



# Full wwPDB X-ray Structure Validation Report

Feb 28, 2014 – 04:00 PM GMT

PDB ID : 2NV1  
Title : Structure of the synthase subunit Pdx1 (YaaD) of PLP synthase from *Bacillus subtilis*  
Authors : Strohmeier, M.; Tews, I.; Sinning, I.  
Deposited on : 2006-11-10  
Resolution : 2.08 Å(reported)

This is a full wwPDB 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 <http://wwpdb.org/ValidationPDFNotes.html>

---

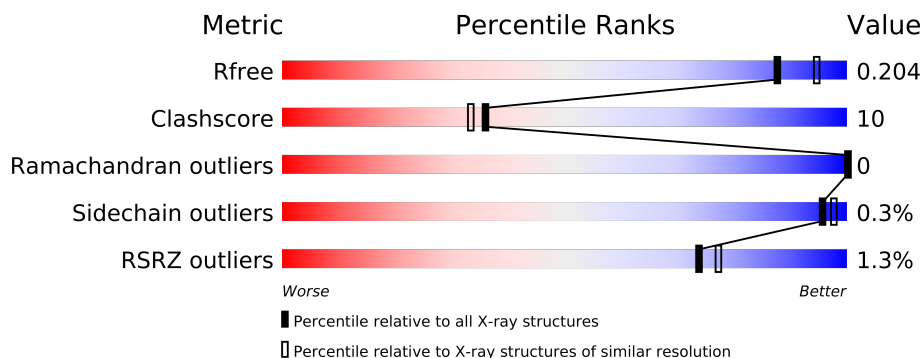
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.15 2013  
Xtriage (Phenix) : dev-1323  
EDS : stable22639  
Percentile statistics : 21963  
Refmac : 5.8.0049  
CCP4 : 6.3.0 (Settle)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : stable22683

# 1 Overall quality at a glance

The reported resolution of this entry is 2.08 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))
$R_{free}$	66092	3396 (2.10-2.06)
Clashscore	79885	4085 (2.10-2.06)
Ramachandran outliers	78287	4045 (2.10-2.06)
Sidechain outliers	78261	4046 (2.10-2.06)
RSRZ outliers	66119	3397 (2.10-2.06)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	305	
1	B	305	
1	C	305	
1	D	305	
1	E	305	
1	F	305	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
3	MG	A	3003	-	X
3	MG	A	3004	-	X

*Continued on next page...*

*Continued from previous page...*

Mol	Type	Chain	Res	Geometry	Electron density
3	MG	A	3009	-	X
3	MG	B	3010	-	X
3	MG	C	3015	-	X
3	MG	C	3022	-	X
3	MG	D	3023	-	X
3	MG	D	3027	-	X
3	MG	E	3032	-	X
3	MG	F	3033	-	X
4	EDO	A	3005	-	X
4	EDO	A	3006	-	X
4	EDO	B	3011	-	X
4	EDO	B	3012	-	X
4	EDO	C	3017	-	X
4	EDO	C	3018	-	X
4	EDO	C	3019	-	X
4	EDO	D	3024	-	X
4	EDO	E	3029	-	X
4	EDO	F	3034	-	X
4	EDO	F	3035	-	X

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 13822 atoms, of which 0 are hydrogen and 0 are deuterium.

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 Pyridoxal biosynthesis lyase pdxS.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	259	Total	C	N	O	S	0	2	0
			1930	1209	330	375	16			
1	B	252	Total	C	N	O	S	0	2	0
			1875	1177	322	362	14			
1	C	256	Total	C	N	O	S	0	2	0
			1915	1199	329	371	16			
1	D	256	Total	C	N	O	S	0	1	0
			1907	1196	327	368	16			
1	E	256	Total	C	N	O	S	0	2	0
			1910	1196	326	371	17			
1	F	250	Total	C	N	O	S	0	1	0
			1850	1161	317	358	14			

There are 66 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	MET	-	CLONING ARTIFACT	UNP P37527
A	-1	ALA	-	CLONING ARTIFACT	UNP P37527
A	0	SER	-	CLONING ARTIFACT	UNP P37527
A	295	LEU	-	EXPRESSION TAG	UNP P37527
A	296	GLU	-	EXPRESSION TAG	UNP P37527
A	297	HIS	-	EXPRESSION TAG	UNP P37527
A	298	HIS	-	EXPRESSION TAG	UNP P37527
A	299	HIS	-	EXPRESSION TAG	UNP P37527
A	300	HIS	-	EXPRESSION TAG	UNP P37527
A	301	HIS	-	EXPRESSION TAG	UNP P37527
A	302	HIS	-	EXPRESSION TAG	UNP P37527
B	-2	MET	-	CLONING ARTIFACT	UNP P37527
B	-1	ALA	-	CLONING ARTIFACT	UNP P37527
B	0	SER	-	CLONING ARTIFACT	UNP P37527
B	295	LEU	-	EXPRESSION TAG	UNP P37527
B	296	GLU	-	EXPRESSION TAG	UNP P37527
B	297	HIS	-	EXPRESSION TAG	UNP P37527

