



Full wwPDB X-ray Structure Validation Report ⓘ

Dec 17, 2023 – 01:00 am GMT

PDB ID : 2WYM
Title : Structure of a metallo- β -lactamase
Authors : Garces, F.; Fernandez, F.J.; Penya-Soler, E.; Aguilar, J.; Baldoma, L.; Coll, M.; Badia, J.; Vega, M.C.
Deposited on : 2009-11-16
Resolution : 2.60 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

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>.

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

MolProbity : 4.02b-467
Mogul : 1.8.4, CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.36
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) : 2.36

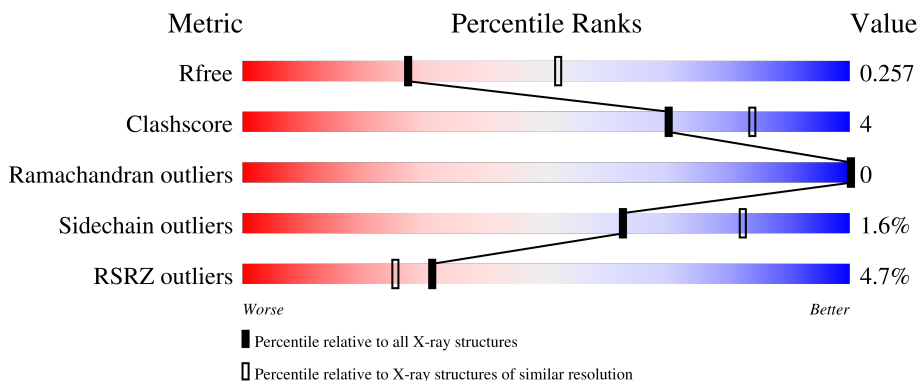
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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.



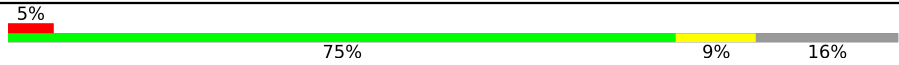
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	3163 (2.60-2.60)
Clashscore	141614	3518 (2.60-2.60)
Ramachandran outliers	138981	3455 (2.60-2.60)
Sidechain outliers	138945	3455 (2.60-2.60)
RSRZ outliers	127900	3104 (2.60-2.60)

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 ≥ 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	360	 4% 76% 8% 16%
1	B	360	 5% 74% 9% 17%
1	D	360	 3% 74% 9% 17%
1	E	360	 4% 75% 8% 17%
2	C	360	 2% 74% 9% 17%

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Mol	Chain	Length	Quality of chain
2	F	360	

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
5	FLC	D	1341	-	-	-	X

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 14722 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 L-ASCORBATE-6-PHOSPHATE LACTONASE ULAG.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	303	2435	1563	413	445	14	0	0	0
1	B	300	2403	1542	409	438	14	0	0	0
1	D	300	2413	1550	411	438	14	0	1	0
1	E	300	2417	1554	411	438	14	0	1	0

- Molecule 2 is a protein called L-ASCORBATE-6-PHOSPHATE LACTONASE ULAG.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	C	298	2389	1533	407	435	14	0	0	0
2	F	301	2411	1548	410	440	13	0	0	0

- Molecule 3 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

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

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



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O 6 3 3	0	0
4	A	1	Total C O 6 3 3	0	0
4	B	1	Total C O 6 3 3	0	0
4	C	1	Total C O 6 3 3	0	0
4	D	1	Total C O 6 3 3	0	0
4	E	1	Total C O 6 3 3	0	0
4	F	1	Total C O 6 3 3	0	0

- Molecule 5 is CITRATE ANION (three-letter code: FLC) (formula: $C_6H_5O_7$).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	D	1	Total	C O	0	0
			13	6 7		

