



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 07:03 PM UTC

PDB ID : 2DG2 / pdb\_00002dg2  
Title : Crystal Structure of Mouse Apolipoprotein A-I Binding Protein  
Authors : Shumilin, I.A.; Jha, K.N.; Zheng, H.; Chruszcz, M.; Cymborowski, M.; Herr, J.C.; Minor, W.  
Deposited on : 2006-03-08  
Resolution : 2.45 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

<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 : 4-5-2 with Phenix2.0  
Mogul : 2022.3.0, CSD as543be (2022)  
Xtriage (Phenix) : 2.0  
EDS : 3.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
CCP4 : 9.0.010 (Gargrove)  
Density-Fitness : 1.0.12  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

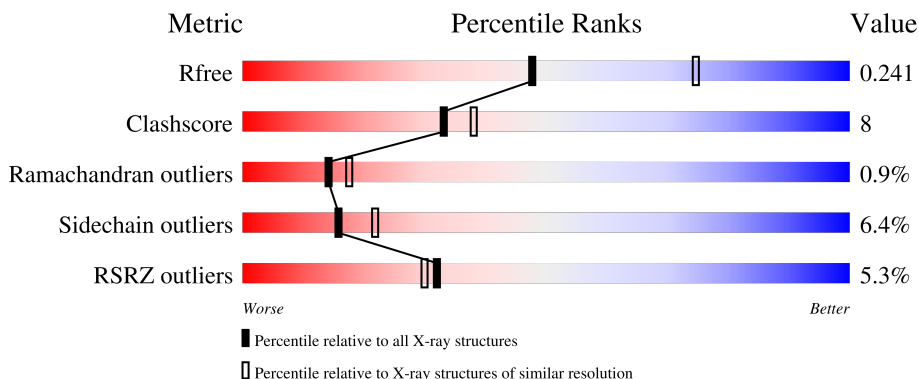
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.45 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.



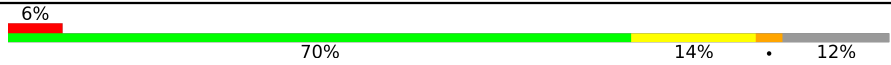
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	180053	1190 (2.46-2.46)
Clashscore	190562	1229 (2.46-2.46)
Ramachandran outliers	187476	1218 (2.46-2.46)
Sidechain outliers	187428	1218 (2.46-2.46)
RSRZ outliers	180081	1190 (2.46-2.46)

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	265	 4% 70% 14% • 12%
1	B	265	 5% 71% 14% • 12%
1	C	265	 5% 68% 16% • 12%
1	D	265	 3% 69% 15% • 12%
1	E	265	 5% 70% 14% • 12%

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Mol	Chain	Length	Quality of chain
1	F	265	 <p>A horizontal bar chart representing the quality of the chain. The bar is divided into four segments: a small red segment at the beginning labeled '6%', a large green segment labeled '70%', a yellow segment labeled '14%', and a small grey segment at the end labeled '12%'. A small black dot is visible on the grey segment.</p>

## 2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 11077 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 Apolipoprotein A-I binding protein.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	S	Se			
1	A	233	1805	1168	290	336	5	6	0	0	0
1	B	233	1805	1168	290	336	5	6	0	0	0
1	C	233	1805	1168	290	336	5	6	0	0	0
1	D	233	1805	1168	290	336	5	6	0	0	0
1	E	233	1805	1168	290	336	5	6	0	0	0
1	F	233	1805	1168	290	336	5	6	0	0	0

There are 84 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	MET	-	initiating methionine	GB 37231544
A	22	MSE	MET	modified residue	GB 37231544
A	54	MSE	MET	modified residue	GB 37231544
A	74	MSE	MET	modified residue	GB 37231544
A	131	MSE	MET	modified residue	GB 37231544
A	139	MSE	MET	modified residue	GB 37231544
A	144	MSE	MET	modified residue	GB 37231544
A	145	MSE	MET	modified residue	GB 37231544
A	259	HIS	-	expression tag	GB 37231544
A	260	HIS	-	expression tag	GB 37231544
A	261	HIS	-	expression tag	GB 37231544
A	262	HIS	-	expression tag	GB 37231544
A	263	HIS	-	expression tag	GB 37231544
A	264	HIS	-	expression tag	GB 37231544
B	0	MET	-	initiating methionine	GB 37231544
B	22	MSE	MET	modified residue	GB 37231544
B	54	MSE	MET	modified residue	GB 37231544

