



# Full wwPDB X-ray Structure Validation Report ⓘ

Sep 2, 2023 – 06:19 PM EDT

PDB ID : 3QK8  
Title : Crystal structure of enoyl-coA hydratase EchA15 from *Mycobacterium marinum* in complex with an unknown ligand  
Authors : Seattle Structural Genomics Center for Infectious Disease (SSGCID)  
Deposited on : 2011-01-31  
Resolution : 1.60 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](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 : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.35  
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

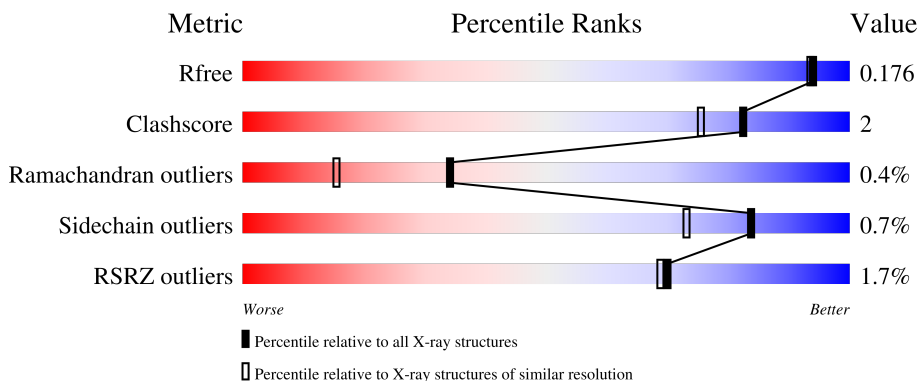
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*


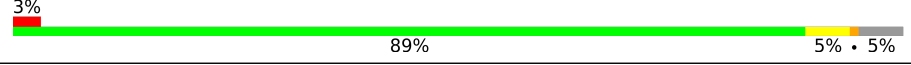
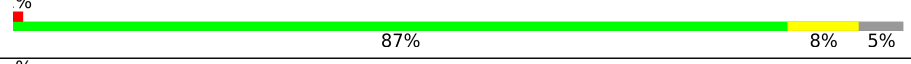
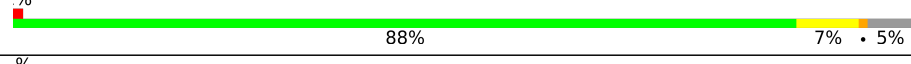
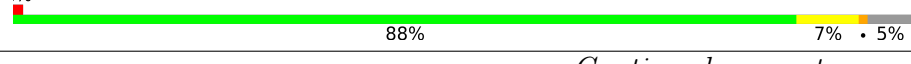
The reported resolution of this entry is 1.60 Å.

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.



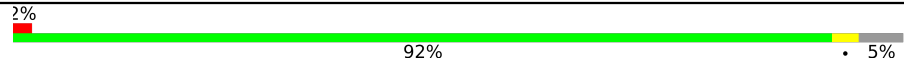
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	130704	3398 (1.60-1.60)
Clashscore	141614	3665 (1.60-1.60)
Ramachandran outliers	138981	3564 (1.60-1.60)
Sidechain outliers	138945	3563 (1.60-1.60)
RSRZ outliers	127900	3321 (1.60-1.60)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments 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	272	 2% 89% 6% 5%
1	B	272	 3% 89% 5% 5%
1	C	272	 % 87% 8% 5%
1	D	272	 % 88% 7% 5%
1	E	272	 % 88% 7% 5%

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Mol	Chain	Length	Quality of chain
1	F	272	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	UNL	E	291	-	-	X	-

## 2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 13426 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 Enoyl-CoA hydratase EchA15.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	259	2012	1277	351	375	9	0	12	0
1	B	259	2003	1270	351	373	9	0	9	0
1	C	259	2027	1288	351	378	10	0	13	0
1	D	259	2001	1271	354	368	8	0	7	0
1	E	259	1997	1265	350	373	9	0	7	0
1	F	259	1981	1258	345	368	10	0	7	0