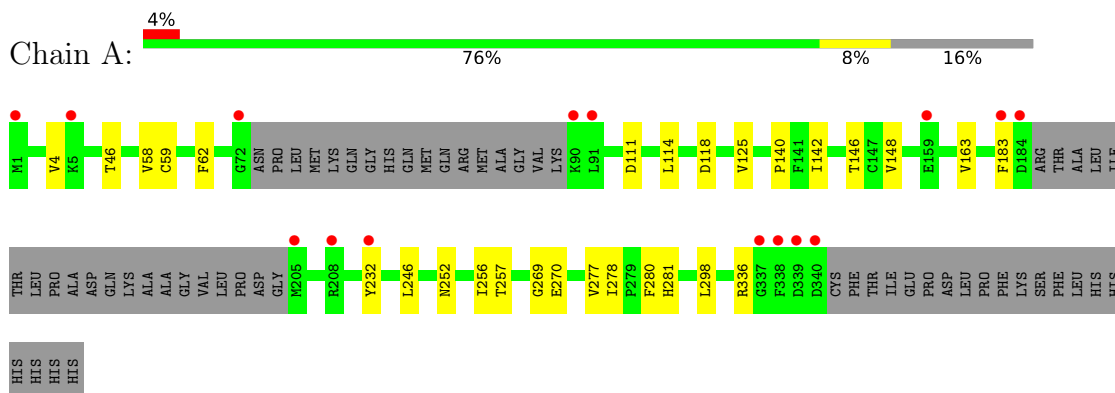
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	38	Total	O	0	0
			38	38		
6	B	27	Total	O	0	0
			27	27		
6	C	37	Total	O	0	0
			37	37		
6	D	52	Total	O	0	0
			52	52		
6	E	18	Total	O	0	0
			18	18		
6	F	21	Total	O	0	0
			21	21		

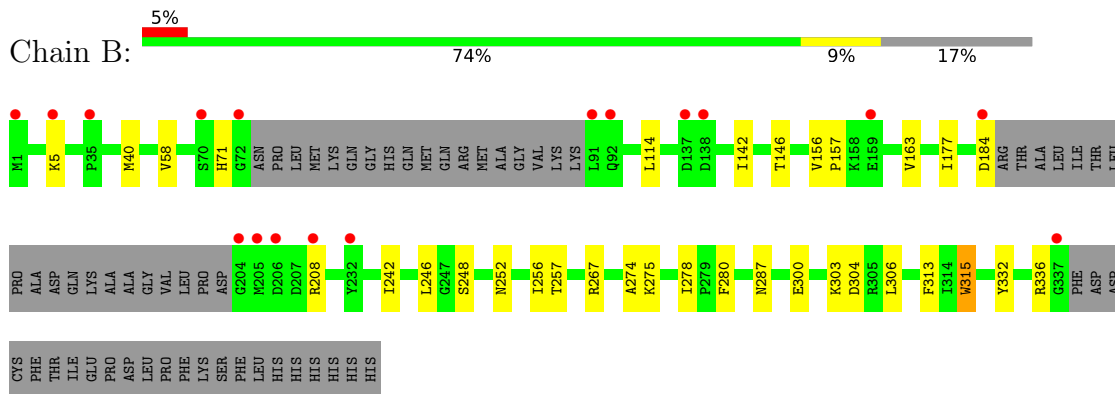
3 Residue-property plots [i](#)

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.

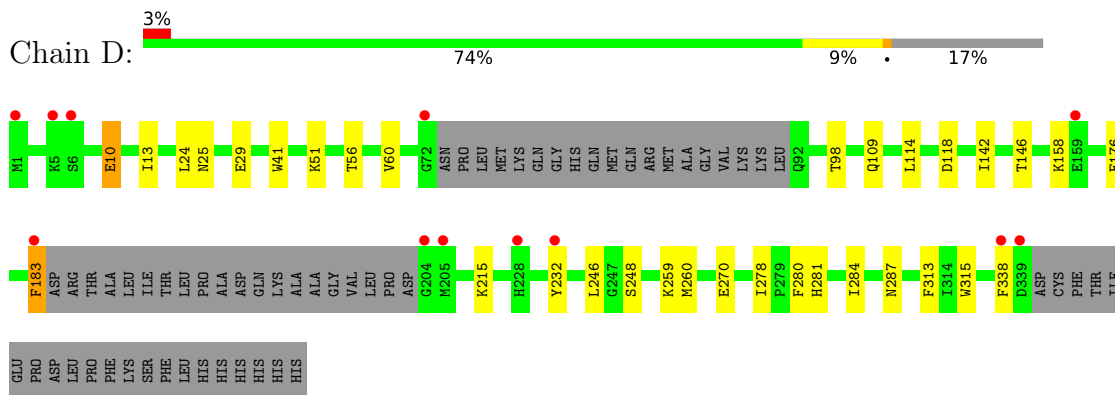
- Molecule 1: L-ASCORBATE-6-PHOSPHATE LACTONASE ULAG