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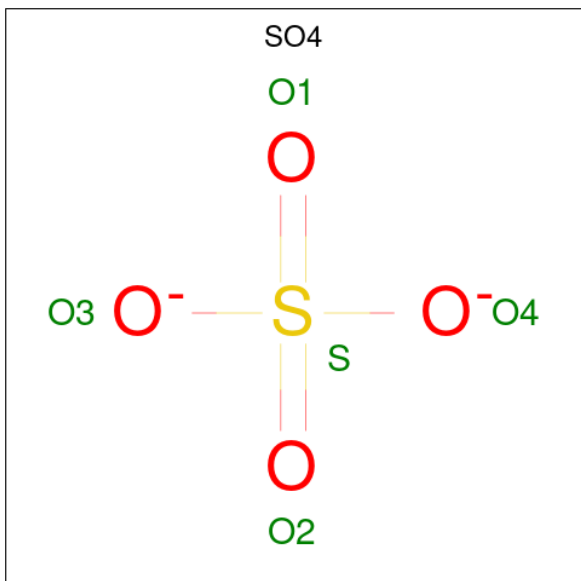
Chain	Residue	Modelled	Actual	Comment	Reference
B	74	MSE	MET	modified residue	GB 37231544
B	131	MSE	MET	modified residue	GB 37231544
B	139	MSE	MET	modified residue	GB 37231544
B	144	MSE	MET	modified residue	GB 37231544
B	145	MSE	MET	modified residue	GB 37231544
B	259	HIS	-	expression tag	GB 37231544
B	260	HIS	-	expression tag	GB 37231544
B	261	HIS	-	expression tag	GB 37231544
B	262	HIS	-	expression tag	GB 37231544
B	263	HIS	-	expression tag	GB 37231544
B	264	HIS	-	expression tag	GB 37231544
C	0	MET	-	initiating methionine	GB 37231544
C	22	MSE	MET	modified residue	GB 37231544
C	54	MSE	MET	modified residue	GB 37231544
C	74	MSE	MET	modified residue	GB 37231544
C	131	MSE	MET	modified residue	GB 37231544
C	139	MSE	MET	modified residue	GB 37231544
C	144	MSE	MET	modified residue	GB 37231544
C	145	MSE	MET	modified residue	GB 37231544
C	259	HIS	-	expression tag	GB 37231544
C	260	HIS	-	expression tag	GB 37231544
C	261	HIS	-	expression tag	GB 37231544
C	262	HIS	-	expression tag	GB 37231544
C	263	HIS	-	expression tag	GB 37231544
C	264	HIS	-	expression tag	GB 37231544
D	0	MET	-	initiating methionine	GB 37231544
D	22	MSE	MET	modified residue	GB 37231544
D	54	MSE	MET	modified residue	GB 37231544
D	74	MSE	MET	modified residue	GB 37231544
D	131	MSE	MET	modified residue	GB 37231544
D	139	MSE	MET	modified residue	GB 37231544
D	144	MSE	MET	modified residue	GB 37231544
D	145	MSE	MET	modified residue	GB 37231544
D	259	HIS	-	expression tag	GB 37231544
D	260	HIS	-	expression tag	GB 37231544
D	261	HIS	-	expression tag	GB 37231544
D	262	HIS	-	expression tag	GB 37231544
D	263	HIS	-	expression tag	GB 37231544
D	264	HIS	-	expression tag	GB 37231544
E	0	MET	-	initiating methionine	GB 37231544
E	22	MSE	MET	modified residue	GB 37231544
E	54	MSE	MET	modified residue	GB 37231544

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Chain	Residue	Modelled	Actual	Comment	Reference
E	74	MSE	MET	modified residue	GB 37231544
E	131	MSE	MET	modified residue	GB 37231544
E	139	MSE	MET	modified residue	GB 37231544
E	144	MSE	MET	modified residue	GB 37231544
E	145	MSE	MET	modified residue	GB 37231544
E	259	HIS	-	expression tag	GB 37231544
E	260	HIS	-	expression tag	GB 37231544
E	261	HIS	-	expression tag	GB 37231544
E	262	HIS	-	expression tag	GB 37231544
E	263	HIS	-	expression tag	GB 37231544
E	264	HIS	-	expression tag	GB 37231544
F	0	MET	-	initiating methionine	GB 37231544
F	22	MSE	MET	modified residue	GB 37231544
F	54	MSE	MET	modified residue	GB 37231544
F	74	MSE	MET	modified residue	GB 37231544
F	131	MSE	MET	modified residue	GB 37231544
F	139	MSE	MET	modified residue	GB 37231544
F	144	MSE	MET	modified residue	GB 37231544
F	145	MSE	MET	modified residue	GB 37231544
F	259	HIS	-	expression tag	GB 37231544
F	260	HIS	-	expression tag	GB 37231544
F	261	HIS	-	expression tag	GB 37231544
F	262	HIS	-	expression tag	GB 37231544
F	263	HIS	-	expression tag	GB 37231544
F	264	HIS	-	expression tag	GB 37231544