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-3	GLY	-	expression tag	UNP B2HM22
A	-2	PRO	-	expression tag	UNP B2HM22
A	-1	GLY	-	expression tag	UNP B2HM22
A	0	SER	-	expression tag	UNP B2HM22
B	-3	GLY	-	expression tag	UNP B2HM22
B	-2	PRO	-	expression tag	UNP B2HM22
B	-1	GLY	-	expression tag	UNP B2HM22
B	0	SER	-	expression tag	UNP B2HM22
C	-3	GLY	-	expression tag	UNP B2HM22
C	-2	PRO	-	expression tag	UNP B2HM22
C	-1	GLY	-	expression tag	UNP B2HM22
C	0	SER	-	expression tag	UNP B2HM22
D	-3	GLY	-	expression tag	UNP B2HM22
D	-2	PRO	-	expression tag	UNP B2HM22
D	-1	GLY	-	expression tag	UNP B2HM22
D	0	SER	-	expression tag	UNP B2HM22
E	-3	GLY	-	expression tag	UNP B2HM22

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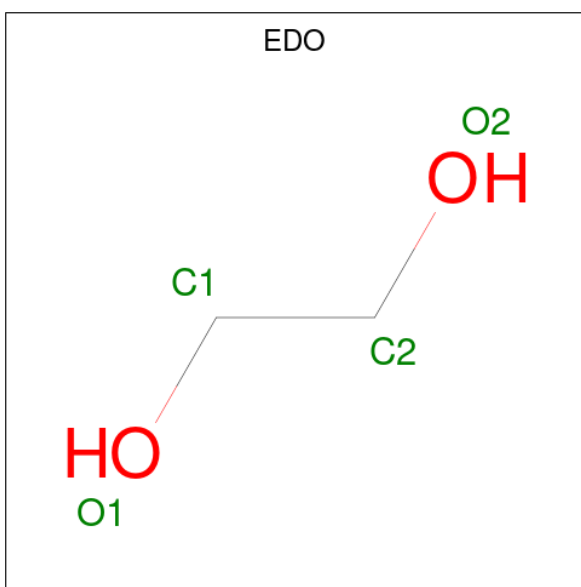
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Chain	Residue	Modelled	Actual	Comment	Reference
E	-2	PRO	-	expression tag	UNP B2HM22
E	-1	GLY	-	expression tag	UNP B2HM22
E	0	SER	-	expression tag	UNP B2HM22
F	-3	GLY	-	expression tag	UNP B2HM22
F	-2	PRO	-	expression tag	UNP B2HM22
F	-1	GLY	-	expression tag	UNP B2HM22
F	0	SER	-	expression tag	UNP B2HM22

- Molecule 2 is UNKNOWN LIGAND (three-letter code: UNL) (formula: ).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total C O 9 7 2	0	0
2	C	1	Total C O 9 7 2	0	0
2	D	1	Total C O 9 7 2	0	0
2	E	1	Total C O 8 6 2	0	0
2	F	1	Total C O 9 7 2	0	0

- Molecule 3 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C<sub>2</sub>H<sub>6</sub>O<sub>2</sub>).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C O 4 2 2	0	0
3	A	1	Total C O 4 2 2	0	0
3	A	1	Total C O 8 4 4	0	1
3	B	1	Total C O 4 2 2	0	0
3	B	1	Total C O 4 2 2	0	0
3	B	1	Total C O 4 2 2	0	0
3	C	1	Total C O 4 2 2	0	0
3	C	1	Total C O 4 2 2	0	0
3	C	1	Total C O 4 2 2	0	0
3	D	1	Total C O 4 2 2	0	0
3	D	1	Total C O 4 2 2	0	0
3	D	1	Total C O 4 2 2	0	0
3	D	1	Total C O 4 2 2	0	0
3	E	1	Total C O 4 2 2	0	0
3	F	1	Total C O 4 2 2	0	0
3	F	1	Total C O 4 2 2	0	0

- Molecule 4 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	E	1	Total Cl 1 1	0	0

- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	212	Total O 212 212	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	223	Total 223	O 223	0	1
5	C	226	Total 226	O 226	0	0
5	D	186	Total 186	O 186	0	0
5	E	232	Total 232	O 232	0	0
5	F	213	Total 213	O 213	0	0

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

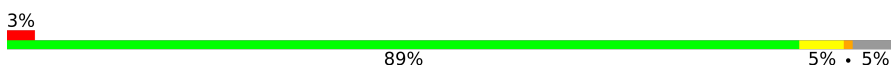
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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.

