wwPDB X-ray Structure Validation Summary Report (i)

Sep 17, 2023 – 01:08 PM EDT

PDB ID	:	4Y0E
Title	:	X-ray Crystal Structure of a putative dioxygenase from Mycobacterium abscessus
Authors	:	Seattle Structural Genomics Center for Infectious Disease (SSGCID)
Deposited on	:	2015-02-06
Resolution	:	1.90 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 (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 (i)) were used in the production of this report:

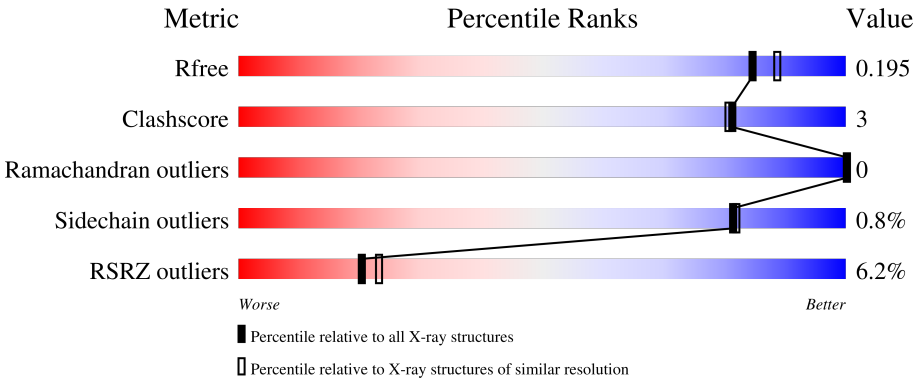
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35.1

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 1.90 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	6207 (1.90-1.90)
Clashscore	141614	6847 (1.90-1.90)
Ramachandran outliers	138981	6760 (1.90-1.90)
Sidechain outliers	138945	6760 (1.90-1.90)
RSRZ outliers	127900	6082 (1.90-1.90)

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	338	5% 84% 5% 11%
1	B	338	5% 83% 5% 12%
1	C	338	2% 84% 6% 10%
1	D	338	9% 81% 7% 12%
1	E	338	7% 83% 6% 12%

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Mol	Chain	Length	Quality of chain
1	F	338	6% 84% 6% 10%
1	G	338	5% 85% 11%
1	H	338	6% 86% 5% 9%

2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 21163 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 Putative dioxygenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	301	Total	C	N	O		0	7	0
			2346	1494	421	431				
1	B	297	Total	C	N	O		0	7	0
			2368	1501	429	438				
1	C	304	Total	C	N	O		0	8	0
			2403	1522	432	449				
1	D	298	Total	C	N	O		0	10	0
			2369	1502	428	439				
1	E	299	Total	C	N	O	S	0	8	0
			2363	1495	424	443	1			
1	F	305	Total	C	N	O		0	6	0
			2384	1511	428	445				
1	G	302	Total	C	N	O		0	7	0
			2355	1501	416	438				
1	H	308	Total	C	N	O		0	5	0
			2403	1522	430	451				

There are 184 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-20	MET	-	initiating methionine	UNP B1MIR1
A	-19	ALA	-	expression tag	UNP B1MIR1
A	-18	HIS	-	expression tag	UNP B1MIR1
A	-17	HIS	-	expression tag	UNP B1MIR1
A	-16	HIS	-	expression tag	UNP B1MIR1
A	-15	HIS	-	expression tag	UNP B1MIR1
A	-14	HIS	-	expression tag	UNP B1MIR1
A	-13	HIS	-	expression tag	UNP B1MIR1
A	-12	MET	-	expression tag	UNP B1MIR1
A	-11	GLY	-	expression tag	UNP B1MIR1
A	-10	THR	-	expression tag	UNP B1MIR1
A	-9	LEU	-	expression tag	UNP B1MIR1
A	-8	GLU	-	expression tag	UNP B1MIR1

