1	C	365	
1	D	365	

## 2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 10360 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.

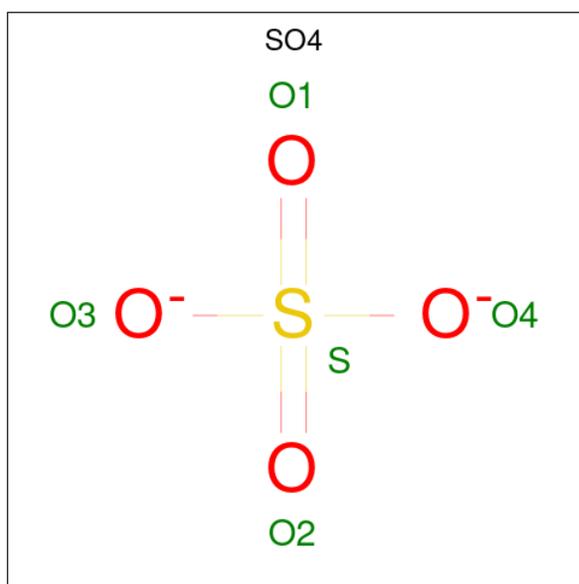
- Molecule 1 is a protein called Autotransporter adhesin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	Se			
1	A	334	2577	1629	440	498	10	0	0	0
1	B	328	2530	1601	432	488	9	0	0	0
1	C	329	2543	1607	435	492	9	0	0	0
1	D	322	2499	1576	428	486	9	0	2	0

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	3215	SER	-	expression tag	UNP A0A3Q0KY79
A	3216	ASN	-	expression tag	UNP A0A3Q0KY79
A	3217	ALA	-	expression tag	UNP A0A3Q0KY79
A	3218	MSE	-	expression tag	UNP A0A3Q0KY79
A	3351	ALA	CYS	engineered mutation	UNP A0A3Q0KY79
B	3215	SER	-	expression tag	UNP A0A3Q0KY79
B	3216	ASN	-	expression tag	UNP A0A3Q0KY79
B	3217	ALA	-	expression tag	UNP A0A3Q0KY79
B	3218	MSE	-	expression tag	UNP A0A3Q0KY79
B	3351	ALA	CYS	engineered mutation	UNP A0A3Q0KY79
C	3215	SER	-	expression tag	UNP A0A3Q0KY79
C	3216	ASN	-	expression tag	UNP A0A3Q0KY79
C	3217	ALA	-	expression tag	UNP A0A3Q0KY79
C	3218	MSE	-	expression tag	UNP A0A3Q0KY79
C	3351	ALA	CYS	engineered mutation	UNP A0A3Q0KY79
D	3215	SER	-	expression tag	UNP A0A3Q0KY79
D	3216	ASN	-	expression tag	UNP A0A3Q0KY79
D	3217	ALA	-	expression tag	UNP A0A3Q0KY79
D	3218	MSE	-	expression tag	UNP A0A3Q0KY79
D	3351	ALA	CYS	engineered mutation	UNP A0A3Q0KY79

- 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 5 4 1	0	0
2	A	1	Total O S 5 4 1	0	0
2	A	1	Total O S 5 4 1	0	0
2	A	1	Total O S 5 4 1	0	0
2	A	1	Total O S 5 4 1	0	0
2	B	1	Total O S 5 4 1	0	0
2	B	1	Total O S 5 4 1	0	0
2	B	1	Total O S 5 4 1	0	0
2	B	1	Total O S 10 8 2	0	1
2	B	1	Total O S 5 4 1	0	0
2	C	1	Total O S 5 4 1	0	0
2	C	1	Total O S 10 8 2	0	1
2	C	1	Total O S 5 4 1	0	0

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	C	1	Total	O	S	0	0
			5	4	1		
2	D	1	Total	O	S	0	0
			5	4	1		
2	D	1	Total	O	S	0	0
			5	4	1		
2	D	1	Total	O	S	0	1
			10	8	2		
2	D	1	Total	O	S	0	0
			5	4	1		

