



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 11:44 AM UTC

PDB ID : 5Y51 / pdb_00005y51
Title : Crystal structure of PytH_H230A
Authors : Xu, D.Q.; Ran, T.T.; He, J.; Wang, W.W.
Deposited on : 2017-08-06
Resolution : 2.30 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

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>.

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

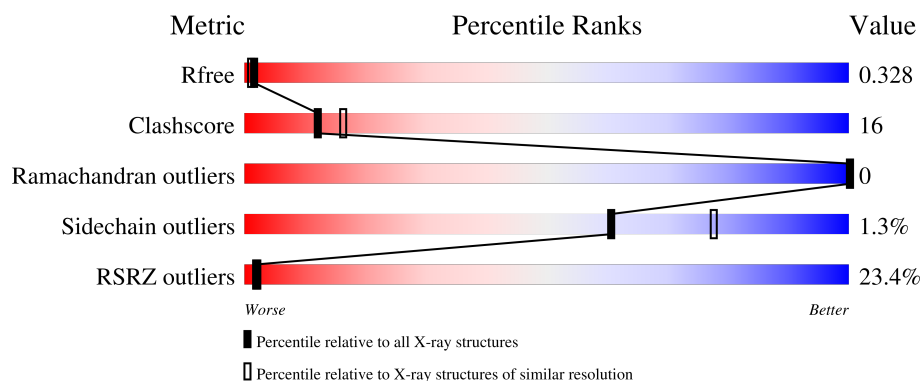
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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	6319 (2.30-2.30)
Clashscore	190562	6919 (2.30-2.30)
Ramachandran outliers	187476	6854 (2.30-2.30)
Sidechain outliers	187428	6854 (2.30-2.30)
RSRZ outliers	180081	6325 (2.30-2.30)

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 ≥ 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	288	3% 69% 16% 14%
1	B	288	2% 68% 17% 14%
1	C	288	7% 70% 17% 13%
1	D	288	6% 69% 17% 13%
1	E	288	39% 53% 32% 13%

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Mol	Chain	Length	Quality of chain
1	F	288	 A horizontal bar chart showing the quality of chain F. The bar is divided into four segments: red (65%), green (51%), yellow (33%), and grey (14%). The segments are stacked horizontally, with the red segment starting from the left and ending at 65%, the green segment starting at 65% and ending at 51%, the yellow segment starting at 51% and ending at 33%, and the grey segment starting at 33% and ending at 14%. The percentages are labeled above or below the segments.

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 11414 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 Pyrethroid hydrolase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	248	Total	C	N	O	S	0	0	0
			1888	1204	325	352	7			
1	B	249	Total	C	N	O	S	0	0	0
			1892	1206	326	353	7			
1	C	251	Total	C	N	O	S	0	0	0
			1899	1210	325	357	7			
1	D	251	Total	C	N	O	S	0	0	0
			1899	1210	325	357	7			
1	E	250	Total	C	N	O	S	0	0	0
			1885	1200	324	354	7			
1	F	248	Total	C	N	O	S	0	0	0
			1888	1204	325	352	7			

There are 54 discrepancies between the modelled and reference sequences:

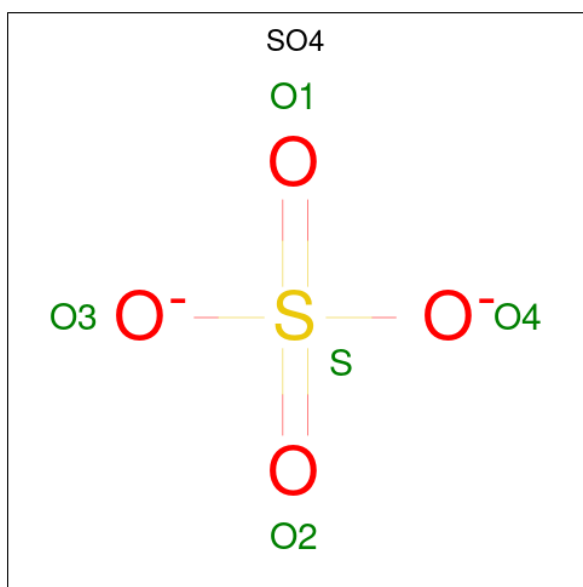
Chain	Residue	Modelled	Actual	Comment	Reference
A	230	ALA	HIS	engineered mutation	UNP D0VUS3
A	281	LEU	-	expression tag	UNP D0VUS3
A	282	GLU	-	expression tag	UNP D0VUS3
A	283	HIS	-	expression tag	UNP D0VUS3
A	284	HIS	-	expression tag	UNP D0VUS3
A	285	HIS	-	expression tag	UNP D0VUS3
A	286	HIS	-	expression tag	UNP D0VUS3
A	287	HIS	-	expression tag	UNP D0VUS3
A	288	HIS	-	expression tag	UNP D0VUS3
B	230	ALA	HIS	engineered mutation	UNP D0VUS3
B	281	LEU	-	expression tag	UNP D0VUS3
B	282	GLU	-	expression tag	UNP D0VUS3
B	283	HIS	-	expression tag	UNP D0VUS3
B	284	HIS	-	expression tag	UNP D0VUS3
B	285	HIS	-	expression tag	UNP D0VUS3
B	286	HIS	-	expression tag	UNP D0VUS3
B	287	HIS	-	expression tag	UNP D0VUS3

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Chain	Residue	Modelled	Actual	Comment	Reference
B	288	HIS	-	expression tag	UNP D0VUS3
C	230	ALA	HIS	engineered mutation	UNP D0VUS3
C	281	LEU	-	expression tag	UNP D0VUS3
C	282	GLU	-	expression tag	UNP D0VUS3
C	283	HIS	-	expression tag	UNP D0VUS3
C	284	HIS	-	expression tag	UNP D0VUS3
C	285	HIS	-	expression tag	UNP D0VUS3
C	286	HIS	-	expression tag	UNP D0VUS3
C	287	HIS	-	expression tag	UNP D0VUS3
C	288	HIS	-	expression tag	UNP D0VUS3
D	230	ALA	HIS	engineered mutation	UNP D0VUS3
D	281	LEU	-	expression tag	UNP D0VUS3
D	282	GLU	-	expression tag	UNP D0VUS3
D	283	HIS	-	expression tag	UNP D0VUS3
D	284	HIS	-	expression tag	UNP D0VUS3
D	285	HIS	-	expression tag	UNP D0VUS3
D	286	HIS	-	expression tag	UNP D0VUS3
D	287	HIS	-	expression tag	UNP D0VUS3
D	288	HIS	-	expression tag	UNP D0VUS3
E	230	ALA	HIS	engineered mutation	UNP D0VUS3
E	281	LEU	-	expression tag	UNP D0VUS3
E	282	GLU	-	expression tag	UNP D0VUS3
E	283	HIS	-	expression tag	UNP D0VUS3
E	284	HIS	-	expression tag	UNP D0VUS3
E	285	HIS	-	expression tag	UNP D0VUS3
E	286	HIS	-	expression tag	UNP D0VUS3
E	287	HIS	-	expression tag	UNP D0VUS3
E	288	HIS	-	expression tag	UNP D0VUS3
F	230	ALA	HIS	engineered mutation	UNP D0VUS3
F	281	LEU	-	expression tag	UNP D0VUS3
F	282	GLU	-	expression tag	UNP D0VUS3
F	283	HIS	-	expression tag	UNP D0VUS3
F	284	HIS	-	expression tag	UNP D0VUS3
F	285	HIS	-	expression tag	UNP D0VUS3
F	286	HIS	-	expression tag	UNP D0VUS3
F	287	HIS	-	expression tag	UNP D0VUS3
F	288	HIS	-	expression tag	UNP D0VUS3

