



wwPDB X-ray Structure Validation Summary Report

Apr 22, 2014 – 01:13 AM EDT

PDB ID : 4O1Q
Title : Crystal Structure of the Q103N-MauG/pre-MethylamineDehydrogenase Complex
Authors : Yukl, E.T.; Wilmot, C.W.
Deposited on : 2013-12-16
Resolution : 2.59 Å(reported)

This is a wwPDB validation summary report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

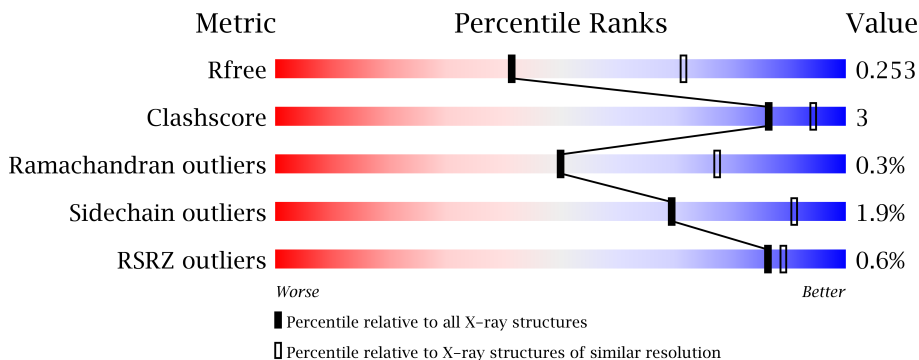
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.16 November 2013
Xtriage (Phenix) : dev-1439
EDS : stable22978
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) : stable22978

1 Overall quality at a glance

The reported resolution of this entry is 2.59 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	1718 (2.60-2.60)
Clashscore	79885	2154 (2.60-2.60)
Ramachandran outliers	78287	2113 (2.60-2.60)
Sidechain outliers	78261	2113 (2.60-2.60)
RSRZ outliers	66119	1718 (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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 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	373	
1	B	373	
2	C	137	
2	E	137	
3	D	385	
3	F	385	

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

Mol	Type	Chain	Res	Geometry	Electron density
6	EDO	A	404	-	X
8	PGE	C	201	-	X

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Mol	Type	Chain	Res	Geometry	Electron density
9	MES	D	401	-	X
9	MES	F	401	-	X

2 Entry composition

There are 11 unique types of molecules in this entry. The entry contains 13884 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 Methylamine utilization protein MauG.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	354	Total	C	N	O	S	0	1	0
			2742	1711	492	528	11			
1	B	355	Total	C	N	O	S	0	1	0
			2751	1716	493	531	11			

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-5	HIS	-	EXPRESSION TAG	UNP Q51658
A	-4	HIS	-	EXPRESSION TAG	UNP Q51658
A	-3	HIS	-	EXPRESSION TAG	UNP Q51658
A	-2	HIS	-	EXPRESSION TAG	UNP Q51658
A	-1	HIS	-	EXPRESSION TAG	UNP Q51658
A	0	HIS	-	EXPRESSION TAG	UNP Q51658
A	103	ASN	GLN	ENGINEERED MUTATION	UNP Q51658
B	-5	HIS	-	EXPRESSION TAG	UNP Q51658
B	-4	HIS	-	EXPRESSION TAG	UNP Q51658
B	-3	HIS	-	EXPRESSION TAG	UNP Q51658
B	-2	HIS	-	EXPRESSION TAG	UNP Q51658
B	-1	HIS	-	EXPRESSION TAG	UNP Q51658
B	0	HIS	-	EXPRESSION TAG	UNP Q51658
B	103	ASN	GLN	ENGINEERED MUTATION	UNP Q51658