- Molecule 3 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	8	Total	Cl	0	1
			9	9		
3	B	2	Total	Cl	0	0
			2	2		
3	C	5	Total	Cl	0	0
			5	5		
3	D	7	Total	Cl	0	0
			7	7		

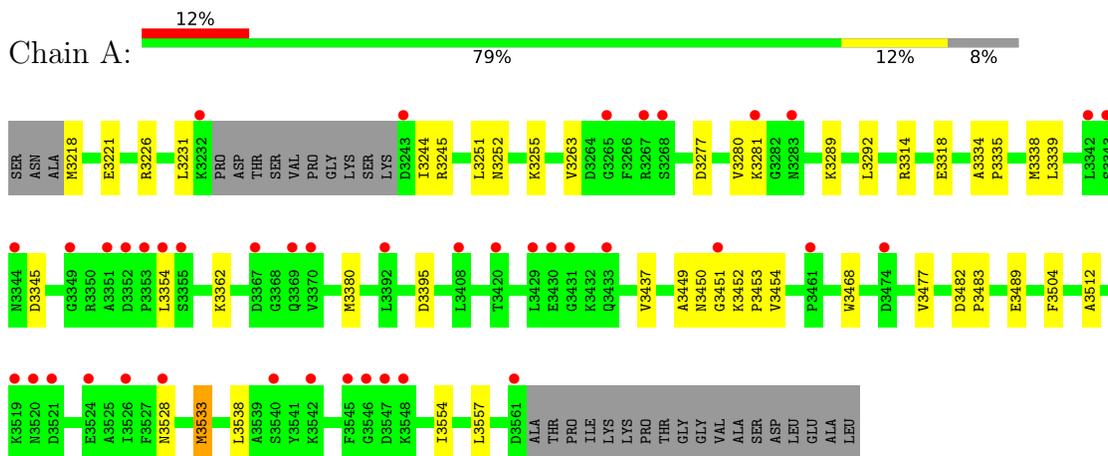
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	15	Total	O	0	1
			16	16		
4	B	17	Total	O	0	0
			17	17		
4	C	24	Total	O	0	0
			24	24		
4	D	26	Total	O	0	0
			26	26		

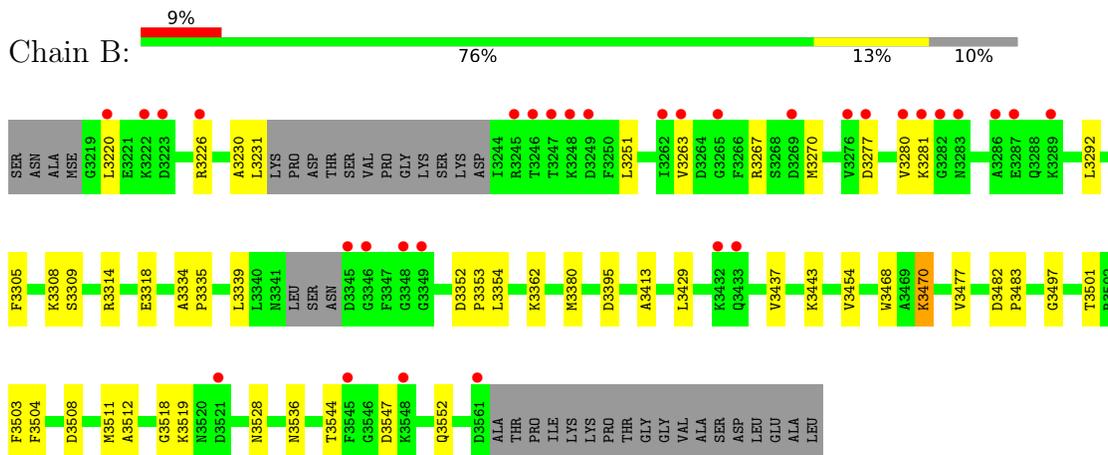
### 3 Residue-property plots [i](#)

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.