- Molecule 2 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



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

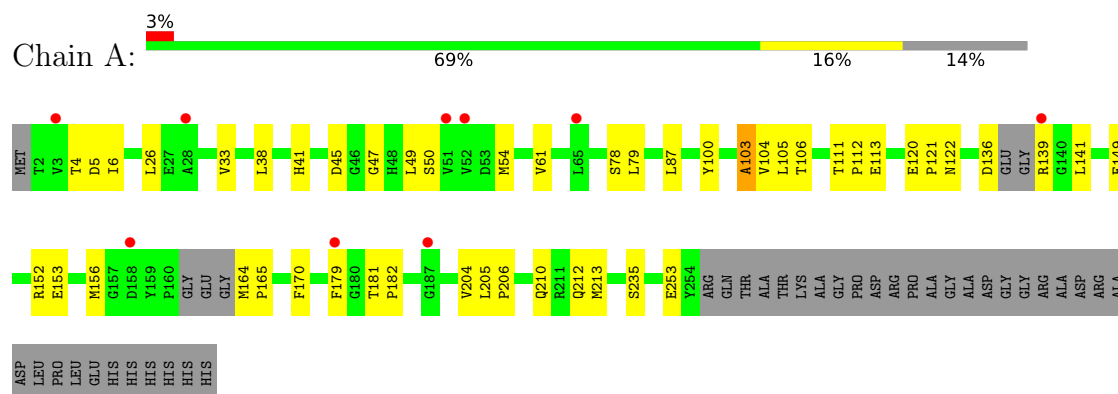
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	9	Total	O	0	0
			9	9		
3	B	7	Total	O	0	0
			7	7		
3	C	3	Total	O	0	0
			3	3		
3	D	9	Total	O	0	0
			9	9		
3	E	4	Total	O	0	0
			4	4		
3	F	1	Total	O	0	0
			1	1		

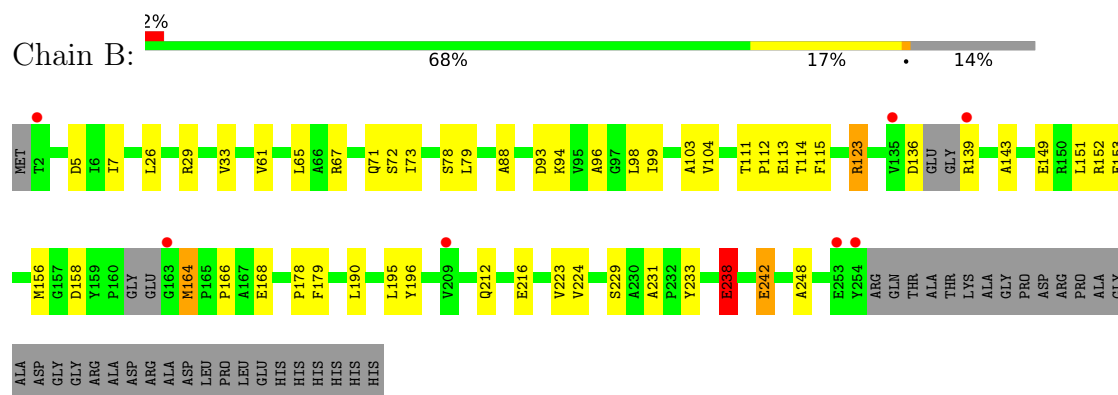
3 Residue-property plots [i](#)

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.

