



# Full wwPDB X-ray Structure Validation Report ⓘ

May 22, 2020 – 12:22 am BST

PDB ID : 2YII  
Title : Manipulating the regioselectivity of phenylalanine aminomutase: new insights into the reaction mechanism of MIO-dependent enzymes from structure-guided directed evolution  
Authors : Wu, B.; Szymanski, W.; Wybenga, G.G.; Heberling, M.M.; Bartsch, S.; Wildeman, S.; Poelarends, G.J.; Feringa, B.L.; Dijkstra, B.W.; Janssen, D.B.  
Deposited on : 2011-05-13  
Resolution : 2.18 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.

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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 : 2.11  
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) : 2.11

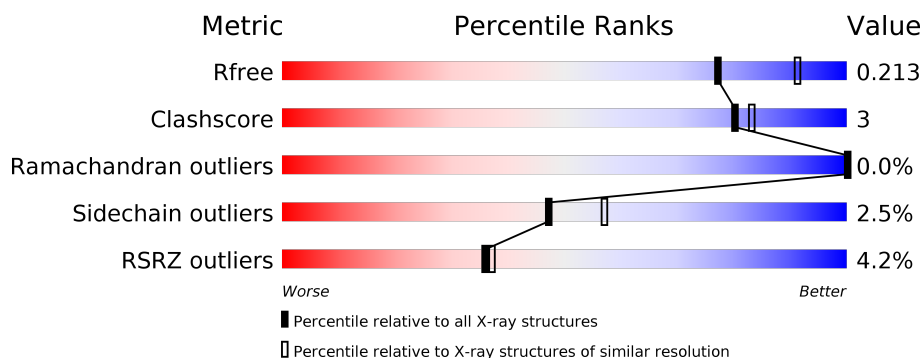
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.18 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	6864 (2.20-2.16)
Clashscore	141614	7689 (2.20-2.16)
Ramachandran outliers	138981	7564 (2.20-2.16)
Sidechain outliers	138945	7564 (2.20-2.16)
RSRZ outliers	127900	6738 (2.20-2.16)

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 on 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	705	<div> <div>5%</div> <div> <div></div> <div>85%</div> <div>5% • 9%</div> </div> </div>
1	B	705	<div> <div>4%</div> <div> <div></div> <div>83%</div> <div>9% • 8%</div> </div> </div>
1	C	705	<div> <div>3%</div> <div> <div></div> <div>83%</div> <div>9% • 8%</div> </div> </div>
1	D	705	<div> <div>4%</div> <div> <div></div> <div>85%</div> <div>6% • 9%</div> </div> </div>

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 20965 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 PHENYLALANINE AMMONIA-LYASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	644	Total	C	N	O	S	0	0	0
			5004	3176	862	943	23			
1	B	650	Total	C	N	O	S	0	0	0
			5051	3203	871	954	23			
1	C	646	Total	C	N	O	S	0	0	0
			5015	3183	864	945	23			
1	D	645	Total	C	N	O	S	0	0	0
			5011	3179	862	947	23			

There are 92 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	expression tag	UNP Q68G84
A	-18	GLY	-	expression tag	UNP Q68G84
A	-17	SER	-	expression tag	UNP Q68G84
A	-16	SER	-	expression tag	UNP Q68G84
A	-15	HIS	-	expression tag	UNP Q68G84
A	-14	HIS	-	expression tag	UNP Q68G84
A	-13	HIS	-	expression tag	UNP Q68G84
A	-12	HIS	-	expression tag	UNP Q68G84
A	-11	HIS	-	expression tag	UNP Q68G84
A	-10	HIS	-	expression tag	UNP Q68G84
A	-9	SER	-	expression tag	UNP Q68G84
A	-8	SER	-	expression tag	UNP Q68G84
A	-7	GLY	-	expression tag	UNP Q68G84
A	-6	LEU	-	expression tag	UNP Q68G84
A	-5	VAL	-	expression tag	UNP Q68G84
A	-4	PRO	-	expression tag	UNP Q68G84
A	-3	ARG	-	expression tag	UNP Q68G84
A	-2	GLY	-	expression tag	UNP Q68G84
A	-1	SER	-	expression tag	UNP Q68G84
A	0	HIS	-	expression tag	UNP Q68G84
A	175	MDO	ALA	chromophore	UNP Q68G84

