



# wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 10, 2017 – 08:01 AM EDT

PDB ID : 2GSZ  
Title : Structure of A. aeolicus PilT with 6 monomers per asymmetric unit  
Authors : Forest, K.T.; Satyshur, K.A.  
Deposited on : unknown  
Resolution : 4.20 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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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	:	1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20030345
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	rb-20030345

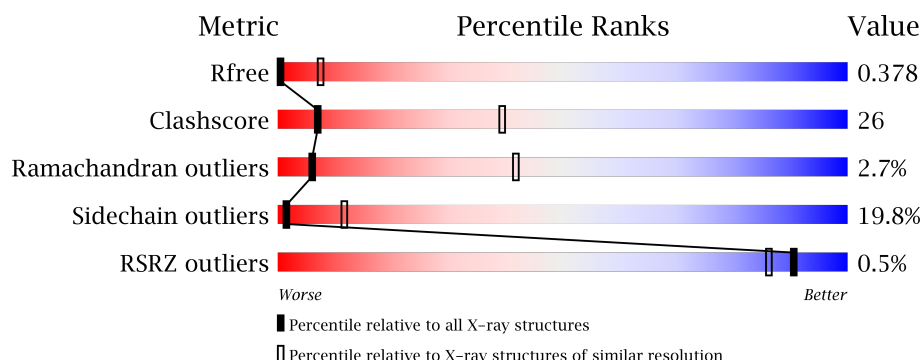
# 1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 4.20 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))
$R_{free}$	100719	1177 (4.80-3.60)
Clashscore	112137	1025 (4.72-3.66)
Ramachandran outliers	110173	1024 (4.76-3.62)
Sidechain outliers	110143	1008 (4.76-3.62)
RSRZ outliers	101464	1188 (4.80-3.60)

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. 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	363	<div> <div>46%</div> <div>37%</div> <div>11%</div> <div>6%</div> </div>
1	B	363	<div> <div>44%</div> <div>42%</div> <div>9%</div> <div>6%</div> </div>
1	C	363	<div> <div>46%</div> <div>38%</div> <div>10%</div> <div>6%</div> </div>
1	D	363	<div> <div>43%</div> <div>42%</div> <div>9%</div> <div>6%</div> </div>
1	E	363	<div> <div>42%</div> <div>41%</div> <div>10%</div> <div>6%</div> </div>

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Mol	Chain	Length	Quality of chain
1	F	363	

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	375	-	-	X	-
2	SO4	C	375	-	-	X	-
2	SO4	E	375	-	-	X	-

## 2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 16344 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 twitching motility protein PilT.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	343	Total	C	N	O	S	Se	0	0	0
			2717	1731	471	505	1	9			
1	B	343	Total	C	N	O	S	Se	0	0	0
			2717	1731	471	505	1	9			
1	C	343	Total	C	N	O	S	Se	0	0	0
			2717	1731	471	505	1	9			
1	D	343	Total	C	N	O	S	Se	0	0	0
			2717	1731	471	505	1	9			
1	E	343	Total	C	N	O	S	Se	0	0	0
			2717	1731	471	505	1	9			
1	F	343	Total	C	N	O	S	Se	0	0	0
			2717	1731	471	505	1	9			

There are 102 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	68	MSE	MET	MODIFIED RESIDUE	GB 2983313
A	136	MSE	MET	MODIFIED RESIDUE	GB 2983313
A	156	MSE	MET	MODIFIED RESIDUE	GB 2983313
A	218	MSE	MET	MODIFIED RESIDUE	GB 2983313
A	318	MSE	MET	MODIFIED RESIDUE	GB 2983313
A	327	MSE	MET	MODIFIED RESIDUE	GB 2983313
A	330	MSE	MET	MODIFIED RESIDUE	GB 2983313
A	349	MSE	MET	MODIFIED RESIDUE	GB 2983313
A	361	MSE	MET	MODIFIED RESIDUE	GB 2983313
A	367	LEU	-	EXPRESSION TAG	GB 2983313
A	368	GLU	-	EXPRESSION TAG	GB 2983313
A	369	HIS	-	EXPRESSION TAG	GB 2983313
A	370	HIS	-	EXPRESSION TAG	GB 2983313
A	371	HIS	-	EXPRESSION TAG	GB 2983313
A	372	HIS	-	EXPRESSION TAG	GB 2983313
A	373	HIS	-	EXPRESSION TAG	GB 2983313
A	374	HIS	-	EXPRESSION TAG	GB 2983313