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-7	ALA	-	expression tag	UNP B1MIR1
A	-6	GLN	-	expression tag	UNP B1MIR1
A	-5	THR	-	expression tag	UNP B1MIR1
A	-4	GLN	-	expression tag	UNP B1MIR1
A	-3	GLY	-	expression tag	UNP B1MIR1
A	-2	PRO	-	expression tag	UNP B1MIR1
A	-1	GLY	-	expression tag	UNP B1MIR1
A	0	SER	-	expression tag	UNP B1MIR1
A	1	MET	-	expression tag	UNP B1MIR1
A	2	VAL	-	expression tag	UNP B1MIR1
B	-20	MET	-	initiating methionine	UNP B1MIR1
B	-19	ALA	-	expression tag	UNP B1MIR1
B	-18	HIS	-	expression tag	UNP B1MIR1
B	-17	HIS	-	expression tag	UNP B1MIR1
B	-16	HIS	-	expression tag	UNP B1MIR1
B	-15	HIS	-	expression tag	UNP B1MIR1
B	-14	HIS	-	expression tag	UNP B1MIR1
B	-13	HIS	-	expression tag	UNP B1MIR1
B	-12	MET	-	expression tag	UNP B1MIR1
B	-11	GLY	-	expression tag	UNP B1MIR1
B	-10	THR	-	expression tag	UNP B1MIR1
B	-9	LEU	-	expression tag	UNP B1MIR1
B	-8	GLU	-	expression tag	UNP B1MIR1
B	-7	ALA	-	expression tag	UNP B1MIR1
B	-6	GLN	-	expression tag	UNP B1MIR1
B	-5	THR	-	expression tag	UNP B1MIR1
B	-4	GLN	-	expression tag	UNP B1MIR1
B	-3	GLY	-	expression tag	UNP B1MIR1
B	-2	PRO	-	expression tag	UNP B1MIR1
B	-1	GLY	-	expression tag	UNP B1MIR1
B	0	SER	-	expression tag	UNP B1MIR1
B	1	MET	-	expression tag	UNP B1MIR1
B	2	VAL	-	expression tag	UNP B1MIR1
C	-20	MET	-	initiating methionine	UNP B1MIR1
C	-19	ALA	-	expression tag	UNP B1MIR1
C	-18	HIS	-	expression tag	UNP B1MIR1
C	-17	HIS	-	expression tag	UNP B1MIR1
C	-16	HIS	-	expression tag	UNP B1MIR1
C	-15	HIS	-	expression tag	UNP B1MIR1
C	-14	HIS	-	expression tag	UNP B1MIR1
C	-13	HIS	-	expression tag	UNP B1MIR1
C	-12	MET	-	expression tag	UNP B1MIR1

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-11	GLY	-	expression tag	UNP B1MIR1
C	-10	THR	-	expression tag	UNP B1MIR1
C	-9	LEU	-	expression tag	UNP B1MIR1
C	-8	GLU	-	expression tag	UNP B1MIR1
C	-7	ALA	-	expression tag	UNP B1MIR1
C	-6	GLN	-	expression tag	UNP B1MIR1
C	-5	THR	-	expression tag	UNP B1MIR1
C	-4	GLN	-	expression tag	UNP B1MIR1
C	-3	GLY	-	expression tag	UNP B1MIR1
C	-2	PRO	-	expression tag	UNP B1MIR1
C	-1	GLY	-	expression tag	UNP B1MIR1
C	0	SER	-	expression tag	UNP B1MIR1
C	1	MET	-	expression tag	UNP B1MIR1
C	2	VAL	-	expression tag	UNP B1MIR1
D	-20	MET	-	initiating methionine	UNP B1MIR1
D	-19	ALA	-	expression tag	UNP B1MIR1
D	-18	HIS	-	expression tag	UNP B1MIR1
D	-17	HIS	-	expression tag	UNP B1MIR1
D	-16	HIS	-	expression tag	UNP B1MIR1
D	-15	HIS	-	expression tag	UNP B1MIR1
D	-14	HIS	-	expression tag	UNP B1MIR1
D	-13	HIS	-	expression tag	UNP B1MIR1
D	-12	MET	-	expression tag	UNP B1MIR1
D	-11	GLY	-	expression tag	UNP B1MIR1
D	-10	THR	-	expression tag	UNP B1MIR1
D	-9	LEU	-	expression tag	UNP B1MIR1
D	-8	GLU	-	expression tag	UNP B1MIR1
D	-7	ALA	-	expression tag	UNP B1MIR1
D	-6	GLN	-	expression tag	UNP B1MIR1
D	-5	THR	-	expression tag	UNP B1MIR1
D	-4	GLN	-	expression tag	UNP B1MIR1
D	-3	GLY	-	expression tag	UNP B1MIR1
D	-2	PRO	-	expression tag	UNP B1MIR1
D	-1	GLY	-	expression tag	UNP B1MIR1
D	0	SER	-	expression tag	UNP B1MIR1
D	1	MET	-	expression tag	UNP B1MIR1
D	2	VAL	-	expression tag	UNP B1MIR1
E	-20	MET	-	initiating methionine	UNP B1MIR1
E	-19	ALA	-	expression tag	UNP B1MIR1
E	-18	HIS	-	expression tag	UNP B1MIR1
E	-17	HIS	-	expression tag	UNP B1MIR1
E	-16	HIS	-	expression tag	UNP B1MIR1