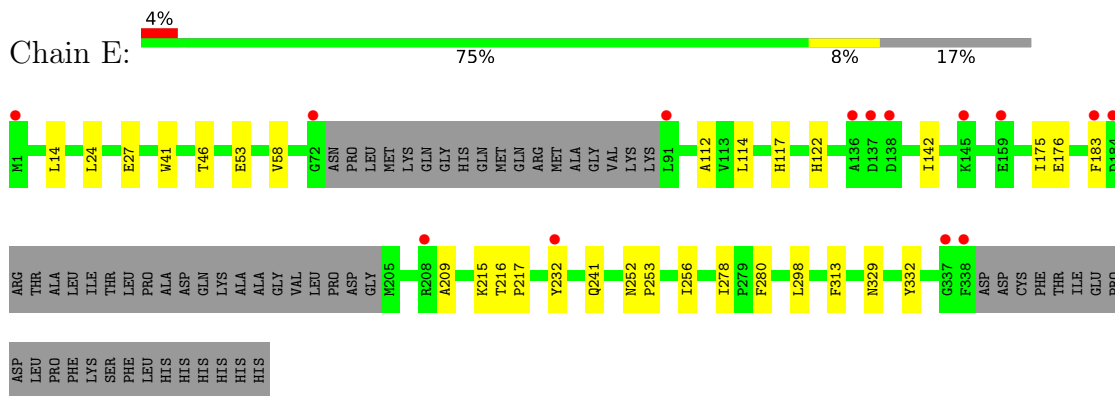
- Molecule 1: L-ASCORBATE-6-PHOSPHATE LACTONASE ULAG



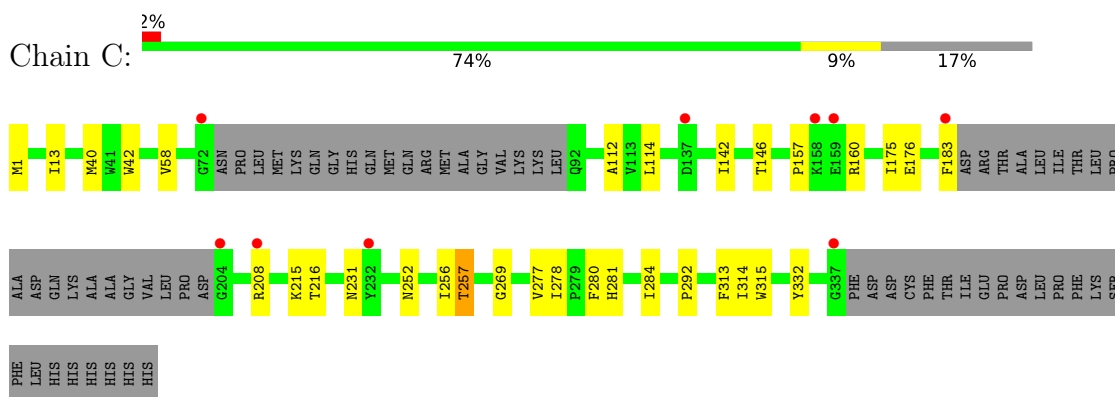
- Molecule 1: L-ASCORBATE-6-PHOSPHATE LACTONASE ULAG



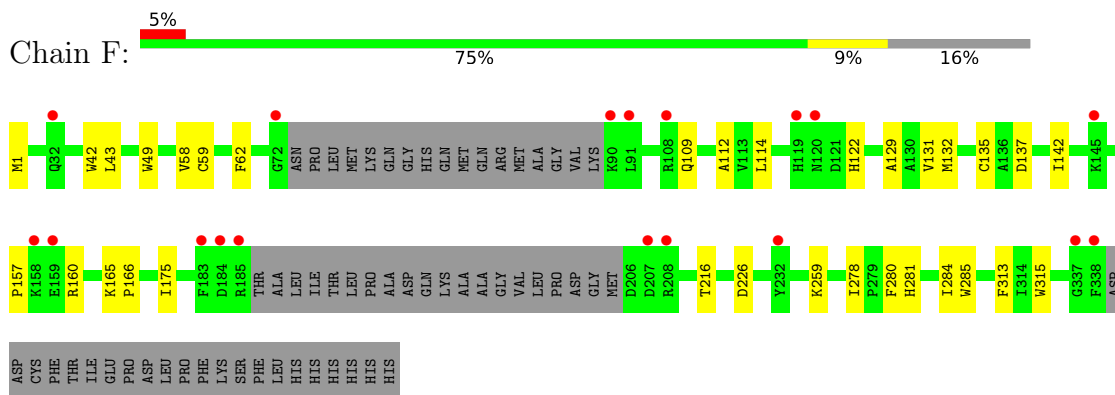
- Molecule 1: L-ASCORBATE-6-PHOSPHATE LACTONASE ULAG