- Molecule 2 is a protein called Methylamine dehydrogenase light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	125	Total	C	N	O	S	0	0	0
			955	590	161	191	13			
2	E	125	Total	C	N	O	S	0	1	0
			958	592	161	191	14			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	-5	HIS	-	EXPRESSION TAG	UNP A1BBA0
C	-4	HIS	-	EXPRESSION TAG	UNP A1BBA0
C	-3	HIS	-	EXPRESSION TAG	UNP A1BBA0
C	-2	HIS	-	EXPRESSION TAG	UNP A1BBA0
C	-1	HIS	-	EXPRESSION TAG	UNP A1BBA0
C	0	HIS	-	EXPRESSION TAG	UNP A1BBA0
E	-5	HIS	-	EXPRESSION TAG	UNP A1BBA0
E	-4	HIS	-	EXPRESSION TAG	UNP A1BBA0
E	-3	HIS	-	EXPRESSION TAG	UNP A1BBA0
E	-2	HIS	-	EXPRESSION TAG	UNP A1BBA0
E	-1	HIS	-	EXPRESSION TAG	UNP A1BBA0
E	0	HIS	-	EXPRESSION TAG	UNP A1BBA0

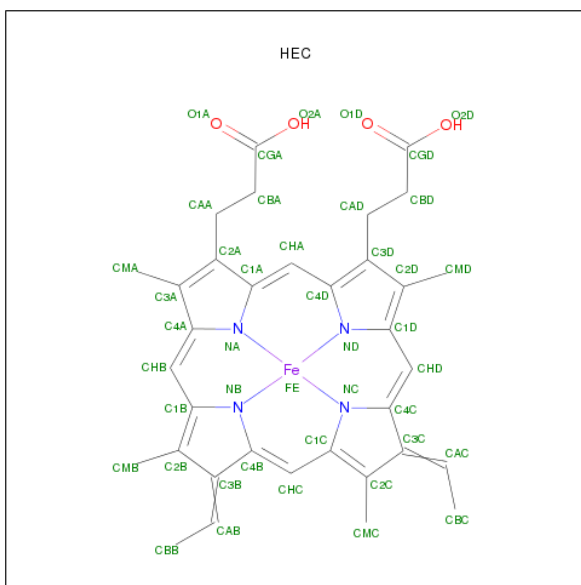
- Molecule 3 is a protein called Methylamine dehydrogenase heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	D	376	Total	C	N	O	S	0	0	0
			2923	1853	502	560	8			
3	F	376	Total	C	N	O	S	0	1	0
			2931	1857	503	563	8			

- Molecule 4 is CALCIUM ION (three-letter code: CA) (formula: Ca).

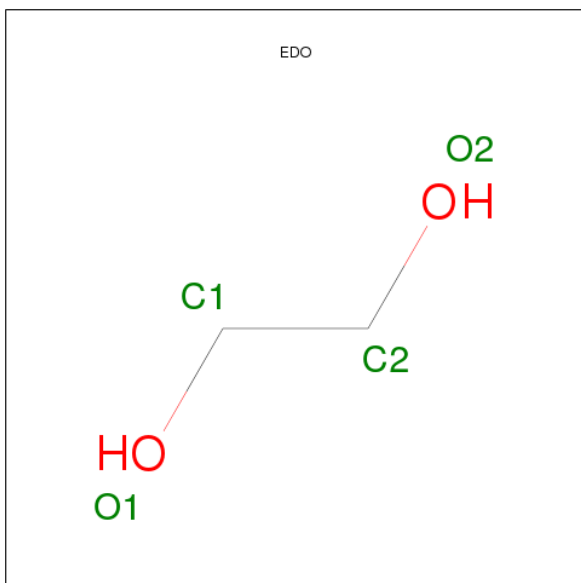
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	1	Total	Ca	0	0
			1	1		
4	A	1	Total	Ca	0	0
			1	1		

- Molecule 5 is HEME C (three-letter code: HEC) (formula: C₃₄H₃₄FeN₄O₄).