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Chain	Residue	Modelled	Actual	Comment	Reference
E	-15	HIS	-	expression tag	UNP B1MIR1
E	-14	HIS	-	expression tag	UNP B1MIR1
E	-13	HIS	-	expression tag	UNP B1MIR1
E	-12	MET	-	expression tag	UNP B1MIR1
E	-11	GLY	-	expression tag	UNP B1MIR1
E	-10	THR	-	expression tag	UNP B1MIR1
E	-9	LEU	-	expression tag	UNP B1MIR1
E	-8	GLU	-	expression tag	UNP B1MIR1
E	-7	ALA	-	expression tag	UNP B1MIR1
E	-6	GLN	-	expression tag	UNP B1MIR1
E	-5	THR	-	expression tag	UNP B1MIR1
E	-4	GLN	-	expression tag	UNP B1MIR1
E	-3	GLY	-	expression tag	UNP B1MIR1
E	-2	PRO	-	expression tag	UNP B1MIR1
E	-1	GLY	-	expression tag	UNP B1MIR1
E	0	SER	-	expression tag	UNP B1MIR1
E	1	MET	-	expression tag	UNP B1MIR1
E	2	VAL	-	expression tag	UNP B1MIR1
F	-20	MET	-	initiating methionine	UNP B1MIR1
F	-19	ALA	-	expression tag	UNP B1MIR1
F	-18	HIS	-	expression tag	UNP B1MIR1
F	-17	HIS	-	expression tag	UNP B1MIR1
F	-16	HIS	-	expression tag	UNP B1MIR1
F	-15	HIS	-	expression tag	UNP B1MIR1
F	-14	HIS	-	expression tag	UNP B1MIR1
F	-13	HIS	-	expression tag	UNP B1MIR1
F	-12	MET	-	expression tag	UNP B1MIR1
F	-11	GLY	-	expression tag	UNP B1MIR1
F	-10	THR	-	expression tag	UNP B1MIR1
F	-9	LEU	-	expression tag	UNP B1MIR1
F	-8	GLU	-	expression tag	UNP B1MIR1
F	-7	ALA	-	expression tag	UNP B1MIR1
F	-6	GLN	-	expression tag	UNP B1MIR1
F	-5	THR	-	expression tag	UNP B1MIR1
F	-4	GLN	-	expression tag	UNP B1MIR1
F	-3	GLY	-	expression tag	UNP B1MIR1
F	-2	PRO	-	expression tag	UNP B1MIR1
F	-1	GLY	-	expression tag	UNP B1MIR1
F	0	SER	-	expression tag	UNP B1MIR1
F	1	MET	-	expression tag	UNP B1MIR1
F	2	VAL	-	expression tag	UNP B1MIR1
G	-20	MET	-	initiating methionine	UNP B1MIR1

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Chain	Residue	Modelled	Actual	Comment	Reference
G	-19	ALA	-	expression tag	UNP B1MIR1
G	-18	HIS	-	expression tag	UNP B1MIR1
G	-17	HIS	-	expression tag	UNP B1MIR1
G	-16	HIS	-	expression tag	UNP B1MIR1
G	-15	HIS	-	expression tag	UNP B1MIR1
G	-14	HIS	-	expression tag	UNP B1MIR1
G	-13	HIS	-	expression tag	UNP B1MIR1
G	-12	MET	-	expression tag	UNP B1MIR1
G	-11	GLY	-	expression tag	UNP B1MIR1
G	-10	THR	-	expression tag	UNP B1MIR1
G	-9	LEU	-	expression tag	UNP B1MIR1
G	-8	GLU	-	expression tag	UNP B1MIR1
G	-7	ALA	-	expression tag	UNP B1MIR1
G	-6	GLN	-	expression tag	UNP B1MIR1
G	-5	THR	-	expression tag	UNP B1MIR1
G	-4	GLN	-	expression tag	UNP B1MIR1
G	-3	GLY	-	expression tag	UNP B1MIR1
G	-2	PRO	-	expression tag	UNP B1MIR1
G	-1	GLY	-	expression tag	UNP B1MIR1
G	0	SER	-	expression tag	UNP B1MIR1
G	1	MET	-	expression tag	UNP B1MIR1
G	2	VAL	-	expression tag	UNP B1MIR1
H	-20	MET	-	initiating methionine	UNP B1MIR1
H	-19	ALA	-	expression tag	UNP B1MIR1
H	-18	HIS	-	expression tag	UNP B1MIR1
H	-17	HIS	-	expression tag	UNP B1MIR1
H	-16	HIS	-	expression tag	UNP B1MIR1
H	-15	HIS	-	expression tag	UNP B1MIR1
H	-14	HIS	-	expression tag	UNP B1MIR1
H	-13	HIS	-	expression tag	UNP B1MIR1
H	-12	MET	-	expression tag	UNP B1MIR1
H	-11	GLY	-	expression tag	UNP B1MIR1
H	-10	THR	-	expression tag	UNP B1MIR1
H	-9	LEU	-	expression tag	UNP B1MIR1
H	-8	GLU	-	expression tag	UNP B1MIR1
H	-7	ALA	-	expression tag	UNP B1MIR1
H	-6	GLN	-	expression tag	UNP B1MIR1
H	-5	THR	-	expression tag	UNP B1MIR1
H	-4	GLN	-	expression tag	UNP B1MIR1
H	-3	GLY	-	expression tag	UNP B1MIR1
H	-2	PRO	-	expression tag	UNP B1MIR1
H	-1	GLY	-	expression tag	UNP B1MIR1

