Full wwPDB X-ray Structure Validation Report (i)

Oct 31, 2024 – 12:29 PM JST

PDB ID	:	7XRT
Title	:	Bacteroides thetaiotaomicron ferulic acid esterase (BT_4077)
Authors	:	Du, G.M.; Wang, Y.L.; Xin, F.J.
Deposited on	:	2022-05-11
Resolution	:	2.01 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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 (i) 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 (1)) were used in the production of this report:

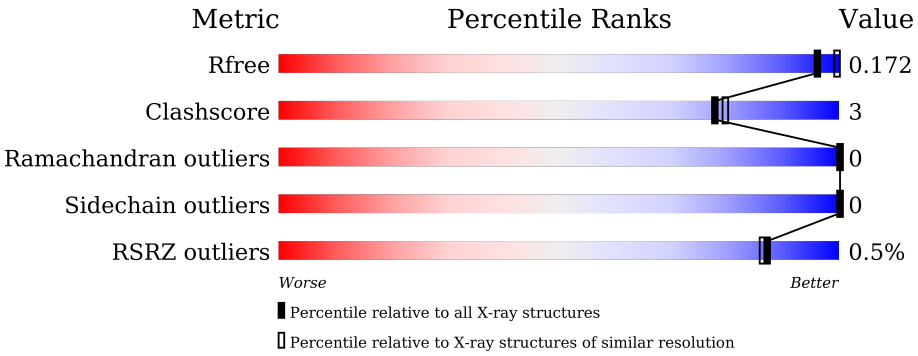
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	3.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.003 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.39

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.01 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}	164625	9409 (2.00-2.00)
Clashscore	180529	10737 (2.00-2.00)
Ramachandran outliers	177936	10628 (2.00-2.00)
Sidechain outliers	177891	10627 (2.00-2.00)
RSRZ outliers	164620	9409 (2.00-2.00)

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 <=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	291	89% · 8%
1	B	291	82% 10% 8%
1	C	291	87% 5% 8%
1	D	291	85% 7% 8%
1	E	291	86% 6% 8%
1	F	291	87% 5% 8%

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Mol	Chain	Length	Quality of chain
1	G	291	2% 84% 8% 8%
1	H	291	% 84% 8% 8%
1	I	291	85% 7% 8%
1	J	291	86% 6% 8%

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 23462 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 Ferulic acid esterase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	268	Total	C	N	O	S	0	0	0
			2153	1385	361	395	12			
1	B	268	Total	C	N	O	S	0	1	0
			2157	1388	361	396	12			
1	C	268	Total	C	N	O	S	0	0	0
			2157	1388	361	396	12			
1	D	268	Total	C	N	O	S	0	0	0
			2140	1377	358	393	12			
1	E	268	Total	C	N	O	S	0	0	0
			2153	1385	360	396	12			
1	F	268	Total	C	N	O	S	0	0	0
			2153	1385	360	396	12			
1	G	268	Total	C	N	O	S	0	0	0
			2144	1378	360	394	12			
1	H	268	Total	C	N	O	S	0	0	0
			2144	1378	360	394	12			
1	I	268	Total	C	N	O	S	0	0	0
			2149	1383	360	394	12			
1	J	268	Total	C	N	O	S	0	0	0
			2149	1383	360	394	12			

There are 230 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	MET	-	initiating methionine	UNP Q8A0E4
A	-1	GLY	-	expression tag	UNP Q8A0E4
A	0	SER	-	expression tag	UNP Q8A0E4
A	1	SER	-	expression tag	UNP Q8A0E4
A	2	HIS	-	expression tag	UNP Q8A0E4
A	3	HIS	-	expression tag	UNP Q8A0E4
A	4	HIS	-	expression tag	UNP Q8A0E4
A	5	HIS	-	expression tag	UNP Q8A0E4
A	6	HIS	-	expression tag	UNP Q8A0E4

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Chain	Residue	Modelled	Actual	Comment	Reference
A	7	HIS	-	expression tag	UNP Q8A0E4
A	8	SER	-	expression tag	UNP Q8A0E4
A	9	SER	-	expression tag	UNP Q8A0E4
A	10	GLY	-	expression tag	UNP Q8A0E4
A	11	LEU	-	expression tag	UNP Q8A0E4
A	12	VAL	-	expression tag	UNP Q8A0E4
A	13	PRO	-	expression tag	UNP Q8A0E4
A	14	ARG	-	expression tag	UNP Q8A0E4
A	15	GLY	-	expression tag	UNP Q8A0E4
A	16	SER	-	expression tag	UNP Q8A0E4
A	17	HIS	-	expression tag	UNP Q8A0E4
A	18	MET	-	expression tag	UNP Q8A0E4
A	19	LEU	-	expression tag	UNP Q8A0E4
A	20	GLU	-	expression tag	UNP Q8A0E4
B	-2	MET	-	initiating methionine	UNP Q8A0E4
B	-1	GLY	-	expression tag	UNP Q8A0E4
B	0	SER	-	expression tag	UNP Q8A0E4
B	1	SER	-	expression tag	UNP Q8A0E4
B	2	HIS	-	expression tag	UNP Q8A0E4
B	3	HIS	-	expression tag	UNP Q8A0E4
B	4	HIS	-	expression tag	UNP Q8A0E4
B	5	HIS	-	expression tag	UNP Q8A0E4
B	6	HIS	-	expression tag	UNP Q8A0E4
B	7	HIS	-	expression tag	UNP Q8A0E4
B	8	SER	-	expression tag	UNP Q8A0E4
B	9	SER	-	expression tag	UNP Q8A0E4
B	10	GLY	-	expression tag	UNP Q8A0E4
B	11	LEU	-	expression tag	UNP Q8A0E4
B	12	VAL	-	expression tag	UNP Q8A0E4
B	13	PRO	-	expression tag	UNP Q8A0E4
B	14	ARG	-	expression tag	UNP Q8A0E4
B	15	GLY	-	expression tag	UNP Q8A0E4
B	16	SER	-	expression tag	UNP Q8A0E4
B	17	HIS	-	expression tag	UNP Q8A0E4
B	18	MET	-	expression tag	UNP Q8A0E4
B	19	LEU	-	expression tag	UNP Q8A0E4
B	20	GLU	-	expression tag	UNP Q8A0E4
C	-2	MET	-	initiating methionine	UNP Q8A0E4
C	-1	GLY	-	expression tag	UNP Q8A0E4
C	0	SER	-	expression tag	UNP Q8A0E4
C	1	SER	-	expression tag	UNP Q8A0E4
C	2	HIS	-	expression tag	UNP Q8A0E4