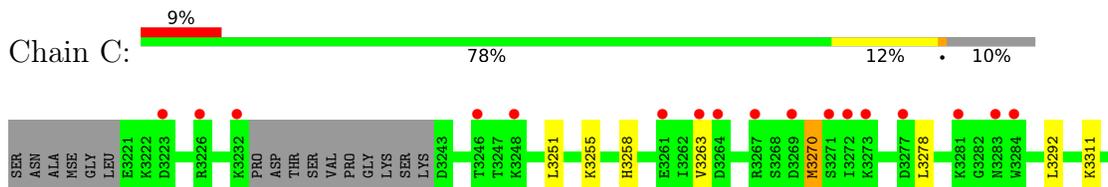
- Molecule 1: Autotransporter adhesin



- Molecule 1: Autotransporter adhesin

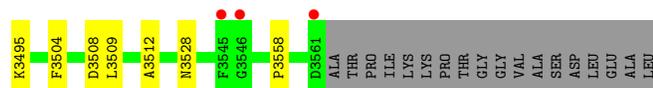
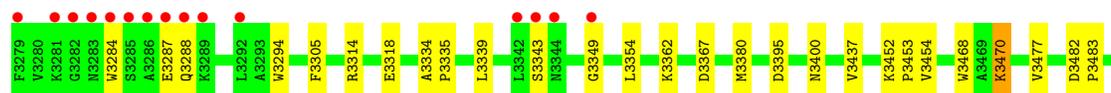
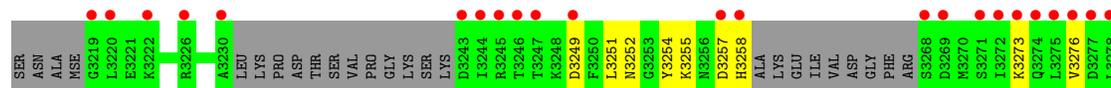
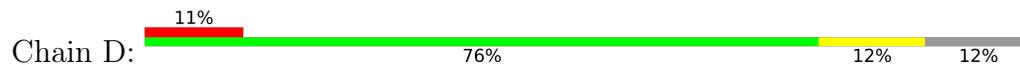


- Molecule 1: Autotransporter adhesin





● Molecule 1: Autotransporter adhesin



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	61.38Å 160.66Å 71.79Å 90.00° 101.28° 90.00°	Depositor
Resolution (Å)	29.87 – 2.80 29.87 – 2.80	Depositor EDS
% Data completeness (in resolution range)	97.5 (29.87-2.80) 97.6 (29.87-2.80)	Depositor EDS
$R_{merge}$	0.11	Depositor
$R_{sym}$	0.11	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.31 (at 2.80Å)	Xtrriage
Refinement program	REFMAC 5.8.0257	Depositor
R, $R_{free}$	0.189 , 0.230 0.196 , 0.228	Depositor DCC
$R_{free}$ test set	1691 reflections (5.17%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	54.5	Xtrriage
Anisotropy	0.172	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , 63.3	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	10360	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	70.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.71% 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: CL, 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	0.65	0/2612	0.73	2/3502 (0.1%)
1	B	0.65	0/2564	0.74	0/3437
1	C	0.65	0/2577	0.74	3/3454 (0.1%)
1	D	0.65	0/2532	0.74	0/3395
All	All	0.65	0/10285	0.74	5/13788 (0.0%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	3218	MSE	CG-SE-CE	5.81	111.69	98.90
1	C	3422	MSE	CG-SE-CE	5.37	110.71	98.90
1	C	3270	MSE	CG-SE-CE	5.27	110.49	98.90
1	C	3533	MSE	CG-SE-CE	5.18	110.30	98.90
1	A	3533	MSE	CG-SE-CE	5.18	110.29	98.90

