



# Full wwPDB X-ray Structure Validation Report ⓘ

Sep 14, 2022 – 01:32 pm BST

PDB ID : 7Z06  
Title : Structure of YwlG (Q2FF14) from *Staphylococcus aureus*  
Authors : Schneider, S.; Scheidler, C.M.; Sieber, S.A.  
Deposited on : 2022-02-22  
Resolution : 1.74 Å(reported)

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We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

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<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 : 1.8.4, CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.30  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0267  
CCP4 : 7.1.010 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.30

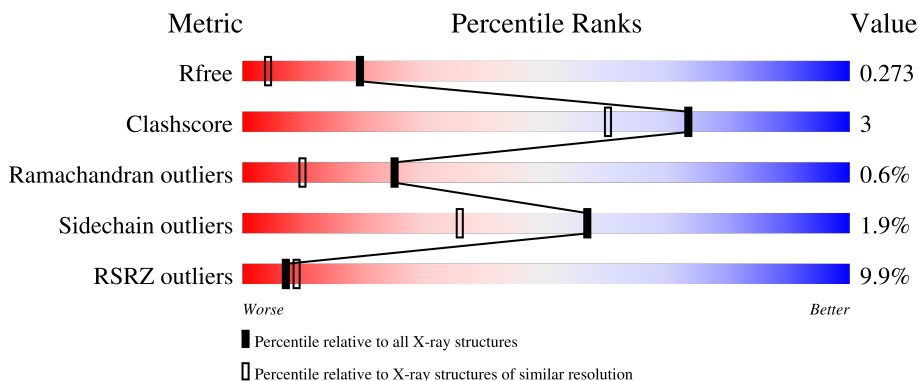
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.74 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	3764 (1.76-1.72)
Clashscore	141614	3923 (1.76-1.72)
Ramachandran outliers	138981	3878 (1.76-1.72)
Sidechain outliers	138945	3878 (1.76-1.72)
RSRZ outliers	127900	3705 (1.76-1.72)

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	196	 8% 86% 6% • 8%
1	B	196	 10% 84% 6% • 10%
1	C	196	 7% 84% 6% • 9%
1	D	196	 11% 83% 6% • 10%
1	E	196	 10% 84% • • 12%

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Mol	Chain	Length	Quality of chain
1	F	196	<p>8% 82% 5% • 12%</p>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	SO4	B	203	-	-	X	-
2	SO4	C	204	-	-	X	-
2	SO4	E	203	-	-	X	-

## 2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 8557 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 UPF0340 protein SAUSA300\_2068.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	181	1382	876	231	264	11	0	1	0
1	B	177	1352	857	226	258	11	0	1	0
1	C	179	1380	877	230	262	11	0	3	0
1	D	176	1332	845	223	253	11	0	1	0
1	E	173	1305	825	219	250	11	0	0	0
1	F	172	1320	838	221	250	11	0	1	0

There are 138 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-21	MET	-	initiating methionine	UNP Q2FF14
A	-20	ALA	-	expression tag	UNP Q2FF14
A	-19	SER	-	expression tag	UNP Q2FF14
A	-18	TRP	-	expression tag	UNP Q2FF14
A	-17	SER	-	expression tag	UNP Q2FF14
A	-16	HIS	-	expression tag	UNP Q2FF14
A	-15	PRO	-	expression tag	UNP Q2FF14
A	-14	GLN	-	expression tag	UNP Q2FF14
A	-13	PHE	-	expression tag	UNP Q2FF14
A	-12	GLU	-	expression tag	UNP Q2FF14
A	-11	LYS	-	expression tag	UNP Q2FF14
A	-10	GLY	-	expression tag	UNP Q2FF14
A	-9	ALA	-	expression tag	UNP Q2FF14
A	-8	VAL	-	expression tag	UNP Q2FF14
A	-7	THR	-	expression tag	UNP Q2FF14
A	-6	SER	-	expression tag	UNP Q2FF14
A	-5	LEU	-	expression tag	UNP Q2FF14