- Molecule 2 is SULFATE ION (CCD ID: 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	B	1	Total O S 5 4 1	0	0
2	C	1	Total O S 5 4 1	0	0
2	D	1	Total O S 5 4 1	0	0
2	E	1	Total O S 5 4 1	0	0
2	F	1	Total O S 5 4 1	0	0

- Molecule 3 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total Cl 1 1	0	0
3	B	1	Total Cl 1 1	0	0
3	C	1	Total Cl 1 1	0	0
3	D	1	Total Cl 1 1	0	0
3	E	1	Total Cl 1 1	0	0
3	F	1	Total Cl 1 1	0	0

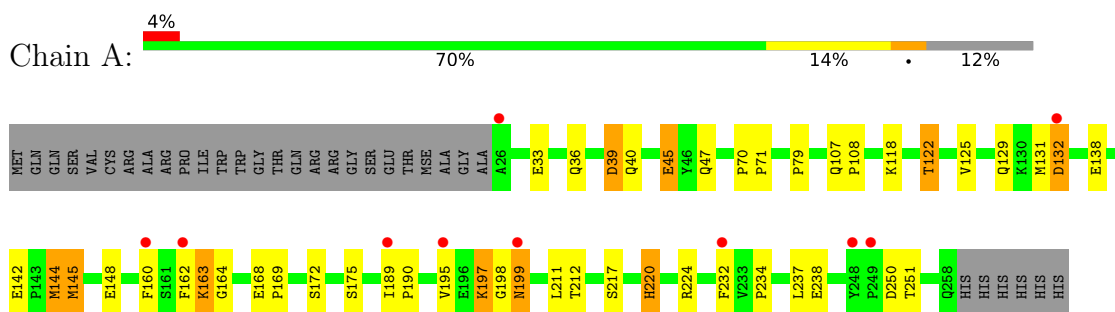
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	44	Total O 44 44	0	0
4	B	41	Total O 41 41	0	0
4	C	41	Total O 41 41	0	0
4	D	26	Total O 26 26	0	0
4	E	30	Total O 30 30	0	0
4	F	29	Total O 29 29	0	0

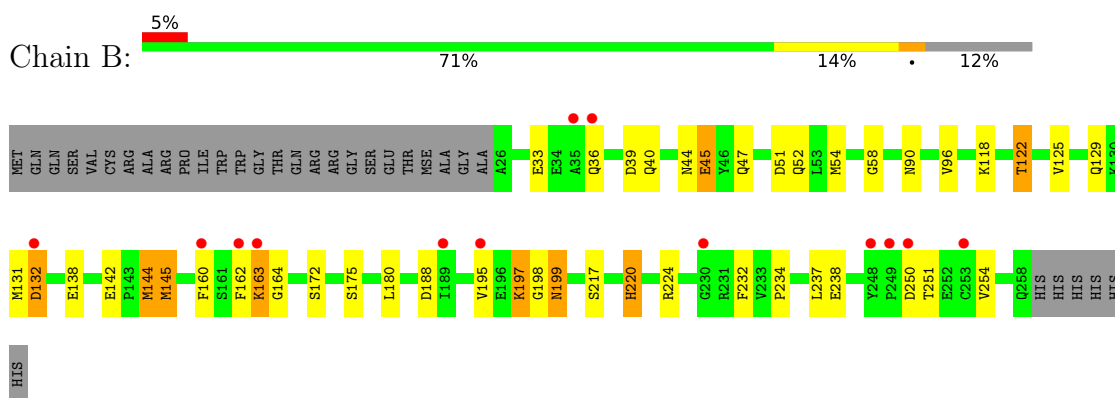
### 3 Residue-property plots [i](#)

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.