- Molecule 2: L-ASCORBATE-6-PHOSPHATE LACTONASE ULAG



- Molecule 2: L-ASCORBATE-6-PHOSPHATE LACTONASE ULAG



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	103.22Å 178.21Å 111.56Å 90.00° 103.96° 90.00°	Depositor
Resolution (Å)	14.97 – 2.60 14.97 – 2.60	Depositor EDS
% Data completeness (in resolution range)	100.0 (14.97-2.60) 100.0 (14.97-2.60)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.90 (at 2.61Å)	Xtrriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.207 , 0.255 0.210 , 0.257	Depositor DCC
R_{free} test set	3011 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å ²)	39.3	Xtrriage
Anisotropy	0.127	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 39.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	14722	wwPDB-VP
Average B, all atoms (Å ²)	40.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.50% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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: FME, GOL, FLC, MN

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	0.33	0/2510	0.46	0/3410
1	B	0.33	0/2477	0.45	0/3366
1	D	0.33	0/2492	0.46	0/3386
1	E	0.33	0/2496	0.44	0/3392
2	C	0.33	0/2453	0.45	0/3334
2	F	0.33	0/2476	0.46	0/3367
All	All	0.33	0/14904	0.45	0/20255

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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	2435	0	2322	16	0
1	B	2403	0	2295	22	0
1	D	2413	0	2300	18	0
1	E	2417	0	2308	19	0
2	C	2389	0	2279	21	0
2	F	2411	0	2286	16	0
3	A	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
3	E	1	0	0	0	0
3	F	1	0	0	0	0
4	A	12	0	16	0	0
4	B	6	0	8	0	0
4	C	6	0	8	0	0
4	D	6	0	8	0	0
4	E	6	0	8	3	0
4	F	6	0	8	0	0
5	D	13	0	5	0	0
6	A	38	0	0	0	0
6	B	27	0	0	1	0
6	C	37	0	0	0	0
6	D	52	0	0	0	0
6	E	18	0	0	0	0
6	F	21	0	0	0	0
All	All	14722	0	13851	102	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 4.