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-4	TYR	-	expression tag	UNP Q2FF14
A	-3	LYS	-	expression tag	UNP Q2FF14
A	-2	LYS	-	expression tag	UNP Q2FF14
A	-1	ALA	-	expression tag	UNP Q2FF14
A	0	GLY	-	expression tag	UNP Q2FF14
A	1	PHE	-	expression tag	UNP Q2FF14
B	-21	MET	-	initiating methionine	UNP Q2FF14
B	-20	ALA	-	expression tag	UNP Q2FF14
B	-19	SER	-	expression tag	UNP Q2FF14
B	-18	TRP	-	expression tag	UNP Q2FF14
B	-17	SER	-	expression tag	UNP Q2FF14
B	-16	HIS	-	expression tag	UNP Q2FF14
B	-15	PRO	-	expression tag	UNP Q2FF14
B	-14	GLN	-	expression tag	UNP Q2FF14
B	-13	PHE	-	expression tag	UNP Q2FF14
B	-12	GLU	-	expression tag	UNP Q2FF14
B	-11	LYS	-	expression tag	UNP Q2FF14
B	-10	GLY	-	expression tag	UNP Q2FF14
B	-9	ALA	-	expression tag	UNP Q2FF14
B	-8	VAL	-	expression tag	UNP Q2FF14
B	-7	THR	-	expression tag	UNP Q2FF14
B	-6	SER	-	expression tag	UNP Q2FF14
B	-5	LEU	-	expression tag	UNP Q2FF14
B	-4	TYR	-	expression tag	UNP Q2FF14
B	-3	LYS	-	expression tag	UNP Q2FF14
B	-2	LYS	-	expression tag	UNP Q2FF14
B	-1	ALA	-	expression tag	UNP Q2FF14
B	0	GLY	-	expression tag	UNP Q2FF14
B	1	PHE	-	expression tag	UNP Q2FF14
C	-21	MET	-	initiating methionine	UNP Q2FF14
C	-20	ALA	-	expression tag	UNP Q2FF14
C	-19	SER	-	expression tag	UNP Q2FF14
C	-18	TRP	-	expression tag	UNP Q2FF14
C	-17	SER	-	expression tag	UNP Q2FF14
C	-16	HIS	-	expression tag	UNP Q2FF14
C	-15	PRO	-	expression tag	UNP Q2FF14
C	-14	GLN	-	expression tag	UNP Q2FF14
C	-13	PHE	-	expression tag	UNP Q2FF14
C	-12	GLU	-	expression tag	UNP Q2FF14
C	-11	LYS	-	expression tag	UNP Q2FF14
C	-10	GLY	-	expression tag	UNP Q2FF14
C	-9	ALA	-	expression tag	UNP Q2FF14

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-8	VAL	-	expression tag	UNP Q2FF14
C	-7	THR	-	expression tag	UNP Q2FF14
C	-6	SER	-	expression tag	UNP Q2FF14
C	-5	LEU	-	expression tag	UNP Q2FF14
C	-4	TYR	-	expression tag	UNP Q2FF14
C	-3	LYS	-	expression tag	UNP Q2FF14
C	-2	LYS	-	expression tag	UNP Q2FF14
C	-1	ALA	-	expression tag	UNP Q2FF14
C	0	GLY	-	expression tag	UNP Q2FF14
C	1	PHE	-	expression tag	UNP Q2FF14
D	-21	MET	-	initiating methionine	UNP Q2FF14
D	-20	ALA	-	expression tag	UNP Q2FF14
D	-19	SER	-	expression tag	UNP Q2FF14
D	-18	TRP	-	expression tag	UNP Q2FF14
D	-17	SER	-	expression tag	UNP Q2FF14
D	-16	HIS	-	expression tag	UNP Q2FF14
D	-15	PRO	-	expression tag	UNP Q2FF14
D	-14	GLN	-	expression tag	UNP Q2FF14
D	-13	PHE	-	expression tag	UNP Q2FF14
D	-12	GLU	-	expression tag	UNP Q2FF14
D	-11	LYS	-	expression tag	UNP Q2FF14
D	-10	GLY	-	expression tag	UNP Q2FF14
D	-9	ALA	-	expression tag	UNP Q2FF14
D	-8	VAL	-	expression tag	UNP Q2FF14
D	-7	THR	-	expression tag	UNP Q2FF14
D	-6	SER	-	expression tag	UNP Q2FF14
D	-5	LEU	-	expression tag	UNP Q2FF14
D	-4	TYR	-	expression tag	UNP Q2FF14
D	-3	LYS	-	expression tag	UNP Q2FF14
D	-2	LYS	-	expression tag	UNP Q2FF14
D	-1	ALA	-	expression tag	UNP Q2FF14
D	0	GLY	-	expression tag	UNP Q2FF14
D	1	PHE	-	expression tag	UNP Q2FF14
E	-21	MET	-	initiating methionine	UNP Q2FF14
E	-20	ALA	-	expression tag	UNP Q2FF14
E	-19	SER	-	expression tag	UNP Q2FF14
E	-18	TRP	-	expression tag	UNP Q2FF14
E	-17	SER	-	expression tag	UNP Q2FF14
E	-16	HIS	-	expression tag	UNP Q2FF14
E	-15	PRO	-	expression tag	UNP Q2FF14
E	-14	GLN	-	expression tag	UNP Q2FF14
E	-13	PHE	-	expression tag	UNP Q2FF14