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Chain	Residue	Modelled	Actual	Comment	Reference
A	175	MDO	SER	chromophore	UNP Q68G84
A	175	MDO	GLY	chromophore	UNP Q68G84
B	-19	MET	-	expression tag	UNP Q68G84
B	-18	GLY	-	expression tag	UNP Q68G84
B	-17	SER	-	expression tag	UNP Q68G84
B	-16	SER	-	expression tag	UNP Q68G84
B	-15	HIS	-	expression tag	UNP Q68G84
B	-14	HIS	-	expression tag	UNP Q68G84
B	-13	HIS	-	expression tag	UNP Q68G84
B	-12	HIS	-	expression tag	UNP Q68G84
B	-11	HIS	-	expression tag	UNP Q68G84
B	-10	HIS	-	expression tag	UNP Q68G84
B	-9	SER	-	expression tag	UNP Q68G84
B	-8	SER	-	expression tag	UNP Q68G84
B	-7	GLY	-	expression tag	UNP Q68G84
B	-6	LEU	-	expression tag	UNP Q68G84
B	-5	VAL	-	expression tag	UNP Q68G84
B	-4	PRO	-	expression tag	UNP Q68G84
B	-3	ARG	-	expression tag	UNP Q68G84
B	-2	GLY	-	expression tag	UNP Q68G84
B	-1	SER	-	expression tag	UNP Q68G84
B	0	HIS	-	expression tag	UNP Q68G84
B	175	MDO	ALA	chromophore	UNP Q68G84
B	175	MDO	SER	chromophore	UNP Q68G84
B	175	MDO	GLY	chromophore	UNP Q68G84
C	-19	MET	-	expression tag	UNP Q68G84
C	-18	GLY	-	expression tag	UNP Q68G84
C	-17	SER	-	expression tag	UNP Q68G84
C	-16	SER	-	expression tag	UNP Q68G84
C	-15	HIS	-	expression tag	UNP Q68G84
C	-14	HIS	-	expression tag	UNP Q68G84
C	-13	HIS	-	expression tag	UNP Q68G84
C	-12	HIS	-	expression tag	UNP Q68G84
C	-11	HIS	-	expression tag	UNP Q68G84
C	-10	HIS	-	expression tag	UNP Q68G84
C	-9	SER	-	expression tag	UNP Q68G84
C	-8	SER	-	expression tag	UNP Q68G84
C	-7	GLY	-	expression tag	UNP Q68G84
C	-6	LEU	-	expression tag	UNP Q68G84
C	-5	VAL	-	expression tag	UNP Q68G84
C	-4	PRO	-	expression tag	UNP Q68G84
C	-3	ARG	-	expression tag	UNP Q68G84

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-2	GLY	-	expression tag	UNP Q68G84
C	-1	SER	-	expression tag	UNP Q68G84
C	0	HIS	-	expression tag	UNP Q68G84
C	175	MDO	ALA	chromophore	UNP Q68G84
C	175	MDO	SER	chromophore	UNP Q68G84
C	175	MDO	GLY	chromophore	UNP Q68G84
D	-19	MET	-	expression tag	UNP Q68G84
D	-18	GLY	-	expression tag	UNP Q68G84
D	-17	SER	-	expression tag	UNP Q68G84
D	-16	SER	-	expression tag	UNP Q68G84
D	-15	HIS	-	expression tag	UNP Q68G84
D	-14	HIS	-	expression tag	UNP Q68G84
D	-13	HIS	-	expression tag	UNP Q68G84
D	-12	HIS	-	expression tag	UNP Q68G84
D	-11	HIS	-	expression tag	UNP Q68G84
D	-10	HIS	-	expression tag	UNP Q68G84
D	-9	SER	-	expression tag	UNP Q68G84
D	-8	SER	-	expression tag	UNP Q68G84
D	-7	GLY	-	expression tag	UNP Q68G84
D	-6	LEU	-	expression tag	UNP Q68G84
D	-5	VAL	-	expression tag	UNP Q68G84
D	-4	PRO	-	expression tag	UNP Q68G84
D	-3	ARG	-	expression tag	UNP Q68G84
D	-2	GLY	-	expression tag	UNP Q68G84
D	-1	SER	-	expression tag	UNP Q68G84
D	0	HIS	-	expression tag	UNP Q68G84
D	175	MDO	ALA	chromophore	UNP Q68G84
D	175	MDO	SER	chromophore	UNP Q68G84
D	175	MDO	GLY	chromophore	UNP Q68G84

- Molecule 2 is BETA-MERCAPTOETHANOL (three-letter code: BME) (formula: C<sub>2</sub>H<sub>6</sub>OS).



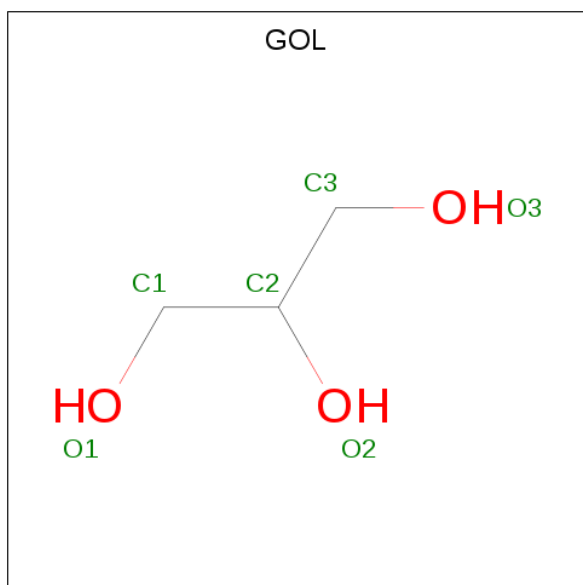
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	O	S	0	0
			4	2	1	1		
2	A	1	Total	C	O	S	0	0
			4	2	1	1		
2	B	1	Total	C	O	S	0	0
			4	2	1	1		
2	B	1	Total	C	O	S	0	0
			4	2	1	1		
2	C	1	Total	C	O	S	0	0
			4	2	1	1		
2	C	1	Total	C	O	S	0	0
			4	2	1	1		
2	D	1	Total	C	O	S	0	0
			4	2	1	1		
2	D	1	Total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

- Molecule 3 is FORMIC ACID (three-letter code: FMT) (formula: CH<sub>2</sub>O<sub>2</sub>).