All (102) 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:E:332:TYR:HD1	4:E:1340:GOL:H31	1.40	0.86
1:B:267:ARG:HH22	2:C:257:THR:HB	1.60	0.67
2:F:278:ILE:HG12	2:F:313:PHE:HB3	1.80	0.64
1:E:183:PHE:CE2	1:E:232:TYR:HB2	2.36	0.61
2:C:40:MET:HG2	2:C:315:TRP:HH2	1.67	0.59
1:A:183:PHE:CE1	1:A:232:TYR:HB2	2.37	0.59
1:B:58:VAL:HG13	1:B:114:LEU:HD13	1.87	0.57
2:F:58:VAL:HG22	2:F:112:ALA:HB3	1.87	0.56
1:B:114:LEU:HG	1:B:142:ILE:HB	1.87	0.56
1:B:146:THR:CG2	1:B:208:ARG:HA	2.36	0.56
1:E:175:ILE:HG12	1:E:216:THR:HG22	1.89	0.55
1:D:246:LEU:HD23	1:D:278:ILE:HB	1.90	0.54
2:C:114:LEU:HG	2:C:142:ILE:HB	1.90	0.53
1:B:40:MET:HG3	1:B:315:TRP:CH2	2.42	0.53
2:C:175:ILE:HG12	2:C:216:THR:HG22	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:148:VAL:HG21	1:A:163:VAL:HG22	1.89	0.53
2:C:278:ILE:HG12	2:C:313:PHE:HB3	1.92	0.53
2:C:13:ILE:HG22	1:D:13:ILE:HG22	1.92	0.52
1:B:300:GLU:HB2	6:B:2018:HOH:O	2.09	0.52
1:B:313:PHE:CZ	1:B:332:TYR:HB2	2.45	0.52
1:D:176:GLU:HB2	1:D:215:LYS:HB2	1.92	0.51
1:E:332:TYR:CD1	4:E:1340:GOL:H31	2.32	0.51
2:C:40:MET:HG2	2:C:315:TRP:CH2	2.44	0.51
1:B:146:THR:HG22	1:B:208:ARG:HA	1.91	0.51
1:B:252:ASN:HB3	1:B:256:ILE:O	2.10	0.51
1:D:98:THR:HB	1:D:284:ILE:HD12	1.94	0.50
1:E:58:VAL:HG22	1:E:112:ALA:HB3	1.93	0.50
1:A:114:LEU:HG	1:A:142:ILE:HB	1.95	0.49
1:A:257:THR:HG23	1:A:257:THR:O	2.13	0.49
1:A:269:GLY:HA3	1:A:277:VAL:HG21	1.95	0.49
1:E:176:GLU:HB3	1:E:215:LYS:HB2	1.95	0.48
1:D:24:LEU:HD11	1:D:41:TRP:CD1	2.48	0.48
1:E:332:TYR:CD1	4:E:1340:GOL:H12	2.48	0.48
1:B:257:THR:HG22	2:C:231:ASN:HD21	1.77	0.48
1:E:241:GLN:O	1:E:241:GLN:HG3	2.14	0.47
2:F:58:VAL:HG13	2:F:114:LEU:HD13	1.97	0.47
1:B:336:ARG:HD2	1:E:253:PRO:HA	1.97	0.47
2:C:58:VAL:HG22	2:C:112:ALA:HB3	1.97	0.47
2:F:175:ILE:HG12	2:F:216:THR:HG22	1.97	0.47
1:A:246:LEU:HD23	1:A:278:ILE:HB	1.97	0.46
1:D:29:GLU:HG3	1:D:109:GLN:OE1	2.16	0.46
2:C:176:GLU:HB3	2:C:215:LYS:HB2	1.98	0.46
1:A:46:THR:HG23	1:A:281:HIS:CD2	2.51	0.46
1:A:298:LEU:HD11	1:E:298:LEU:HD11	1.98	0.46
1:E:278:ILE:HG12	1:E:313:PHE:HB3	1.98	0.45
1:B:257:THR:HG22	2:C:231:ASN:ND2	2.31	0.45
2:C:269:GLY:HA3	2:C:277:VAL:HG21	1.97	0.45
1:E:114:LEU:HG	1:E:142:ILE:HB	1.98	0.45
1:A:4:VAL:HG13	2:F:129:ALA:HA	1.98	0.45
1:A:118:ASP:HB3	1:A:146:THR:HG23	1.97	0.45
1:D:114:LEU:HG	1:D:142:ILE:HB	1.98	0.45
1:D:248:SER:O	1:D:260:MET:HB2	2.17	0.45
1:B:303:LYS:HG3	1:B:304:ASP:N	2.32	0.45
1:E:117:HIS:HB3	1:E:209:ALA:HB2	1.99	0.45
2:C:252:ASN:HB3	2:C:256:ILE:O	2.17	0.45
1:B:242:ILE:O	1:B:274:ALA:HA	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:252:ASN:HB3	1:E:256:ILE:O	2.17	0.44
2:C:313:PHE:CZ	2:C:332:TYR:HB2	2.52	0.44
1:B:246:LEU:HD23	1:B:278:ILE:HB	1.98	0.44
1:A:270:GLU:OE2	1:B:336:ARG:NH2	2.42	0.43
1:B:114:LEU:HD21	1:B:177:ILE:HD13	2.00	0.43
2:F:122:HIS:CE1	2:F:226:ASP:HB2	2.53	0.43
2:C:42:TRP:HB2	2:C:315:TRP:CZ3	2.52	0.43
1:A:111:ASP:O	1:A:140:PRO:HD2	2.18	0.43
1:E:24:LEU:HD11	1:E:41:TRP:CD1	2.54	0.43
1:E:253:PRO:HB2	1:E:256:ILE:HD12	2.00	0.43
1:B:156:VAL:HA	1:B:157:PRO:HD2	1.90	0.42
1:A:59:CYS:SG	1:A:62:PHE:HB2	2.60	0.42
1:A:336:ARG:NH2	1:D:270:GLU:OE2	2.51	0.42
1:D:118:ASP:HB3	1:D:146:THR:HG23	2.01	0.42
2:F:137:ASP:HA	2:F:160:ARG:NH2	2.33	0.42
1:A:58:VAL:HG13	1:A:114:LEU:HD13	2.00	0.42
1:B:71:HIS:CE1	1:E:27:GLU:HG3	2.54	0.42
2:F:132:MET:HE3	2:F:157:PRO:HD2	2.02	0.42
2:F:59:CYS:SG	2:F:62:PHE:HB2	2.60	0.42
2:F:259:LYS:HE3	2:F:281:HIS:CE1	2.55	0.42
1:D:183:PHE:CE2	1:D:232:TYR:HB2	2.55	0.42
1:D:25:ASN:O	1:D:29:GLU:HB2	2.20	0.42
1:D:158:LYS:HE3	1:D:158:LYS:HB2	1.91	0.42
2:F:42:TRP:HB2	2:F:315:TRP:CZ3	2.55	0.42
2:C:281:HIS:O	2:C:284:ILE:HG22	2.21	0.41
1:D:287:ASN:OD1	1:D:287:ASN:N	2.53	0.41
1:A:252:ASN:HB3	1:A:256:ILE:O	2.21	0.41
1:D:259:LYS:HE3	1:D:281:HIS:CE1	2.55	0.41
1:E:46:THR:HG1	1:E:122:HIS:CE1	2.38	0.41
1:E:53:GLU:OE2	1:E:217:PRO:HB2	2.20	0.41
1:B:146:THR:HG21	1:B:208:ARG:HA	2.02	0.41
2:C:146:THR:HG21	2:C:208:ARG:HG3	2.02	0.41
2:F:114:LEU:HG	2:F:142:ILE:HB	2.03	0.41
1:B:5:LYS:HA	1:B:5:LYS:HD2	1.90	0.41
2:C:292:PRO:HB2	2:C:314:ILE:HG12	2.01	0.41
2:C:157:PRO:HB2	2:C:160:ARG:HB2	2.03	0.41
1:D:10:GLU:H	1:D:10:GLU:CD	2.23	0.41
1:D:278:ILE:HG12	1:D:313:PHE:HB3	2.03	0.41
2:F:165:LYS:HG2	2:F:166:PRO:HD2	2.02	0.41
2:C:146:THR:HG22	2:C:208:ARG:HA	2.03	0.40
2:F:43:LEU:HD11	2:F:49:TRP:HB2	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:146:THR:CG2	2:C:208:ARG:HA	2.51	0.40
1:B:40:MET:HG3	1:B:315:TRP:HH2	1.87	0.40
1:D:51:LYS:HA	1:D:56:THR:O	2.21	0.40
2:F:131:VAL:O	2:F:135:CYS:HB2	2.21	0.40
2:F:284:ILE:HG23	2:F:285:TRP:CD1	2.56	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	297/360 (82%)	288 (97%)	9 (3%)	0	100	100
1	B	294/360 (82%)	286 (97%)	8 (3%)	0	100	100
1	D	295/360 (82%)	282 (96%)	13 (4%)	0	100	100
1	E	295/360 (82%)	288 (98%)	7 (2%)	0	100	100
2	C	292/360 (81%)	284 (97%)	8 (3%)	0	100	100
2	F	295/360 (82%)	282 (96%)	13 (4%)	0	100	100
All	All	1768/2160 (82%)	1710 (97%)	58 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	260/308 (84%)	258 (99%)	2 (1%)	81	92
1	B	256/308 (83%)	248 (97%)	8 (3%)	40	66
1	D	257/308 (83%)	251 (98%)	6 (2%)	50	75
1	E	258/308 (84%)	255 (99%)	3 (1%)	71	87
2	C	253/307 (82%)	250 (99%)	3 (1%)	71	87
2	F	254/307 (83%)	252 (99%)	2 (1%)	81	92
All	All	1538/1846 (83%)	1514 (98%)	24 (2%)	62	82