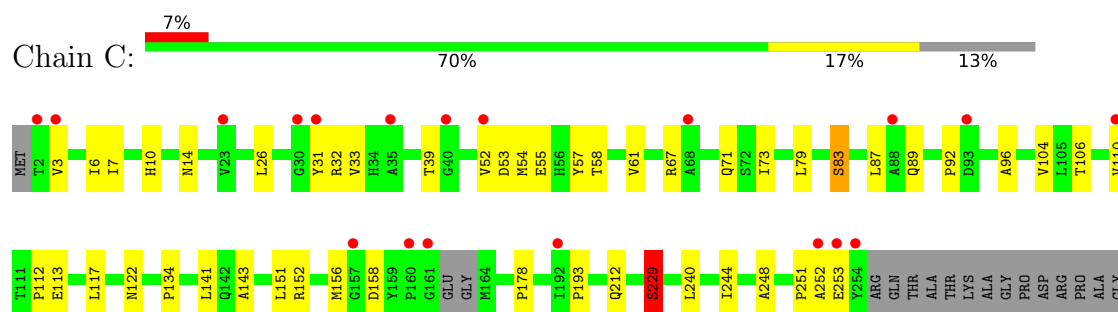
• Molecule 1: Pyrethroid hydrolase



• Molecule 1: Pyrethroid hydrolase

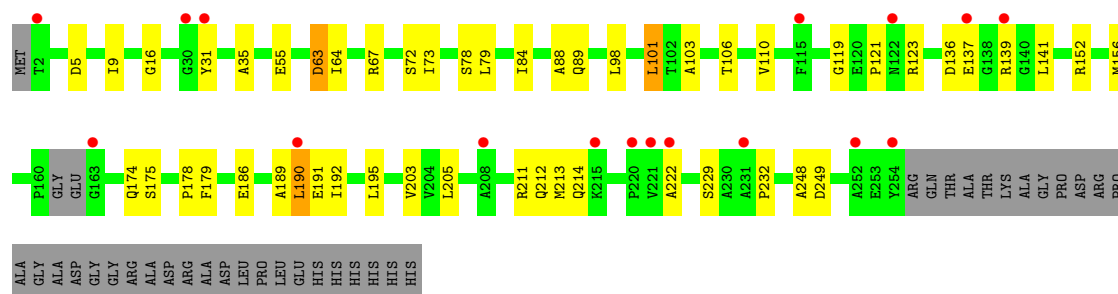


• Molecule 1: Pyrethroid hydrolase

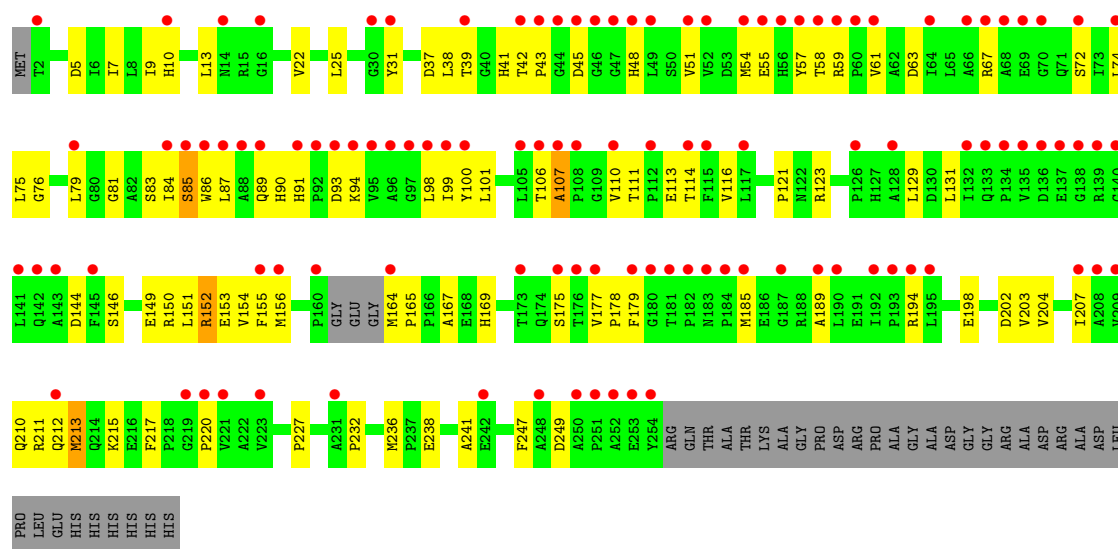


ALA
ASP
GLY
GLY
ARG
ALA
ASP
ARG
ALA
ASP
LEU
LEU
PRO
GLU
GLU
HIS
HIS
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• Molecule 1: Pyrethroid hydrolase