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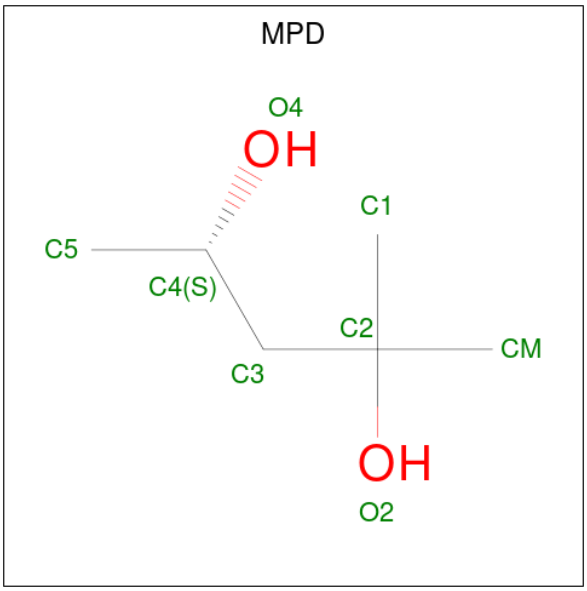
Chain	Residue	Modelled	Actual	Comment	Reference
H	0	SER	-	expression tag	UNP B1MIR1
H	1	MET	-	expression tag	UNP B1MIR1
H	2	VAL	-	expression tag	UNP B1MIR1

- Molecule 2 is FE (III) ION (three-letter code: FE) (formula: Fe).

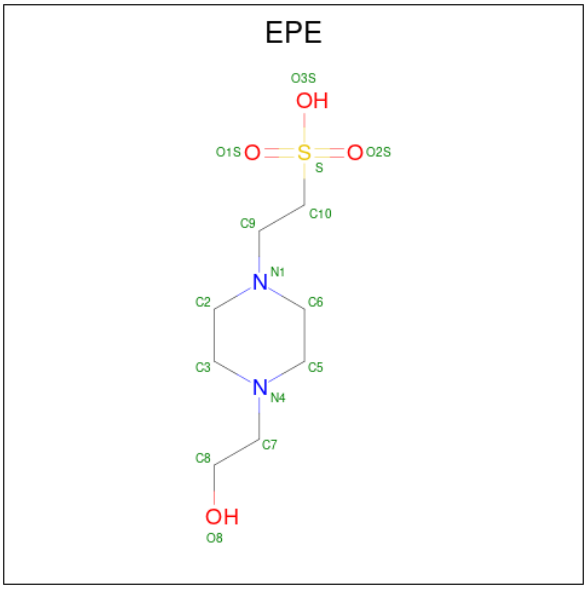
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Fe 1 1	0	0
2	B	1	Total Fe 1 1	0	0
2	C	1	Total Fe 1 1	0	0
2	D	1	Total Fe 1 1	0	0
2	E	1	Total Fe 1 1	0	0
2	F	1	Total Fe 1 1	0	0
2	G	1	Total Fe 1 1	0	0
2	H	1	Total Fe 1 1	0	0

- 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	B	1	Total C O 8 6 2	0	0
3	C	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

- Molecule 4 is 4-(2-HYDROXYETHYL)-1-PIPERAZINE ETHANESULFONIC ACID (three-letter code: EPE) (formula: $C_8H_{18}N_2O_4S$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C N O S 15 8 2 4 1	0	0
4	B	1	Total C N O S 15 8 2 4 1	0	0
4	C	1	Total C N O S 15 8 2 4 1	0	0
4	D	1	Total C N O S 15 8 2 4 1	0	0
4	E	1	Total C N O S 15 8 2 4 1	0	0

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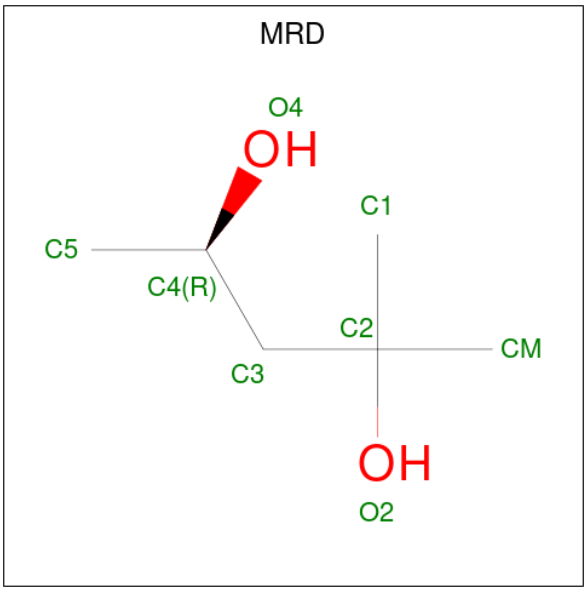
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	F	1	Total C N O S 15 8 2 4 1	0	0
4	G	1	Total C N O S 15 8 2 4 1	0	0
4	H	1	Total C N O S 15 8 2 4 1	0	0

- Molecule 5 is (4R)-2-METHYLPENTANE-2,4-DIOL (three-letter code: MRD) (formula: $C_6H_{14}O_2$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	G	1	Total C O 8 6 2	0	0
5	H	1	Total C O 8 6 2	0	0

- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	195	Total O 195 195	0	0
6	B	282	Total O 282 282	0	0
6	C	311	Total O 311 311	0	0
6	D	260	Total O 260 260	0	0