All (24) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	125	VAL
1	A	280	PHE
1	B	163	VAL
1	B	184	ASP
1	B	248	SER
1	B	275	LYS
1	B	280	PHE
1	B	287	ASN
1	B	306	LEU
1	B	315	TRP
2	C	183	PHE
2	C	257	THR
2	C	280	PHE
1	D	10	GLU
1	D	60	VAL
1	D	183	PHE
1	D	280	PHE
1	D	315	TRP
1	D	338	PHE
1	E	14	LEU
1	E	280	PHE
1	E	329	ASN
2	F	109	GLN
2	F	280	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	117	HIS

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Mol	Chain	Res	Type
1	D	293	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](#)

2 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
2	FME	C	1	2	8,9,10	0.72	0	7,9,11	3.73	3 (42%)
2	FME	F	1	2	8,9,10	0.73	0	7,9,11	3.55	2 (28%)

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	FME	C	1	2	-	4/7/9/11	-
2	FME	F	1	2	-	4/7/9/11	-

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	1	FME	CA-N-CN	-8.60	109.60	122.82
2	F	1	FME	CA-N-CN	-7.98	110.55	122.82
2	F	1	FME	CE-SD-CG	4.17	114.73	100.40
2	C	1	FME	CE-SD-CG	3.93	113.88	100.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	1	FME	O-C-CA	-2.04	119.43	124.78

There are no chirality outliers.