*Continued on next page...*

*Continued from previous page...*

Chain	Residue	Modelled	Actual	Comment	Reference
B	298	HIS	-	EXPRESSION TAG	UNP P37527
B	299	HIS	-	EXPRESSION TAG	UNP P37527
B	300	HIS	-	EXPRESSION TAG	UNP P37527
B	301	HIS	-	EXPRESSION TAG	UNP P37527
B	302	HIS	-	EXPRESSION TAG	UNP P37527
C	-2	MET	-	CLONING ARTIFACT	UNP P37527
C	-1	ALA	-	CLONING ARTIFACT	UNP P37527
C	0	SER	-	CLONING ARTIFACT	UNP P37527
C	295	LEU	-	EXPRESSION TAG	UNP P37527
C	296	GLU	-	EXPRESSION TAG	UNP P37527
C	297	HIS	-	EXPRESSION TAG	UNP P37527
C	298	HIS	-	EXPRESSION TAG	UNP P37527
C	299	HIS	-	EXPRESSION TAG	UNP P37527
C	300	HIS	-	EXPRESSION TAG	UNP P37527
C	301	HIS	-	EXPRESSION TAG	UNP P37527
C	302	HIS	-	EXPRESSION TAG	UNP P37527
D	-2	MET	-	CLONING ARTIFACT	UNP P37527
D	-1	ALA	-	CLONING ARTIFACT	UNP P37527
D	0	SER	-	CLONING ARTIFACT	UNP P37527
D	295	LEU	-	EXPRESSION TAG	UNP P37527
D	296	GLU	-	EXPRESSION TAG	UNP P37527
D	297	HIS	-	EXPRESSION TAG	UNP P37527
D	298	HIS	-	EXPRESSION TAG	UNP P37527
D	299	HIS	-	EXPRESSION TAG	UNP P37527
D	300	HIS	-	EXPRESSION TAG	UNP P37527
D	301	HIS	-	EXPRESSION TAG	UNP P37527
D	302	HIS	-	EXPRESSION TAG	UNP P37527
E	-2	MET	-	CLONING ARTIFACT	UNP P37527
E	-1	ALA	-	CLONING ARTIFACT	UNP P37527
E	0	SER	-	CLONING ARTIFACT	UNP P37527
E	295	LEU	-	EXPRESSION TAG	UNP P37527
E	296	GLU	-	EXPRESSION TAG	UNP P37527
E	297	HIS	-	EXPRESSION TAG	UNP P37527
E	298	HIS	-	EXPRESSION TAG	UNP P37527
E	299	HIS	-	EXPRESSION TAG	UNP P37527
E	300	HIS	-	EXPRESSION TAG	UNP P37527
E	301	HIS	-	EXPRESSION TAG	UNP P37527
E	302	HIS	-	EXPRESSION TAG	UNP P37527
F	-2	MET	-	CLONING ARTIFACT	UNP P37527
F	-1	ALA	-	CLONING ARTIFACT	UNP P37527
F	0	SER	-	CLONING ARTIFACT	UNP P37527
F	295	LEU	-	EXPRESSION TAG	UNP P37527

*Continued on next page...*

*Continued from previous page...*

Chain	Residue	Modelled	Actual	Comment	Reference
F	296	GLU	-	EXPRESSION TAG	UNP P37527
F	297	HIS	-	EXPRESSION TAG	UNP P37527
F	298	HIS	-	EXPRESSION TAG	UNP P37527
F	299	HIS	-	EXPRESSION TAG	UNP P37527
F	300	HIS	-	EXPRESSION TAG	UNP P37527
F	301	HIS	-	EXPRESSION TAG	UNP P37527
F	302	HIS	-	EXPRESSION TAG	UNP P37527

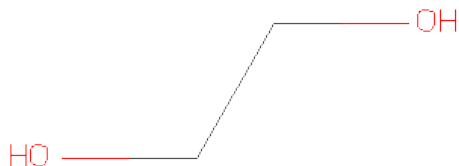
- Molecule 2 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	D	2	Total Cl 2 2	0	0
2	E	2	Total Cl 2 2	0	0
2	B	2	Total Cl 2 2	0	0
2	C	2	Total Cl 2 2	0	0
2	A	2	Total Cl 2 2	0	0
2	F	2	Total Cl 2 2	0	0

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

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

- Molecule 4 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
4	A	1	Total	C	O	0	0
			4	2	2		
4	A	1	Total	C	O	0	0
			4	2	2		
4	B	1	Total	C	O	0	0
			4	2	2		
4	B	1	Total	C	O	0	0
			4	2	2		
4	C	1	Total	C	O	0	0
			4	2	2		
4	C	1	Total	C	O	0	0
			4	2	2		
4	C	1	Total	C	O	0	0
			4	2	2		
4	D	1	Total	C	O	0	0
			4	2	2		
4	E	1	Total	C	O	0	0
			4	2	2		
4	F	1	Total	C	O	0	0
			4	2	2		
4	F	1	Total	C	O	0	0
			4	2	2		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	381	Total	O	0	0
			381	381		

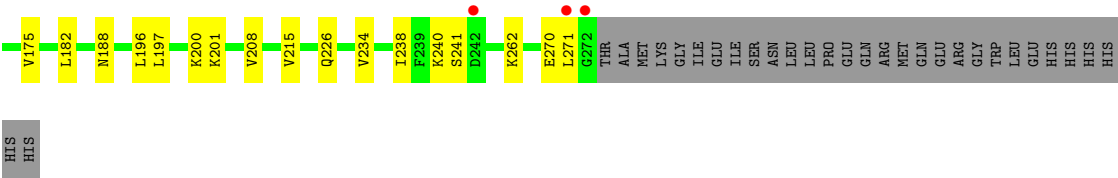
*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	425	Total 425	O 425	0	0
5	C	373	Total 373	O 373	0	0
5	D	388	Total 388	O 388	0	0
5	E	398	Total 398	O 398	0	0
5	F	402	Total 402	O 402	0	0