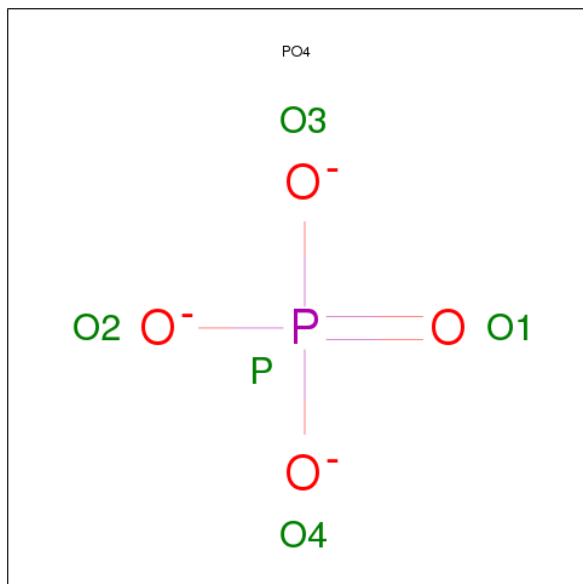
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	A	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
5	A	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
5	B	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
5	B	1	Total 43	C 34	Fe 1	N 4	O 4	0	0

- Molecule 6 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $\text{C}_2\text{H}_6\text{O}_2$).



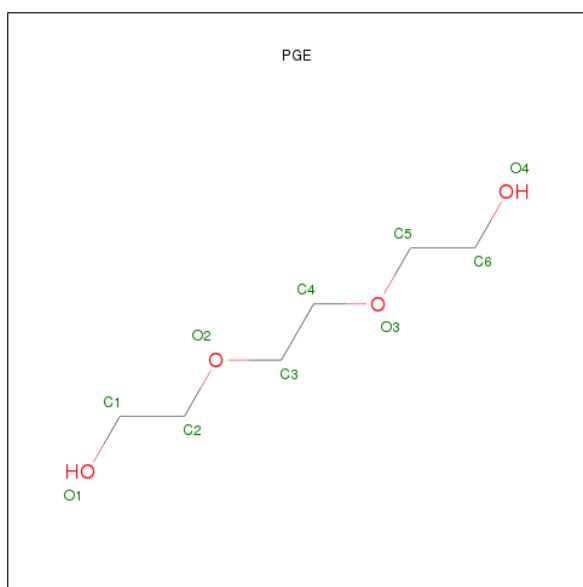
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			4	2	2		
6	A	1	Total	C	O	0	0
			4	2	2		
6	B	1	Total	C	O	0	0
			4	2	2		

- Molecule 7 is PHOSPHATE ION (three-letter code: PO4) (formula: O₄P).



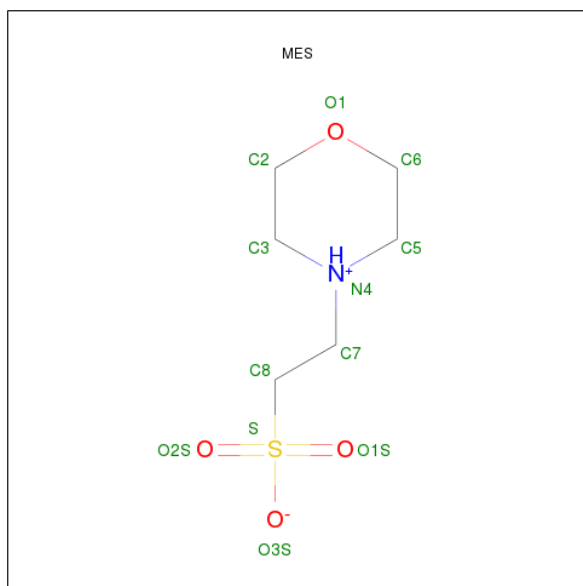
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	B	1	Total	O	P	0	0
			5	4	1		

- Molecule 8 is TRIETHYLENE GLYCOL (three-letter code: PGE) (formula: C₆H₁₄O₄).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	C	1	Total	C	O	0	0
			10	6	4		

- Molecule 9 is 2-(N-MORPHOLINO)-ETHANESULFONICACID (three-letter code: MES) (formula: $C_6H_{13}NO_4S$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
9	D	1	Total	C	N	O	S	0	0
			12	6	1	4	1		
9	F	1	Total	C	N	O	S	0	0
			12	6	1	4	1		

- Molecule 10 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	F	1	Total	Na	0	0
			1	1		

- Molecule 11 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
11	A	63	Total	O	0	0
			63	63		
11	B	97	Total	O	0	0
			97	97		
11	C	29	Total	O	0	0
			29	29		
11	D	65	Total	O	0	0
			65	65		
11	E	27	Total	O	0	0
			27	27		
11	F	116	Total	O	0	1
			117	117		

