



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 15, 2017 – 02:03 am GMT

PDB ID : 3SLE  
Title : Crystal Structure of the P107C-MauG/pre-Methylamine Dehydrogenase Complex  
Authors : Yukl, E.T.; Wilmot, C.M.  
Deposited on : 2011-06-24  
Resolution : 2.52 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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/validation/2016/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 : 1.7.2 (RC1), CSD as538be (2017)  
Xtriage (Phenix) : 1.9-1692  
EDS : trunk28620  
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : recalc28949

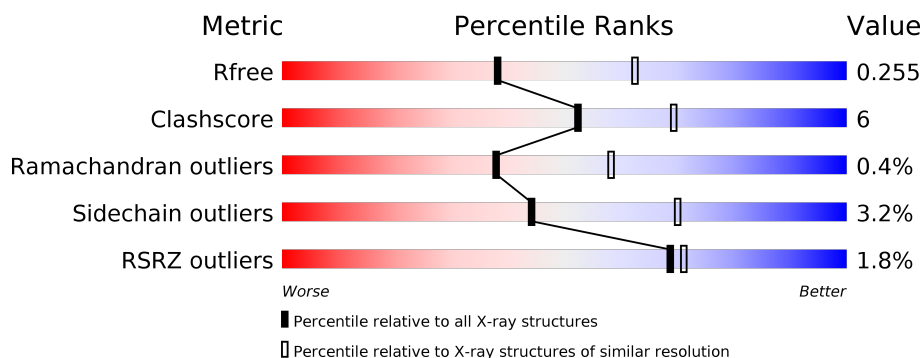
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.52 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))
$R_{free}$	100719	4636 (2.54-2.50)
Clashscore	112137	5382 (2.54-2.50)
Ramachandran outliers	110173	5282 (2.54-2.50)
Sidechain outliers	110143	5284 (2.54-2.50)
RSRZ outliers	101464	4669 (2.54-2.50)

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. 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	373	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 1%, yellow 1%, green 98%);"></div> <div style="display: flex; justify-content: space-between; margin-top: 5px;"> <span>%</span> <span>83%</span> <span>10%</span> <span>• 5%</span> </div> </div>
1	B	373	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 1%, yellow 1%, green 98%);"></div> <div style="display: flex; justify-content: space-between; margin-top: 5px;"> <span>%</span> <span>83%</span> <span>11%</span> <span>• 5%</span> </div> </div>
2	C	137	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 1%, yellow 1%, green 98%);"></div> <div style="display: flex; justify-content: space-between; margin-top: 5px;"> <span>%</span> <span>81%</span> <span>12%</span> <span>• 6%</span> </div> </div>
2	E	137	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, green 73%, yellow 16%, orange 9%, grey 2%);"></div> <div style="display: flex; justify-content: space-between; margin-top: 5px;"> <span></span> <span>73%</span> <span>16%</span> <span>• 9%</span> </div> </div>
3	D	385	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 3%, orange 1%, yellow 1%, green 95%);"></div> <div style="display: flex; justify-content: space-between; margin-top: 5px;"> <span>3%</span> <span>78%</span> <span>19%</span> <span>• •</span> </div> </div>
3	F	385	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 3%, orange 1%, yellow 1%, green 95%);"></div> <div style="display: flex; justify-content: space-between; margin-top: 5px;"> <span>3%</span> <span>85%</span> <span>12%</span> <span>•</span> </div> </div>

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	0AF	C	57	-	-	X	-
2	0AF	E	57	-	-	X	-
6	ACT	B	403	-	-	-	X

## 2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 13939 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 Methylamine utilization protein MauG.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	354	Total	C	N	O	S	0	1	0
			2744	1710	492	530	12			
1	B	355	Total	C	N	O	S	0	5	0
			2788	1736	500	540	12			

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	107	CSD	PRO	ENGINEERED MUTATION	UNP Q51658
A	368	HIS	-	EXPRESSION TAG	UNP Q51658
A	369	HIS	-	EXPRESSION TAG	UNP Q51658
A	370	HIS	-	EXPRESSION TAG	UNP Q51658
A	371	HIS	-	EXPRESSION TAG	UNP Q51658
A	372	HIS	-	EXPRESSION TAG	UNP Q51658
A	373	HIS	-	EXPRESSION TAG	UNP Q51658
B	107	CSD	PRO	ENGINEERED MUTATION	UNP Q51658
B	368	HIS	-	EXPRESSION TAG	UNP Q51658
B	369	HIS	-	EXPRESSION TAG	UNP Q51658
B	370	HIS	-	EXPRESSION TAG	UNP Q51658
B	371	HIS	-	EXPRESSION TAG	UNP Q51658
B	372	HIS	-	EXPRESSION TAG	UNP Q51658
B	373	HIS	-	EXPRESSION TAG	UNP Q51658

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	129	Total	C	N	O	S	0	0	0
			994	614	173	194	13			
2	E	125	Total	C	N	O	S	0	4	0
			972	601	162	193	16			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	132	HIS	-	EXPRESSION TAG	UNP P22619
C	133	HIS	-	EXPRESSION TAG	UNP P22619
C	134	HIS	-	EXPRESSION TAG	UNP P22619
C	135	HIS	-	EXPRESSION TAG	UNP P22619
C	136	HIS	-	EXPRESSION TAG	UNP P22619
C	137	HIS	-	EXPRESSION TAG	UNP P22619
E	132	HIS	-	EXPRESSION TAG	UNP P22619
E	133	HIS	-	EXPRESSION TAG	UNP P22619
E	134	HIS	-	EXPRESSION TAG	UNP P22619
E	135	HIS	-	EXPRESSION TAG	UNP P22619
E	136	HIS	-	EXPRESSION TAG	UNP P22619
E	137	HIS	-	EXPRESSION TAG	UNP P22619