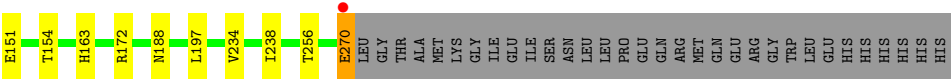






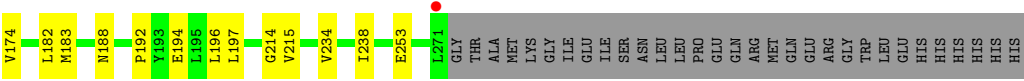
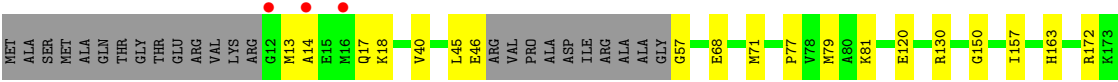
• Molecule 1: Pyridoxal biosynthesis lyase pdxS

Chain E:



• Molecule 1: Pyridoxal biosynthesis lyase pdxS

Chain F:



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	101.06Å 106.20Å 182.33Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.68 – 2.08 46.76 – 2.08	Depositor EDS
% Data completeness (in resolution range)	98.6 (48.68-2.08) 98.6 (46.76-2.08)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.10	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.81 (at 2.08Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, $R_{free}$	0.142 , 0.191 0.156 , 0.204	Depositor DCC
$R_{free}$ test set	5782 reflections (5.22%)	DCC
Wilson B-factor (Å <sup>2</sup> )	25.1	Xtriage
Anisotropy	0.043	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , 78.7	EDS
Estimated twinning fraction	0.017 for k,h,-l	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 116580 reflections	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	13822	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	41.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 15.31% of the height of the origin peak. No significant pseudotranslation is detected.*

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

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MG, EDO, 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	0.76	0/1960	0.76	1/2643 (0.0%)
1	B	0.76	0/1905	0.76	0/2570
1	C	0.75	0/1945	0.73	1/2620 (0.0%)
1	D	0.75	0/1932	0.74	1/2604 (0.0%)
1	E	0.80	0/1940	0.74	1/2616 (0.0%)
1	F	0.82	0/1876	0.77	1/2532 (0.0%)
All	All	0.77	0/11558	0.75	5/15585 (0.0%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	172	ARG	NE-CZ-NH1	5.79	123.20	120.30
1	E	172	ARG	NE-CZ-NH1	5.29	122.94	120.30
1	D	24	ASP	CB-CG-OD2	-5.24	113.58	118.30
1	C	63	ASP	CB-CG-OD1	5.13	122.92	118.30
1	A	182	LEU	CB-CG-CD1	-5.12	102.29	111.00

There are no chirality outliers.

There are no planarity outliers.

### 5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1930	0	1942	37	0
1	B	1875	0	1882	25	0
1	C	1915	0	1933	47	0
1	D	1907	0	1931	46	0
1	E	1910	0	1920	39	0
1	F	1850	0	1862	35	1
2	A	2	0	0	2	0
2	B	2	0	0	1	0
2	C	2	0	0	1	0
2	D	2	0	0	1	0
2	E	2	0	0	2	0
2	F	2	0	0	1	0
3	A	3	0	0	0	0
3	B	1	0	0	0	0
3	C	3	0	0	0	0
3	D	2	0	0	0	0
3	E	2	0	0	0	0
3	F	1	0	0	0	0
4	A	8	0	12	0	0
4	B	8	0	12	0	1
4	C	12	0	16	9	0
4	D	4	0	6	0	0
4	E	4	0	5	0	0
4	F	8	0	12	3	0
5	A	381	0	0	25	0
5	B	425	0	0	18	1
5	C	373	0	0	21	1
5	D	388	0	0	28	0
5	E	398	0	0	25	1
5	F	402	0	0	21	1
All	All	13822	0	11533	238	3

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 10.

All (238) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:211:ALA:HB3	5:B:4411:HOH:O	1.29	1.32
1:D:14:ALA:HB2	5:D:4401:HOH:O	1.40	1.21
1:A:264:ILE:HG23	5:A:4372:HOH:O	1.41	1.19
1:F:120:GLU:HG3	5:F:4169:HOH:O	1.48	1.12
1:A:13:MET:HE1	5:A:4170:HOH:O	1.52	1.06
1:A:226:GLN:HB2	5:A:4379:HOH:O	1.61	0.99