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

- Molecule 4 is GLYCEROL (three-letter code: GOL) (formula:  $C_3H_8O_3$ ).



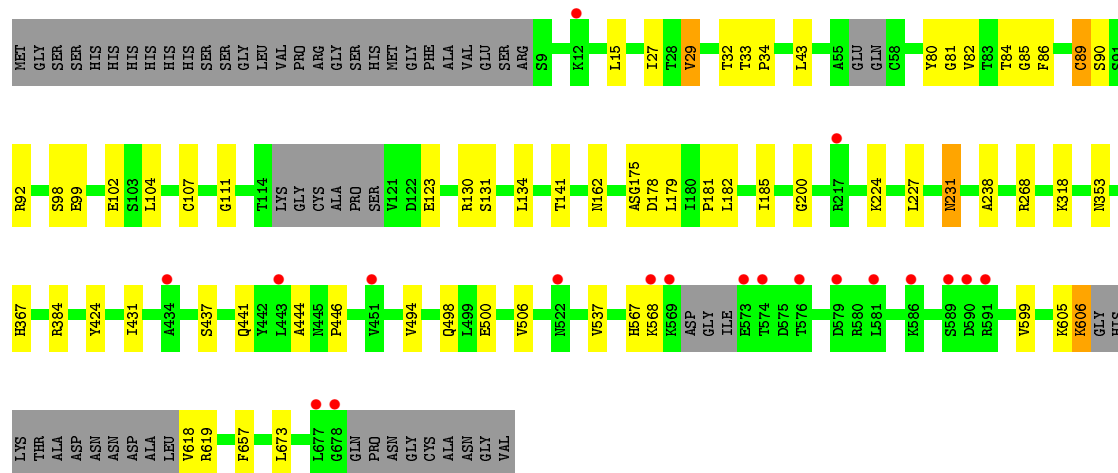
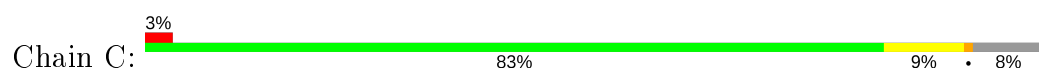
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	B	1	Total	C	O	0	0
			6	3	3		

- Molecule 5 is water.

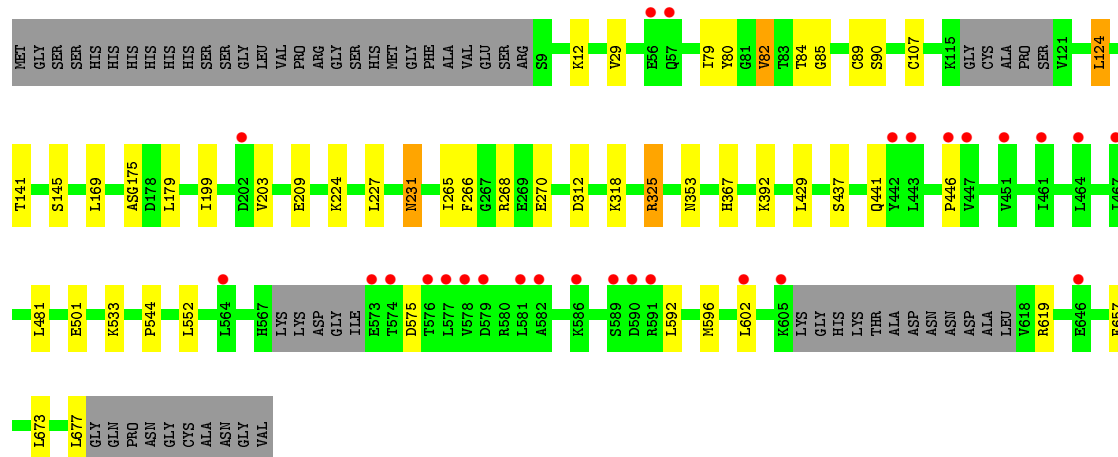
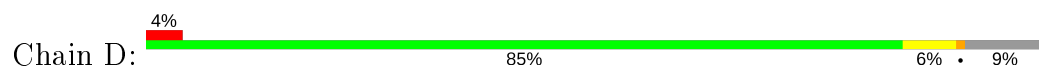
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	241	Total	O	0	0
			241	241		
5	B	193	Total	O	0	0
			193	193		
5	C	228	Total	O	0	0
			228	228		
5	D	172	Total	O	0	0
			172	172		







• Molecule 1: PHENYLALANINE AMMONIA-LYASE



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	99.45Å 146.00Å 99.68Å 90.00° 99.51° 90.00°	Depositor
Resolution (Å)	98.31 – 2.18 48.26 – 2.18	Depositor EDS
% Data completeness (in resolution range)	97.9 (98.31-2.18) 98.0 (48.26-2.18)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.06 (at 2.18Å)	Xtriage
Refinement program	REFMAC 5.5.0102	Depositor
R, $R_{free}$	0.179 , 0.214 0.180 , 0.213	Depositor DCC
$R_{free}$ test set	7140 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	28.1	Xtriage
Anisotropy	0.052	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , 40.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.017 for l,-k,h	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	20965	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.53% 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