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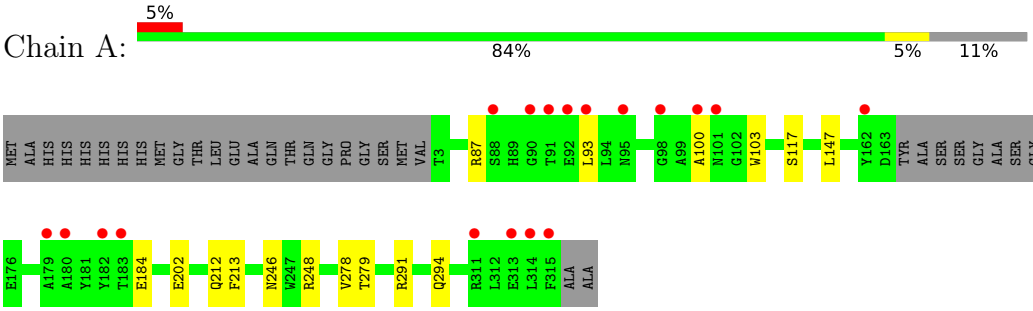
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	E	255	Total O 255 255	0	0
6	F	250	Total O 250 250	0	0
6	G	186	Total O 186 186	0	0
6	H	241	Total O 241 241	0	0

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.

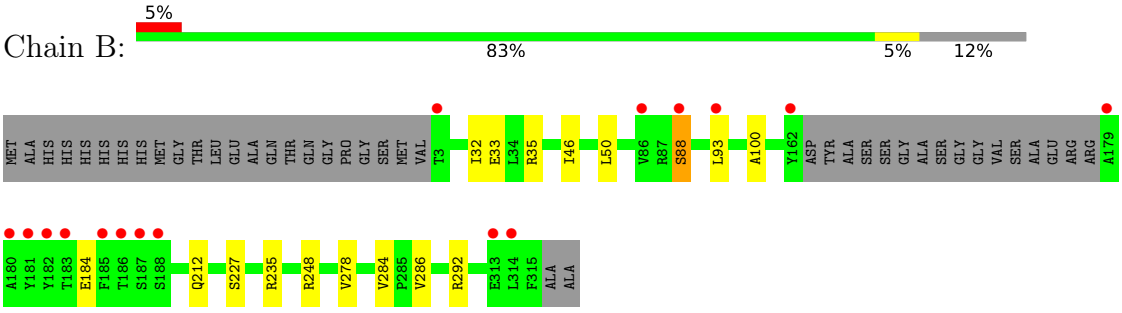
• Molecule 1: Putative dioxygenase

Chain A:



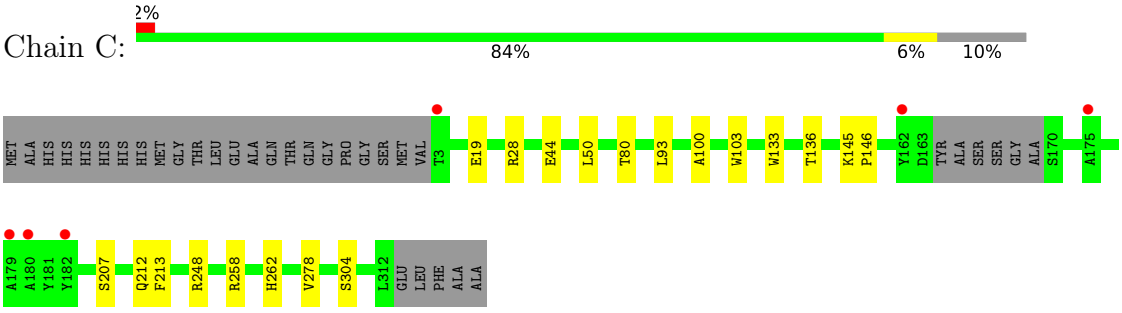
• Molecule 1: Putative dioxygenase

Chain B:



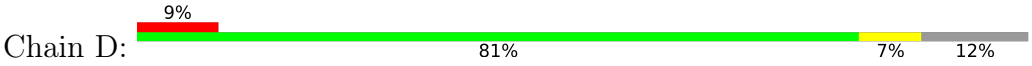
• Molecule 1: Putative dioxygenase

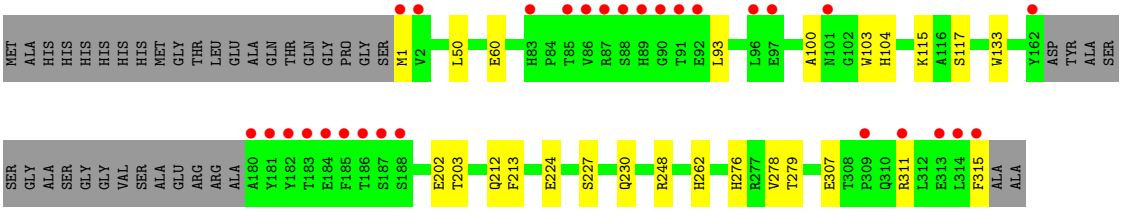
Chain C:



• Molecule 1: Putative dioxygenase

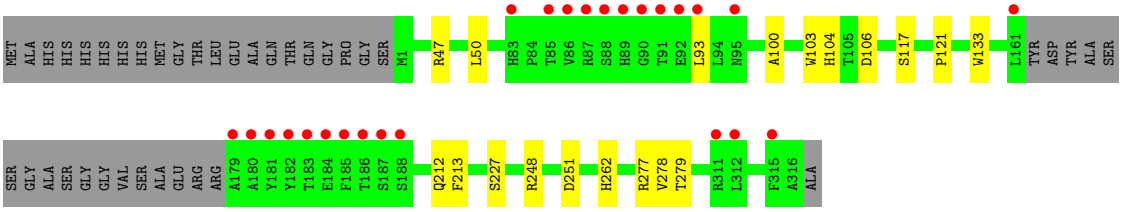
Chain D:





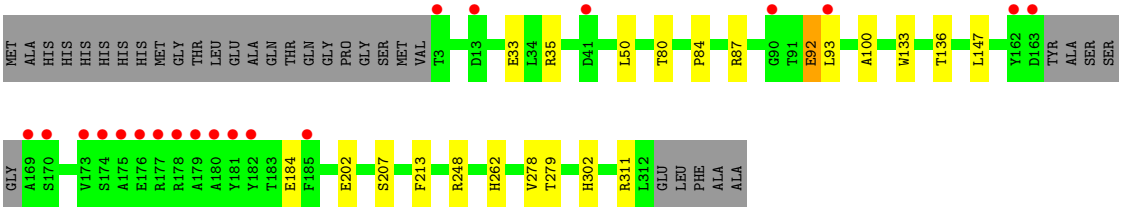
• Molecule 1: Putative dioxygenase

Chain E:



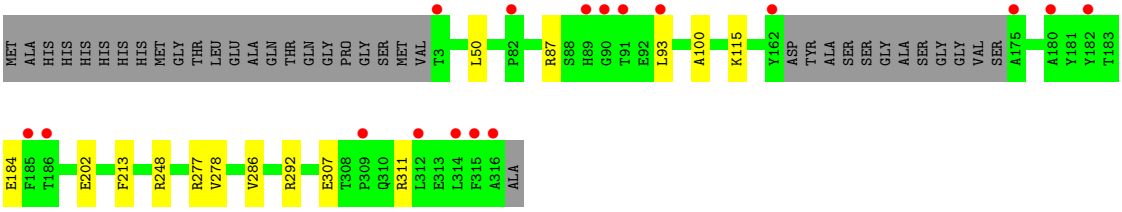
• Molecule 1: Putative dioxygenase

Chain F:



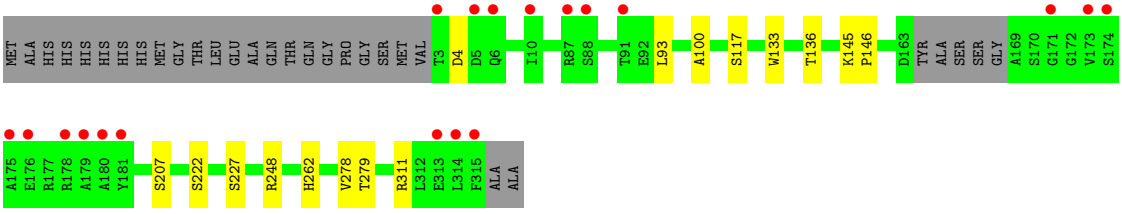
• Molecule 1: Putative dioxygenase

Chain G:



• Molecule 1: Putative dioxygenase

Chain H:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	103.90Å 92.98Å 136.98Å 90.00° 96.11° 90.00°	Depositor
Resolution (Å)	45.40 – 1.90 45.40 – 1.90	Depositor EDS
% Data completeness (in resolution range)	94.0 (45.40-1.90) 94.0 (45.40-1.90)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.32 (at 1.89Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.160 , 0.195 0.159 , 0.195	Depositor DCC
R_{free} test set	9514 reflections (4.96%)	wwPDB-VP
Wilson B-factor (Å^2)	18.7	Xtriage
Anisotropy	0.019	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 56.9	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	0.96	EDS
Total number of atoms	21163	wwPDB-VP
Average B, all atoms (Å^2)	28.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 59.10 % 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 1.8553e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

[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: MRD, MPD, FE, EPE

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	0.35	0/2427	0.52	0/3315
1	B	0.38	0/2445	0.54	0/3332
1	C	0.41	0/2483	0.55	0/3384
1	D	0.43	0/2454	0.57	0/3345
1	E	0.39	0/2440	0.55	0/3327
1	F	0.36	0/2458	0.55	0/3353
1	G	0.32	0/2433	0.50	0/3324
1	H	0.36	0/2475	0.54	0/3377
All	All	0.38	0/19615	0.54	0/26757

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	2346	0	2254	10	0
1	B	2368	0	2314	11	0
1	C	2403	0	2335	13	0
1	D	2369	0	2308	20	0
1	E	2363	0	2305	13	1

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	F	2384	0	2310	15	0
1	G	2355	0	2259	10	0
1	H	2403	0	2309	6	1
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
3	A	8	0	14	0	0
3	B	8	0	14	1	0
3	C	8	0	14	1	0
3	D	8	0	14	2	0
3	E	8	0	14	2	0
3	F	8	0	14	1	0
4	A	15	0	17	2	0
4	B	15	0	17	2	0
4	C	15	0	17	3	0
4	D	15	0	17	3	0
4	E	15	0	17	3	0
4	F	15	0	17	2	0
4	G	15	0	17	2	0
4	H	15	0	17	1	0
5	G	8	0	14	2	0
5	H	8	0	14	0	0
6	A	195	0	0	3	0
6	B	282	0	0	0	0
6	C	311	0	0	1	0
6	D	260	0	0	2	0
6	E	255	0	0	2	0
6	F	250	0	0	2	0
6	G	186	0	0	2	0
6	H	241	0	0	1	0
All	All	21163	0	18642	98	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 3.