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:C:17[B]:GLN:OE1	5:C:4325:HOH:O	1.80	0.99
1:C:194:GLU:HB2	4:C:3017:EDO:H12	1.45	0.95
1:C:192:PRO:HB3	4:C:3017:EDO:H22	1.50	0.94
1:C:16:MET:HE3	5:C:4301:HOH:O	1.68	0.94
1:F:14:ALA:HB2	5:F:4401:HOH:O	1.69	0.93
1:B:143:ALA:HA	5:B:4437:HOH:O	1.70	0.92
1:E:13:MET:HE1	5:E:4378:HOH:O	1.71	0.90
1:D:226:GLN:NE2	5:D:4094:HOH:O	2.04	0.88
1:A:226:GLN:OE1	5:A:4169:HOH:O	1.93	0.87
1:F:253[B]:GLU:OE1	5:F:4314:HOH:O	1.92	0.86
1:C:17[B]:GLN:HE22	1:C:79:MET:CE	1.89	0.86
1:C:17[B]:GLN:HE22	1:C:79:MET:HE1	1.43	0.84
1:B:126:VAL:HG22	5:B:4377:HOH:O	1.79	0.83
1:B:232:VAL:HG22	5:B:4411:HOH:O	1.78	0.82
1:B:125:PHE:HB2	5:B:4437:HOH:O	1.79	0.82
2:B:3007:CL:CL	5:B:4100:HOH:O	2.35	0.81
1:C:16:MET:HE1	5:C:4336:HOH:O	1.83	0.78
1:E:10:LYS:HE2	5:E:4437:HOH:O	1.83	0.78
1:D:45:LEU:HD21	1:D:81:LYS:HE3	1.65	0.77
1:B:72:ASN:HB3	5:B:4433:HOH:O	1.85	0.77
1:A:179:GLU:HG2	5:A:4238:HOH:O	1.85	0.76
1:E:66:ILE:HB	5:E:4397:HOH:O	1.84	0.76
1:F:194:GLU:H	4:F:3034:EDO:H22	1.50	0.76
1:F:14:ALA:HA	5:F:4392:HOH:O	1.85	0.76
1:E:66:ILE:HD12	5:E:4397:HOH:O	1.85	0.75
1:A:79:MET:HE3	5:A:4359:HOH:O	1.85	0.74
1:A:197:LEU:HD12	5:A:4349:HOH:O	1.89	0.73
1:C:7:GLU:N	5:C:4280:HOH:O	2.22	0.72
1:E:14:ALA:HB2	5:E:4363:HOH:O	1.88	0.72
1:F:46:GLU:C	5:F:4347:HOH:O	2.27	0.72
1:D:8:ARG:N	5:D:4397:HOH:O	2.22	0.72
2:E:3025:CL:CL	5:E:4141:HOH:O	2.44	0.72
1:D:197:LEU:HD12	5:D:4319:HOH:O	1.89	0.71
2:E:3026:CL:CL	5:E:4428:HOH:O	2.44	0.71
1:A:14:ALA:HA	1:A:17[B]:GLN:HE21	1.55	0.71
2:C:3013:CL:CL	5:C:4107:HOH:O	2.46	0.70
1:B:45:LEU:HD21	1:B:81:LYS:HE2	1.73	0.69
1:E:13:MET:HA	1:E:16[A]:MET:CE	2.23	0.69
1:E:197:LEU:HD12	5:E:4392:HOH:O	1.92	0.69
2:A:3001:CL:CL	5:A:4103:HOH:O	2.47	0.69
1:E:36:GLU:HB2	5:E:4274:HOH:O	1.91	0.68
1:C:45:LEU:HD21	1:C:81:LYS:HE3	1.75	0.68

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:C:194:GLU:CB	4:C:3017:EDO:H12	2.22	0.67
1:D:240:LYS:NZ	5:D:4366:HOH:O	2.26	0.67
1:D:188:ASN:ND2	5:D:4212:HOH:O	2.27	0.67
1:A:238:ILE:HG12	5:A:4290:HOH:O	1.95	0.67
1:A:218:PRO:CB	5:A:4372:HOH:O	2.44	0.66
1:E:13:MET:HA	1:E:16[A]:MET:HE3	1.79	0.65
1:D:188:ASN:HB2	5:D:4419:HOH:O	1.96	0.65
2:F:3030:CL:CL	5:F:4096:HOH:O	2.51	0.65
1:A:194:GLU:OE2	5:A:4121:HOH:O	2.15	0.65
1:E:46:GLU:HG3	1:E:66:ILE:HD12	1.78	0.64
1:A:45:LEU:HD21	1:A:81:LYS:HE3	1.80	0.64
1:F:13:MET:CA	5:F:4313:HOH:O	2.46	0.64
1:F:183:MET:HG3	5:F:4379:HOH:O	1.97	0.63
1:C:24:ASP:OD1	4:C:3019:EDO:O1	2.17	0.62
1:D:262:LYS:NZ	5:D:4216:HOH:O	2.27	0.62
1:E:197:LEU:CD1	5:E:4392:HOH:O	2.45	0.62
1:D:234:VAL:HG21	1:D:238:ILE:HD11	1.82	0.61
1:F:150:GLY:H	1:F:163:HIS:HD2	1.48	0.61
1:B:17:GLN:HG3	5:B:4410:HOH:O	1.99	0.61
1:D:16:MET:HE3	5:D:4391:HOH:O	1.99	0.61
1:A:234:VAL:HG21	1:A:238:ILE:HD11	1.83	0.60
1:C:17[B]:GLN:NE2	1:C:79:MET:HE1	2.15	0.60
1:A:81:LYS:NZ	5:A:4087:HOH:O	2.29	0.59
1:D:14:ALA:O	1:D:17:GLN:HG2	2.01	0.59
1:D:130:ARG:HG3	1:D:149:LYS:HD2	1.85	0.59
1:C:192:PRO:CB	4:C:3017:EDO:H22	2.30	0.59
1:B:18:LYS:HD2	5:B:4417:HOH:O	2.02	0.59
1:E:46:GLU:HG3	1:E:66:ILE:CD1	2.34	0.58
1:A:218:PRO:HB2	5:A:4372:HOH:O	2.03	0.58
1:F:192:PRO:HB3	4:F:3034:EDO:H12	1.85	0.58
2:D:3020:CL:CL	5:D:4113:HOH:O	2.54	0.58
1:C:120:GLU:HG3	5:C:4292:HOH:O	2.03	0.58
1:C:240:LYS:HD3	1:C:240:LYS:N	2.19	0.57
1:E:10:LYS:HG2	5:E:4437:HOH:O	2.04	0.57
1:A:214:GLY:HA2	5:A:4301:HOH:O	2.06	0.56
1:E:256:THR:HB	5:E:4441:HOH:O	2.05	0.55
1:F:18:LYS:HB3	5:F:4371:HOH:O	2.05	0.55
1:E:124:PRO:HA	5:E:4437:HOH:O	2.06	0.55
1:A:46:GLU:HG3	1:A:66:ILE:CD1	2.37	0.55
1:A:46:GLU:HG3	1:A:66:ILE:HD12	1.89	0.55
1:D:13:MET:HA	1:D:16:MET:HE2	1.89	0.55
1:B:144:SER:N	5:B:4437:HOH:O	2.38	0.54