3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

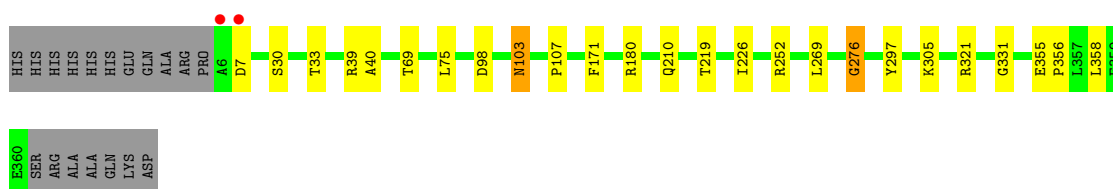
- Molecule 1: Methylamine utilization protein MauG

Chain A: 



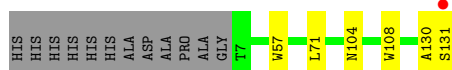
- Molecule 1: Methylamine utilization protein MauG

Chain B: 



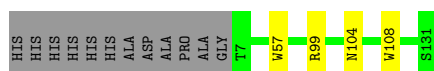
- Molecule 2: Methylamine dehydrogenase light chain

Chain C: 



- Molecule 2: Methylamine dehydrogenase light chain

Chain E: 



- Molecule 3: Methylamine dehydrogenase heavy chain

Chain D: 



- Molecule 3: Methylamine dehydrogenase heavy chain

Chain F: 

ASP	ALA	PRO	GLU	ALA	GLU	THR	GLN	ALA	Q11	E12	R20	R45	E67	I92	A93	H94	I102	E112	V117	S157	I228	W242	K260	R289	R293	K307	L316	D384	W385	G386
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4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	55.53Å 83.52Å 107.78Å 109.94° 91.54° 105.78°	Depositor
Resolution (Å)	44.49 – 2.59 44.49 – 2.59	Depositor EDS
% Data completeness (in resolution range)	98.2 (44.49-2.59) 98.2 (44.49-2.59)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	0.12	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.45 (at 2.58Å)	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
R, R_{free}	0.198 , 0.254 0.195 , 0.253	Depositor DCC
R_{free} test set	2653 reflections (5.26%)	DCC
Wilson B-factor (Å ²)	40.2	Xtriage
Anisotropy	0.545	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 13.9	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 53091 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	13884	wwPDB-VP
Average B, all atoms (Å ²)	52.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.02% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities 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: PGE, 0AF, NA, PO4, EDO, MES, HEC, CA

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	0.32	0/2806	0.51	0/3808
1	B	0.33	0/2815	0.52	0/3820
2	C	0.32	0/964	0.51	0/1315
2	E	0.31	0/970	0.52	0/1323
3	D	0.29	0/3000	0.51	0/4088
3	F	0.31	0/3008	0.54	0/4099
All	All	0.31	0/13563	0.52	0/18453

There are no bond length outliers.

There are no bond angle outliers.

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	2742	0	0	6	0
1	B	2751	0	0	12	0
2	C	955	0	0	3	0
2	E	958	0	0	3	0
3	D	2923	0	0	7	0
3	F	2931	0	0	8	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	1	0	0	0	0
4	B	1	0	0	0	0
5	A	86	0	0	0	0
5	B	86	0	0	0	0
6	A	8	0	12	0	0
6	B	4	0	6	0	0
7	B	5	0	0	0	0
8	C	10	0	14	0	0
9	D	12	0	13	0	0
9	F	12	0	13	0	0
10	F	1	0	0	0	0
11	A	63	0	0	1	0
11	B	97	0	0	4	0
11	C	29	0	0	0	0
11	D	65	0	0	1	0
11	E	27	0	0	1	0
11	F	117	0	0	1	0
All	All	13884	0	58	35	0

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 3.