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Chain	Residue	Modelled	Actual	Comment	Reference
C	3	HIS	-	expression tag	UNP Q8A0E4
C	4	HIS	-	expression tag	UNP Q8A0E4
C	5	HIS	-	expression tag	UNP Q8A0E4
C	6	HIS	-	expression tag	UNP Q8A0E4
C	7	HIS	-	expression tag	UNP Q8A0E4
C	8	SER	-	expression tag	UNP Q8A0E4
C	9	SER	-	expression tag	UNP Q8A0E4
C	10	GLY	-	expression tag	UNP Q8A0E4
C	11	LEU	-	expression tag	UNP Q8A0E4
C	12	VAL	-	expression tag	UNP Q8A0E4
C	13	PRO	-	expression tag	UNP Q8A0E4
C	14	ARG	-	expression tag	UNP Q8A0E4
C	15	GLY	-	expression tag	UNP Q8A0E4
C	16	SER	-	expression tag	UNP Q8A0E4
C	17	HIS	-	expression tag	UNP Q8A0E4
C	18	MET	-	expression tag	UNP Q8A0E4
C	19	LEU	-	expression tag	UNP Q8A0E4
C	20	GLU	-	expression tag	UNP Q8A0E4
D	-2	MET	-	initiating methionine	UNP Q8A0E4
D	-1	GLY	-	expression tag	UNP Q8A0E4
D	0	SER	-	expression tag	UNP Q8A0E4
D	1	SER	-	expression tag	UNP Q8A0E4
D	2	HIS	-	expression tag	UNP Q8A0E4
D	3	HIS	-	expression tag	UNP Q8A0E4
D	4	HIS	-	expression tag	UNP Q8A0E4
D	5	HIS	-	expression tag	UNP Q8A0E4
D	6	HIS	-	expression tag	UNP Q8A0E4
D	7	HIS	-	expression tag	UNP Q8A0E4
D	8	SER	-	expression tag	UNP Q8A0E4
D	9	SER	-	expression tag	UNP Q8A0E4
D	10	GLY	-	expression tag	UNP Q8A0E4
D	11	LEU	-	expression tag	UNP Q8A0E4
D	12	VAL	-	expression tag	UNP Q8A0E4
D	13	PRO	-	expression tag	UNP Q8A0E4
D	14	ARG	-	expression tag	UNP Q8A0E4
D	15	GLY	-	expression tag	UNP Q8A0E4
D	16	SER	-	expression tag	UNP Q8A0E4
D	17	HIS	-	expression tag	UNP Q8A0E4
D	18	MET	-	expression tag	UNP Q8A0E4
D	19	LEU	-	expression tag	UNP Q8A0E4
D	20	GLU	-	expression tag	UNP Q8A0E4
E	-2	MET	-	initiating methionine	UNP Q8A0E4

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Chain	Residue	Modelled	Actual	Comment	Reference
E	-1	GLY	-	expression tag	UNP Q8A0E4
E	0	SER	-	expression tag	UNP Q8A0E4
E	1	SER	-	expression tag	UNP Q8A0E4
E	2	HIS	-	expression tag	UNP Q8A0E4
E	3	HIS	-	expression tag	UNP Q8A0E4
E	4	HIS	-	expression tag	UNP Q8A0E4
E	5	HIS	-	expression tag	UNP Q8A0E4
E	6	HIS	-	expression tag	UNP Q8A0E4
E	7	HIS	-	expression tag	UNP Q8A0E4
E	8	SER	-	expression tag	UNP Q8A0E4
E	9	SER	-	expression tag	UNP Q8A0E4
E	10	GLY	-	expression tag	UNP Q8A0E4
E	11	LEU	-	expression tag	UNP Q8A0E4
E	12	VAL	-	expression tag	UNP Q8A0E4
E	13	PRO	-	expression tag	UNP Q8A0E4
E	14	ARG	-	expression tag	UNP Q8A0E4
E	15	GLY	-	expression tag	UNP Q8A0E4
E	16	SER	-	expression tag	UNP Q8A0E4
E	17	HIS	-	expression tag	UNP Q8A0E4
E	18	MET	-	expression tag	UNP Q8A0E4
E	19	LEU	-	expression tag	UNP Q8A0E4
E	20	GLU	-	expression tag	UNP Q8A0E4
F	-2	MET	-	initiating methionine	UNP Q8A0E4
F	-1	GLY	-	expression tag	UNP Q8A0E4
F	0	SER	-	expression tag	UNP Q8A0E4
F	1	SER	-	expression tag	UNP Q8A0E4
F	2	HIS	-	expression tag	UNP Q8A0E4
F	3	HIS	-	expression tag	UNP Q8A0E4
F	4	HIS	-	expression tag	UNP Q8A0E4
F	5	HIS	-	expression tag	UNP Q8A0E4
F	6	HIS	-	expression tag	UNP Q8A0E4
F	7	HIS	-	expression tag	UNP Q8A0E4
F	8	SER	-	expression tag	UNP Q8A0E4
F	9	SER	-	expression tag	UNP Q8A0E4
F	10	GLY	-	expression tag	UNP Q8A0E4
F	11	LEU	-	expression tag	UNP Q8A0E4
F	12	VAL	-	expression tag	UNP Q8A0E4
F	13	PRO	-	expression tag	UNP Q8A0E4
F	14	ARG	-	expression tag	UNP Q8A0E4
F	15	GLY	-	expression tag	UNP Q8A0E4
F	16	SER	-	expression tag	UNP Q8A0E4
F	17	HIS	-	expression tag	UNP Q8A0E4