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:D:271:LEU:HD13	5:D:4361:HOH:O	2.06	0.54
1:B:15:GLU:O	1:B:18:LYS:HB2	2.07	0.54
1:E:13:MET:O	1:E:16[B]:MET:HG2	2.07	0.54
1:E:10:LYS:CD	5:E:4437:HOH:O	2.55	0.54
1:C:191:ALA:O	4:C:3018:EDO:C1	2.55	0.54
1:E:6:THR:HG23	1:E:9:VAL:H	1.71	0.54
1:E:16[B]:MET:CE	5:E:4353:HOH:O	2.56	0.54
1:B:46:GLU:HB3	5:B:4416:HOH:O	2.08	0.54
1:E:22:ILE:HG12	1:E:41:ALA:HB3	1.90	0.54
1:E:234:VAL:HG21	1:E:238:ILE:HD11	1.91	0.53
1:B:13:MET:O	1:B:16[B]:MET:CG	2.56	0.53
1:F:45:LEU:HD21	1:F:81:LYS:HE3	1.91	0.53
1:E:13:MET:HA	1:E:16[A]:MET:HE2	1.91	0.53
1:B:194:GLU:HG3	5:B:4423:HOH:O	2.09	0.52
1:E:188:ASN:ND2	5:E:4232:HOH:O	2.42	0.52
1:F:150:GLY:H	1:F:163:HIS:CD2	2.26	0.52
1:F:57:GLY:N	5:F:4382:HOH:O	2.42	0.52
1:C:226:GLN:NE2	5:C:4059:HOH:O	2.37	0.52
1:C:198:GLN:NE2	1:C:202:ASP:OD1	2.43	0.52
1:D:17:GLN:NE2	1:D:145:MET:SD	2.83	0.51
1:A:226:GLN:NE2	5:A:4129:HOH:O	2.42	0.51
1:D:201:LYS:HG3	5:D:4319:HOH:O	2.10	0.51
1:F:17:GLN:CD	5:F:4392:HOH:O	2.49	0.51
1:C:246:LYS:NZ	5:C:4395:HOH:O	2.43	0.51
1:C:81:LYS:NZ	4:C:3019:EDO:H12	2.25	0.51
1:F:130:ARG:HG2	1:F:163:HIS:CE1	2.45	0.51
2:A:3001:CL:CL	5:A:4328:HOH:O	2.56	0.51
1:C:13:MET:HG2	5:C:4379:HOH:O	2.09	0.51
1:D:47:ARG:CB	5:D:4244:HOH:O	2.59	0.51
1:C:10:LYS:HA	1:C:13:MET:HE3	1.93	0.50
1:A:68:GLU:HA	1:A:71:MET:HE2	1.93	0.50
1:D:45:LEU:CD2	1:D:81:LYS:HE3	2.37	0.50
1:D:168:ASN:CG	5:D:4356:HOH:O	2.49	0.50
1:B:249:LYS:O	1:B:253[B]:GLU:HG2	2.11	0.50
1:A:55:ALA:N	5:A:4302:HOH:O	2.44	0.50
1:B:127:CYS:CA	5:B:4377:HOH:O	2.60	0.50
1:C:100:TYR:HD2	5:C:4320:HOH:O	1.93	0.49
1:C:240:LYS:NZ	5:C:4262:HOH:O	2.24	0.49
1:E:10:LYS:CE	5:E:4437:HOH:O	2.50	0.49
1:D:100:TYR:HD2	5:D:4420:HOH:O	1.94	0.49
1:D:57:GLY:HA3	5:D:4272:HOH:O	2.12	0.49
1:C:46:GLU:O	1:C:47:ARG:CB	2.61	0.49