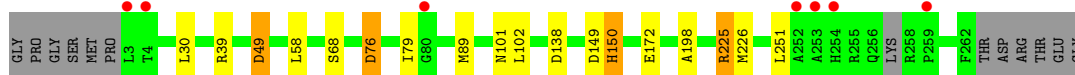
- Molecule 1: Enoyl-CoA hydratase EchA15

Chain A: 




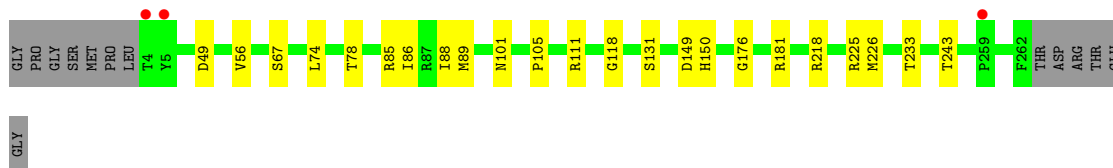
- Molecule 1: Enoyl-CoA hydratase EchA15

Chain B: 




- Molecule 1: Enoyl-CoA hydratase EchA15

Chain C: 




- Molecule 1: Enoyl-CoA hydratase EchA15

Chain D: 



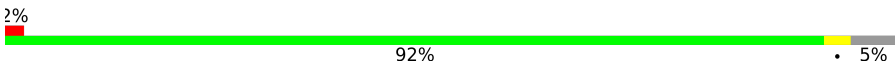
- Molecule 1: Enoyl-CoA hydratase EchA15

Chain E: 





## ● Molecule 1: Enoyl-CoA hydratase EchA15

Chain F:  2% 92% 5%



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	73.99Å 129.53Å 78.61Å 90.00° 108.57° 90.00°	Depositor
Resolution (Å)	48.88 – 1.60 48.88 – 1.60	Depositor EDS
% Data completeness (in resolution range)	98.4 (48.88-1.60) 98.4 (48.88-1.60)	Depositor EDS
$R_{merge}$	0.04	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.76 (at 1.60Å)	Xtrriage
Refinement program	REFMAC	Depositor
R, $R_{free}$	0.137 , 0.164 0.151 , 0.176	Depositor DCC
$R_{free}$ test set	9122 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	12.9	Xtrriage
Anisotropy	0.154	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 41.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	13426	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	14.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.85% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

## 5 Model quality i

### 5.1 Standard geometry i

Bond lengths and bond angles in the following residue types are not validated in this section: EDO, UNL, CL

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	0.79	1/2088 (0.0%)	0.84	3/2840 (0.1%)
1	B	0.81	0/2067	0.84	5/2810 (0.2%)
1	C	0.76	0/2103	0.85	6/2860 (0.2%)
1	D	0.76	0/2063	0.84	6/2804 (0.2%)
1	E	0.78	0/2059	0.90	5/2802 (0.2%)
1	F	0.78	0/2042	0.87	5/2780 (0.2%)
All	All	0.78	1/12422 (0.0%)	0.86	30/16896 (0.2%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	177	GLU	CB-CG	-5.22	1.42	1.52