All (8) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	C	1	FME	O1-CN-N-CA
2	C	1	FME	CA-CB-CG-SD
2	F	1	FME	O1-CN-N-CA
2	C	1	FME	N-CA-CB-CG
2	F	1	FME	N-CA-CB-CG
2	C	1	FME	CB-CG-SD-CE
2	F	1	FME	CB-CG-SD-CE
2	F	1	FME	CA-CB-CG-SD

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 14 ligands modelled in this entry, 6 are monoatomic - leaving 8 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	GOL	A	1343	-	5,5,5	0.36	0	5,5,5	0.33	0
4	GOL	E	1340	-	5,5,5	0.43	0	5,5,5	0.25	0
5	FLC	D	1341	-	12,12,12	0.96	0	17,17,17	1.30	1 (5%)
4	GOL	A	1342	-	5,5,5	0.38	0	5,5,5	0.30	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	GOL	B	1339	-	5,5,5	0.36	0	5,5,5	0.32	0
4	GOL	D	1342	-	5,5,5	0.35	0	5,5,5	0.29	0
4	GOL	F	1340	-	5,5,5	0.34	0	5,5,5	0.27	0
4	GOL	C	1339	-	5,5,5	0.38	0	5,5,5	0.25	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	GOL	A	1343	-	-	4/4/4/4	-
4	GOL	E	1340	-	-	2/4/4/4	-
5	FLC	D	1341	-	-	5/16/16/16	-
4	GOL	A	1342	-	-	2/4/4/4	-
4	GOL	B	1339	-	-	3/4/4/4	-
4	GOL	D	1342	-	-	2/4/4/4	-
4	GOL	F	1340	-	-	0/4/4/4	-
4	GOL	C	1339	-	-	2/4/4/4	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	D	1341	FLC	OB2-CBC-CB	3.12	118.48	113.05

There are no chirality outliers.

All (20) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	C	1339	GOL	C1-C2-C3-O3
4	E	1340	GOL	O1-C1-C2-C3
4	A	1343	GOL	O1-C1-C2-O2
4	A	1342	GOL	O1-C1-C2-C3
4	A	1343	GOL	O1-C1-C2-C3
4	A	1343	GOL	C1-C2-C3-O3
4	B	1339	GOL	O1-C1-C2-C3
4	B	1339	GOL	C1-C2-C3-O3
4	D	1342	GOL	C1-C2-C3-O3

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Mol	Chain	Res	Type	Atoms
4	C	1339	GOL	O2-C2-C3-O3
4	E	1340	GOL	O1-C1-C2-O2
5	D	1341	FLC	CA-CB-CBC-OB1
5	D	1341	FLC	CG-CB-CBC-OB2
4	A	1343	GOL	O2-C2-C3-O3
5	D	1341	FLC	OHB-CB-CG-CGC
5	D	1341	FLC	CA-CB-CBC-OB2
5	D	1341	FLC	CG-CB-CBC-OB1
4	A	1342	GOL	O1-C1-C2-O2
4	D	1342	GOL	O2-C2-C3-O3
4	B	1339	GOL	O1-C1-C2-O2

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	E	1340	GOL	3	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, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	303/360 (84%)	0.00	15 (4%) 28 23	25, 39, 54, 66	0
1	B	300/360 (83%)	0.08	17 (5%) 23 18	23, 40, 54, 62	0
1	D	300/360 (83%)	-0.15	12 (4%) 38 31	20, 33, 47, 60	0
1	E	300/360 (83%)	0.15	14 (4%) 31 25	28, 44, 60, 64	0
2	C	297/360 (82%)	-0.07	9 (3%) 50 43	22, 38, 53, 57	0
2	F	300/360 (83%)	0.26	18 (6%) 21 16	23, 46, 61, 67	0
All	All	1800/2160 (83%)	0.04	85 (4%) 31 25	20, 40, 59, 67	0