*Continued on next page...*



*Continued from previous page...*

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:C:11:ARG:HB3	5:C:4305:HOH:O	2.11	0.49
1:A:218:PRO:HB3	5:A:4372:HOH:O	2.11	0.49
1:C:47:ARG:O	5:C:4289:HOH:O	2.20	0.49
1:E:29:GLU:HG3	5:E:4446:HOH:O	2.13	0.49
1:B:232:VAL:HA	5:B:4411:HOH:O	2.12	0.48
1:F:17:GLN:OE1	5:F:4392:HOH:O	2.20	0.48
1:F:14:ALA:HB3	5:F:4386:HOH:O	2.14	0.48
1:D:197:LEU:CD1	5:D:4319:HOH:O	2.54	0.48
1:C:186:ALA:HB1	4:C:3018:EDO:H12	1.96	0.48
1:D:241:SER:HB2	5:D:4412:HOH:O	2.13	0.48
1:D:234:VAL:CG2	1:D:238:ILE:HD11	2.43	0.48
1:D:57:GLY:CA	5:D:4272:HOH:O	2.61	0.47
1:A:157:ILE:HD13	1:A:215:VAL:HA	1.96	0.47
1:F:163:HIS:HE1	5:F:4136:HOH:O	1.97	0.47
1:F:68:GLU:HA	1:F:71:MET:CE	2.45	0.47
1:F:234:VAL:HG21	1:F:238:ILE:HD11	1.96	0.47
1:B:153:GLY:C	5:B:4345:HOH:O	2.51	0.47
1:E:45:LEU:HD21	1:E:81:LYS:HE2	1.97	0.47
1:F:188:ASN:HB3	5:F:4404:HOH:O	2.14	0.47
1:D:120:GLU:HG3	5:D:4308:HOH:O	2.15	0.47
1:D:100:TYR:HE2	5:D:4401:HOH:O	1.97	0.47
1:D:14:ALA:O	1:D:17:GLN:CG	2.62	0.47
1:C:214:GLY:HA2	5:C:4216:HOH:O	2.15	0.47
1:D:182:LEU:HD22	1:D:196:LEU:HD13	1.96	0.47
1:D:13:MET:HG3	5:D:4388:HOH:O	2.14	0.46
1:F:174:VAL:HG13	1:F:182:LEU:HD21	1.96	0.46
1:A:270:GLU:HB2	5:A:4331:HOH:O	2.16	0.46
1:A:14:ALA:HA	1:A:17[B]:GLN:NE2	2.27	0.46
1:A:194:GLU:HB2	5:A:4175:HOH:O	2.16	0.46
1:E:67:VAL:HG12	1:E:71:MET:CE	2.45	0.46
1:B:151:GLU:O	5:B:4270:HOH:O	2.21	0.46
1:E:101:ILE:HD12	1:E:123:VAL:HG11	1.97	0.46
1:F:214:GLY:HA2	5:F:4140:HOH:O	2.15	0.46
1:C:17[B]:GLN:CD	5:C:4325:HOH:O	2.42	0.45
1:C:191:ALA:O	4:C:3018:EDO:H11	2.16	0.45
1:F:68:GLU:HA	1:F:71:MET:HE2	1.98	0.45
1:B:18:LYS:HE2	5:B:4279:HOH:O	2.15	0.45
1:D:18:LYS:N	5:D:4289:HOH:O	2.48	0.45
1:A:151:GLU:HG2	1:A:154:THR:HG21	1.98	0.45
1:D:175:VAL:O	1:D:200:LYS:NZ	2.49	0.45
1:F:253[B]:GLU:CD	5:F:4314:HOH:O	2.50	0.45
1:A:130:ARG:HG3	1:A:149:LYS:HD2	1.98	0.45

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:D:68:GLU:HA	1:D:71:MET:HE2	1.99	0.45
1:A:55:ALA:N	5:A:4368:HOH:O	2.50	0.45
1:C:150:GLY:H	1:C:163:HIS:HD2	1.63	0.45
1:D:270:GLU:HG2	5:E:4221:HOH:O	2.16	0.45
1:B:40:VAL:O	1:B:77:PRO:HD2	2.16	0.44
1:D:145:MET:HG3	1:D:208:VAL:HG23	2.00	0.44
1:C:40:VAL:O	1:C:77:PRO:HD2	2.17	0.44
1:C:234:VAL:HG21	1:C:238:ILE:HD11	1.99	0.44
1:F:194:GLU:HB2	4:F:3034:EDO:O1	2.17	0.44
1:C:201:LYS:NZ	5:C:4318:HOH:O	2.50	0.44
1:A:178:SER:OG	1:A:180:ASP:OD1	2.31	0.44
1:A:13:MET:CE	5:A:4170:HOH:O	2.33	0.44
1:C:17[B]:GLN:NE2	1:C:79:MET:CE	2.70	0.44
1:D:71:MET:HA	1:D:78:VAL:HG21	1.99	0.44
1:E:79:MET:HG2	1:E:100:TYR:HB2	2.00	0.44
1:F:197:LEU:HD12	5:F:4403:HOH:O	2.18	0.44
1:E:36:GLU:HB3	5:E:4431:HOH:O	2.18	0.43
1:F:57:GLY:HA2	5:F:4382:HOH:O	2.18	0.43
1:A:55:ALA:HB2	5:A:4368:HOH:O	2.18	0.43
1:C:67:VAL:O	1:C:71:MET:HG3	2.18	0.43
1:C:178:SER:OG	1:C:180:ASP:OD1	2.36	0.43
1:D:16:MET:CE	5:D:4391:HOH:O	2.62	0.43
1:F:194:GLU:OE2	5:F:4080:HOH:O	2.21	0.43
1:C:198:GLN:HG2	5:C:4125:HOH:O	2.19	0.43
1:E:16[B]:MET:SD	5:E:4353:HOH:O	2.62	0.43
1:D:240:LYS:CD	1:D:240:LYS:N	2.82	0.43
1:D:157:ILE:HD13	1:D:215:VAL:HA	2.01	0.43
1:D:201:LYS:HE3	5:D:4319:HOH:O	2.18	0.43
1:D:122:THR:HG23	5:D:4176:HOH:O	2.19	0.43
1:E:101:ILE:CD1	1:E:123:VAL:HG11	2.48	0.43
1:E:151:GLU:HG2	1:E:154:THR:HG21	2.01	0.43
1:E:67:VAL:HG12	1:E:71:MET:HE2	2.02	0.42
1:C:174:VAL:HG13	1:C:182:LEU:HD21	2.00	0.42
1:C:57:GLY:N	5:C:4281:HOH:O	2.51	0.42
1:D:9:VAL:O	1:D:13:MET:HG2	2.19	0.42
1:C:57:GLY:HA3	5:C:4374:HOH:O	2.19	0.42
1:B:67:VAL:HG12	1:B:71:MET:CE	2.49	0.42
1:C:225:MET:HE2	5:C:4155:HOH:O	2.20	0.42
1:B:250:ALA:HA	1:B:267:LEU:HD22	2.01	0.42
1:B:241:SER:HB2	5:B:4395:HOH:O	2.19	0.42
1:E:63:ASP:HB3	5:E:4397:HOH:O	2.19	0.42
1:B:22:ILE:HG12	1:B:41:ALA:HB3	2.01	0.42

*Continued on next page...*

Continued from previous page...