All (30) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	85	ARG	NE-CZ-NH2	-10.04	115.28	120.30
1	E	85	ARG	NE-CZ-NH1	9.60	125.10	120.30
1	D	85	ARG	NE-CZ-NH1	9.44	125.02	120.30
1	A	85	ARG	NE-CZ-NH1	9.11	124.86	120.30
1	D	85	ARG	NE-CZ-NH2	-9.02	115.79	120.30
1	F	85	ARG	NE-CZ-NH1	8.08	124.34	120.30
1	B	138[A]	ASP	C-N-CA	7.64	138.35	122.30
1	B	138[B]	ASP	C-N-CA	7.64	138.35	122.30
1	F	85	ARG	NE-CZ-NH2	-7.35	116.62	120.30
1	C	149	ASP	CB-CG-OD1	7.11	124.70	118.30
1	E	225[A]	ARG	NE-CZ-NH1	7.04	123.82	120.30
1	E	225[B]	ARG	NE-CZ-NH1	7.04	123.82	120.30
1	F	225	ARG	NE-CZ-NH1	6.88	123.74	120.30
1	C	85	ARG	NE-CZ-NH1	6.88	123.74	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	85	ARG	NE-CZ-NH2	-6.47	117.07	120.30
1	C	181	ARG	NE-CZ-NH1	6.38	123.49	120.30
1	C	218	ARG	NE-CZ-NH2	-5.80	117.40	120.30
1	D	226	MET	CG-SD-CE	5.73	109.37	100.20
1	E	181	ARG	NE-CZ-NH2	-5.69	117.45	120.30
1	F	103	ASP	CB-CG-OD2	-5.64	113.22	118.30
1	A	192	ASP	CB-CG-OD1	5.56	123.31	118.30
1	C	111	ARG	NE-CZ-NH1	5.37	122.98	120.30
1	C	85	ARG	NE-CZ-NH2	-5.35	117.62	120.30
1	B	225[A]	ARG	NE-CZ-NH1	5.34	122.97	120.30
1	B	225[B]	ARG	NE-CZ-NH1	5.34	122.97	120.30
1	B	76	ASP	CB-CG-OD2	-5.30	113.53	118.30
1	D	225[A]	ARG	NE-CZ-NH1	5.26	122.93	120.30
1	D	225[B]	ARG	NE-CZ-NH1	5.26	122.93	120.30
1	D	218	ARG	NE-CZ-NH2	-5.11	117.75	120.30
1	F	87	ARG	NE-CZ-NH1	-5.06	117.77	120.30

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	2012	0	1998	12	0
1	B	2003	0	1977	12	0
1	C	2027	0	2032	12	0
1	D	2001	0	2007	15	0
1	E	1997	0	1978	11	0
1	F	1981	0	1963	3	0
2	A	9	0	0	0	0
2	C	9	0	0	0	0
2	D	9	0	0	0	0
2	E	8	0	0	2	0
2	F	9	0	0	0	0
3	A	16	0	24	0	0
3	B	12	0	18	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	C	12	0	18	1	0
3	D	16	0	24	1	0
3	E	4	0	6	0	0
3	F	8	0	12	0	0
4	E	1	0	0	0	0
5	A	212	0	0	2	2
5	B	223	0	0	4	0
5	C	226	0	0	0	0
5	D	186	0	0	4	0
5	E	232	0	0	2	2
5	F	213	0	0	0	0
All	All	13426	0	12057	60	2

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 2.