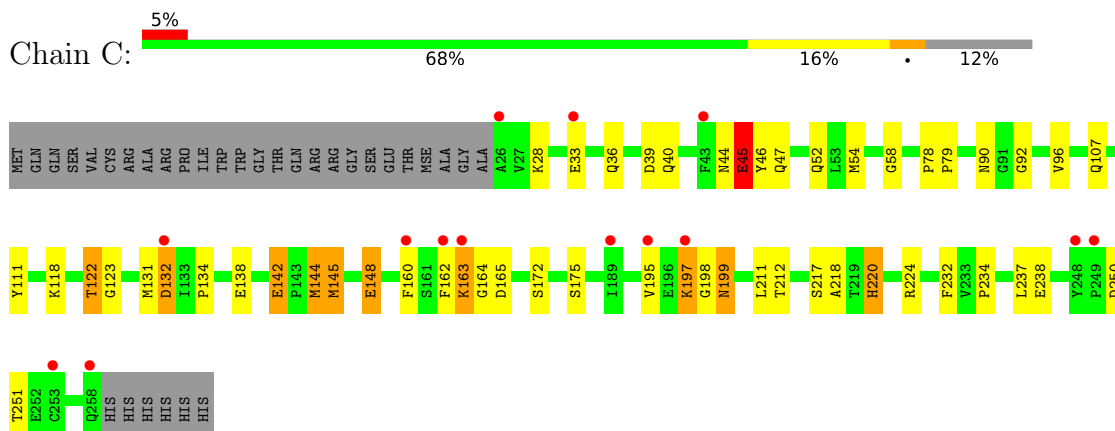
- Molecule 1: Apolipoprotein A-I binding protein



- Molecule 1: Apolipoprotein A-I binding protein



- Molecule 1: Apolipoprotein A-I binding protein





## 4 Data and refinement statistics i

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	104.86Å 125.75Å 163.62Å 90.00° 106.56° 90.00°	Depositor
Resolution (Å)	80.00 – 2.45 80.00 – 2.45	Depositor EDS
% Data completeness (in resolution range)	98.3 (80.00-2.45) 98.3 (80.00-2.45)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.51 (at 2.45Å)	Xtrriage
Refinement program	REFMAC 5.2.0005	Depositor
R, $R_{free}$	0.206 , 0.228 0.219 , 0.241	Depositor DCC
$R_{free}$ test set	3740 reflections (4.91%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	44.6	Xtrriage
Anisotropy	0.219	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 41.7	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.51$ , $\langle L^2 \rangle = 0.34$	Xtrriage
Estimated twinning fraction	0.000 for h,-k,-h-l	Xtrriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	11077	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	43.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 84.37 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.6955e-07. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<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	1.29	6/1850 (0.3%)	1.11	4/2510 (0.2%)
1	B	1.29	8/1850 (0.4%)	1.12	7/2510 (0.3%)
1	C	1.29	10/1850 (0.5%)	1.13	8/2510 (0.3%)
1	D	1.30	8/1850 (0.4%)	1.12	5/2510 (0.2%)
1	E	1.29	8/1850 (0.4%)	1.13	5/2510 (0.2%)
1	F	1.30	7/1850 (0.4%)	1.12	5/2510 (0.2%)
All	All	1.29	47/11100 (0.4%)	1.12	34/15060 (0.2%)

The worst 5 of 47 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	144	MSE	SE-CE	9.03	2.22	1.95
1	B	144	MSE	SE-CE	8.70	2.21	1.95
1	F	144	MSE	SE-CE	8.48	2.21	1.95
1	C	144	MSE	SE-CE	8.12	2.19	1.95
1	A	144	MSE	SE-CE	7.62	2.18	1.95

The worst 5 of 34 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	163	LYS	N-CA-C	6.90	124.79	114.09
1	F	163	LYS	N-CA-C	6.81	124.64	114.09
1	E	163	LYS	N-CA-C	6.62	124.71	114.64
1	C	163	LYS	N-CA-C	6.54	124.58	114.64
1	F	220	HIS	CB-CG-CD2	-6.54	122.69	131.20

There are no chirality outliers.

There are no planarity outliers.

## 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	1805	0	1790	31	0
1	B	1805	0	1790	24	0
1	C	1805	0	1790	33	0
1	D	1805	0	1790	26	0
1	E	1805	0	1790	34	0
1	F	1805	0	1790	27	1
2	A	5	0	0	1	0
2	B	5	0	0	0	0
2	C	5	0	0	0	0
2	D	5	0	0	0	0
2	E	5	0	0	0	0
2	F	5	0	0	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
3	E	1	0	0	0	0
3	F	1	0	0	1	0
4	A	44	0	0	13	0
4	B	41	0	0	9	0
4	C	41	0	0	12	0
4	D	26	0	0	6	0
4	E	30	0	0	16	0
4	F	29	0	0	5	1
All	All	11077	0	10740	169	1

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 8.