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, FMT, MDO, BME

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	0.38	0/5075	0.52	0/6882
1	B	0.39	0/5121	0.53	1/6942 (0.0%)
1	C	0.55	1/5086 (0.0%)	0.53	0/6896
1	D	0.39	0/5082	0.53	0/6893
All	All	0.44	1/20364 (0.0%)	0.53	1/27613 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2
1	B	0	2
1	C	0	2
1	D	0	2
All	All	0	8

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	89	CYS	C-N	28.00	1.98	1.34

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	384	ARG	NE-CZ-NH2	-5.61	117.50	120.30

There are no chirality outliers.

All (8) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	175	MDO	Mainchain,Peptide
1	B	175	MDO	Mainchain,Peptide
1	C	175	MDO	Mainchain,Peptide
1	D	175	MDO	Mainchain,Peptide

## 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	5004	0	5072	26	0
1	B	5051	0	5114	37	0
1	C	5015	0	5085	36	0
1	D	5011	0	5072	26	0
2	A	8	0	10	0	0
2	B	8	0	10	1	0
2	C	8	0	10	2	0
2	D	8	0	10	1	0
3	A	3	0	1	0	0
3	B	3	0	1	0	0
3	C	3	0	1	1	0
3	D	3	0	1	0	0
4	B	6	0	8	0	0
5	A	241	0	0	1	0
5	B	193	0	0	1	0
5	C	228	0	0	1	0
5	D	172	0	0	1	0
All	All	20965	0	20395	110	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 (110) 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:89:CYS:C	1:C:90:SER:N	1.98	1.17
1:A:89:CYS:C	1:A:90:SER:N	2.02	1.11
1:D:89:CYS:C	1:D:90:SER:N	2.03	1.10