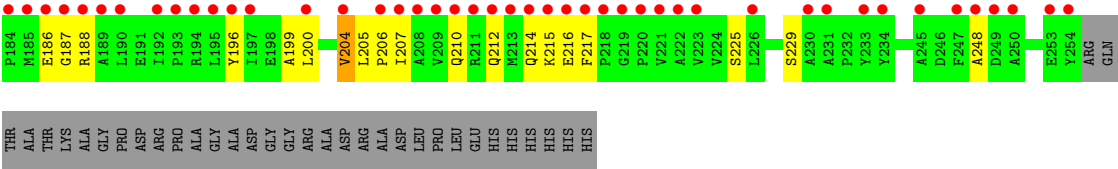


• Molecule 1: Pyrethroid hydrolase



• Molecule 1: Pyrethroid hydrolase





4 Data and refinement statistics

Property	Value	Source
Space group	P 4 ₂ 2 ₁ 2	Depositor
Cell constants a, b, c, α , β , γ	168.38Å 168.38Å 123.86Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.82 – 2.30 19.82 – 2.30	Depositor EDS
% Data completeness (in resolution range)	94.8 (19.82-2.30) 94.8 (19.82-2.30)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.04 (at 2.30Å)	Xtriage
Refinement program	PHENIX (dev_2247: ???)	Depositor
R, R_{free}	0.269 , 0.330 0.270 , 0.328	Depositor DCC
R_{free} test set	3788 reflections (4.78%)	wwPDB-VP
Wilson B-factor (Å ²)	34.5	Xtriage
Anisotropy	0.536	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 31.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	11414	wwPDB-VP
Average B, all atoms (Å ²)	41.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 11.12% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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 ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: SO4

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.60	1/1938 (0.1%)	0.70	3/2652 (0.1%)
1	B	0.63	1/1942 (0.1%)	0.66	0/2657
1	C	0.62	2/1950 (0.1%)	0.70	1/2670 (0.0%)
1	D	0.59	2/1950 (0.1%)	0.67	1/2670 (0.0%)
1	E	0.62	1/1936 (0.1%)	0.75	2/2652 (0.1%)
1	F	0.54	0/1938	0.88	11/2652 (0.4%)
All	All	0.60	7/11654 (0.1%)	0.73	18/15953 (0.1%)

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	107	ALA	C-N	6.68	1.40	1.33
1	C	83	SER	C-O	-5.95	1.17	1.24
1	D	64	ILE	C-O	-5.75	1.17	1.24
1	A	103	ALA	C-O	-5.42	1.16	1.23
1	C	229	SER	C-O	-5.27	1.18	1.24

The worst 5 of 18 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	235	SER	CA-C-N	-9.98	113.09	122.37
1	A	235	SER	C-N-CA	-9.98	113.09	122.37
1	F	133	GLN	CA-C-N	9.62	129.72	119.90
1	F	133	GLN	C-N-CA	9.62	129.72	119.90
1	F	133	GLN	N-CA-C	7.03	121.79	109.48

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	1888	0	1858	34	0
1	B	1892	0	1861	36	0
1	C	1899	0	1860	37	0
1	D	1899	0	1860	35	0
1	E	1885	0	1835	105	0
1	F	1888	0	1858	108	0
2	A	5	0	0	0	0
2	B	5	0	0	1	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	9	0	0	0	0
3	B	7	0	0	0	0
3	C	3	0	0	0	0
3	D	9	0	0	2	0
3	E	4	0	0	3	0
3	F	1	0	0	0	0
All	All	11414	0	11132	352	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 16.