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Chain	Residue	Modelled	Actual	Comment	Reference
F	18	MET	-	expression tag	UNP Q8A0E4
F	19	LEU	-	expression tag	UNP Q8A0E4
F	20	GLU	-	expression tag	UNP Q8A0E4
G	-2	MET	-	initiating methionine	UNP Q8A0E4
G	-1	GLY	-	expression tag	UNP Q8A0E4
G	0	SER	-	expression tag	UNP Q8A0E4
G	1	SER	-	expression tag	UNP Q8A0E4
G	2	HIS	-	expression tag	UNP Q8A0E4
G	3	HIS	-	expression tag	UNP Q8A0E4
G	4	HIS	-	expression tag	UNP Q8A0E4
G	5	HIS	-	expression tag	UNP Q8A0E4
G	6	HIS	-	expression tag	UNP Q8A0E4
G	7	HIS	-	expression tag	UNP Q8A0E4
G	8	SER	-	expression tag	UNP Q8A0E4
G	9	SER	-	expression tag	UNP Q8A0E4
G	10	GLY	-	expression tag	UNP Q8A0E4
G	11	LEU	-	expression tag	UNP Q8A0E4
G	12	VAL	-	expression tag	UNP Q8A0E4
G	13	PRO	-	expression tag	UNP Q8A0E4
G	14	ARG	-	expression tag	UNP Q8A0E4
G	15	GLY	-	expression tag	UNP Q8A0E4
G	16	SER	-	expression tag	UNP Q8A0E4
G	17	HIS	-	expression tag	UNP Q8A0E4
G	18	MET	-	expression tag	UNP Q8A0E4
G	19	LEU	-	expression tag	UNP Q8A0E4
G	20	GLU	-	expression tag	UNP Q8A0E4
H	-2	MET	-	initiating methionine	UNP Q8A0E4
H	-1	GLY	-	expression tag	UNP Q8A0E4
H	0	SER	-	expression tag	UNP Q8A0E4
H	1	SER	-	expression tag	UNP Q8A0E4
H	2	HIS	-	expression tag	UNP Q8A0E4
H	3	HIS	-	expression tag	UNP Q8A0E4
H	4	HIS	-	expression tag	UNP Q8A0E4
H	5	HIS	-	expression tag	UNP Q8A0E4
H	6	HIS	-	expression tag	UNP Q8A0E4
H	7	HIS	-	expression tag	UNP Q8A0E4
H	8	SER	-	expression tag	UNP Q8A0E4
H	9	SER	-	expression tag	UNP Q8A0E4
H	10	GLY	-	expression tag	UNP Q8A0E4
H	11	LEU	-	expression tag	UNP Q8A0E4
H	12	VAL	-	expression tag	UNP Q8A0E4
H	13	PRO	-	expression tag	UNP Q8A0E4

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Chain	Residue	Modelled	Actual	Comment	Reference
H	14	ARG	-	expression tag	UNP Q8A0E4
H	15	GLY	-	expression tag	UNP Q8A0E4
H	16	SER	-	expression tag	UNP Q8A0E4
H	17	HIS	-	expression tag	UNP Q8A0E4
H	18	MET	-	expression tag	UNP Q8A0E4
H	19	LEU	-	expression tag	UNP Q8A0E4
H	20	GLU	-	expression tag	UNP Q8A0E4
I	-2	MET	-	initiating methionine	UNP Q8A0E4
I	-1	GLY	-	expression tag	UNP Q8A0E4
I	0	SER	-	expression tag	UNP Q8A0E4
I	1	SER	-	expression tag	UNP Q8A0E4
I	2	HIS	-	expression tag	UNP Q8A0E4
I	3	HIS	-	expression tag	UNP Q8A0E4
I	4	HIS	-	expression tag	UNP Q8A0E4
I	5	HIS	-	expression tag	UNP Q8A0E4
I	6	HIS	-	expression tag	UNP Q8A0E4
I	7	HIS	-	expression tag	UNP Q8A0E4
I	8	SER	-	expression tag	UNP Q8A0E4
I	9	SER	-	expression tag	UNP Q8A0E4
I	10	GLY	-	expression tag	UNP Q8A0E4
I	11	LEU	-	expression tag	UNP Q8A0E4
I	12	VAL	-	expression tag	UNP Q8A0E4
I	13	PRO	-	expression tag	UNP Q8A0E4
I	14	ARG	-	expression tag	UNP Q8A0E4
I	15	GLY	-	expression tag	UNP Q8A0E4
I	16	SER	-	expression tag	UNP Q8A0E4
I	17	HIS	-	expression tag	UNP Q8A0E4
I	18	MET	-	expression tag	UNP Q8A0E4
I	19	LEU	-	expression tag	UNP Q8A0E4
I	20	GLU	-	expression tag	UNP Q8A0E4
J	-2	MET	-	initiating methionine	UNP Q8A0E4
J	-1	GLY	-	expression tag	UNP Q8A0E4
J	0	SER	-	expression tag	UNP Q8A0E4
J	1	SER	-	expression tag	UNP Q8A0E4
J	2	HIS	-	expression tag	UNP Q8A0E4
J	3	HIS	-	expression tag	UNP Q8A0E4
J	4	HIS	-	expression tag	UNP Q8A0E4
J	5	HIS	-	expression tag	UNP Q8A0E4
J	6	HIS	-	expression tag	UNP Q8A0E4
J	7	HIS	-	expression tag	UNP Q8A0E4
J	8	SER	-	expression tag	UNP Q8A0E4
J	9	SER	-	expression tag	UNP Q8A0E4