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Chain	Residue	Modelled	Actual	Comment	Reference
B	68	MSE	MET	MODIFIED RESIDUE	GB 2983313
B	136	MSE	MET	MODIFIED RESIDUE	GB 2983313
B	156	MSE	MET	MODIFIED RESIDUE	GB 2983313
B	218	MSE	MET	MODIFIED RESIDUE	GB 2983313
B	318	MSE	MET	MODIFIED RESIDUE	GB 2983313
B	327	MSE	MET	MODIFIED RESIDUE	GB 2983313
B	330	MSE	MET	MODIFIED RESIDUE	GB 2983313
B	349	MSE	MET	MODIFIED RESIDUE	GB 2983313
B	361	MSE	MET	MODIFIED RESIDUE	GB 2983313
B	367	LEU	-	EXPRESSION TAG	GB 2983313
B	368	GLU	-	EXPRESSION TAG	GB 2983313
B	369	HIS	-	EXPRESSION TAG	GB 2983313
B	370	HIS	-	EXPRESSION TAG	GB 2983313
B	371	HIS	-	EXPRESSION TAG	GB 2983313
B	372	HIS	-	EXPRESSION TAG	GB 2983313
B	373	HIS	-	EXPRESSION TAG	GB 2983313
B	374	HIS	-	EXPRESSION TAG	GB 2983313
C	68	MSE	MET	MODIFIED RESIDUE	GB 2983313
C	136	MSE	MET	MODIFIED RESIDUE	GB 2983313
C	156	MSE	MET	MODIFIED RESIDUE	GB 2983313
C	218	MSE	MET	MODIFIED RESIDUE	GB 2983313
C	318	MSE	MET	MODIFIED RESIDUE	GB 2983313
C	327	MSE	MET	MODIFIED RESIDUE	GB 2983313
C	330	MSE	MET	MODIFIED RESIDUE	GB 2983313
C	349	MSE	MET	MODIFIED RESIDUE	GB 2983313
C	361	MSE	MET	MODIFIED RESIDUE	GB 2983313
C	367	LEU	-	EXPRESSION TAG	GB 2983313
C	368	GLU	-	EXPRESSION TAG	GB 2983313
C	369	HIS	-	EXPRESSION TAG	GB 2983313
C	370	HIS	-	EXPRESSION TAG	GB 2983313
C	371	HIS	-	EXPRESSION TAG	GB 2983313
C	372	HIS	-	EXPRESSION TAG	GB 2983313
C	373	HIS	-	EXPRESSION TAG	GB 2983313
C	374	HIS	-	EXPRESSION TAG	GB 2983313
D	68	MSE	MET	MODIFIED RESIDUE	GB 2983313
D	136	MSE	MET	MODIFIED RESIDUE	GB 2983313
D	156	MSE	MET	MODIFIED RESIDUE	GB 2983313
D	218	MSE	MET	MODIFIED RESIDUE	GB 2983313
D	318	MSE	MET	MODIFIED RESIDUE	GB 2983313
D	327	MSE	MET	MODIFIED RESIDUE	GB 2983313
D	330	MSE	MET	MODIFIED RESIDUE	GB 2983313
D	349	MSE	MET	MODIFIED RESIDUE	GB 2983313