All (60) 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)
2:E:291:UNL:C4	2:E:291:UNL:C6	2.40	0.91
1:A:55[B]:ARG:HH12	1:D:263:THR:CG2	1.85	0.89
1:A:233[B]:THR:HG21	5:B:681:HOH:O	1.81	0.81
1:A:55[B]:ARG:HH12	1:D:263:THR:HG21	1.47	0.78
1:E:74:LEU:O	1:E:78[B]:THR:HG23	1.90	0.72
1:A:55[B]:ARG:NH1	1:D:263:THR:HG21	2.06	0.70
1:C:243[A]:THR:OG1	1:D:82:TYR:HE2	1.81	0.64
1:C:233[A]:THR:HG21	5:D:932:HOH:O	1.98	0.62
5:B:300:HOH:O	1:F:226[B]:MET:HE1	1.98	0.62
1:C:74:LEU:O	1:C:78[B]:THR:HG23	2.00	0.61
1:B:172:GLU:OE1	5:B:1091:HOH:O	2.16	0.60
1:A:101:ASN:HA	1:A:225[B]:ARG:HH21	1.67	0.58
1:C:233[B]:THR:HG22	1:D:233:THR:N	2.19	0.57
1:B:58:LEU:HD11	1:B:198:ALA:HB1	1.86	0.56
1:A:188[B]:CYS:SG	5:A:737:HOH:O	2.58	0.56
1:B:101:ASN:HA	1:B:225[A]:ARG:HH21	1.72	0.55
1:D:25:LEU:HD21	1:D:41:LEU:HD21	1.90	0.53
1:B:39:ARG:HD3	1:B:39:ARG:C	2.30	0.52
1:A:39:ARG:HD3	1:A:39:ARG:C	2.32	0.50
1:C:101:ASN:HA	1:C:225[B]:ARG:HH21	1.75	0.50
1:D:58:LEU:HD22	5:D:1156:HOH:O	2.12	0.49
1:D:27:SER:OG	1:D:31:ASN:HA	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:39:ARG:HD3	1:E:39:ARG:C	2.35	0.47
1:C:78[B]:THR:HG22	1:C:88:ILE:HD13	1.96	0.47
1:D:83:GLU:HG2	5:D:1006:HOH:O	2.14	0.47
1:D:49:ASP:CG	1:D:102:LEU:HD12	2.36	0.46
1:D:101:ASN:HA	1:D:225[A]:ARG:HH21	1.80	0.46
1:B:89[B]:MET:HE3	3:B:301:EDO:H21	1.96	0.46
5:B:300:HOH:O	1:F:226[B]:MET:CE	2.59	0.46
1:A:25[A]:LEU:HD21	1:A:41:LEU:HD21	1.98	0.46
1:D:93:ARG:HD3	3:D:301:EDO:H12	1.98	0.46
1:E:251:LEU:O	1:E:255:ARG:HG2	2.16	0.46
1:A:55[B]:ARG:NH1	1:D:263:THR:CG2	2.64	0.45
1:B:79:ILE:CD1	1:B:251:LEU:CD1	2.95	0.45
1:E:117:ALA:HB1	5:E:1002:HOH:O	2.16	0.44
1:B:79:ILE:HD11	1:B:251:LEU:CD1	2.46	0.44
1:E:49:ASP:CG	1:E:102:LEU:HD12	2.37	0.44
1:C:86:ILE:HD12	1:C:89[B]:MET:HE1	2.00	0.44
1:B:30:LEU:HB2	1:B:68:SER:HB3	1.99	0.44
1:A:60[B]:ARG:NH1	5:A:1259:HOH:O	2.30	0.43
1:A:149:ASP:O	1:A:150:HIS:HB3	2.19	0.43
1:D:149:ASP:O	1:D:150:HIS:HB3	2.19	0.42
1:C:67:SER:HB3	1:C:118:GLY:HA3	2.00	0.42
1:E:101:ASN:HA	1:E:225[A]:ARG:HH21	1.83	0.42
1:B:226[B]:MET:HA	1:B:226[B]:MET:HE2	2.01	0.42
1:F:149:ASP:O	1:F:150:HIS:HB3	2.19	0.42
1:B:49:ASP:CG	1:B:102:LEU:HD12	2.40	0.42
1:B:79:ILE:CD1	1:B:251:LEU:HD12	2.50	0.42
1:B:149:ASP:O	1:B:150:HIS:HB3	2.20	0.42
1:D:10:SER:OG	1:D:37:MET:HA	2.19	0.42
5:D:1117:HOH:O	1:E:50:ARG:HG2	2.18	0.41
1:E:83:GLU:HG2	5:E:778:HOH:O	2.20	0.41
1:C:89[B]:MET:HE3	3:C:301:EDO:H21	2.01	0.41
1:C:226[A]:MET:HA	1:C:226[A]:MET:HE2	2.03	0.41
1:C:56:VAL:HG22	1:C:105:PRO:HG2	2.04	0.40
1:E:88:ILE:HG21	2:E:291:UNL:C4	2.52	0.40
1:A:27:SER:HB2	1:A:28:PRO:CD	2.52	0.40
1:C:131:SER:O	1:C:176:GLY:HA3	2.22	0.40
1:E:167:TYR:CZ	1:E:174:LEU:HD13	2.57	0.40
1:E:27:SER:OG	1:E:31:ASN:HA	2.22	0.40

All (2) 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)
5:A:1069:HOH:O	5:E:313:HOH:O[1_554]	2.14	0.06
5:A:300:HOH:O	5:E:1175:HOH:O[1_554]	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	269/272 (99%)	262 (97%)	6 (2%)	1 (0%)	34	15
1	B	264/272 (97%)	259 (98%)	4 (2%)	1 (0%)	34	15
1	C	270/272 (99%)	266 (98%)	3 (1%)	1 (0%)	34	15
1	D	264/272 (97%)	261 (99%)	2 (1%)	1 (0%)	34	15
1	E	264/272 (97%)	259 (98%)	4 (2%)	1 (0%)	34	15
1	F	264/272 (97%)	260 (98%)	3 (1%)	1 (0%)	34	15
All	All	1595/1632 (98%)	1567 (98%)	22 (1%)	6 (0%)	34	15