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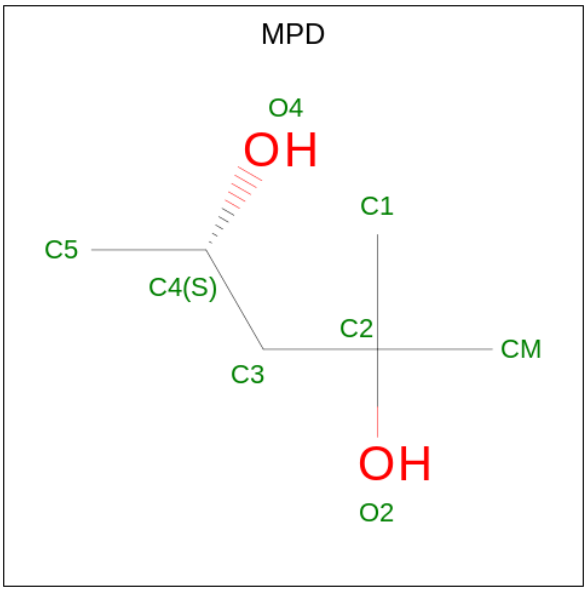
Chain	Residue	Modelled	Actual	Comment	Reference
J	10	GLY	-	expression tag	UNP Q8A0E4
J	11	LEU	-	expression tag	UNP Q8A0E4
J	12	VAL	-	expression tag	UNP Q8A0E4
J	13	PRO	-	expression tag	UNP Q8A0E4
J	14	ARG	-	expression tag	UNP Q8A0E4
J	15	GLY	-	expression tag	UNP Q8A0E4
J	16	SER	-	expression tag	UNP Q8A0E4
J	17	HIS	-	expression tag	UNP Q8A0E4
J	18	MET	-	expression tag	UNP Q8A0E4
J	19	LEU	-	expression tag	UNP Q8A0E4
J	20	GLU	-	expression tag	UNP Q8A0E4

- Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Ca 1 1	0	0
2	B	1	Total Ca 1 1	0	0
2	C	1	Total Ca 1 1	0	0
2	D	1	Total Ca 1 1	0	0
2	E	1	Total Ca 1 1	0	0
2	F	1	Total Ca 1 1	0	0
2	G	1	Total Ca 1 1	0	0
2	H	1	Total Ca 1 1	0	0
2	I	1	Total Ca 1 1	0	0
2	J	1	Total Ca 1 1	0	0

- Molecule 3 is (4S)-2-METHYL-2,4-PENTANEDIOL (three-letter code: MPD) (formula: $C_6H_{14}O_2$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C O 8 6 2	0	0
3	D	1	Total C O 8 6 2	0	0
3	E	1	Total C O 8 6 2	0	0
3	F	1	Total C O 8 6 2	0	0
3	G	1	Total C O 8 6 2	0	0
3	G	1	Total C O 8 6 2	0	0
3	H	1	Total C O 8 6 2	0	0
3	I	1	Total C O 8 6 2	0	0
3	J	1	Total C O 8 6 2	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	212	Total O 212 212	0	0
4	B	212	Total O 212 212	0	0
4	C	238	Total O 238 238	0	0

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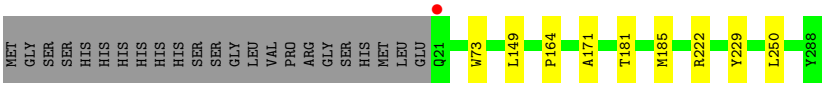
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	D	135	Total O 135 135	0	0
4	E	212	Total O 212 212	0	0
4	F	203	Total O 203 203	0	0
4	G	148	Total O 148 148	0	0
4	H	147	Total O 147 147	0	0
4	I	200	Total O 200 200	0	0
4	J	174	Total O 174 174	0	0

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.

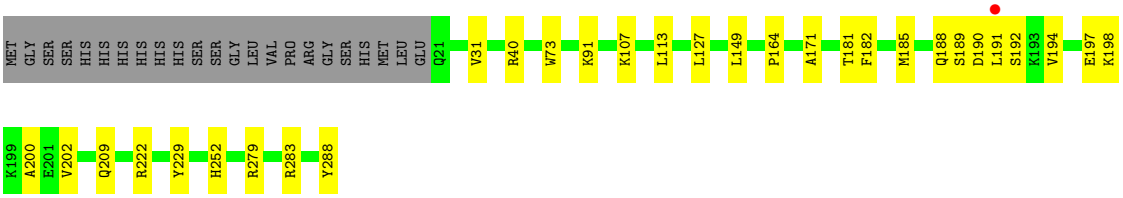
• Molecule 1: Ferulic acid esterase

Chain A:



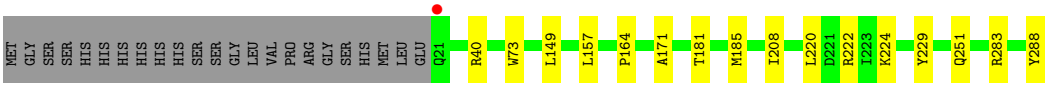
• Molecule 1: Ferulic acid esterase

Chain B:



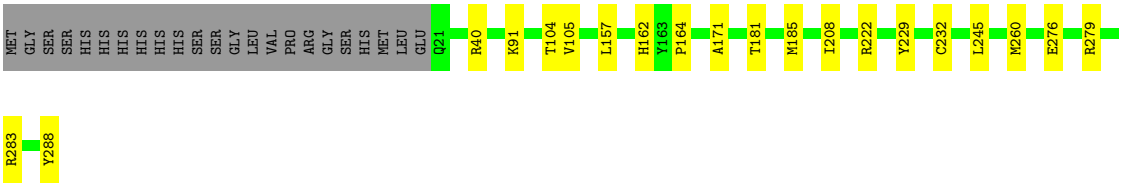
• Molecule 1: Ferulic acid esterase

Chain C:



• Molecule 1: Ferulic acid esterase

Chain D:

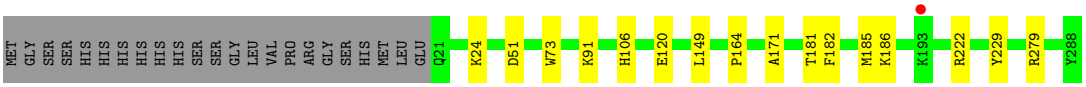


• Molecule 1: Ferulic acid esterase

Chain E:

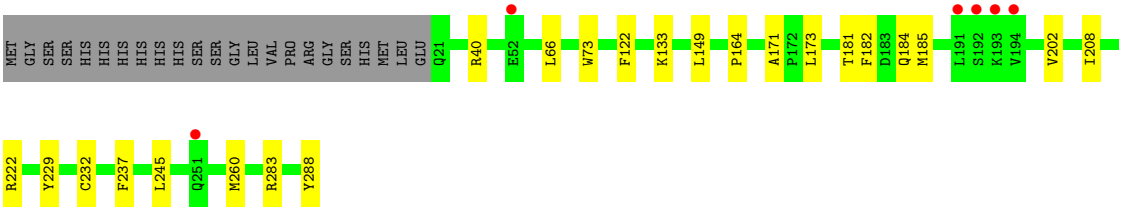
• Molecule 1: Ferulic acid esterase

Chain F:



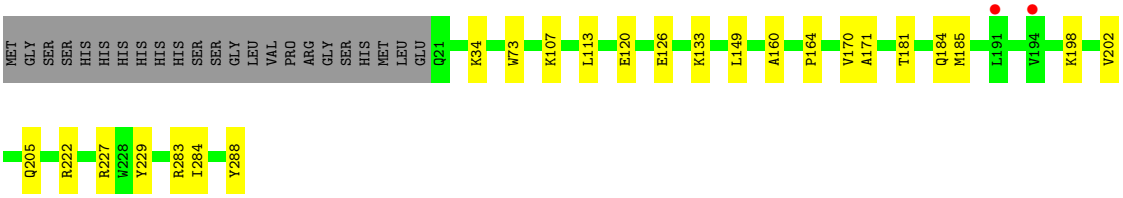
• Molecule 1: Ferulic acid esterase

Chain G:



• Molecule 1: Ferulic acid esterase

Chain H:



• Molecule 1: Ferulic acid esterase

Chain I:

• Molecule 1: Ferulic acid esterase

Chain J:

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	113.39Å 160.16Å 192.06Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.35 – 2.01 29.35 – 2.01	Depositor EDS
% Data completeness (in resolution range)	98.6 (29.35-2.01) 98.6 (29.35-2.01)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	4.59 (at 2.01Å)	Xtriage
Refinement program	PHENIX 1.15.2_3472	Depositor
R, R_{free}	0.152 , 0.172 0.152 , 0.172	Depositor DCC
R_{free} test set	11491 reflections (4.92%)	wwPDB-VP
Wilson B-factor (Å^2)	29.8	Xtriage
Anisotropy	0.519	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.33 , 50.7	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.97	EDS
Total number of atoms	23462	wwPDB-VP
Average B, all atoms (Å^2)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.44% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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: MPD, CA

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	0.41	0/2211	0.56	0/2991
1	B	0.43	0/2218	0.59	0/3001
1	C	0.40	0/2215	0.54	0/2995
1	D	0.34	0/2198	0.51	0/2977
1	E	0.41	0/2211	0.56	0/2991
1	F	0.38	0/2211	0.55	0/2991
1	G	0.34	0/2202	0.51	0/2979
1	H	0.36	0/2202	0.54	0/2979
1	I	0.38	0/2207	0.53	0/2986
1	J	0.36	0/2207	0.53	0/2986
All	All	0.38	0/22082	0.54	0/29876