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:173:VAL:C	1:B:174:SER:N	2.11	1.04
1:C:506:VAL:HG21	1:C:599:VAL:HG21	1.39	1.02
1:B:89:CYS:C	1:B:90:SER:N	2.14	1.00
1:C:82:VAL:HG22	1:C:224:LYS:HB2	1.66	0.77
1:C:605:LYS:O	1:C:606:LYS:HB3	1.84	0.74
1:A:587:ARG:HH11	1:A:587:ARG:HG2	1.52	0.73
1:B:407:SER:OG	1:B:410:LEU:HB2	1.90	0.71
1:D:199:ILE:HB	1:D:203:VAL:HG22	1.76	0.68
1:B:384:ARG:NH2	1:B:468:SER:OG	2.27	0.67
1:D:592:LEU:HG	1:D:596:MET:CE	2.24	0.67
1:B:179:LEU:HD11	2:B:1175:BME:S2	2.35	0.65
1:A:318:LYS:HB3	1:B:90:SER:HB2	1.78	0.64
1:C:446:PRO:HD3	1:D:446:PRO:HD3	1.80	0.63
1:C:437:SER:O	1:C:441:GLN:HG2	1.98	0.63
1:D:592:LEU:HG	1:D:596:MET:HE2	1.80	0.62
1:C:29:VAL:HG23	1:C:141:THR:HG21	1.80	0.62
1:A:224:LYS:HE2	1:A:356:PRO:HD2	1.83	0.60
1:C:90:SER:HB2	1:D:318:LYS:HB3	1.83	0.60
1:D:501:GLU:OE1	1:D:619:ARG:HD2	2.03	0.59
1:A:294:TRP:CH2	1:A:624:LYS:HE2	2.38	0.57
3:C:1680:FMT:O1	1:D:325:ARG:NH2	2.37	0.57
1:A:227:LEU:O	1:A:231:ASN:HB2	2.03	0.57
1:A:587:ARG:HG2	1:A:587:ARG:NH1	2.19	0.57
1:A:587:ARG:HD2	5:A:2216:HOH:O	2.05	0.57
1:D:544:PRO:HG2	1:D:596:MET:HE3	1.87	0.57
1:B:506:VAL:HG21	1:B:599:VAL:HG11	1.88	0.56
1:D:29:VAL:HG12	1:D:141:THR:HG21	1.88	0.55
1:A:545:CYS:SG	1:A:589:SER:HA	2.46	0.55
1:C:84:THR:HG22	1:C:85:GLY:O	2.06	0.55
1:D:12:LYS:HE2	1:D:677:LEU:HB3	1.88	0.54
1:C:182:LEU:HD23	1:C:185:ILE:HD12	1.90	0.54
1:C:98:SER:O	1:C:102:GLU:HG3	2.07	0.54
1:B:403:ILE:O	1:B:407:SER:HB2	2.07	0.54
1:B:563:ILE:O	1:B:567:HIS:HB3	2.09	0.53
1:C:318:LYS:HB3	1:D:90:SER:HB2	1.91	0.53
1:A:29:VAL:HG12	1:A:141:THR:HG21	1.91	0.52
1:C:506:VAL:CG2	1:C:599:VAL:HG21	2.27	0.52
1:B:227:LEU:O	1:B:231:ASN:HB2	2.09	0.52
1:D:79:ILE:HB	1:D:82:VAL:HG22	1.92	0.52
1:B:545:CYS:SG	1:B:589:SER:HA	2.49	0.52
1:A:446:PRO:HD3	1:B:446:PRO:HD3	1.91	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:145:SER:O	1:D:224:LYS:HE3	2.10	0.51
1:B:110:ALA:HB1	1:D:429:LEU:HD23	1.92	0.51
1:B:29:VAL:HG12	1:B:141:THR:HG21	1.94	0.51
1:B:572:ILE:HG13	1:B:573:GLU:H	1.77	0.50
1:D:592:LEU:HG	1:D:596:MET:HE1	1.92	0.50
1:B:43:LEU:O	1:B:130:ARG:NH2	2.45	0.50
1:B:501:GLU:OE1	1:B:619:ARG:HD2	2.11	0.49
1:C:178:ASP:HB3	1:C:181:PRO:HG2	1.92	0.49
1:B:178:ASP:HB3	1:B:181:PRO:HG2	1.93	0.49
1:A:650:GLN:HG3	1:C:111:GLY:O	2.13	0.49
1:A:94:THR:HG22	1:A:96:ARG:H	1.78	0.49
1:B:130:ARG:HD2	5:B:2044:HOH:O	2.13	0.49
1:C:179:LEU:HD11	2:C:1175:BME:S2	2.53	0.48
1:C:43:LEU:HG	1:C:134:LEU:HD22	1.95	0.48
1:D:227:LEU:O	1:D:231:ASN:HB2	2.14	0.48
1:B:374:SER:HA	1:B:463:SER:HB2	1.95	0.48
1:C:227:LEU:O	1:C:231:ASN:HB2	2.14	0.48
1:D:80:TYR:HB3	1:D:367:HIS:CD2	2.50	0.47
1:B:51:VAL:HG21	1:B:159:LEU:HD13	1.96	0.47
1:D:437:SER:O	1:D:441:GLN:HG2	2.15	0.47
1:A:512:SER:HB2	1:A:529:LEU:HD21	1.96	0.47
1:D:544:PRO:CG	1:D:596:MET:HE3	2.45	0.46
1:C:27:ILE:CD1	1:C:43:LEU:HB2	2.45	0.46
1:A:369:ALA:HA	1:A:371:PHE:CE2	2.50	0.46
1:A:437:SER:O	1:A:441:GLN:HG2	2.17	0.45
1:D:124:LEU:HD13	1:D:169:LEU:HD12	1.98	0.45
1:B:255:GLU:HG2	1:B:331:LEU:HD13	1.99	0.45
1:A:179:LEU:HD23	1:C:431:ILE:HD13	1.99	0.45
1:A:85:GLY:HA2	1:C:424:TYR:OH	2.17	0.45
1:A:528:LEU:HG	1:A:555:LEU:HD22	1.98	0.44
1:C:567:HIS:O	1:C:568:LYS:HB2	2.18	0.44
1:B:598:ALA:O	1:B:602:LEU:HB2	2.17	0.44
1:C:130:ARG:HD2	5:C:2052:HOH:O	2.16	0.44
1:D:270:GLU:HB2	5:D:2071:HOH:O	2.17	0.44
1:D:179:LEU:HD11	2:D:1175:BME:S2	2.58	0.44
1:C:131:SER:HB2	1:C:238:ALA:HB1	1.99	0.43
1:C:384:ARG:HG2	1:C:444:ALA:HA	2.00	0.43
1:C:15:LEU:HD21	1:C:673:LEU:HD12	2.01	0.43
1:B:163:VAL:HG13	1:B:199:ILE:HD13	2.01	0.43
1:A:422:VAL:HG11	1:C:99:GLU:HG3	2.00	0.43
1:B:182:LEU:HD23	1:B:185:ILE:HD12	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:551:LEU:O	1:B:555:LEU:HG	2.19	0.43
1:A:175:MDO:O2	1:A:179:LEU:HD13	2.20	0.42
1:A:114:THR:HG1	1:C:657:PHE:HZ	1.67	0.42
1:A:90:SER:HB2	1:B:318:LYS:HB3	2.01	0.42
1:B:562:THR:HG23	1:B:566:LEU:HD12	2.00	0.42
1:C:162:ASN:ND2	1:C:200:GLY:HA2	2.34	0.42
1:B:353:ASN:H	1:B:353:ASN:ND2	2.18	0.41
1:C:80:TYR:HB3	1:C:367:HIS:CD2	2.55	0.41
1:A:68:TRP:O	1:A:72:LYS:HG2	2.20	0.41
1:B:70:GLN:OE1	1:B:222:GLN:HB3	2.21	0.41
1:D:265:ILE:O	1:D:266:PHE:HB2	2.21	0.41
1:B:43:LEU:HD22	1:B:134:LEU:HD22	2.01	0.41
1:C:86:PHE:CE2	1:C:104:LEU:HB2	2.55	0.41
1:A:322:TYR:CZ	1:B:459:GLN:HG2	2.55	0.41
1:B:383:VAL:O	1:B:387:VAL:HG23	2.21	0.41
1:C:33:THR:HA	1:C:34:PRO:HD3	1.91	0.41
1:C:86:PHE:HB3	2:C:1175:BME:H11	2.03	0.41
1:D:84:THR:HG22	1:D:85:GLY:O	2.20	0.41
1:A:175:MDO:HB1	1:B:322:TYR:HE2	1.86	0.40
1:C:494:VAL:O	1:C:498:GLN:HG3	2.20	0.40
1:B:114:THR:HG22	1:D:657:PHE:CZ	2.56	0.40
1:B:231:ASN:HA	1:B:231:ASN:HD22	1.73	0.40
1:B:10:HIS:NE2	1:B:255:GLU:OE2	2.55	0.40
1:C:81:GLY:HA3	1:C:227:LEU:HD22	2.03	0.40
1:C:500:GLU:HG3	1:C:537:VAL:HG12	2.03	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles ⓘ