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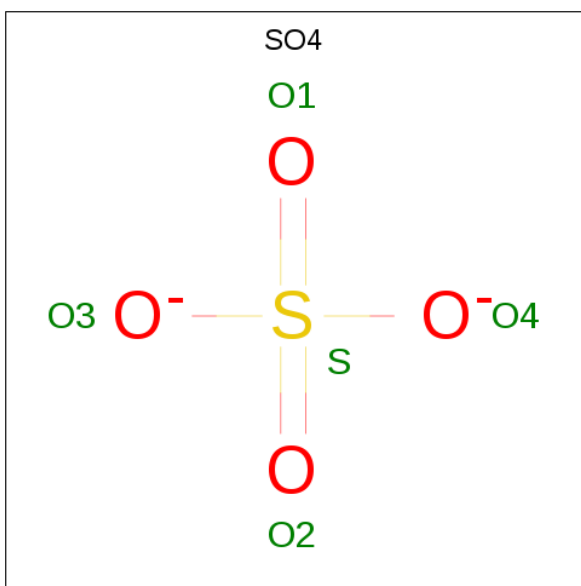
Chain	Residue	Modelled	Actual	Comment	Reference
D	361	MSE	MET	MODIFIED RESIDUE	GB 2983313
D	367	LEU	-	EXPRESSION TAG	GB 2983313
D	368	GLU	-	EXPRESSION TAG	GB 2983313
D	369	HIS	-	EXPRESSION TAG	GB 2983313
D	370	HIS	-	EXPRESSION TAG	GB 2983313
D	371	HIS	-	EXPRESSION TAG	GB 2983313
D	372	HIS	-	EXPRESSION TAG	GB 2983313
D	373	HIS	-	EXPRESSION TAG	GB 2983313
D	374	HIS	-	EXPRESSION TAG	GB 2983313
E	68	MSE	MET	MODIFIED RESIDUE	GB 2983313
E	136	MSE	MET	MODIFIED RESIDUE	GB 2983313
E	156	MSE	MET	MODIFIED RESIDUE	GB 2983313
E	218	MSE	MET	MODIFIED RESIDUE	GB 2983313
E	318	MSE	MET	MODIFIED RESIDUE	GB 2983313
E	327	MSE	MET	MODIFIED RESIDUE	GB 2983313
E	330	MSE	MET	MODIFIED RESIDUE	GB 2983313
E	349	MSE	MET	MODIFIED RESIDUE	GB 2983313
E	361	MSE	MET	MODIFIED RESIDUE	GB 2983313
E	367	LEU	-	EXPRESSION TAG	GB 2983313
E	368	GLU	-	EXPRESSION TAG	GB 2983313
E	369	HIS	-	EXPRESSION TAG	GB 2983313
E	370	HIS	-	EXPRESSION TAG	GB 2983313
E	371	HIS	-	EXPRESSION TAG	GB 2983313
E	372	HIS	-	EXPRESSION TAG	GB 2983313
E	373	HIS	-	EXPRESSION TAG	GB 2983313
E	374	HIS	-	EXPRESSION TAG	GB 2983313
F	68	MSE	MET	MODIFIED RESIDUE	GB 2983313
F	136	MSE	MET	MODIFIED RESIDUE	GB 2983313
F	156	MSE	MET	MODIFIED RESIDUE	GB 2983313
F	218	MSE	MET	MODIFIED RESIDUE	GB 2983313
F	318	MSE	MET	MODIFIED RESIDUE	GB 2983313
F	327	MSE	MET	MODIFIED RESIDUE	GB 2983313
F	330	MSE	MET	MODIFIED RESIDUE	GB 2983313
F	349	MSE	MET	MODIFIED RESIDUE	GB 2983313
F	361	MSE	MET	MODIFIED RESIDUE	GB 2983313
F	367	LEU	-	EXPRESSION TAG	GB 2983313
F	368	GLU	-	EXPRESSION TAG	GB 2983313
F	369	HIS	-	EXPRESSION TAG	GB 2983313
F	370	HIS	-	EXPRESSION TAG	GB 2983313
F	371	HIS	-	EXPRESSION TAG	GB 2983313
F	372	HIS	-	EXPRESSION TAG	GB 2983313
F	373	HIS	-	EXPRESSION TAG	GB 2983313