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

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	2153	0	2080	5	0
1	B	2157	0	2087	19	0
1	C	2157	0	2089	9	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D	2140	0	2049	12	0
1	E	2153	0	2078	10	0
1	F	2153	0	2078	10	0
1	G	2144	0	2058	15	0
1	H	2144	0	2058	13	0
1	I	2149	0	2074	10	0
1	J	2149	0	2074	11	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
2	E	1	0	0	0	0
2	F	1	0	0	0	0
2	G	1	0	0	0	0
2	H	1	0	0	0	0
2	I	1	0	0	0	0
2	J	1	0	0	0	0
3	A	8	0	14	1	0
3	D	8	0	14	1	0
3	E	8	0	14	0	0
3	F	8	0	14	1	0
3	G	16	0	28	0	0
3	H	8	0	14	1	0
3	I	8	0	14	1	0
3	J	8	0	14	1	0
4	A	212	0	0	1	0
4	B	212	0	0	2	0
4	C	238	0	0	2	0
4	D	135	0	0	1	0
4	E	212	0	0	1	0
4	F	203	0	0	2	0
4	G	148	0	0	2	0
4	H	147	0	0	1	0
4	I	200	0	0	0	0
4	J	174	0	0	2	0
All	All	23462	0	20851	116	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 (116) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:113:LEU:HD11	1:B:202:VAL:HG21	1.55	0.89
1:H:133:LYS:NZ	4:H:401:HOH:O	2.20	0.75
1:D:157:LEU:HD21	1:D:208:ILE:HD11	1.71	0.73
1:C:40:ARG:HB3	4:C:444:HOH:O	1.91	0.71
1:C:157:LEU:HD21	1:C:208:ILE:HD11	1.72	0.70
1:F:91:LYS:HE2	1:F:279:ARG:HH21	1.57	0.69
1:J:107:LYS:O	1:J:188:GLN:NE2	2.27	0.67
1:B:91:LYS:HE3	1:B:279:ARG:HH21	1.62	0.64
1:C:251:GLN:NE2	4:C:405:HOH:O	2.33	0.60
1:F:120:GLU:OE1	3:F:302:MPD:H13	2.02	0.60
1:D:91:LYS:NZ	4:D:405:HOH:O	2.33	0.59
1:D:276:GLU:OE1	1:D:279:ARG:NH2	2.35	0.59
1:H:164:PRO:HB2	1:H:222:ARG:HG3	1.84	0.59
1:G:237:PHE:HD1	4:G:508:HOH:O	1.85	0.59
1:J:120:GLU:OE1	3:J:302:MPD:H12	2.04	0.58
1:J:251:GLN:NE2	4:J:401:HOH:O	2.23	0.57
1:G:182:PHE:CE1	1:G:202:VAL:HG12	2.40	0.56
1:F:181:THR:O	1:F:185:MET:HG3	2.04	0.56
1:J:283:ARG:HD2	4:J:489:HOH:O	2.04	0.56
1:F:24:LYS:NZ	1:F:51:ASP:OD2	2.34	0.56
1:H:120:GLU:OE1	3:H:302:MPD:H13	2.06	0.56
1:D:181:THR:O	1:D:185:MET:HG3	2.06	0.55
1:C:181:THR:O	1:C:185:MET:HG3	2.05	0.55
1:J:164:PRO:HB2	1:J:222:ARG:HG3	1.89	0.55
1:A:181:THR:O	1:A:185:MET:HG3	2.07	0.54
1:C:283:ARG:HG2	1:C:288:TYR:CD1	2.42	0.54
1:B:283:ARG:HG2	1:B:288:TYR:CD1	2.42	0.54
1:E:283:ARG:HG2	1:E:288:TYR:CD1	2.43	0.54
1:E:181:THR:O	1:E:185:MET:HG3	2.09	0.53
1:H:283:ARG:HG2	1:H:288:TYR:CD1	2.44	0.53
1:B:113:LEU:HD11	1:B:202:VAL:CG2	2.34	0.52
1:B:107:LYS:O	1:B:188:GLN:NE2	2.35	0.52
1:B:209:GLN:OE1	1:B:252:HIS:NE2	2.41	0.52
1:J:182:PHE:CE2	1:J:186:LYS:HD2	2.44	0.52
1:J:219:LYS:HZ3	1:J:223:ILE:HD11	1.74	0.52
1:J:283:ARG:HG2	1:J:288:TYR:CD1	2.45	0.52
1:I:31:VAL:HG22	1:I:130:HIS:CD2	2.45	0.51
1:J:181:THR:O	1:J:185:MET:HG3	2.10	0.51
1:E:182:PHE:CE2	1:E:186:LYS:HD2	2.46	0.51
1:F:73:TRP:CZ2	1:F:149:LEU:HD23	2.46	0.51
1:J:73:TRP:CZ2	1:J:149:LEU:HD23	2.46	0.50
1:D:164:PRO:HB2	1:D:222:ARG:HG3	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:209:GLN:OE1	1:I:252:HIS:NE2	2.41	0.50
1:B:31:VAL:HG21	1:B:127:LEU:HD23	1.92	0.50
1:F:164:PRO:HB2	1:F:222:ARG:HG3	1.93	0.50
1:H:113:LEU:O	1:H:198:LYS:HE2	2.11	0.49
1:F:106:HIS:HE1	4:F:501:HOH:O	1.95	0.49
1:B:190:ASP:OD1	1:B:192:SER:OG	2.30	0.49
1:D:283:ARG:HG2	1:D:288:TYR:CD1	2.48	0.49
1:H:181:THR:O	1:H:185:MET:HG3	2.13	0.49
1:E:91:LYS:NZ	4:E:403:HOH:O	2.35	0.48
1:H:107:LYS:O	1:H:184:GLN:NE2	2.46	0.48
1:I:182:PHE:CE2	1:I:186:LYS:HD2	2.49	0.48
1:B:181:THR:O	1:B:185:MET:HG3	2.13	0.47
1:G:283:ARG:HG2	1:G:288:TYR:CD1	2.50	0.47
1:D:208:ILE:HD13	1:D:245:LEU:HD13	1.96	0.47
1:C:164:PRO:HB2	1:C:222:ARG:HG3	1.97	0.47
1:B:182:PHE:CE1	1:B:202:VAL:HG23	2.50	0.47
1:G:73:TRP:CZ2	1:G:149:LEU:HD23	2.50	0.46
1:G:181:THR:O	1:G:185:MET:HG3	2.15	0.46
1:F:171:ALA:HA	1:F:229:TYR:O	2.15	0.46
1:I:283:ARG:HG2	1:I:288:TYR:CD1	2.51	0.46
1:D:104:THR:HG22	1:D:105:VAL:HG23	1.98	0.46
1:G:164:PRO:HB2	1:G:222:ARG:HG3	1.97	0.46
1:E:247:ASN:O	1:E:251:GLN:HG3	2.16	0.46
1:E:73:TRP:CZ2	1:E:149:LEU:HD23	2.52	0.45
1:G:40:ARG:HG2	1:G:122:PHE:CZ	2.51	0.45