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	2577	0	2566	34	0
1	B	2530	0	2517	37	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	2543	0	2526	29	0
1	D	2499	0	2474	34	0
2	A	25	0	0	0	0
2	B	30	0	0	0	0
2	C	25	0	0	1	0
2	D	25	0	0	0	0
3	A	9	0	0	0	0
3	B	2	0	0	0	0
3	C	5	0	0	0	0
3	D	7	0	0	0	0
4	A	16	0	0	0	0
4	B	17	0	0	0	0
4	C	24	0	0	0	0
4	D	26	0	0	0	0
All	All	10360	0	10083	114	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 114 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:B:3544:THR:HG23	1:B:3547:ASP:HB3	1.60	0.81
1:B:3354:LEU:HD21	1:B:3380:MSE:HE1	1.77	0.65
1:D:3354:LEU:HD21	1:D:3380:MSE:SE	2.47	0.64
1:B:3267:ARG:HG3	1:B:3270:MSE:HG3	1.81	0.63
1:A:3395:ASP:HB3	1:B:3251:LEU:HD13	1.82	0.61

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	330/365 (90%)	318 (96%)	12 (4%)	0	100	100
1	B	322/365 (88%)	313 (97%)	9 (3%)	0	100	100
1	C	323/365 (88%)	313 (97%)	10 (3%)	0	100	100
1	D	318/365 (87%)	310 (98%)	8 (2%)	0	100	100
All	All	1293/1460 (89%)	1254 (97%)	39 (3%)	0	100	100

There are no Ramachandran outliers to report.

### 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	271/285 (95%)	271 (100%)	0	100	100
1	B	265/285 (93%)	263 (99%)	2 (1%)	81	94
1	C	267/285 (94%)	266 (100%)	1 (0%)	91	97
1	D	263/285 (92%)	261 (99%)	2 (1%)	81	94
All	All	1066/1140 (94%)	1061 (100%)	5 (0%)	88	96

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	3470	LYS
1	B	3508	ASP
1	C	3508	ASP
1	D	3470	LYS
1	D	3508	ASP

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](#)

Of 44 ligands modelled in this entry, 23 are monoatomic - leaving 21 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	$\# Z  > 2$
2	SO4	C	3603	-	4,4,4	0.39	0	6,6,6	0.06	0
2	SO4	B	3602	-	4,4,4	0.38	0	6,6,6	0.05	0
2	SO4	A	3603	-	4,4,4	0.38	0	6,6,6	0.06	0
2	SO4	B	3604[B]	-	4,4,4	0.39	0	6,6,6	0.06	0
2	SO4	B	3605	-	4,4,4	0.38	0	6,6,6	0.05	0
2	SO4	A	3605	-	4,4,4	0.38	0	6,6,6	0.04	0
2	SO4	C	3602[A]	-	4,4,4	0.40	0	6,6,6	0.06	0
2	SO4	A	3601	-	4,4,4	0.39	0	6,6,6	0.05	0
2	SO4	C	3601	-	4,4,4	0.39	0	6,6,6	0.05	0
2	SO4	A	3602	-	4,4,4	0.40	0	6,6,6	0.07	0
2	SO4	D	3602	-	4,4,4	0.38	0	6,6,6	0.05	0
2	SO4	C	3602[B]	-	4,4,4	0.41	0	6,6,6	0.07	0
2	SO4	D	3603[A]	-	4,4,4	0.39	0	6,6,6	0.05	0
2	SO4	C	3604	-	4,4,4	0.37	0	6,6,6	0.06	0
2	SO4	A	3604	-	4,4,4	0.39	0	6,6,6	0.04	0
2	SO4	B	3601	-	4,4,4	0.38	0	6,6,6	0.06	0
2	SO4	B	3603	-	4,4,4	0.39	0	6,6,6	0.05	0
2	SO4	B	3604[A]	-	4,4,4	0.39	0	6,6,6	0.07	0
2	SO4	D	3604	-	4,4,4	0.39	0	6,6,6	0.04	0
2	SO4	D	3603[B]	-	4,4,4	0.39	0	6,6,6	0.04	0
2	SO4	D	3601	-	4,4,4	0.38	0	6,6,6	0.05	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.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	3602[B]	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, 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	324/365 (88%)	0.60	42 (12%) 3 2	42, 71, 123, 172	0
1	B	319/365 (87%)	0.29	32 (10%) 7 4	35, 55, 124, 146	0
1	C	320/365 (87%)	0.37	33 (10%) 6 3	30, 61, 131, 157	0
1	D	313/365 (85%)	0.40	41 (13%) 3 2	29, 48, 151, 173	0
All	All	1276/1460 (87%)	0.42	148 (11%) 4 2	29, 59, 136, 173	0