The worst 5 of 98 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:C:19[B]:GLU:OE2	1:C:28[B]:ARG:NH2	2.18	0.76
1:A:202:GLU:OE2	6:A:662:HOH:O	2.06	0.72
1:E:213:PHE:HZ	4:E:403:EPE:H92	1.57	0.69
1:B:33:GLU:OE1	1:B:35[A]:ARG:NH2	2.22	0.68
1:G:286:VAL:HG12	1:G:292[B]:ARG:HG2	1.75	0.68

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:E:227:SER:OG	1:H:227[B]:SER:OG[1_655]	2.19	0.01

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	305/338 (90%)	301 (99%)	4 (1%)	0	100	100
1	B	300/338 (89%)	294 (98%)	6 (2%)	0	100	100
1	C	308/338 (91%)	303 (98%)	5 (2%)	0	100	100
1	D	304/338 (90%)	299 (98%)	5 (2%)	0	100	100
1	E	303/338 (90%)	298 (98%)	5 (2%)	0	100	100
1	F	307/338 (91%)	302 (98%)	5 (2%)	0	100	100
1	G	305/338 (90%)	299 (98%)	6 (2%)	0	100	100
1	H	309/338 (91%)	305 (99%)	4 (1%)	0	100	100
All	All	2441/2704 (90%)	2401 (98%)	40 (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	237/277 (86%)	235 (99%)	2 (1%)	81	82
1	B	247/277 (89%)	245 (99%)	2 (1%)	81	82
1	C	249/277 (90%)	248 (100%)	1 (0%)	91	91
1	D	246/277 (89%)	243 (99%)	3 (1%)	71	70
1	E	246/277 (89%)	245 (100%)	1 (0%)	91	91
1	F	245/277 (88%)	243 (99%)	2 (1%)	81	82
1	G	238/277 (86%)	237 (100%)	1 (0%)	91	91
1	H	246/277 (89%)	241 (98%)	5 (2%)	55	51
All	All	1954/2216 (88%)	1937 (99%)	17 (1%)	81	79

5 of 17 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	H	222[B]	SER
1	H	311	ARG
1	D	248	ARG
1	E	248	ARG
1	F	92	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	H	230	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 monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 24 ligands modelled in this entry, 8 are monoatomic - leaving 16 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	D	402	-	7,7,7	0.41	0	9,10,10	0.43	0
3	MPD	B	402	-	7,7,7	0.36	0	9,10,10	0.65	0
3	MPD	C	402	-	7,7,7	0.32	0	9,10,10	0.73	0
4	EPE	D	403	-	15,15,15	0.90	1 (6%)	18,20,20	1.76	5 (27%)
5	MRD	G	402	-	7,7,7	0.30	0	9,10,10	0.47	0
4	EPE	H	403	-	15,15,15	0.88	1 (6%)	18,20,20	1.80	6 (33%)
4	EPE	A	403	-	15,15,15	0.89	1 (6%)	18,20,20	1.79	6 (33%)
4	EPE	C	403	-	15,15,15	0.94	1 (6%)	18,20,20	1.82	4 (22%)
4	EPE	G	403	-	15,15,15	0.86	1 (6%)	18,20,20	1.78	5 (27%)
4	EPE	E	403	-	15,15,15	0.91	1 (6%)	18,20,20	1.77	4 (22%)
4	EPE	B	403	-	15,15,15	0.85	1 (6%)	18,20,20	1.69	4 (22%)
3	MPD	A	402	-	7,7,7	0.28	0	9,10,10	0.89	1 (11%)
4	EPE	F	403	-	15,15,15	0.95	1 (6%)	18,20,20	1.77	6 (33%)
3	MPD	F	402	-	7,7,7	0.32	0	9,10,10	0.35	0
5	MRD	H	402	-	7,7,7	0.35	0	9,10,10	0.36	0
3	MPD	E	402	-	7,7,7	0.33	0	9,10,10	0.46	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	D	402	-	-	2/5/5/5	-
3	MPD	B	402	-	-	3/5/5/5	-
3	MPD	C	402	-	-	0/5/5/5	-
4	EPE	D	403	-	-	6/9/19/19	0/1/1/1
5	MRD	G	402	-	-	3/5/5/5	-
4	EPE	H	403	-	-	4/9/19/19	0/1/1/1
4	EPE	A	403	-	-	4/9/19/19	0/1/1/1
4	EPE	C	403	-	-	6/9/19/19	0/1/1/1
4	EPE	G	403	-	-	5/9/19/19	0/1/1/1
4	EPE	E	403	-	-	6/9/19/19	0/1/1/1
4	EPE	B	403	-	-	3/9/19/19	0/1/1/1
3	MPD	A	402	-	-	0/5/5/5	-
4	EPE	F	403	-	-	6/9/19/19	0/1/1/1
3	MPD	F	402	-	-	3/5/5/5	-
5	MRD	H	402	-	-	2/5/5/5	-
3	MPD	E	402	-	-	3/5/5/5	-