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Chain	Residue	Modelled	Actual	Comment	Reference
E	-12	GLU	-	expression tag	UNP Q2FF14
E	-11	LYS	-	expression tag	UNP Q2FF14
E	-10	GLY	-	expression tag	UNP Q2FF14
E	-9	ALA	-	expression tag	UNP Q2FF14
E	-8	VAL	-	expression tag	UNP Q2FF14
E	-7	THR	-	expression tag	UNP Q2FF14
E	-6	SER	-	expression tag	UNP Q2FF14
E	-5	LEU	-	expression tag	UNP Q2FF14
E	-4	TYR	-	expression tag	UNP Q2FF14
E	-3	LYS	-	expression tag	UNP Q2FF14
E	-2	LYS	-	expression tag	UNP Q2FF14
E	-1	ALA	-	expression tag	UNP Q2FF14
E	0	GLY	-	expression tag	UNP Q2FF14
E	1	PHE	-	expression tag	UNP Q2FF14
F	-21	MET	-	initiating methionine	UNP Q2FF14
F	-20	ALA	-	expression tag	UNP Q2FF14
F	-19	SER	-	expression tag	UNP Q2FF14
F	-18	TRP	-	expression tag	UNP Q2FF14
F	-17	SER	-	expression tag	UNP Q2FF14
F	-16	HIS	-	expression tag	UNP Q2FF14
F	-15	PRO	-	expression tag	UNP Q2FF14
F	-14	GLN	-	expression tag	UNP Q2FF14
F	-13	PHE	-	expression tag	UNP Q2FF14
F	-12	GLU	-	expression tag	UNP Q2FF14
F	-11	LYS	-	expression tag	UNP Q2FF14
F	-10	GLY	-	expression tag	UNP Q2FF14
F	-9	ALA	-	expression tag	UNP Q2FF14
F	-8	VAL	-	expression tag	UNP Q2FF14
F	-7	THR	-	expression tag	UNP Q2FF14
F	-6	SER	-	expression tag	UNP Q2FF14
F	-5	LEU	-	expression tag	UNP Q2FF14
F	-4	TYR	-	expression tag	UNP Q2FF14
F	-3	LYS	-	expression tag	UNP Q2FF14
F	-2	LYS	-	expression tag	UNP Q2FF14
F	-1	ALA	-	expression tag	UNP Q2FF14
F	0	GLY	-	expression tag	UNP Q2FF14
F	1	PHE	-	expression tag	UNP Q2FF14

- 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	A	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	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	C	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		
2	D	1	Total	O	S	0	0
			5	4	1		
2	E	1	Total	O	S	0	0
			5	4	1		
2	E	1	Total	O	S	0	0
			5	4	1		
2	E	1	Total	O	S	0	0
			5	4	1		

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	F	1	Total O S 5 4 1	0	0
2	F	1	Total O S 5 4 1	0	0
2	F	1	Total O S 5 4 1	0	0

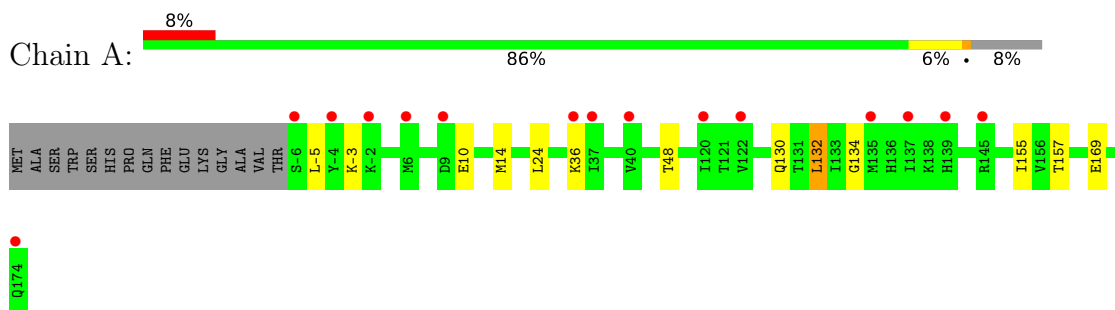
- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	70	Total O 70 70	0	0
3	B	70	Total O 70 70	0	0
3	C	74	Total O 74 74	0	0
3	D	67	Total O 67 67	0	0
3	E	61	Total O 61 61	0	0
3	F	59	Total O 59 59	0	0