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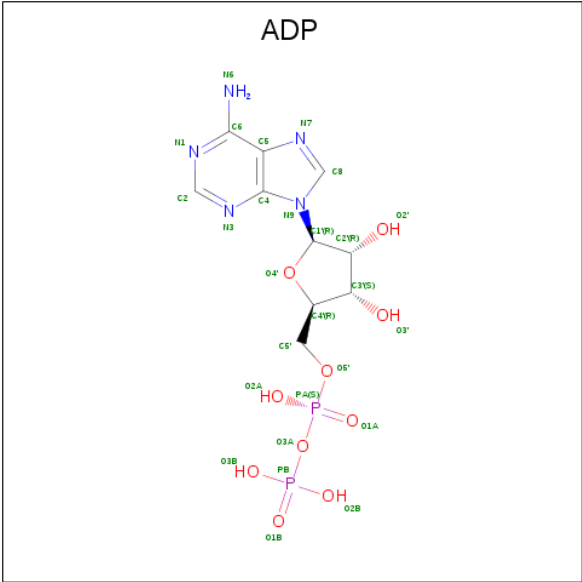
Chain	Residue	Modelled	Actual	Comment	Reference
F	374	HIS	-	EXPRESSION TAG	GB 2983313

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



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

- Molecule 3 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula: C<sub>10</sub>H<sub>15</sub>N<sub>5</sub>O<sub>10</sub>P<sub>2</sub>).



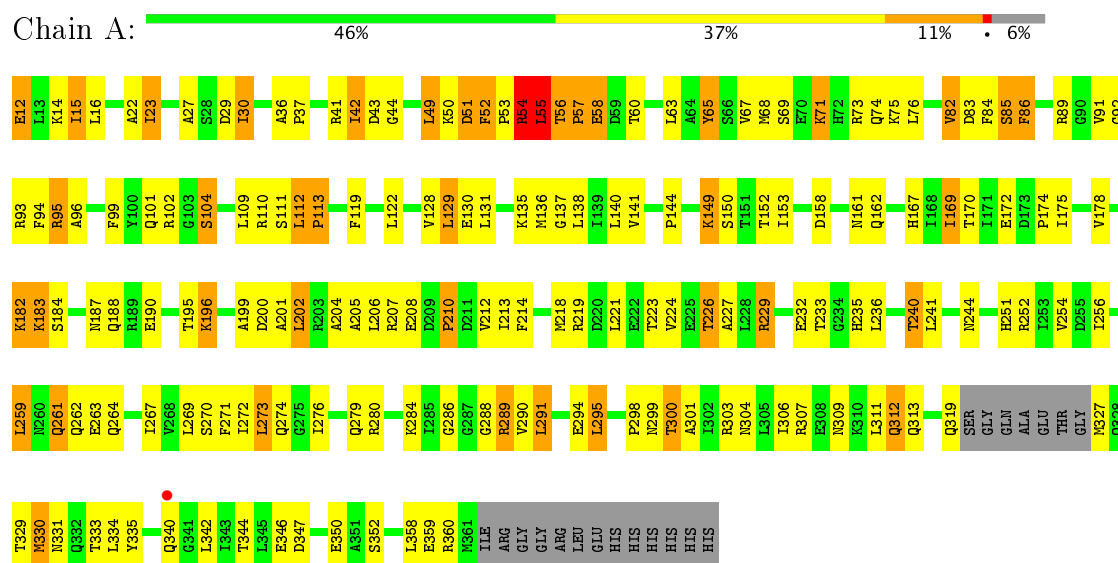
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	F	1	Total	C	N	O	P	0	0
			27	10	5	10	2		