### 5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	633/705 (90%)	621 (98%)	12 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	637/705 (90%)	623 (98%)	13 (2%)	1 (0%)	47	52
1	C	635/705 (90%)	623 (98%)	12 (2%)	0	100	100
1	D	634/705 (90%)	620 (98%)	14 (2%)	0	100	100
All	All	2539/2820 (90%)	2487 (98%)	51 (2%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	573	GLU

### 5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	546/592 (92%)	534 (98%)	12 (2%)	52	62
1	B	551/592 (93%)	536 (97%)	15 (3%)	44	54
1	C	547/592 (92%)	536 (98%)	11 (2%)	55	66
1	D	547/592 (92%)	531 (97%)	16 (3%)	42	51
All	All	2191/2368 (92%)	2137 (98%)	54 (2%)	47	57

All (54) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	32	THR
1	A	59	ARG
1	A	94	THR
1	A	102	GLU
1	A	107	CYS
1	A	121	VAL
1	A	179	LEU
1	A	231	ASN
1	A	268	ARG
1	A	392	LYS

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Mol	Chain	Res	Type
1	A	528	LEU
1	A	575	ASP
1	B	59	ARG
1	B	82	VAL
1	B	84	THR
1	B	97	LEU
1	B	102	GLU
1	B	107	CYS
1	B	231	ASN
1	B	268	ARG
1	B	353	ASN
1	B	392	LYS
1	B	557	GLN
1	B	562	THR
1	B	573	GLU
1	B	602	LEU
1	B	673	LEU
1	C	29	VAL
1	C	32	THR
1	C	92	ARG
1	C	107	CYS
1	C	123	GLU
1	C	231	ASN
1	C	268	ARG
1	C	353	ASN
1	C	606	LYS
1	C	618	VAL
1	C	619	ARG
1	D	82	VAL
1	D	107	CYS
1	D	124	LEU
1	D	209	GLU
1	D	231	ASN
1	D	268	ARG
1	D	312	ASP
1	D	325	ARG
1	D	353	ASN
1	D	392	LYS
1	D	481	LEU
1	D	533	LYS
1	D	552	LEU
1	D	575	ASP

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Mol	Chain	Res	Type
1	D	602	LEU
1	D	673	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	231	ASN
1	B	231	ASN
1	B	557	GLN
1	C	231	ASN
1	D	231	ASN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

4 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
1	MDO	A	175	1,2	12,13,14	2.77	6 (50%)	15,18,20	3.51	4 (26%)
1	MDO	B	175	1,2	12,13,14	2.72	6 (50%)	15,18,20	3.48	4 (26%)
1	MDO	C	175	1,2	12,13,14	2.81	6 (50%)	15,18,20	3.43	4 (26%)
1	MDO	D	175	1,2	12,13,14	2.80	5 (41%)	15,18,20	2.92	4 (26%)

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
1	MDO	A	175	1,2	-	0/4/23/24	0/1/1/1
1	MDO	B	175	1,2	-	2/4/23/24	0/1/1/1
1	MDO	C	175	1,2	-	2/4/23/24	0/1/1/1
1	MDO	D	175	1,2	-	3/4/23/24	0/1/1/1

All (23) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	175	MDO	O2-C2	6.46	1.36	1.23
1	A	175	MDO	O2-C2	6.25	1.36	1.23
1	C	175	MDO	O2-C2	5.92	1.35	1.23
1	B	175	MDO	O2-C2	5.80	1.35	1.23
1	D	175	MDO	O-C	4.25	1.44	1.19
1	B	175	MDO	O-C	4.15	1.43	1.19
1	C	175	MDO	O-C	4.12	1.43	1.19
1	A	175	MDO	O-C	4.10	1.43	1.19
1	C	175	MDO	CA-C1	3.39	1.56	1.51
1	C	175	MDO	C2-N3	-3.24	1.32	1.39
1	B	175	MDO	C2-N3	-3.10	1.32	1.39
1	D	175	MDO	C2-N3	-3.10	1.32	1.39
1	B	175	MDO	CA2-N2	-3.06	1.33	1.39
1	A	175	MDO	CA-C1	3.03	1.55	1.51
1	A	175	MDO	C2-N3	-2.98	1.32	1.39
1	B	175	MDO	CA-C1	2.96	1.55	1.51
1	C	175	MDO	CA2-N2	-2.92	1.33	1.39
1	A	175	MDO	CA2-N2	-2.75	1.34	1.39
1	D	175	MDO	CA2-N2	-2.67	1.34	1.39
1	D	175	MDO	CA-C1	2.60	1.55	1.51
1	C	175	MDO	CA2-C2	-2.33	1.38	1.43
1	B	175	MDO	CA2-C2	-2.27	1.38	1.43
1	A	175	MDO	CA2-C2	-2.18	1.38	1.43