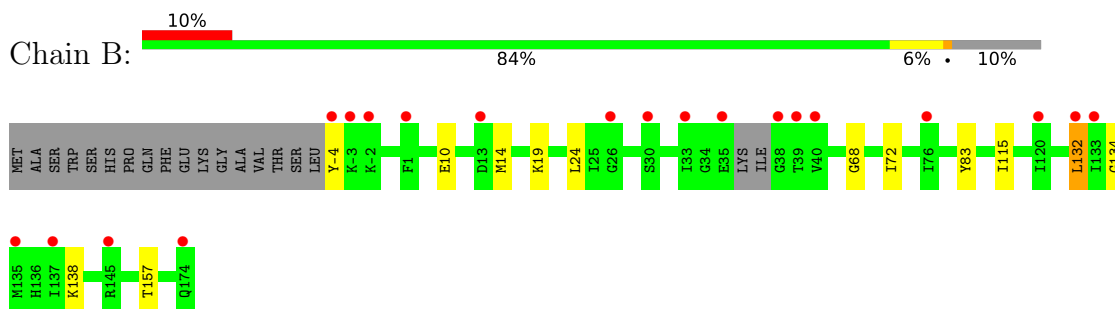
### 3 Residue-property plots [i](#)

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.

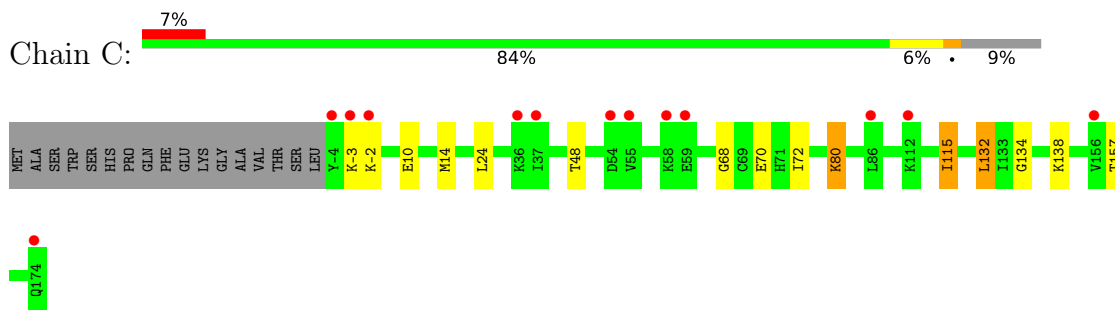
- Molecule 1: UPF0340 protein SAUSA300\_2068



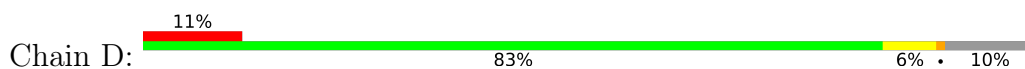
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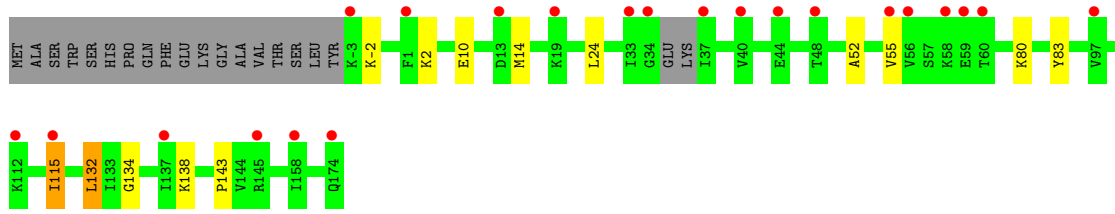


- Molecule 1: UPF0340 protein SAUSA300\_2068

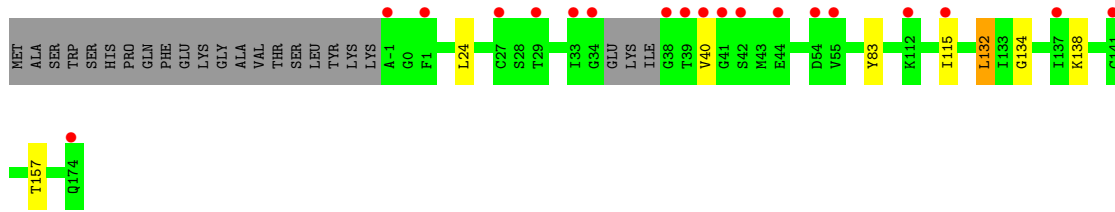
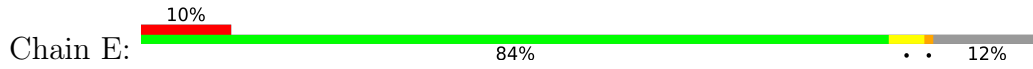