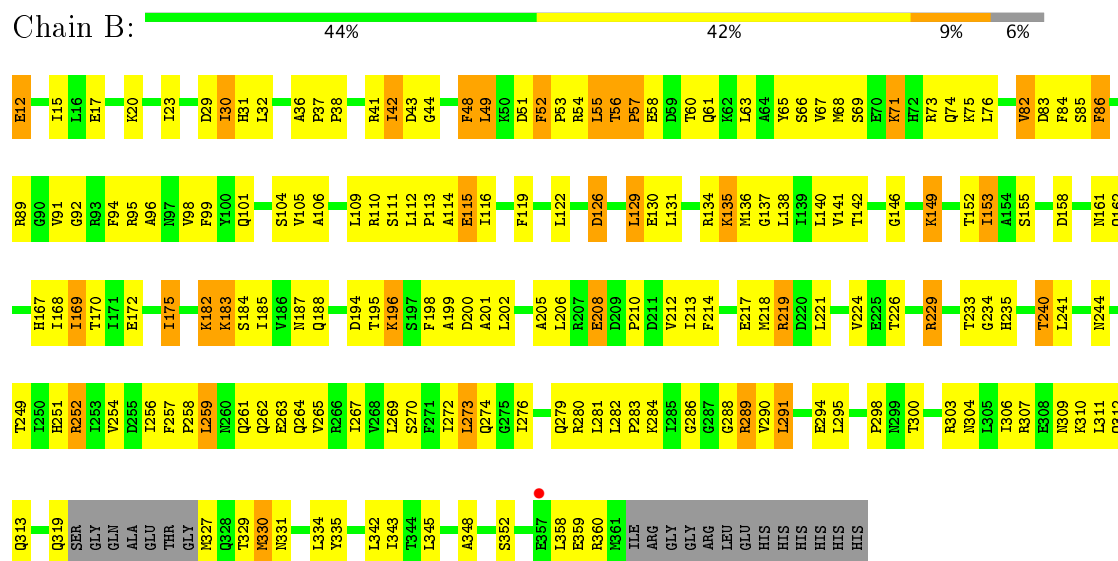
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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: twitching motility protein PilT