The worst 5 of 35 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:39:ARG:NH2	1:B:276:GLY:O	2.31	0.63
1:B:103:ASN:ND2	11:B:597:HOH:O	2.32	0.62
1:A:172:ASP:O	1:A:177:ARG:NH1	2.35	0.59
1:B:107:PRO:CG	11:B:597:HOH:O	2.52	0.57
2:E:99:ARG:NH1	11:E:212:HOH:O	2.38	0.56

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	353/373 (95%)	339 (96%)	13 (4%)	1 (0%)	50	77
1	B	354/373 (95%)	342 (97%)	10 (3%)	2 (1%)	33	63
2	C	122/137 (89%)	115 (94%)	7 (6%)	0	100	100
2	E	123/137 (90%)	116 (94%)	7 (6%)	0	100	100
3	D	374/385 (97%)	356 (95%)	17 (4%)	1 (0%)	50	77
3	F	375/385 (97%)	356 (95%)	18 (5%)	1 (0%)	50	77
All	All	1701/1790 (95%)	1624 (96%)	72 (4%)	5 (0%)	50	77

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	276	GLY
1	B	358	LEU
3	F	102	ILE
1	A	232	GLU
3	D	102	ILE

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	277/292 (95%)	271 (98%)	6 (2%)	64	89
1	B	278/292 (95%)	271 (98%)	7 (2%)	60	86
2	C	104/112 (93%)	103 (99%)	1 (1%)	85	96
2	E	105/112 (94%)	105 (100%)	0	100	100
3	D	304/310 (98%)	298 (98%)	6 (2%)	68	90
3	F	305/310 (98%)	299 (98%)	6 (2%)	68	90
All	All	1373/1428 (96%)	1347 (98%)	26 (2%)	69	91

5 of 26 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	305	LYS
3	D	20	ARG

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Mol	Chain	Res	Type
3	F	260	LYS
1	B	321	ARG
2	C	71	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA ⓘ

There are no RNA chains in this entry.

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

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	0AF	C	57	2	16,16,17	4.66	3 (18%)	19,22,24	2.50	5 (26%)
2	0AF	E	57	2	16,16,17	4.57	3 (18%)	19,22,24	2.37	7 (36%)

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	0AF	C	57	2	-	0/4/6/8	0/2/2/2
2	0AF	E	57	2	-	0/4/6/8	0/2/2/2

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	57	0AF	O-C	17.69	1.23	1.11

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	57	0AF	O-C	17.03	1.23	1.11
2	E	57	0AF	CZ2-CE2	4.24	1.49	1.41
2	E	57	0AF	CD2-CE2	3.78	1.47	1.41
2	C	57	0AF	CZ2-CE2	3.54	1.48	1.41

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	57	0AF	C-CA-N	-8.08	105.76	113.83
2	E	57	0AF	C-CA-N	-7.06	106.78	113.83
2	C	57	0AF	CZ2-CE2-CD2	-3.76	116.87	121.47
2	C	57	0AF	CD1-NE1-CE2	3.53	110.56	107.82
2	E	57	0AF	CD1-NE1-CE2	3.45	110.50	107.82

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 14 ligands modelled in this entry, 3 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	$\# Z > 2$
5	HEC	A	402	1	50,50,50	3.63	26 (52%)	56,82,82	3.25	24 (42%)
5	HEC	A	403	1	50,50,50	3.40	28 (56%)	56,82,82	3.36	25 (44%)
6	EDO	A	404	-	3,3,3	0.54	0	2,2,2	0.30	0
6	EDO	A	405	-	3,3,3	0.52	0	2,2,2	0.35	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	HEC	B	402	1	50,50,50	3.55	26 (52%)	56,82,82	3.26	24 (42%)
5	HEC	B	403	1	50,50,50	3.44	26 (52%)	56,82,82	3.47	24 (42%)
6	EDO	B	404	-	3,3,3	0.51	0	2,2,2	0.34	0
7	PO4	B	405	-	4,4,4	0.30	0	6,6,6	0.28	0
8	PGE	C	201	-	9,9,9	0.52	0	8,8,8	0.28	0
9	MES	D	401	-	12,12,12	1.86	1 (8%)	16,16,16	5.05	9 (56%)
9	MES	F	401	-	12,12,12	2.05	1 (8%)	16,16,16	4.71	6 (37%)