- Molecule 1: UPF0340 protein SAUSA300\_2068

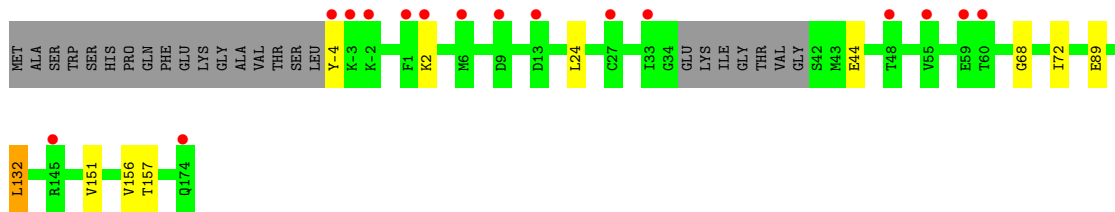
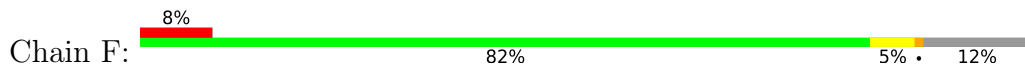




● Molecule 1: UPF0340 protein SAUSA300\_2068



● Molecule 1: UPF0340 protein SAUSA300\_2068



● Molecule 1: UPF0340 protein SAUSA300\_2068



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	54.74Å 136.88Å 79.19Å 90.00° 98.55° 90.00°	Depositor
Resolution (Å)	47.99 – 1.74 47.99 – 1.74	Depositor EDS
% Data completeness (in resolution range)	97.8 (47.99-1.74) 97.8 (47.99-1.74)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	0.96 (at 1.74Å)	Xtriage
Refinement program	REFMAC 5.8.0267	Depositor
R, $R_{free}$	0.250 , 0.275 0.249 , 0.273	Depositor DCC
$R_{free}$ test set	5725 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	30.3	Xtriage
Anisotropy	0.547	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	(Not available) , (Not available)	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	8557	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	18.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.80% 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: 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	0.59	0/1404	0.74	0/1895
1	B	0.63	0/1373	0.76	0/1852
1	C	0.60	0/1405	0.79	0/1897
1	D	0.58	0/1355	0.76	0/1829
1	E	0.62	0/1325	0.76	0/1789
1	F	0.56	0/1341	0.75	0/1809
All	All	0.60	0/8203	0.76	0/11071

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	1382	0	1412	9	0
1	B	1352	0	1375	11	0
1	C	1380	0	1415	13	0
1	D	1332	0	1361	12	0
1	E	1305	0	1324	5	0
1	F	1320	0	1345	10	0
2	A	10	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	15	0	0	4	0
2	C	20	0	0	2	0
2	D	10	0	0	0	0
2	E	15	0	0	3	0
2	F	15	0	0	0	0
3	A	70	0	0	1	0
3	B	70	0	0	1	0
3	C	74	0	0	2	0
3	D	67	0	0	1	0
3	E	61	0	0	1	0
3	F	59	0	0	0	0
All	All	8557	0	8232	54	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 3.