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:17[B]:GLN:OE1	1:A:22:ILE:HD11	2.20	0.42
1:D:240:LYS:N	1:D:240:LYS:HD3	2.35	0.42
1:F:157:ILE:HD13	1:F:215:VAL:HA	2.00	0.42
1:A:253[B]:GLU:CD	5:A:4374:HOH:O	2.59	0.41
1:E:10:LYS:CG	5:E:4437:HOH:O	2.66	0.41
1:C:147:ARG:HA	1:C:210:PHE:O	2.20	0.41
1:D:10:LYS:HE2	5:D:4095:HOH:O	2.20	0.41
1:A:45:LEU:HD21	1:A:81:LYS:CE	2.50	0.41
1:E:270:GLU:HB2	5:E:4429:HOH:O	2.21	0.41
1:C:249:LYS:HG2	5:C:4349:HOH:O	2.20	0.41
1:F:17:GLN:HE22	1:F:79:MET:CE	2.34	0.41
1:F:57:GLY:CA	5:F:4382:HOH:O	2.68	0.41
1:E:130:ARG:HG2	1:E:163:HIS:CE1	2.56	0.41
1:E:17:GLN:NE2	1:E:100:TYR:OH	2.54	0.40
1:C:79:MET:HG2	1:C:100:TYR:HB2	2.04	0.40
1:F:40:VAL:O	1:F:77:PRO:HD2	2.22	0.40
1:D:200:LYS:NZ	5:D:4359:HOH:O	2.53	0.40
1:A:153:GLY:C	5:A:4319:HOH:O	2.59	0.40
1:A:157:ILE:HD11	1:A:215:VAL:HG22	2.02	0.40
1:C:157:ILE:HD13	1:C:215:VAL:HA	2.04	0.40

All (3) 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	Distance(Å)	Clash(Å)
5:C:4168:HOH:O	5:E:4131:HOH:O[2_665]	2.10	0.10
1:F:188:ASN:O	4:B:3011:EDO:O1[2_665]	2.14	0.06
5:B:4100:HOH:O	5:F:4379:HOH:O[2_665]	2.18	0.02

## 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	257/305 (84%)	254 (99%)	3 (1%)	0	100	100
1	B	250/305 (82%)	249 (100%)	1 (0%)	0	100	100

Continued on next page...

*Continued from previous page...*

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	254/305 (83%)	250 (98%)	4 (2%)	0	100	100
1	D	253/305 (83%)	250 (99%)	3 (1%)	0	100	100
1	E	254/305 (83%)	252 (99%)	2 (1%)	0	100	100
1	F	247/305 (81%)	245 (99%)	2 (1%)	0	100	100
All	All	1515/1830 (83%)	1500 (99%)	15 (1%)	0	100	100

There are no Ramachandran outliers to report.

### 5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution. The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	198/237 (84%)	198 (100%)	0	100	100
1	B	190/237 (80%)	189 (100%)	1 (0%)	94	96
1	C	198/237 (84%)	197 (100%)	1 (0%)	94	96
1	D	196/237 (83%)	196 (100%)	0	100	100
1	E	197/237 (83%)	196 (100%)	1 (0%)	94	96
1	F	189/237 (80%)	188 (100%)	1 (0%)	94	96
All	All	1168/1422 (82%)	1164 (100%)	4 (0%)	96	98

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	247	PHE
1	C	240	LYS
1	E	270	GLU
1	F	196	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	209	ASN

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	B	226	GLN
1	C	72	ASN
1	C	163	HIS
1	C	209	ASN
1	D	72	ASN
1	D	188	ASN
1	E	17	GLN
1	E	188	ASN
1	E	226	GLN
1	F	17	GLN
1	F	72	ASN
1	F	163	HIS
1	F	188	ASN

### 5.3.3 RNA ⓘ

There are no RNA chains in this entry.

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

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

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

Of 35 ligands modelled in this entry, 24 are monoatomic - leaving 11 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	$\# Z  > 2$
4	EDO	A	3005	-	3,3,3	0.22	0	2,2,2	0.28	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
4	EDO	A	3006	-	3,3,3	0.48	0	2,2,2	0.44	0
4	EDO	B	3011	-	3,3,3	0.51	0	2,2,2	0.63	0
4	EDO	B	3012	-	3,3,3	0.37	0	2,2,2	0.62	0
4	EDO	C	3017	-	3,3,3	0.77	0	2,2,2	0.33	0
4	EDO	C	3018	-	3,3,3	0.60	0	2,2,2	0.94	0
4	EDO	C	3019	-	3,3,3	0.33	0	2,2,2	0.81	0
4	EDO	D	3024	-	3,3,3	0.36	0	2,2,2	0.74	0
4	EDO	E	3029	-	3,3,3	0.69	0	2,2,2	0.95	0
4	EDO	F	3034	-	3,3,3	0.49	0	2,2,2	0.64	0
4	EDO	F	3035	-	3,3,3	0.37	0	2,2,2	0.90	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
4	EDO	A	3005	-	-	0/1/1/1	0/0/0/0
4	EDO	A	3006	-	-	0/1/1/1	0/0/0/0
4	EDO	B	3011	-	-	0/1/1/1	0/0/0/0
4	EDO	B	3012	-	-	0/1/1/1	0/0/0/0
4	EDO	C	3017	-	-	0/1/1/1	0/0/0/0
4	EDO	C	3018	-	-	0/1/1/1	0/0/0/0
4	EDO	C	3019	-	-	0/1/1/1	0/0/0/0
4	EDO	D	3024	-	-	0/1/1/1	0/0/0/0
4	EDO	E	3029	-	-	0/1/1/1	0/0/0/0
4	EDO	F	3034	-	-	0/1/1/1	0/0/0/0
4	EDO	F	3035	-	-	0/1/1/1	0/0/0/0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