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
5	HEC	A	402	1	-	0/10/54/54	0/0/8/8
5	HEC	A	403	1	-	0/10/54/54	0/0/8/8
6	EDO	A	404	-	-	0/1/1/1	0/0/0/0
6	EDO	A	405	-	-	0/1/1/1	0/0/0/0
5	HEC	B	402	1	-	0/10/54/54	0/0/8/8
5	HEC	B	403	1	-	0/10/54/54	0/0/8/8
6	EDO	B	404	-	-	0/1/1/1	0/0/0/0
7	PO4	B	405	-	-	0/0/0/0	0/0/0/0
8	PGE	C	201	-	-	0/7/7/7	0/0/0/0
9	MES	D	401	-	-	0/6/14/14	0/1/1/1
9	MES	F	401	-	-	0/6/14/14	1/1/1/1

The worst 5 of 108 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	402	HEC	C3C-CAC	13.21	1.52	1.34
5	A	402	HEC	C3B-CAB	13.07	1.52	1.34
5	B	402	HEC	C3B-CAB	12.96	1.52	1.34
5	A	403	HEC	C3B-CAB	12.41	1.51	1.34
5	B	403	HEC	C3B-CAB	12.29	1.51	1.34

The worst 5 of 112 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	D	401	MES	O3S-S-O2S	-11.44	82.58	112.50
9	F	401	MES	O3S-S-O2S	-11.24	83.10	112.50
9	D	401	MES	O3S-S-O1S	-10.79	84.27	112.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	F	401	MES	O3S-S-O1S	-10.50	85.04	112.50
5	B	402	HEC	CBB-CAB-C3B	-9.74	106.07	127.36

There are no chirality outliers.

There are no torsion outliers.

All (1) ring outliers are listed below:

Mol	Chain	Res	Type	Atoms
9	F	401	MES	C2-C3-C5-C6-N4-O1

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, 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	354/373 (94%)	-0.23	3 (0%) 83 85	43, 55, 70, 81	0
1	B	355/373 (95%)	-0.29	2 (0%) 86 89	36, 47, 62, 75	0
2	C	125/137 (91%)	0.02	1 (0%) 83 85	39, 50, 73, 86	0
2	E	125/137 (91%)	0.07	0 100 100	37, 46, 58, 83	0
3	D	376/385 (97%)	-0.08	5 (1%) 74 75	38, 59, 86, 102	0
3	F	376/385 (97%)	-0.26	0 100 100	35, 46, 63, 73	0
All	All	1711/1790 (95%)	-0.18	11 (0%) 86 89	35, 51, 76, 102	0

The worst 5 of 11 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	6	ALA	5.8
1	A	320	ALA	3.6
1	A	6	ALA	2.9
3	D	386	GLY	2.9
1	A	7	ASP	2.9

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

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, 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	RSR	LLDF	B-factors(Å ²)	Q<0.9
2	0AF	C	57	15/16	0.20	1.18	46,49,52,52	0
2	0AF	E	57	15/16	0.21	1.11	44,46,48,48	0

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, 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	RSR	LLDF	B-factors(Å ²)	Q<0.9
9	MES	D	401	12/12	0.30	7.47	105,111,112,113	0
9	MES	F	401	12/12	0.31	7.20	88,96,101,101	0
8	PGE	C	201	10/10	0.24	4.32	60,69,74,74	0
6	EDO	A	404	4/4	0.31	2.77	61,62,62,63	0
5	HEC	B	403	43/43	0.15	1.04	36,37,38,39	0
5	HEC	A	403	43/43	0.15	0.65	44,45,46,47	0
5	HEC	B	402	43/43	0.13	0.44	39,41,44,46	0
4	CA	A	401	1/1	0.09	0.30	61,61,61,61	0
5	HEC	A	402	43/43	0.13	0.24	44,48,52,54	0
7	PO4	B	405	5/5	0.12	0.07	76,77,78,78	0
4	CA	B	401	1/1	0.09	-0.12	33,33,33,33	0
6	EDO	A	405	4/4	0.16	-0.20	60,60,60,61	0
6	EDO	B	404	4/4	0.12	-0.50	59,59,59,60	0
10	NA	F	402	1/1	0.10	-1.11	52,52,52,52	0

6.5 Other polymers ⓘ

There are no such residues in this entry.