The worst 5 of 352 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:194:ARG:NH1	1:E:217:PHE:CE1	2.13	1.16
1:C:54:MET:HE1	1:C:178:PRO:HA	1.15	1.15
1:E:9:ILE:HD11	1:E:38:LEU:HD11	1.18	1.15
1:F:54:MET:HB2	1:F:86:TRP:CH2	1.81	1.14
1:E:9:ILE:HD11	1:E:38:LEU:CD1	1.83	1.08

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	242/288 (84%)	234 (97%)	8 (3%)	0	100	100
1	B	243/288 (84%)	234 (96%)	9 (4%)	0	100	100
1	C	247/288 (86%)	234 (95%)	13 (5%)	0	100	100
1	D	247/288 (86%)	233 (94%)	14 (6%)	0	100	100
1	E	246/288 (85%)	226 (92%)	20 (8%)	0	100	100
1	F	242/288 (84%)	229 (95%)	13 (5%)	0	100	100
All	All	1467/1728 (85%)	1390 (95%)	77 (5%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	199/226 (88%)	198 (100%)	1 (0%)	81	90
1	B	199/226 (88%)	195 (98%)	4 (2%)	48	67
1	C	199/226 (88%)	198 (100%)	1 (0%)	81	90
1	D	199/226 (88%)	195 (98%)	4 (2%)	48	67
1	E	196/226 (87%)	193 (98%)	3 (2%)	57	75
1	F	199/226 (88%)	196 (98%)	3 (2%)	57	75
All	All	1191/1356 (88%)	1175 (99%)	16 (1%)	61	77

5 of 16 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	F	105	LEU
1	F	104	VAL
1	D	190	LEU
1	E	215	LYS
1	D	101	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 17 such sidechains are listed below:

Mol	Chain	Res	Type
1	F	10	HIS
1	F	212	GLN
1	D	90	HIS
1	D	91	HIS
1	D	172	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

6 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	D	301	-	4,4,4	0.22	0	6,6,6	0.47	0
2	SO4	E	301	-	4,4,4	0.32	0	6,6,6	0.31	0
2	SO4	B	301	-	4,4,4	0.38	0	6,6,6	0.26	0
2	SO4	A	301	-	4,4,4	0.23	0	6,6,6	0.25	0
2	SO4	C	301	-	4,4,4	0.21	0	6,6,6	0.06	0
2	SO4	F	301	-	4,4,4	0.20	0	6,6,6	0.36	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	B	301	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, 95th 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 ²)	Q<0.9
1	A	248/288 (86%)	0.54	9 (3%) 46 48	21, 30, 43, 58	0
1	B	249/288 (86%)	0.61	7 (2%) 55 57	20, 31, 45, 66	0
1	C	251/288 (87%)	0.94	19 (7%) 20 21	22, 36, 53, 74	0
1	D	251/288 (87%)	0.79	17 (6%) 23 25	19, 32, 50, 70	0
1	E	250/288 (86%)	1.92	112 (44%) 0 0	26, 49, 66, 89	0
1	F	248/288 (86%)	2.99	187 (75%) 0 0	38, 68, 86, 108	0
All	All	1497/1728 (86%)	1.30	351 (23%) 2 2	19, 37, 75, 108	0

The worst 5 of 351 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	189	ALA	7.6
1	F	86	TRP	6.9
1	F	54	MET	6.7
1	F	139	ARG	6.5
1	F	109	GLY	6.3

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, 95th 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 ²)	Q<0.9
2	SO4	D	301	5/5	0.82	0.13	41,43,47,53	0
2	SO4	F	301	5/5	0.85	0.15	30,39,51,56	0
2	SO4	E	301	5/5	0.92	0.09	39,42,46,47	0
2	SO4	A	301	5/5	0.93	0.08	38,41,43,46	0
2	SO4	C	301	5/5	0.94	0.10	31,34,38,42	0
2	SO4	B	301	5/5	0.95	0.08	31,36,42,42	0

6.5 Other polymers [i](#)

There are no such residues in this entry.