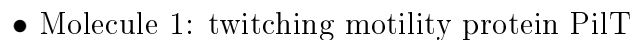


#### • Molecule 1: twitching motility protein PilT

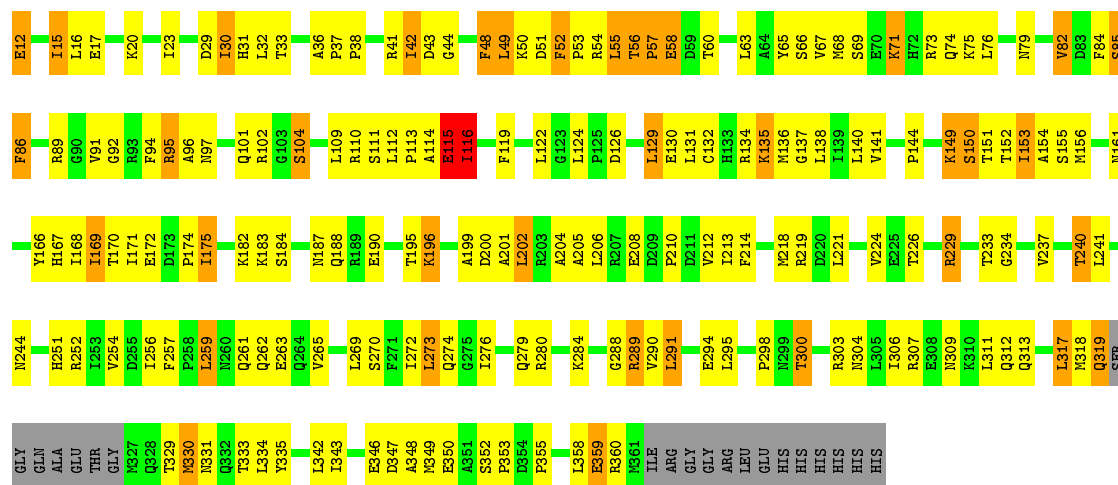


#### • Molecule 1: twitching motility protein PilT





Chain F:  43% 41% 10% • 6%



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	206.11Å 105.24Å 123.02Å 90.00° 111.06° 90.00°	Depositor
Resolution (Å)	25.00 – 4.20 32.48 – 4.20	Depositor EDS
% Data completeness (in resolution range)	94.8 (25.00-4.20) 94.7 (32.48-4.20)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	0.09	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	6.91 (at 4.27Å)	Xtriage
Refinement program	REFMAC	Depositor
R, $R_{free}$	0.343 , 0.406 0.317 , 0.378	Depositor DCC
$R_{free}$ test set	859 reflections (5.29%)	DCC
Wilson B-factor (Å <sup>2</sup> )	115.0	Xtriage
Anisotropy	0.105	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.23 , 9.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.51$ , $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.85	EDS
Total number of atoms	16344	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	124.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.01% 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, ADP

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	0.83	0/2753	0.83	3/3702 (0.1%)
1	B	0.88	3/2753 (0.1%)	0.83	1/3702 (0.0%)
1	C	0.80	0/2753	0.82	2/3702 (0.1%)
1	D	0.80	0/2753	0.90	5/3702 (0.1%)
1	E	0.83	1/2753 (0.0%)	0.91	9/3702 (0.2%)
1	F	0.83	1/2753 (0.0%)	0.85	7/3702 (0.2%)
All	All	0.83	5/16518 (0.0%)	0.86	27/22212 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	B	0	1
1	F	0	2
All	All	0	3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	115	GLU	CD-OE1	13.20	1.40	1.25
1	B	115	GLU	CD-OE2	11.11	1.37	1.25
1	F	115	GLU	CD-OE2	6.81	1.33	1.25
1	E	115	GLU	CG-CD	5.85	1.60	1.51
1	B	115	GLU	CG-CD	5.22	1.59	1.51

The worst 5 of 27 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	289	ARG	NE-CZ-NH1	-15.71	112.44	120.30
1	D	289	ARG	NE-CZ-NH2	15.63	128.12	120.30
1	E	219	ARG	CG-CD-NE	12.56	138.18	111.80
1	E	219	ARG	NE-CZ-NH2	-9.03	115.78	120.30
1	D	289	ARG	CD-NE-CZ	8.79	135.91	123.60

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	115	GLU	Peptide
1	F	114	ALA	Peptide
1	F	115	GLU	Peptide

## 5.2 Too-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 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	2717	0	2798	162	2
1	B	2717	0	2798	152	4
1	C	2717	0	2798	136	0
1	D	2717	0	2797	162	3
1	E	2717	0	2798	180	0
1	F	2717	0	2798	154	0
2	B	5	0	0	6	0
2	C	5	0	0	4	0
2	E	5	0	0	2	0
3	F	27	0	12	7	0
All	All	16344	0	16799	845	5

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 26.

The worst 5 of 845 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:E:136:MSE:SE	1:E:136:MSE:CE	2.14	1.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:136:MSE:CE	1:B:136:MSE:SE	2.14	1.44
1:A:136:MSE:SE	1:A:136:MSE:CE	2.18	1.42
1:A:218:MSE:SE	1:A:218:MSE:CE	2.18	1.41
1:C:136:MSE:CE	1:C:136:MSE:SE	2.19	1.41

All (5) 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:B:310:LYS:NZ	1:D:319:GLN:OE1[4_555]	1.37	0.83
1:A:73:ARG:NH2	1:A:73:ARG:NH2[2_554]	1.77	0.43
1:B:310:LYS:NZ	1:D:319:GLN:CD[4_555]	2.06	0.14
1:A:12:GLU:OE1	1:B:61:GLN:NE2[2_554]	2.07	0.13
1:B:345:LEU:CD2	1:D:24:GLU:O[1_565]	2.12	0.08

## 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	339/363 (93%)	279 (82%)	52 (15%)	8 (2%)	7	44
1	B	339/363 (93%)	276 (81%)	54 (16%)	9 (3%)	6	42
1	C	339/363 (93%)	278 (82%)	51 (15%)	10 (3%)	5	40
1	D	339/363 (93%)	277 (82%)	54 (16%)	8 (2%)	7	44
1	E	339/363 (93%)	280 (83%)	51 (15%)	8 (2%)	7	44
1	F	339/363 (93%)	279 (82%)	49 (14%)	11 (3%)	5	38
All	All	2034/2178 (93%)	1669 (82%)	311 (15%)	54 (3%)	6	42