All (85) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	72	GLY	6.2
1	A	1	MET	5.7
1	D	339	ASP	5.3
1	E	91	LEU	5.2
2	F	338	PHE	5.1
1	B	91	LEU	5.0
2	F	90	LYS	5.0
1	E	338	PHE	4.9
1	E	137	ASP	4.9
1	B	184	ASP	4.8
1	A	232	TYR	4.8
2	F	185	ARG	4.5
2	F	72	GLY	4.5
1	E	184	ASP	4.5
1	A	184	ASP	4.4
1	A	91	LEU	4.4
1	A	72	GLY	4.3
2	C	159	GLU	4.3
2	F	232	TYR	4.3

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Mol	Chain	Res	Type	RSRZ
1	E	1	MET	4.3
1	D	232	TYR	4.1
1	E	72	GLY	4.1
1	D	338	PHE	4.1
2	F	184	ASP	4.0
1	E	159	GLU	4.0
1	D	159	GLU	4.0
1	B	159	GLU	3.9
2	F	159	GLU	3.8
1	A	339	ASP	3.8
2	C	232	TYR	3.7
1	E	232	TYR	3.7
1	D	204	GLY	3.6
1	B	232	TYR	3.6
2	F	91	LEU	3.6
2	C	72	GLY	3.5
1	B	1	MET	3.5
2	C	204	GLY	3.5
2	F	208	ARG	3.4
1	A	90	LYS	3.4
1	A	338	PHE	3.3
1	D	183	PHE	3.3
1	B	337	GLY	3.2
1	D	1	MET	3.2
1	B	206	ASP	3.2
2	C	183	PHE	3.1
2	C	337	GLY	3.1
1	A	159	GLU	3.1
1	E	337	GLY	2.9
1	D	205	MET	2.9
1	E	208	ARG	2.9
1	B	138	ASP	2.9
2	C	137	ASP	2.9
1	B	137	ASP	2.9
1	B	204	GLY	2.8
2	F	158	LYS	2.7
2	F	145	LYS	2.7
2	F	337	GLY	2.6
1	B	92	GLN	2.6
1	B	70	SER	2.6
2	F	119	HIS	2.5
2	F	32	GLN	2.5

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Mol	Chain	Res	Type	RSRZ
1	B	5	LYS	2.5
2	C	158	LYS	2.5
1	D	6	SER	2.5
1	D	72	GLY	2.4
1	E	138	ASP	2.4
1	D	228	HIS	2.4
2	F	120	ASN	2.4
1	A	5	LYS	2.3
1	A	205	MET	2.3
1	E	145	LYS	2.3
1	A	183	PHE	2.3
1	A	208	ARG	2.3
2	F	207	ASP	2.3
1	A	337	GLY	2.3
1	E	183	PHE	2.2
1	B	205	MET	2.2
2	F	108	ARG	2.1
1	D	5	LYS	2.1
1	E	136	ALA	2.1
1	B	208	ARG	2.1
2	F	183	PHE	2.1
1	B	35	PRO	2.1
1	A	340	ASP	2.1
2	C	208	ARG	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, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	FME	C	1	10/11	0.81	0.22	42,42,45,46	0
2	FME	F	1	10/11	0.81	0.23	51,52,54,54	0

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, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	GOL	B	1339	6/6	0.67	0.39	67,68,68,68	0
5	FLC	D	1341	13/13	0.76	0.43	72,73,73,73	0
4	GOL	F	1340	6/6	0.77	0.33	64,65,65,65	0
3	MN	B	1338	1/1	0.85	0.11	63,63,63,63	1
4	GOL	A	1342	6/6	0.86	0.42	52,52,52,52	0
4	GOL	E	1340	6/6	0.88	0.40	38,38,39,39	0
4	GOL	C	1339	6/6	0.88	0.26	64,64,64,64	0
4	GOL	D	1342	6/6	0.88	0.18	46,46,46,47	0
4	GOL	A	1343	6/6	0.89	0.21	60,60,60,60	0
3	MN	A	1341	1/1	0.90	0.12	67,67,67,67	1
3	MN	E	1339	1/1	0.93	0.16	67,67,67,67	1
3	MN	F	1339	1/1	0.94	0.09	67,67,67,67	1
3	MN	C	1338	1/1	0.95	0.04	61,61,61,61	1
3	MN	D	1340	1/1	0.97	0.07	69,69,69,69	1

6.5 Other polymers [i](#)

There are no such residues in this entry.