All (54) 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:D:52:ALA:O	1:D:55:VAL:HG22	1.67	0.93
1:A:157:THR:HG21	1:B:132:LEU:HD21	1.58	0.85
1:C:10:GLU:HG2	1:C:14:MET:HE3	1.59	0.82
1:A:132:LEU:HD21	1:B:157:THR:HG21	1.64	0.80
1:C:157:THR:HG21	1:F:132:LEU:HD21	1.63	0.78
1:C:10:GLU:HG2	1:C:14:MET:CE	2.19	0.72
1:C:80:LYS:HA	1:C:115[A]:ILE:CD1	2.21	0.71
1:C:132:LEU:HD21	1:F:157:THR:HG21	1.74	0.69
1:F:68:GLY:HA3	1:F:72:ILE:HD11	1.75	0.69
1:D:80:LYS:HA	1:D:115[A]:ILE:CD1	2.23	0.69
1:D:132:LEU:HD21	1:E:157:THR:HG21	1.74	0.68
1:C:68:GLY:HA3	1:C:72:ILE:HD11	1.75	0.68
1:E:138:LYS:HE3	3:E:349:HOH:O	1.93	0.67
1:D:10:GLU:HG2	1:D:14:MET:HE3	1.75	0.67
1:D:132:LEU:HB3	2:E:203:SO4:O3	1.97	0.65
1:D:80:LYS:HA	1:D:115[A]:ILE:HD12	1.80	0.64
1:F:-4:TYR:CZ	1:F:2:LYS:HE2	2.33	0.63
1:E:83:TYR:HB2	1:E:115:ILE:HD11	1.81	0.63
1:B:10:GLU:HG2	1:B:14:MET:CE	2.29	0.62
1:B:83:TYR:HB2	1:B:115[A]:ILE:HD11	1.82	0.62
1:C:80:LYS:HA	1:C:115[A]:ILE:HD12	1.82	0.61
1:B:10:GLU:HG2	1:B:14:MET:HE3	1.83	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:10:GLU:HG2	1:D:14:MET:CE	2.32	0.59
1:D:138:LYS:HE3	3:D:353:HOH:O	2.03	0.58
1:A:10:GLU:HG2	1:A:14:MET:HE3	1.85	0.57
1:F:151:VAL:HG23	1:F:156[B]:VAL:CG2	2.37	0.55
1:A:10:GLU:HG2	1:A:14:MET:CE	2.36	0.55
1:B:138:LYS:HE3	3:B:331:HOH:O	2.04	0.55
1:D:52:ALA:O	1:D:55:VAL:CG2	2.49	0.55
1:F:-4:TYR:CG	1:F:2:LYS:HD2	2.42	0.55
1:E:134:GLY:HA3	2:E:203:SO4:O3	2.07	0.53
1:B:134:GLY:HA3	2:B:203:SO4:O3	2.09	0.53
1:D:143:PRO:HG3	1:E:132:LEU:CD1	2.40	0.52
1:B:68:GLY:HA3	1:B:72:ILE:HD11	1.91	0.52
1:A:132:LEU:HB3	2:B:203:SO4:O3	2.10	0.51
1:F:151:VAL:HG23	1:F:156[B]:VAL:HG21	1.93	0.50
1:B:132:LEU:HB3	2:B:203:SO4:O4	2.12	0.50
1:C:134:GLY:HA3	2:C:204:SO4:O3	2.12	0.49
1:A:134:GLY:HA3	2:B:203:SO4:O4	2.13	0.49
1:D:134:GLY:HA3	2:E:203:SO4:O1	2.16	0.46
2:C:204:SO4:O3	1:F:132:LEU:HB3	2.16	0.46
1:B:-4:TYR:CD1	1:B:-4:TYR:C	2.90	0.45
1:A:-3:LYS:O	1:A:48[A]:THR:HG21	2.17	0.45
1:C:138:LYS:HE3	3:C:363:HOH:O	2.17	0.44
1:C:70:GLU:H	1:C:70:GLU:CD	2.22	0.44
1:F:-4:TYR:CE1	1:F:2:LYS:HE2	2.53	0.43
1:C:138:LYS:CE	3:C:363:HOH:O	2.66	0.43
1:C:80:LYS:HD2	1:C:115[B]:ILE:HD12	1.99	0.43
1:F:-4:TYR:CE2	1:F:2:LYS:HE2	2.54	0.42
1:A:169:GLU:OE1	3:A:301:HOH:O	2.21	0.41
1:B:19:LYS:HB3	1:B:19:LYS:HE3	1.95	0.41
1:A:130:GLN:NE2	1:A:155:ILE:HD12	2.35	0.41
1:D:83:TYR:HB2	1:D:115[A]:ILE:HD11	2.03	0.40
1:C:-3:LYS:O	1:C:48[A]:THR:HG21	2.22	0.40

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	180/196 (92%)	173 (96%)	6 (3%)	1 (1%)	25	10
1	B	174/196 (89%)	168 (97%)	5 (3%)	1 (1%)	25	10
1	C	180/196 (92%)	174 (97%)	5 (3%)	1 (1%)	25	10
1	D	173/196 (88%)	167 (96%)	5 (3%)	1 (1%)	25	10
1	E	169/196 (86%)	163 (96%)	5 (3%)	1 (1%)	25	10
1	F	169/196 (86%)	163 (96%)	5 (3%)	1 (1%)	25	10
All	All	1045/1176 (89%)	1008 (96%)	31 (3%)	6 (1%)	25	10