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	175	MDO	CA2-C2-N3	8.86	107.56	103.37
1	B	175	MDO	CA2-C2-N3	8.85	107.56	103.37
1	A	175	MDO	O2-C2-CA2	-8.66	126.10	130.96
1	A	175	MDO	CA2-C2-N3	7.90	107.11	103.37
1	D	175	MDO	CA2-C2-N3	7.79	107.05	103.37
1	C	175	MDO	O2-C2-CA2	-7.35	126.83	130.96
1	B	175	MDO	O2-C2-CA2	-6.90	127.09	130.96

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	175	MDO	O-C-CA3	-5.93	108.47	126.39
1	A	175	MDO	O-C-CA3	-5.80	108.87	126.39
1	D	175	MDO	O-C-CA3	-5.09	111.03	126.39
1	C	175	MDO	O-C-CA3	-5.08	111.05	126.39
1	D	175	MDO	O2-C2-CA2	-4.78	128.28	130.96
1	C	175	MDO	N3-C1-N2	-2.85	109.48	111.45
1	D	175	MDO	N3-C1-N2	-2.73	109.56	111.45
1	B	175	MDO	N3-C1-N2	-2.68	109.60	111.45
1	A	175	MDO	N3-C1-N2	-2.22	109.92	111.45

There are no chirality outliers.

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	B	175	MDO	N2-C1-CA-CB
1	C	175	MDO	N2-C1-CA-CB
1	D	175	MDO	N2-C1-CA-CB
1	B	175	MDO	N3-C1-CA-CB
1	C	175	MDO	N3-C1-CA-CB
1	D	175	MDO	N3-C1-CA-CB
1	D	175	MDO	C-CA3-N3-C2

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	175	MDO	2	0

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

13 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond

length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	FMT	C	1680	-	0,2,2	0.00	-	0,1,1	0.00	-
3	FMT	B	1680	-	0,2,2	0.00	-	0,1,1	0.00	-
2	BME	B	1089	1	3,3,3	0.83	0	1,2,2	0.28	0
3	FMT	D	1679	-	0,2,2	0.00	-	0,1,1	0.00	-
2	BME	A	1175	1	3,3,3	0.65	0	1,2,2	0.26	0
2	BME	B	1175	1	3,3,3	0.68	0	1,2,2	0.37	0
2	BME	C	1175	1	3,3,3	0.61	0	1,2,2	0.04	0
2	BME	D	1175	1	3,3,3	0.65	0	1,2,2	0.33	0
2	BME	D	1089	1	3,3,3	0.64	0	1,2,2	0.23	0
3	FMT	A	1679	-	0,2,2	0.00	-	0,1,1	0.00	-
4	GOL	B	1679	-	5,5,5	0.36	0	5,5,5	0.40	0
2	BME	A	1089	1	3,3,3	0.71	0	1,2,2	0.01	0
2	BME	C	1089	1	3,3,3	0.53	0	1,2,2	0.17	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
2	BME	B	1089	1	-	1/1/1/1	-
2	BME	A	1175	1	-	0/1/1/1	-
2	BME	B	1175	1	-	0/1/1/1	-
2	BME	C	1175	1	-	0/1/1/1	-
2	BME	D	1175	1	-	0/1/1/1	-
2	BME	D	1089	1	-	0/1/1/1	-
4	GOL	B	1679	-	-	2/4/4/4	-
2	BME	A	1089	1	-	0/1/1/1	-
2	BME	C	1089	1	-	0/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	B	1679	GOL	O2-C2-C3-O3

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Mol	Chain	Res	Type	Atoms
4	B	1679	GOL	C1-C2-C3-O3
2	B	1089	BME	O1-C1-C2-S2

There are no ring outliers.

4 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	1680	FMT	1	0
2	B	1175	BME	1	0
2	C	1175	BME	2	0
2	D	1175	BME	1	0

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	B	2
1	A	1
1	D	1
1	C	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B	89:CYS	C	90:SER	N	2.14
1	B	173:VAL	C	174:SER	N	2.11
1	D	89:CYS	C	90:SER	N	2.03
1	A	89:CYS	C	90:SER	N	2.02
1	C	89:CYS	C	90:SER	N	1.98

## 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	643/705 (91%)	0.18	34 (5%) 26 27	16, 31, 54, 67	0
1	B	649/705 (92%)	0.23	28 (4%) 35 36	17, 32, 47, 68	0
1	C	645/705 (91%)	0.10	19 (2%) 51 52	16, 30, 47, 61	0
1	D	644/705 (91%)	0.18	27 (4%) 36 37	17, 31, 54, 71	0
All	All	2581/2820 (91%)	0.17	108 (4%) 36 37	16, 31, 50, 71	0