1:D:162:HIS:CD2	3:D:302:MPD:H53	2.52	0.45
1:G:208:ILE:HD13	1:G:245:LEU:HD13	1.97	0.45
1:B:190:ASP:O	1:B:194:VAL:HG23	2.16	0.45
1:E:164:PRO:HB2	1:E:222:ARG:HG3	1.98	0.45
1:B:40:ARG:HB3	4:B:443:HOH:O	2.16	0.44
1:F:182:PHE:CE2	1:F:186:LYS:HD2	2.52	0.44
1:B:73:TRP:CZ2	1:B:149:LEU:HD23	2.51	0.44
1:G:182:PHE:HE1	1:G:202:VAL:CG1	2.30	0.44
1:H:73:TRP:CZ2	1:H:149:LEU:HD23	2.52	0.44
1:A:250:LEU:O	4:A:401:HOH:O	2.21	0.44
1:B:164:PRO:HB2	1:B:222:ARG:HG3	1.98	0.44
1:G:133:LYS:HD2	4:G:425:HOH:O	2.17	0.44
1:I:181:THR:O	1:I:185:MET:HG3	2.18	0.44
1:B:197:GLU:O	1:B:200:ALA:N	2.51	0.44
1:C:73:TRP:CZ2	1:C:149:LEU:HD23	2.53	0.44
1:C:171:ALA:HA	1:C:229:TYR:O	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:189:SER:O	1:B:191:LEU:HD22	2.17	0.43
1:G:66:LEU:HD13	1:G:184:GLN:HE22	1.84	0.43
1:I:73:TRP:CZ2	1:I:149:LEU:HD23	2.52	0.43
1:I:171:ALA:HA	1:I:229:TYR:O	2.19	0.43
1:B:113:LEU:HD13	1:B:198:LYS:HE3	1.99	0.43
1:E:208:ILE:HD13	1:E:245:LEU:HD13	2.01	0.43
1:A:73:TRP:CZ2	1:A:149:LEU:HD23	2.54	0.43
3:A:302:MPD:H11	3:A:302:MPD:H4	1.78	0.42
1:E:157:LEU:HD21	1:E:208:ILE:HD11	2.01	0.42
1:G:182:PHE:CE1	1:G:202:VAL:CG1	3.03	0.42
1:B:91:LYS:NZ	4:B:405:HOH:O	2.48	0.42
1:G:171:ALA:HA	1:G:229:TYR:O	2.20	0.42
1:I:164:PRO:HB2	1:I:222:ARG:HG3	2.01	0.42
1:B:171:ALA:HA	1:B:229:TYR:O	2.18	0.42
1:H:160:ALA:CB	1:H:170:VAL:HG21	2.49	0.42
1:H:171:ALA:HA	1:H:229:TYR:O	2.19	0.42
1:I:180:TRP:CZ3	1:I:184:GLN:OE1	2.72	0.42
1:H:34:LYS:N	1:H:126:GLU:OE2	2.52	0.42
1:J:171:ALA:HA	1:J:229:TYR:O	2.19	0.42
1:F:106:HIS:CE1	4:F:501:HOH:O	2.72	0.42
1:I:161:LEU:HD11	1:I:208:ILE:HD12	2.02	0.42
1:C:220:LEU:HG	1:C:224:LYS:HE3	2.03	0.41
1:D:171:ALA:HA	1:D:229:TYR:O	2.20	0.41
1:G:149:LEU:HA	1:G:173:LEU:O	2.21	0.41
1:A:171:ALA:HA	1:A:229:TYR:O	2.20	0.41
1:G:232:CYS:O	1:G:260:MET:HA	2.20	0.41
1:D:40:ARG:HD2	1:D:40:ARG:HA	1.92	0.41
1:H:227:ARG:HG3	1:H:284:ILE:HD12	2.02	0.41
1:A:164:PRO:HB2	1:A:222:ARG:HG3	2.01	0.41
1:H:202:VAL:O	1:H:205:GLN:N	2.53	0.41
1:D:232:CYS:O	1:D:260:MET:HA	2.21	0.41
1:E:209:GLN:O	1:E:213:GLU:HG3	2.20	0.41
3:I:302:MPD:HM3	3:I:302:MPD:H4	1.93	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	266/291 (91%)	259 (97%)	7 (3%)	0	100	100
1	B	267/291 (92%)	260 (97%)	7 (3%)	0	100	100
1	C	266/291 (91%)	260 (98%)	6 (2%)	0	100	100
1	D	266/291 (91%)	259 (97%)	7 (3%)	0	100	100
1	E	266/291 (91%)	260 (98%)	6 (2%)	0	100	100
1	F	266/291 (91%)	259 (97%)	7 (3%)	0	100	100
1	G	266/291 (91%)	259 (97%)	7 (3%)	0	100	100
1	H	266/291 (91%)	259 (97%)	7 (3%)	0	100	100
1	I	266/291 (91%)	260 (98%)	6 (2%)	0	100	100
1	J	266/291 (91%)	259 (97%)	7 (3%)	0	100	100
All	All	2661/2910 (91%)	2594 (98%)	67 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	226/250 (90%)	226 (100%)	0	100	100
1	B	227/250 (91%)	227 (100%)	0	100	100
1	C	227/250 (91%)	227 (100%)	0	100	100
1	D	222/250 (89%)	222 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	E	226/250 (90%)	226 (100%)	0	100	100
1	F	226/250 (90%)	226 (100%)	0	100	100
1	G	223/250 (89%)	223 (100%)	0	100	100
1	H	223/250 (89%)	223 (100%)	0	100	100
1	I	225/250 (90%)	225 (100%)	0	100	100
1	J	225/250 (90%)	225 (100%)	0	100	100
All	All	2250/2500 (90%)	2250 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA (i)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains (i)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 19 ligands modelled in this entry, 10 are monoatomic - leaving 9 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	$\#\|Z\|>2$
3	MPD	E	302	-	7,7,7	0.33	0	9,10,10	0.48	0
3	MPD	J	302	-	7,7,7	0.32	0	9,10,10	0.64	0
3	MPD	F	302	-	7,7,7	0.40	0	9,10,10	0.60	0
3	MPD	I	302	-	7,7,7	0.28	0	9,10,10	0.32	0
3	MPD	A	302	-	7,7,7	0.26	0	9,10,10	0.31	0
3	MPD	G	302	-	7,7,7	0.24	0	9,10,10	0.30	0
3	MPD	D	302	-	7,7,7	0.29	0	9,10,10	0.24	0
3	MPD	G	303	-	7,7,7	0.34	0	9,10,10	0.79	0
3	MPD	H	302	-	7,7,7	0.34	0	9,10,10	0.58	0