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	132	LEU
1	B	132	LEU
1	C	132	LEU
1	D	132	LEU
1	E	132	LEU
1	F	132	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	155/166 (93%)	152 (98%)	3 (2%)	57	36
1	B	151/166 (91%)	150 (99%)	1 (1%)	84	75
1	C	155/166 (93%)	150 (97%)	5 (3%)	39	15
1	D	149/166 (90%)	144 (97%)	5 (3%)	37	13
1	E	146/166 (88%)	144 (99%)	2 (1%)	67	50
1	F	148/166 (89%)	145 (98%)	3 (2%)	55	33

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	904/996 (91%)	885 (98%)	19 (2%)	57 30

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	-5	LEU
1	A	24	LEU
1	A	36	LYS
1	B	24	LEU
1	C	-2	LYS
1	C	24	LEU
1	C	80	LYS
1	C	115[A]	ILE
1	C	115[B]	ILE
1	D	-2	LYS
1	D	2	LYS
1	D	24	LEU
1	D	115[A]	ILE
1	D	115[B]	ILE
1	E	24	LEU
1	E	40	VAL
1	F	24	LEU
1	F	44	GLU
1	F	89	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	110	HIS
1	A	130	GLN
1	C	110	HIS
1	C	139	HIS
1	D	110	HIS
1	D	174	GLN
1	E	110	HIS

### 5.3.3 RNA ⓘ

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](#)

17 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	201	-	4,4,4	0.47	0	6,6,6	0.12	0
2	SO4	C	204	-	4,4,4	0.43	0	6,6,6	0.11	0
2	SO4	C	202	-	4,4,4	0.46	0	6,6,6	0.19	0
2	SO4	E	203	-	4,4,4	0.60	0	6,6,6	0.11	0
2	SO4	F	202	-	4,4,4	0.39	0	6,6,6	0.07	0
2	SO4	D	202	-	4,4,4	0.43	0	6,6,6	0.19	0
2	SO4	A	202	-	4,4,4	0.39	0	6,6,6	0.08	0
2	SO4	E	202	-	4,4,4	0.44	0	6,6,6	0.13	0
2	SO4	C	201	-	4,4,4	0.43	0	6,6,6	0.14	0
2	SO4	B	202	-	4,4,4	0.44	0	6,6,6	0.09	0
2	SO4	F	201	-	4,4,4	0.40	0	6,6,6	0.18	0
2	SO4	B	201	-	4,4,4	0.42	0	6,6,6	0.09	0
2	SO4	C	203	-	4,4,4	0.38	0	6,6,6	0.06	0
2	SO4	D	201	-	4,4,4	0.45	0	6,6,6	0.07	0
2	SO4	F	203	-	4,4,4	0.34	0	6,6,6	0.08	0
2	SO4	B	203	-	4,4,4	0.35	0	6,6,6	0.10	0
2	SO4	E	201	-	4,4,4	0.40	0	6,6,6	0.09	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 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	204	SO4	2	0
2	E	203	SO4	3	0
2	B	203	SO4	4	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	181/196 (92%)	0.71	15 (8%) <b>11</b> <b>14</b>	8, 15, 26, 40	0
1	B	177/196 (90%)	0.87	20 (11%) <b>5</b> <b>6</b>	9, 16, 30, 47	0
1	C	179/196 (91%)	0.56	13 (7%) <b>15</b> <b>19</b>	9, 14, 25, 41	0
1	D	176/196 (89%)	0.83	22 (12%) <b>3</b> <b>4</b>	9, 16, 27, 48	0
1	E	173/196 (88%)	0.87	19 (10%) <b>5</b> <b>6</b>	10, 17, 27, 48	0
1	F	172/196 (87%)	0.76	16 (9%) <b>8</b> <b>10</b>	10, 16, 29, 59	0
All	All	1058/1176 (89%)	0.77	105 (9%) <b>7</b> <b>9</b>	8, 16, 28, 59	0

All (105) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	-4	TYR	10.6
1	E	40	VAL	8.9
1	B	-4	TYR	6.1
1	D	37	ILE	5.6
1	D	174	GLN	5.2
1	F	174	GLN	5.0
1	C	-4	TYR	5.0
1	A	174	GLN	4.8
1	B	39	THR	4.8
1	E	39	THR	4.5
1	F	33	ILE	4.1
1	F	2	LYS	4.1
1	D	40	VAL	4.0
1	D	55	VAL	3.8
1	B	33	ILE	3.8
1	B	174	GLN	3.8
1	A	37	ILE	3.7
1	B	40	VAL	3.7
1	C	174	GLN	3.6