The worst 5 of 148 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	3344	ASN	11.0
1	A	3546	GLY	10.6
1	D	3281	LYS	8.1
1	D	3344	ASN	8.1
1	D	3268	SER	7.0

### 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	SO4	D	3602	5/5	0.67	0.28	116,120,129,132	0
3	CL	A	3606	1/1	0.69	0.11	88,88,88,88	0
3	CL	D	3609	1/1	0.72	0.18	85,85,85,85	0
3	CL	D	3611	1/1	0.73	0.32	73,73,73,73	0
3	CL	D	3610	1/1	0.77	0.38	86,86,86,86	0
2	SO4	A	3605	5/5	0.79	0.35	114,117,129,137	0
2	SO4	C	3604	5/5	0.80	0.41	95,98,109,114	0
3	CL	C	3608	1/1	0.81	0.16	83,83,83,83	0
3	CL	C	3606	1/1	0.82	0.17	90,90,90,90	0
2	SO4	B	3604[A]	5/5	0.83	0.31	53,57,61,61	5
2	SO4	B	3604[B]	5/5	0.83	0.31	67,67,75,76	5
3	CL	C	3605	1/1	0.84	0.15	81,81,81,81	0
3	CL	C	3607	1/1	0.84	0.20	74,74,74,74	0
2	SO4	A	3602	5/5	0.85	0.31	88,96,98,101	0
2	SO4	B	3605	5/5	0.85	0.20	103,110,124,128	0
3	CL	C	3609	1/1	0.86	0.13	86,86,86,86	0
3	CL	A	3609	1/1	0.86	0.15	72,72,72,72	0
3	CL	A	3608	1/1	0.87	0.34	98,98,98,98	0
2	SO4	B	3602	5/5	0.88	0.27	108,109,116,119	0
3	CL	D	3607	1/1	0.88	0.11	69,69,69,69	0
2	SO4	D	3603[A]	5/5	0.88	0.24	59,61,65,69	5
2	SO4	D	3603[B]	5/5	0.88	0.24	50,52,56,56	5
3	CL	B	3607	1/1	0.88	0.12	79,79,79,79	0
3	CL	D	3605	1/1	0.89	0.14	77,77,77,77	0
3	CL	A	3610	1/1	0.91	0.20	81,81,81,81	0
2	SO4	C	3601	5/5	0.91	0.41	110,113,118,121	0
3	CL	A	3613[B]	1/1	0.92	0.12	61,61,61,61	1
2	SO4	A	3604	5/5	0.92	0.14	95,103,110,114	0
2	SO4	B	3603	5/5	0.92	0.32	100,102,107,108	0
2	SO4	C	3602[A]	5/5	0.92	0.21	44,46,52,52	5
2	SO4	C	3602[B]	5/5	0.92	0.21	27,30,31,37	5
3	CL	A	3613[A]	1/1	0.92	0.12	53,53,53,53	1
3	CL	D	3608	1/1	0.93	0.13	86,86,86,86	0
3	CL	A	3612	1/1	0.93	0.07	84,84,84,84	0
3	CL	A	3611	1/1	0.94	0.12	79,79,79,79	0
2	SO4	A	3603	5/5	0.94	0.12	76,86,100,101	0
3	CL	D	3606	1/1	0.94	0.06	72,72,72,72	0
2	SO4	D	3604	5/5	0.94	0.26	92,92,95,100	0
2	SO4	D	3601	5/5	0.95	0.14	67,70,76,79	0
3	CL	B	3606	1/1	0.95	0.07	67,67,67,67	0
2	SO4	A	3601	5/5	0.95	0.12	77,80,84,84	0
2	SO4	C	3603	5/5	0.97	0.19	80,86,88,94	0
2	SO4	B	3601	5/5	0.98	0.10	50,58,63,65	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
3	CL	A	3607	1/1	0.99	0.05	70,70,70,70	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.