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	150	HIS
1	B	150	HIS
1	C	150	HIS
1	D	150	HIS
1	E	150	HIS
1	F	150	HIS

#### 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	211/218 (97%)	210 (100%)	1 (0%)	88	80
1	B	208/218 (95%)	206 (99%)	2 (1%)	76	61
1	C	215/218 (99%)	214 (100%)	1 (0%)	88	80
1	D	210/218 (96%)	209 (100%)	1 (0%)	88	80
1	E	209/218 (96%)	207 (99%)	2 (1%)	76	61
1	F	206/218 (94%)	205 (100%)	1 (0%)	88	80
All	All	1259/1308 (96%)	1251 (99%)	8 (1%)	84	77

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	49	ASP
1	B	49	ASP
1	B	76	ASP
1	C	49	ASP
1	D	49	ASP
1	E	15	PRO
1	E	49	ASP
1	F	49	ASP

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

Mol	Chain	Res	Type
1	B	248	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 23 ligands modelled in this entry, 5 are unknown and 1 is monoatomic - leaving 17 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	EDO	D	269	-	3,3,3	0.61	0	2,2,2	0.72	0
3	EDO	F	301	-	3,3,3	0.57	0	2,2,2	0.45	0
3	EDO	A	269[A]	-	3,3,3	0.45	0	2,2,2	0.29	0
3	EDO	B	301	-	3,3,3	0.46	0	2,2,2	0.28	0
3	EDO	D	305	-	3,3,3	0.63	0	2,2,2	0.10	0
3	EDO	F	297	-	3,3,3	0.29	0	2,2,2	0.48	0
3	EDO	C	297	-	3,3,3	0.37	0	2,2,2	0.32	0
3	EDO	C	301	-	3,3,3	0.58	0	2,2,2	0.32	0
3	EDO	C	305	-	3,3,3	0.59	0	2,2,2	0.11	0
3	EDO	D	301	-	3,3,3	0.39	0	2,2,2	1.36	0
3	EDO	D	297	-	3,3,3	0.36	0	2,2,2	0.59	0
3	EDO	B	297	-	3,3,3	0.35	0	2,2,2	0.39	0
3	EDO	B	305	-	3,3,3	0.84	0	2,2,2	0.36	0
3	EDO	E	297	-	3,3,3	0.51	0	2,2,2	0.12	0
3	EDO	A	305	-	3,3,3	0.77	0	2,2,2	0.26	0
3	EDO	A	269[B]	-	3,3,3	0.39	0	2,2,2	0.51	0
3	EDO	A	297	-	3,3,3	0.38	0	2,2,2	0.30	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	EDO	D	269	-	-	1/1/1/1	-
3	EDO	F	301	-	-	1/1/1/1	-
3	EDO	A	269[A]	-	-	1/1/1/1	-
3	EDO	B	301	-	-	0/1/1/1	-
3	EDO	D	305	-	-	1/1/1/1	-
3	EDO	F	297	-	-	0/1/1/1	-
3	EDO	C	297	-	-	0/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	EDO	C	301	-	-	0/1/1/1	-
3	EDO	C	305	-	-	1/1/1/1	-
3	EDO	D	301	-	-	1/1/1/1	-
3	EDO	D	297	-	-	1/1/1/1	-
3	EDO	B	297	-	-	0/1/1/1	-
3	EDO	B	305	-	-	1/1/1/1	-
3	EDO	E	297	-	-	1/1/1/1	-
3	EDO	A	305	-	-	1/1/1/1	-
3	EDO	A	269[B]	-	-	1/1/1/1	-
3	EDO	A	297	-	-	1/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (12) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	E	297	EDO	O1-C1-C2-O2
3	A	269[B]	EDO	O1-C1-C2-O2
3	D	301	EDO	O1-C1-C2-O2
3	D	297	EDO	O1-C1-C2-O2
3	D	269	EDO	O1-C1-C2-O2
3	A	269[A]	EDO	O1-C1-C2-O2
3	B	305	EDO	O1-C1-C2-O2
3	C	305	EDO	O1-C1-C2-O2
3	D	305	EDO	O1-C1-C2-O2
3	A	305	EDO	O1-C1-C2-O2
3	F	301	EDO	O1-C1-C2-O2
3	A	297	EDO	O1-C1-C2-O2

There are no ring outliers.