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	F	403	EPE	C10-S	3.27	1.82	1.77
4	C	403	EPE	C10-S	3.26	1.82	1.77
4	E	403	EPE	C10-S	3.09	1.81	1.77
4	D	403	EPE	C10-S	3.06	1.81	1.77
4	A	403	EPE	C10-S	3.05	1.81	1.77

The worst 5 of 41 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	C	403	EPE	C5-N4-C3	4.42	118.77	108.83
4	E	403	EPE	C5-N4-C3	4.24	118.38	108.83
4	H	403	EPE	C5-N4-C3	4.24	118.36	108.83
4	G	403	EPE	C5-N4-C3	4.16	118.20	108.83
4	A	403	EPE	C5-N4-C3	4.14	118.14	108.83

There are no chirality outliers.

5 of 56 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	402	MPD	O2-C2-C3-C4
4	B	403	EPE	N4-C7-C8-O8
4	C	403	EPE	C9-C10-S-O2S
4	D	403	EPE	N4-C7-C8-O8
4	E	403	EPE	N4-C7-C8-O8

There are no ring outliers.

14 monomers are involved in 27 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	D	402	MPD	2	0
3	B	402	MPD	1	0
3	C	402	MPD	1	0
4	D	403	EPE	3	0
5	G	402	MRD	2	0
4	H	403	EPE	1	0
4	A	403	EPE	2	0
4	C	403	EPE	3	0
4	G	403	EPE	2	0
4	E	403	EPE	3	0
4	B	403	EPE	2	0
4	F	403	EPE	2	0
3	F	402	MPD	1	0
3	E	402	MPD	2	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	301/338 (89%)	-0.06	18 (5%)	21	24	10, 30, 60, 88	0
1	B	297/338 (87%)	-0.27	16 (5%)	25	29	11, 22, 52, 80	0
1	C	304/338 (89%)	-0.14	6 (1%)	65	68	8, 18, 45, 67	0
1	D	298/338 (88%)	0.04	29 (9%)	7	9	9, 19, 54, 75	0
1	E	299/338 (88%)	0.04	25 (8%)	11	12	11, 21, 59, 71	0
1	F	305/338 (90%)	0.07	20 (6%)	18	20	11, 24, 57, 74	0
1	G	302/338 (89%)	0.03	17 (5%)	24	27	12, 34, 63, 89	0
1	H	308/338 (91%)	-0.11	19 (6%)	20	23	13, 24, 64, 96	0
All	All	2414/2704 (89%)	-0.05	150 (6%)	20	23	8, 23, 59, 96	0

The worst 5 of 150 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	91	THR	7.6
1	E	182	TYR	7.3
1	E	186	THR	6.7
1	D	87	ARG	6.2
1	H	91	THR	5.9

6.2 Non-standard residues in protein, DNA, RNA chains

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

6.3 Carbohydrates

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	B	402	8/8	0.68	0.27	39,44,47,49	0
4	EPE	B	403	15/15	0.68	0.23	95,95,96,96	0
4	EPE	D	403	15/15	0.69	0.28	85,88,98,98	0
4	EPE	E	403	15/15	0.73	0.32	81,82,88,88	0
5	MRD	G	402	8/8	0.74	0.25	51,54,58,60	0
4	EPE	A	403	15/15	0.78	0.30	91,93,98,100	0
5	MRD	H	402	8/8	0.80	0.19	33,41,42,43	0
3	MPD	A	402	8/8	0.81	0.22	43,48,54,56	0
4	EPE	H	403	15/15	0.82	0.21	76,77,81,83	0
4	EPE	G	403	15/15	0.85	0.27	86,87,88,89	0
3	MPD	F	402	8/8	0.85	0.23	30,40,46,46	0
3	MPD	D	402	8/8	0.88	0.17	29,33,37,40	0
4	EPE	F	403	15/15	0.88	0.23	65,76,80,82	0
3	MPD	C	402	8/8	0.89	0.15	27,37,40,40	0
4	EPE	C	403	15/15	0.90	0.18	51,68,79,80	0
3	MPD	E	402	8/8	0.94	0.12	21,26,33,37	0
2	FE	A	401	1/1	0.97	0.04	33,33,33,33	0
2	FE	G	401	1/1	0.98	0.03	38,38,38,38	0
2	FE	H	401	1/1	0.98	0.03	30,30,30,30	0
2	FE	E	401	1/1	0.99	0.04	29,29,29,29	0
2	FE	F	401	1/1	0.99	0.03	26,26,26,26	0
2	FE	B	401	1/1	0.99	0.03	29,29,29,29	0
2	FE	C	401	1/1	0.99	0.03	23,23,23,23	0
2	FE	D	401	1/1	0.99	0.03	25,25,25,25	0

6.5 Other polymers (i)

There are no such residues in this entry.