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
3	MPD	E	302	-	-	0/5/5/5	-
3	MPD	J	302	-	-	2/5/5/5	-
3	MPD	F	302	-	-	1/5/5/5	-
3	MPD	I	302	-	-	1/5/5/5	-
3	MPD	A	302	-	-	1/5/5/5	-
3	MPD	G	302	-	-	5/5/5/5	-
3	MPD	D	302	-	-	2/5/5/5	-
3	MPD	G	303	-	-	1/5/5/5	-
3	MPD	H	302	-	-	1/5/5/5	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (14) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	G	302	MPD	C1-C2-C3-C4
3	G	302	MPD	O2-C2-C3-C4
3	I	302	MPD	C2-C3-C4-C5
3	G	302	MPD	C2-C3-C4-C5
3	G	303	MPD	C2-C3-C4-C5
3	G	302	MPD	C2-C3-C4-O4
3	G	302	MPD	CM-C2-C3-C4
3	J	302	MPD	O2-C2-C3-C4

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Mol	Chain	Res	Type	Atoms
3	A	302	MPD	C2-C3-C4-C5
3	D	302	MPD	C2-C3-C4-C5
3	F	302	MPD	C2-C3-C4-C5
3	H	302	MPD	C2-C3-C4-C5
3	J	302	MPD	C2-C3-C4-C5
3	D	302	MPD	C2-C3-C4-O4

There are no ring outliers.

6 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	J	302	MPD	1	0
3	F	302	MPD	1	0
3	I	302	MPD	1	0
3	A	302	MPD	1	0
3	D	302	MPD	1	0
3	H	302	MPD	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

6.1 Protein, DNA and RNA chains

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^{th} 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	268/291 (92%)	-0.69	1 (0%) 89 88	23, 31, 59, 105	0
1	B	268/291 (92%)	-0.59	1 (0%) 89 88	19, 30, 71, 97	1 (0%)
1	C	268/291 (92%)	-0.71	1 (0%) 89 88	21, 31, 55, 95	0
1	D	268/291 (92%)	-0.38	0 100 100	26, 43, 83, 125	0
1	E	268/291 (92%)	-0.66	0 100 100	21, 31, 65, 100	0
1	F	268/291 (92%)	-0.60	1 (0%) 89 88	23, 32, 68, 96	0
1	G	268/291 (92%)	-0.40	6 (2%) 62 60	26, 40, 82, 129	0
1	H	268/291 (92%)	-0.44	2 (0%) 84 83	27, 41, 76, 110	0
1	I	268/291 (92%)	-0.59	1 (0%) 89 88	22, 33, 72, 100	0
1	J	268/291 (92%)	-0.48	0 100 100	25, 38, 73, 106	0
All	All	2680/2910 (92%)	-0.55	13 (0%) 87 86	19, 35, 72, 129	1 (0%)

All (13) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	G	52	GLU	3.7
1	G	194	VAL	3.1
1	B	191	LEU	2.9
1	A	21	GLN	2.6
1	G	193	LYS	2.6
1	G	191	LEU	2.5
1	G	192	SER	2.5
1	H	194	VAL	2.4
1	G	251	GLN	2.4
1	C	21	GLN	2.3
1	I	184	GLN	2.3
1	F	193	LYS	2.1
1	H	191	LEU	2.1

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^{th} 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
3	MPD	I	302	8/8	0.76	0.21	72,76,79,84	0
3	MPD	G	303	8/8	0.78	0.22	84,87,87,90	0
3	MPD	D	302	8/8	0.82	0.19	76,81,90,90	0
3	MPD	G	302	8/8	0.82	0.22	63,70,79,80	0
3	MPD	H	302	8/8	0.83	0.15	59,67,69,76	0
3	MPD	E	302	8/8	0.84	0.21	60,73,79,79	0
3	MPD	A	302	8/8	0.85	0.17	60,71,77,77	0
3	MPD	J	302	8/8	0.85	0.16	66,74,78,80	0
3	MPD	F	302	8/8	0.86	0.17	53,58,66,68	0
2	CA	B	301	1/1	0.98	0.09	15,15,15,15	0
2	CA	E	301	1/1	0.99	0.10	13,13,13,13	0
2	CA	F	301	1/1	0.99	0.09	17,17,17,17	0
2	CA	G	301	1/1	0.99	0.12	21,21,21,21	0
2	CA	H	301	1/1	0.99	0.10	15,15,15,15	0
2	CA	I	301	1/1	0.99	0.08	16,16,16,16	0
2	CA	A	301	1/1	0.99	0.09	14,14,14,14	0
2	CA	D	301	1/1	0.99	0.10	21,21,21,21	0
2	CA	J	301	1/1	1.00	0.09	16,16,16,16	0
2	CA	C	301	1/1	1.00	0.10	14,14,14,14	0

6.5 Other polymers (i)

There are no such residues in this entry.