3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	301	EDO	1	0
3	C	301	EDO	1	0
3	D	301	EDO	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<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	259/272 (95%)	-0.28	5 (1%) 66 65	6, 12, 26, 51	0
1	B	259/272 (95%)	-0.21	7 (2%) 54 52	5, 12, 26, 38	0
1	C	259/272 (95%)	-0.32	3 (1%) 79 78	6, 12, 27, 36	0
1	D	259/272 (95%)	-0.30	4 (1%) 73 73	6, 14, 29, 38	0
1	E	259/272 (95%)	-0.36	3 (1%) 79 78	5, 11, 26, 37	0
1	F	259/272 (95%)	-0.24	5 (1%) 66 65	6, 12, 32, 46	0
All	All	1554/1632 (95%)	-0.28	27 (1%) 70 69	5, 12, 28, 51	0

All (27) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	259	PRO	5.0
1	B	3	LEU	4.5
1	B	259	PRO	4.5
1	A	257	LYS	4.4
1	B	4	THR	4.3
1	A	259	PRO	4.0
1	B	252	ALA	3.3
1	F	72	PHE	3.2
1	B	253	ALA	3.1
1	F	4	THR	2.9
1	E	259	PRO	2.9
1	A	254	HIS	2.8
1	D	259	PRO	2.7
1	F	257	LYS	2.7
1	E	4	THR	2.6
1	D	263	THR	2.6
1	E	254	HIS	2.5
1	C	5	TYR	2.4
1	D	257	LYS	2.4

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Mol	Chain	Res	Type	RSRZ
1	C	259	PRO	2.3
1	C	4	THR	2.3
1	A	260	ALA	2.2
1	A	258	ARG	2.2
1	B	254	HIS	2.1
1	B	80	GLY	2.0
1	F	260	ALA	2.0
1	D	7	ASP	2.0

## 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<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
3	EDO	B	305	4/4	0.69	0.18	39,40,42,43	0
3	EDO	A	305	4/4	0.76	0.14	37,38,38,38	0
3	EDO	D	269	4/4	0.83	0.18	21,23,27,29	0
3	EDO	A	269[A]	4/4	0.85	0.21	12,16,17,19	4
3	EDO	A	269[B]	4/4	0.85	0.21	17,18,19,22	4
3	EDO	E	297	4/4	0.87	0.10	35,35,35,38	0
3	EDO	D	301	4/4	0.89	0.13	23,25,27,33	0
3	EDO	D	305	4/4	0.90	0.10	37,38,39,41	0
2	UNL	C	291	9/-	0.92	0.13	16,21,25,26	0
2	UNL	D	291	9/-	0.92	0.15	18,23,25,27	0
2	UNL	A	291	9/-	0.92	0.14	15,20,23,24	0
3	EDO	C	305	4/4	0.92	0.14	40,40,40,41	0
3	EDO	F	301	4/4	0.92	0.12	20,24,26,27	0
3	EDO	A	297	4/4	0.93	0.12	25,26,29,33	0
2	UNL	F	291	9/-	0.93	0.15	16,21,24,25	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
3	EDO	B	301	4/4	0.94	0.13	18,23,24,26	0
2	UNL	E	291	8/-	0.94	0.16	15,21,26,29	0
3	EDO	C	301	4/4	0.94	0.12	19,23,24,25	0
3	EDO	D	297	4/4	0.96	0.12	23,27,30,32	0
3	EDO	C	297	4/4	0.96	0.11	19,19,25,31	0
3	EDO	F	297	4/4	0.96	0.10	20,21,26,28	0
3	EDO	B	297	4/4	0.96	0.12	24,26,30,33	0
4	CL	E	269	1/1	0.98	0.05	22,22,22,22	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.