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Mol	Chain	Res	Type	RSRZ
1	D	112	LYS	3.5
1	F	6	MET	3.5
1	E	29	THR	3.5
1	B	120	ILE	3.4
1	D	58	LYS	3.4
1	E	27	CYS	3.3
1	A	137	ILE	3.3
1	A	145	ARG	3.2
1	E	34	GLY	3.2
1	C	37	ILE	3.2
1	E	41	GLY	3.2
1	E	-1	ALA	3.2
1	A	40	VAL	3.2
1	B	133	ILE	3.1
1	E	33	ILE	3.1
1	B	13	ASP	3.1
1	B	-3	LYS	3.0
1	F	145	ARG	2.9
1	A	36	LYS	2.9
1	C	112	LYS	2.9
1	E	1	PHE	2.8
1	A	-6	SER	2.8
1	B	1	PHE	2.8
1	F	13	ASP	2.8
1	D	115[A]	ILE	2.8
1	E	38	GLY	2.8
1	B	145	ARG	2.8
1	D	1	PHE	2.8
1	F	48	THR	2.7
1	D	19	LYS	2.7
1	D	44	GLU	2.7
1	F	9	ASP	2.7
1	E	54	ASP	2.7
1	A	6	MET	2.7
1	D	48	THR	2.7
1	E	141	CYS	2.6
1	F	-3	LYS	2.6
1	C	-3	LYS	2.6
1	E	44	GLU	2.6
1	D	97	VAL	2.6
1	F	59	GLU	2.6
1	D	33	ILE	2.5

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Mol	Chain	Res	Type	RSRZ
1	F	1	PHE	2.5
1	B	137	ILE	2.5
1	E	55	VAL	2.5
1	E	174	GLN	2.5
1	A	120	ILE	2.5
1	A	122	VAL	2.5
1	E	137	ILE	2.5
1	E	42	SER	2.4
1	C	58	LYS	2.4
1	C	-2	LYS	2.4
1	D	60	THR	2.4
1	D	137	ILE	2.3
1	F	-2	LYS	2.3
1	E	115	ILE	2.3
1	D	59	GLU	2.3
1	B	38	GLY	2.3
1	D	13	ASP	2.3
1	D	-3	LYS	2.3
1	A	135	MET	2.3
1	D	34	GLY	2.3
1	C	55	VAL	2.2
1	B	132	LEU	2.2
1	E	112	LYS	2.2
1	D	145	ARG	2.2
1	F	27	CYS	2.2
1	C	54	ASP	2.2
1	B	30	SER	2.2
1	F	55	VAL	2.2
1	A	-4	TYR	2.1
1	B	26	GLY	2.1
1	C	86	LEU	2.1
1	B	35	GLU	2.1
1	B	-2	LYS	2.1
1	A	139	HIS	2.1
1	B	135	MET	2.1
1	F	60	THR	2.1
1	D	158	ILE	2.1
1	C	36	LYS	2.1
1	C	156	VAL	2.1
1	A	9	ASP	2.1
1	B	76	ILE	2.1
1	A	-2	LYS	2.0

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Mol	Chain	Res	Type	RSRZ
1	C	59	GLU	2.0
1	D	56	VAL	2.0

## 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	F	203	5/5	0.91	0.16	59,67,67,74	0
2	SO4	C	203	5/5	0.93	0.15	78,78,82,86	0
2	SO4	E	203	5/5	0.94	0.43	22,27,37,37	5
2	SO4	B	203	5/5	0.95	0.55	39,47,60,64	5
2	SO4	B	201	5/5	0.95	0.22	56,57,59,63	0
2	SO4	B	202	5/5	0.96	0.17	41,42,49,50	0
2	SO4	F	201	5/5	0.96	0.14	44,46,47,51	0
2	SO4	C	204	5/5	0.96	0.29	30,40,47,48	5
2	SO4	E	202	5/5	0.97	0.19	41,43,51,51	0
2	SO4	A	202	5/5	0.97	0.14	47,49,52,58	0
2	SO4	C	202	5/5	0.97	0.17	43,46,49,50	0
2	SO4	F	202	5/5	0.97	0.15	67,71,75,76	0
2	SO4	D	201	5/5	0.97	0.19	58,61,67,69	0
2	SO4	E	201	5/5	0.98	0.13	58,59,65,69	0
2	SO4	A	201	5/5	0.98	0.17	39,43,45,50	0
2	SO4	D	202	5/5	0.98	0.13	43,49,53,53	0
2	SO4	C	201	5/5	0.99	0.14	49,53,59,60	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.