The worst 5 of 169 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:144:MSE:SE	1:E:144:MSE:CE	2.16	1.42
1:A:144:MSE:SE	1:A:144:MSE:CE	2.18	1.40
1:C:144:MSE:SE	1:C:144:MSE:CE	2.19	1.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:144:MSE:SE	1:F:144:MSE:CE	2.20	1.39
1:B:144:MSE:CE	1:B:144:MSE:SE	2.21	1.38

All (1) 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:F:132:ASP:CB	4:F:1014:HOH:O[2_555]	2.16	0.04

## 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	231/265 (87%)	214 (93%)	15 (6%)	2 (1%)	14 17
1	B	231/265 (87%)	214 (93%)	15 (6%)	2 (1%)	14 17
1	C	231/265 (87%)	210 (91%)	18 (8%)	3 (1%)	9 9
1	D	231/265 (87%)	212 (92%)	17 (7%)	2 (1%)	14 17
1	E	231/265 (87%)	210 (91%)	19 (8%)	2 (1%)	14 17
1	F	231/265 (87%)	209 (90%)	20 (9%)	2 (1%)	14 17
All	All	1386/1590 (87%)	1269 (92%)	104 (8%)	13 (1%)	14 17

5 of 13 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	45	GLU
1	B	45	GLU
1	C	45	GLU
1	D	45	GLU
1	E	45	GLU

### 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	199/220 (90%)	186 (94%)	13 (6%)	15	21
1	B	199/220 (90%)	187 (94%)	12 (6%)	17	26
1	C	199/220 (90%)	186 (94%)	13 (6%)	15	21
1	D	199/220 (90%)	186 (94%)	13 (6%)	15	21
1	E	199/220 (90%)	186 (94%)	13 (6%)	15	21
1	F	199/220 (90%)	186 (94%)	13 (6%)	15	21
All	All	1194/1320 (90%)	1117 (94%)	77 (6%)	16	22

5 of 77 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	132	ASP
1	F	138	GLU
1	E	148	GLU
1	F	36	GLN
1	F	197	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 11 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	244	ASN
1	E	117	ASN
1	F	244	ASN
1	E	244	ASN
1	C	244	ASN

### 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 oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 12 ligands modelled in this entry, 6 are monoatomic - leaving 6 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	A	1001	-	4,4,4	0.17	0	6,6,6	0.28	0
2	SO4	B	1003	-	4,4,4	0.20	0	6,6,6	0.18	0
2	SO4	F	1011	-	4,4,4	0.21	0	6,6,6	0.25	0
2	SO4	C	1005	-	4,4,4	0.27	0	6,6,6	0.24	0
2	SO4	E	1009	-	4,4,4	0.22	0	6,6,6	0.30	0
2	SO4	D	1007	-	4,4,4	0.21	0	6,6,6	0.20	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	A	1001	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	227/265 (85%)	0.14	10 (4%) 39 38	18, 39, 70, 79	0
1	B	227/265 (85%)	0.18	13 (5%) 29 26	18, 39, 70, 79	0
1	C	227/265 (85%)	0.33	14 (6%) 26 24	18, 39, 70, 79	0
1	D	227/265 (85%)	0.35	8 (3%) 47 47	18, 39, 70, 79	0
1	E	227/265 (85%)	0.37	12 (5%) 32 30	18, 39, 70, 80	0
1	F	227/265 (85%)	0.36	15 (6%) 24 22	18, 39, 70, 79	0
All	All	1362/1590 (85%)	0.29	72 (5%) 32 30	18, 39, 71, 80	0

The worst 5 of 72 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	132	ASP	4.1
1	E	249	PRO	3.9
1	D	132	ASP	3.8
1	C	253	CYS	3.7
1	D	249	PRO	3.4

### 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 oligosaccharides 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	C	1005	5/5	0.70	0.19	127,127,133,133	0
3	CL	A	1002	1/1	0.73	0.15	101,101,101,101	0
3	CL	F	1012	1/1	0.73	0.24	81,81,81,81	0
2	SO4	E	1009	5/5	0.78	0.21	122,129,129,132	0
2	SO4	F	1011	5/5	0.78	0.23	130,134,137,139	0
2	SO4	A	1001	5/5	0.79	0.19	114,124,126,127	0
2	SO4	D	1007	5/5	0.80	0.19	128,129,132,133	0
3	CL	B	1004	1/1	0.84	0.11	89,89,89,89	0
3	CL	E	1010	1/1	0.84	0.12	100,100,100,100	0
2	SO4	B	1003	5/5	0.84	0.18	113,120,122,124	0
3	CL	D	1008	1/1	0.86	0.16	96,96,96,96	0
3	CL	C	1006	1/1	0.88	0.10	89,89,89,89	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.