5 of 54 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	114	ALA
1	A	199	ALA
1	C	50	LYS
1	C	55	LEU
1	D	55	LEU

### 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	297/303 (98%)	237 (80%)	60 (20%)	1	11
1	B	297/303 (98%)	241 (81%)	56 (19%)	2	13
1	C	297/303 (98%)	237 (80%)	60 (20%)	1	11
1	D	297/303 (98%)	242 (82%)	55 (18%)	2	14
1	E	297/303 (98%)	236 (80%)	61 (20%)	1	10
1	F	297/303 (98%)	237 (80%)	60 (20%)	1	11
All	All	1782/1818 (98%)	1430 (80%)	352 (20%)	1	12

5 of 352 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	252	ARG
1	D	149	LYS
1	F	200	ASP
1	C	273	LEU
1	D	23	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 33 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	264	GLN
1	D	261	GLN
1	F	261	GLN
1	C	304	ASN

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Mol	Chain	Res	Type
1	D	74	GLN

### 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 carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

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	B	375	-	4,4,4	1.61	1 (25%)	6,6,6	1.49	1 (16%)
2	SO4	C	375	-	4,4,4	0.29	0	6,6,6	0.55	0
2	SO4	E	375	-	4,4,4	2.35	1 (25%)	6,6,6	0.64	0
3	ADP	F	500	-	25,29,29	1.63	5 (20%)	24,45,45	1.86	3 (12%)

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	B	375	-	-	0/0/0/0	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	SO4	C	375	-	-	0/0/0/0	0/0/0/0
2	SO4	E	375	-	-	0/0/0/0	0/0/0/0
3	ADP	F	500	-	-	0/12/32/32	0/3/3/3

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	F	500	ADP	C4-N3	2.12	1.38	1.35
3	F	500	ADP	C2-N3	2.37	1.36	1.32
2	B	375	SO4	O2-S	2.56	1.59	1.45
3	F	500	ADP	PB-O3A	2.75	1.64	1.60
2	E	375	SO4	O2-S	4.13	1.68	1.45

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	F	500	ADP	N3-C2-N1	-6.86	122.89	128.86
3	F	500	ADP	C4-C5-N7	-3.10	106.41	109.41
3	F	500	ADP	C2-N1-C6	2.21	122.64	118.77
2	B	375	SO4	O4-S-O2	2.55	123.31	109.26

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 19 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	375	SO4	6	0
2	C	375	SO4	4	0
2	E	375	SO4	2	0
3	F	500	ADP	7	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	334/363 (92%)	-0.23	1 (0%) 93 91	82, 118, 160, 176	0
1	B	334/363 (92%)	-0.24	1 (0%) 93 91	82, 118, 160, 176	0
1	C	334/363 (92%)	-0.23	4 (1%) 79 71	82, 118, 160, 176	0
1	D	334/363 (92%)	-0.15	1 (0%) 93 91	82, 118, 160, 176	0
1	E	334/363 (92%)	-0.12	4 (1%) 79 71	82, 118, 160, 176	0
1	F	334/363 (92%)	-0.20	0 100 100	82, 118, 160, 176	0
All	All	2004/2178 (92%)	-0.19	11 (0%) 90 86	82, 118, 160, 176	0

The worst 5 of 11 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	90	GLY	2.9
1	E	339	LYS	2.8
1	C	91	VAL	2.5
1	E	357	GLU	2.4
1	E	345	LEU	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 carbohydrates 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. 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	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
3	ADP	F	500	27/27	0.71	0.36	0.57	153,177,179,179	0
2	SO4	E	375	5/5	0.87	0.27	0.02	148,148,148,149	0
2	SO4	B	375	5/5	0.90	0.19	-0.39	88,88,89,90	0
2	SO4	C	375	5/5	0.96	0.17	-0.67	112,113,114,115	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.