## 5.7 Other polymers ⓘ

There are no such residues in this entry.

## 5.8 Polymer linkage issues

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	259/305 (84%)	-0.50	5 (1%) 64 67	28, 34, 63, 78	0
1	B	252/305 (82%)	-0.68	3 (1%) 75 79	27, 34, 58, 82	0
1	C	256/305 (83%)	-0.58	1 (0%) 90 92	28, 34, 59, 70	0
1	D	256/305 (83%)	-0.53	4 (1%) 68 72	27, 34, 62, 77	0
1	E	256/305 (83%)	-0.59	3 (1%) 75 79	27, 34, 61, 74	0
1	F	250/305 (81%)	-0.55	4 (1%) 68 72	28, 34, 54, 85	0
All	All	1529/1830 (83%)	-0.57	20 (1%) 74 77	27, 34, 60, 85	0

All (20) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	56	GLY	4.6
1	A	55	ALA	4.3
1	B	12	GLY	4.1
1	A	6	THR	4.0
1	D	272	GLY	3.4
1	D	9	VAL	3.1
1	D	242	ASP	3.0
1	B	11	ARG	2.9
1	E	16[A]	MET	2.8
1	F	271	LEU	2.7
1	A	7	GLU	2.5
1	A	9	VAL	2.4
1	B	14	ALA	2.3
1	F	12	GLY	2.3
1	E	13	MET	2.3
1	E	270	GLU	2.2
1	C	9	VAL	2.2
1	F	14	ALA	2.1
1	F	16	MET	2.1

*Continued on next page...*



*Continued from previous page...*

Mol	Chain	Res	Type	RSRZ
1	D	271	LEU	2.0

## 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 carbohydrates in this entry.

## 6.4 Ligands ⓘ

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
4	EDO	B	3011	4/4	0.44	20.35	84,85,86,87	0
3	MG	A	3009	1/1	0.16	16.93	61,61,61,61	0
4	EDO	D	3024	4/4	0.21	12.31	38,43,46,53	0
3	MG	A	3003	1/1	0.27	10.81	61,61,61,61	0
4	EDO	C	3019	4/4	0.21	9.53	57,60,61,63	0
4	EDO	B	3012	4/4	0.21	8.91	37,44,47,56	0
3	MG	D	3027	1/1	0.25	8.74	66,66,66,66	0
3	MG	C	3022	1/1	0.19	8.52	61,61,61,61	0
4	EDO	C	3018	4/4	0.16	8.32	44,45,47,50	0
4	EDO	A	3006	4/4	0.27	8.29	73,74,74,75	0
4	EDO	E	3029	4/4	0.18	8.20	39,41,44,49	0
3	MG	E	3032	1/1	0.18	6.30	63,63,63,63	0
4	EDO	A	3005	4/4	0.16	5.19	39,40,44,46	0
4	EDO	F	3035	4/4	0.13	5.17	41,43,45,48	0
3	MG	B	3010	1/1	0.19	5.06	58,58,58,58	0
4	EDO	C	3017	4/4	0.22	4.02	37,39,48,50	0
3	MG	A	3004	1/1	0.17	4.01	67,67,67,67	0
3	MG	F	3033	1/1	0.14	3.49	60,60,60,60	0
3	MG	D	3023	1/1	0.18	3.24	64,64,64,64	0

*Continued on next page...*

*Continued from previous page...*

Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
3	MG	C	3015	1/1	0.10	3.16	65,65,65,65	0
4	EDO	F	3034	4/4	0.19	2.16	32,39,46,47	0
3	MG	C	3016	1/1	0.13	0.54	65,65,65,65	0
2	CL	C	3013	1/1	0.07	-0.26	46,46,46,46	0
2	CL	F	3030	1/1	0.06	-0.64	47,47,47,47	0
2	CL	D	3021	1/1	0.07	-0.67	53,53,53,53	0
2	CL	F	3031	1/1	0.06	-0.86	51,51,51,51	0
2	CL	A	3002	1/1	0.06	-0.97	58,58,58,58	0
2	CL	D	3020	1/1	0.05	-1.15	51,51,51,51	0
2	CL	A	3001	1/1	0.06	-1.17	56,56,56,56	0
3	MG	E	3028	1/1	0.07	-1.32	56,56,56,56	0
2	CL	C	3014	1/1	0.04	-1.39	54,54,54,54	0
2	CL	E	3026	1/1	0.06	-1.39	51,51,51,51	0
2	CL	B	3008	1/1	0.04	-1.50	54,54,54,54	0
2	CL	E	3025	1/1	0.04	-2.03	51,51,51,51	0
2	CL	B	3007	1/1	0.03	-2.82	50,50,50,50	0

## 6.5 Other polymers ⓘ

There are no such residues in this entry.