All (108) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	57	GLN	5.8
1	B	571	GLY	4.5
1	B	570	ASP	4.4
1	D	576	THR	4.4
1	C	678	GLY	4.3
1	A	520	LEU	4.3
1	D	57	GLN	4.2
1	D	56	GLU	4.1
1	B	56	GLU	4.1
1	D	577	LEU	3.9
1	A	576	THR	3.9
1	B	572	ILE	3.9
1	A	584	PHE	3.7
1	A	589	SER	3.6
1	A	566	LEU	3.6
1	C	573	GLU	3.6
1	C	591	ARG	3.6
1	B	202	ASP	3.6
1	B	574	THR	3.5
1	D	573	GLU	3.5
1	A	202	ASP	3.5

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Mol	Chain	Res	Type	RSRZ
1	C	569	LYS	3.5
1	A	564	LEU	3.5
1	B	573	GLU	3.5
1	D	574	THR	3.4
1	A	47	HIS	3.2
1	A	523	ASP	3.2
1	B	75	ASP	3.1
1	D	605	LYS	3.1
1	D	591	ARG	3.0
1	D	451	VAL	3.0
1	B	523	ASP	3.0
1	A	522	ASN	3.0
1	A	581	LEU	3.0
1	B	567	HIS	2.9
1	A	605	LYS	2.9
1	C	574	THR	2.9
1	A	568	LYS	2.9
1	A	519	GLY	2.8
1	C	586	LYS	2.8
1	C	677	LEU	2.8
1	D	586	LYS	2.8
1	A	57	GLN	2.8
1	C	576	THR	2.8
1	B	55	ALA	2.8
1	A	451	VAL	2.7
1	A	580	ARG	2.7
1	A	447	VAL	2.7
1	B	677	LEU	2.7
1	B	589	SER	2.6
1	C	568	LYS	2.6
1	D	564	LEU	2.6
1	A	121	VAL	2.6
1	A	567	HIS	2.6
1	C	451	VAL	2.5
1	B	447	VAL	2.5
1	C	590	ASP	2.5
1	A	56	GLU	2.5
1	D	202	ASP	2.5
1	D	467	ILE	2.5
1	A	217	ARG	2.5
1	B	8	ARG	2.5
1	B	12	LYS	2.5

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Mol	Chain	Res	Type	RSRZ
1	B	25	LYS	2.5
1	A	565	ALA	2.5
1	D	579	ASP	2.4
1	A	518	CYS	2.4
1	C	522	ASN	2.4
1	B	569	LYS	2.4
1	A	590	ASP	2.4
1	C	217	ARG	2.4
1	A	577	LEU	2.3
1	D	443	LEU	2.3
1	D	602	LEU	2.3
1	C	12	LYS	2.3
1	D	581	LEU	2.3
1	B	121	VAL	2.3
1	A	514	LEU	2.3
1	D	447	VAL	2.3
1	D	589	SER	2.3
1	B	437	SER	2.2
1	D	461	ILE	2.2
1	B	576	THR	2.2
1	A	449	THR	2.2
1	B	565	ALA	2.2
1	A	591	ARG	2.2
1	C	581	LEU	2.1
1	D	464	LEU	2.1
1	C	589	SER	2.1
1	B	449	THR	2.1
1	D	578	VAL	2.1
1	D	582	ALA	2.1
1	C	579	ASP	2.1
1	A	515	ALA	2.1
1	A	586	LYS	2.1
1	D	442	TYR	2.1
1	C	443	LEU	2.0
1	B	442	TYR	2.0
1	D	646	GLU	2.0
1	B	58	CYS	2.0
1	D	446	PRO	2.0
1	A	562	THR	2.0
1	B	444	ALA	2.0
1	C	434	ALA	2.0
1	A	575	ASP	2.0

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Mol	Chain	Res	Type	RSRZ
1	A	674	GLN	2.0
1	B	451	VAL	2.0
1	D	590	ASP	2.0

## 6.2 Non-standard residues in protein, DNA, RNA chains [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
1	MDO	B	175	13/14	0.92	0.13	26,27,31,35	0
1	MDO	A	175	13/14	0.93	0.12	22,24,27,32	0
1	MDO	D	175	13/14	0.93	0.15	22,23,26,31	0
1	MDO	C	175	13/14	0.94	0.13	22,24,27,32	0

## 6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
2	BME	D	1175	4/4	0.85	0.17	43,44,44,44	0
2	BME	B	1175	4/4	0.87	0.16	45,45,46,46	0
2	BME	C	1175	4/4	0.91	0.16	41,43,43,43	0
4	GOL	B	1679	6/6	0.93	0.11	37,38,38,39	0
2	BME	D	1089	4/4	0.94	0.10	30,31,32,34	0
2	BME	A	1175	4/4	0.94	0.13	43,43,43,43	0
2	BME	A	1089	4/4	0.94	0.13	33,34,35,35	0
3	FMT	C	1680	3/3	0.95	0.10	37,37,37,38	0
2	BME	C	1089	4/4	0.95	0.13	31,31,32,34	0
3	FMT	B	1680	3/3	0.96	0.14	43,43,43,44	0
3	FMT	D	1679	3/3	0.97	0.09	32,32,32,32	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	BME	B	1089	4/4	0.97	0.11	39,39,39,40	0
3	FMT	A	1679	3/3	0.97	0.12	31,31,32,33	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.