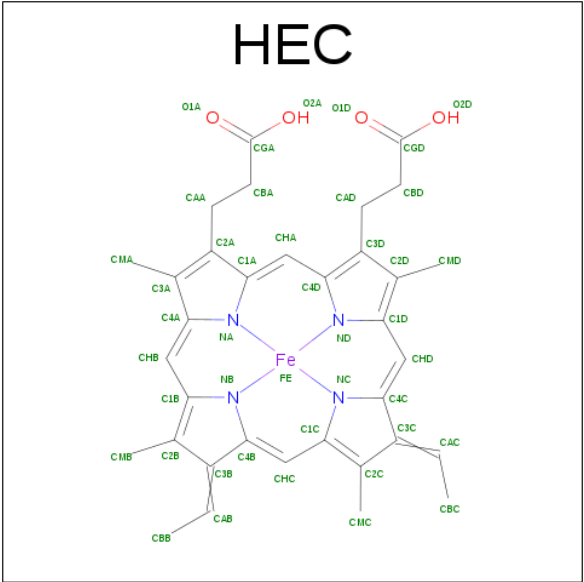
- Molecule 3 is a protein called Methylamine dehydrogenase heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	D	376	Total	C	N	O	S	0	1	0
			2929	1857	502	562	8			
3	F	376	Total	C	N	O	S	0	1	0
			2926	1855	502	560	9			

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

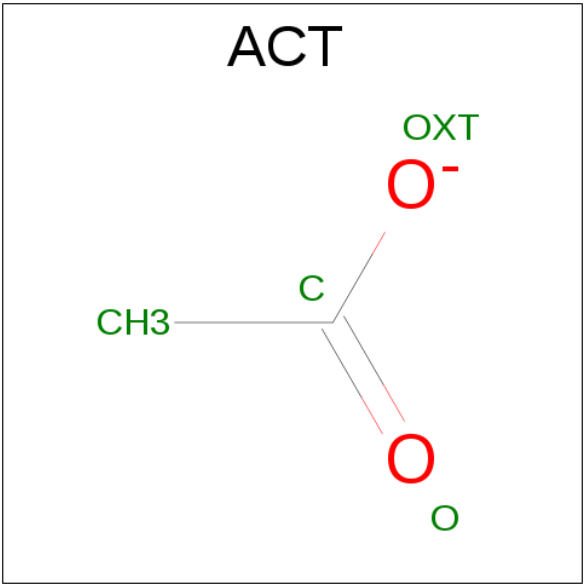
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	1	Total	Ca	0	0
			1	1		
4	A	1	Total	Ca	0	0
			1	1		

- Molecule 5 is HEME C (three-letter code: HEC) (formula: C<sub>34</sub>H<sub>34</sub>FeN<sub>4</sub>O<sub>4</sub>).



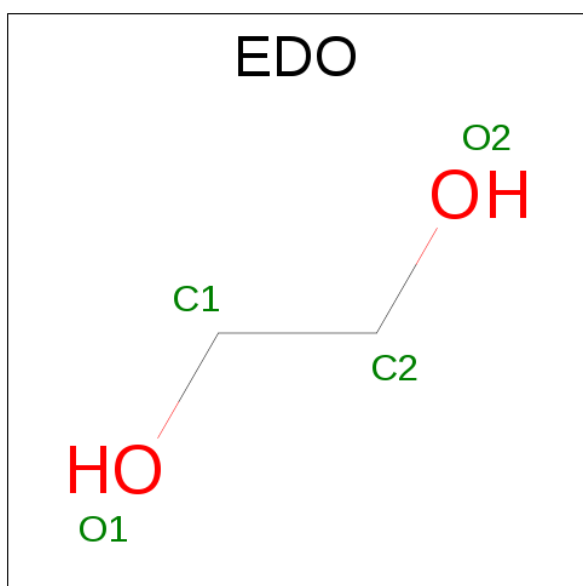
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	A	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
5	A	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
5	B	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
5	B	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		

- Molecule 6 is ACETATE ION (three-letter code: ACT) (formula: C<sub>2</sub>H<sub>3</sub>O<sub>2</sub>).



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

- Molecule 7 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula:  $C_2H_6O_2$ ).



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

- Molecule 8 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	A	66	Total O 66 66	0	0
8	B	105	Total O 105 105	0	0
8	C	18	Total O 18 18	0	0
8	D	52	Total O 52 52	0	0

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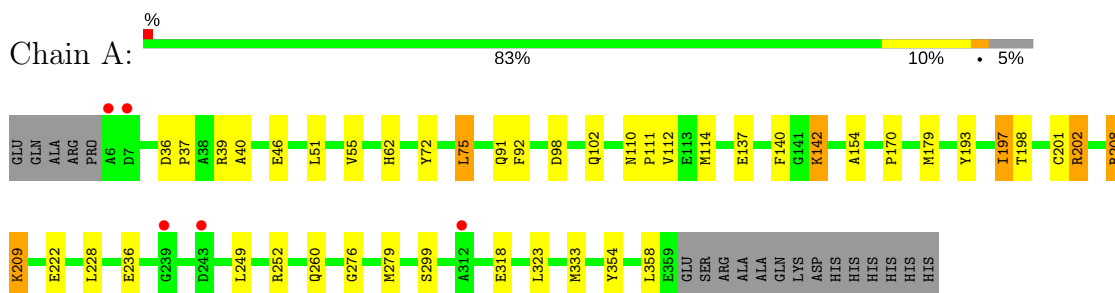
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	E	30	Total 30	O 30	0	0
8	F	117	Total 117	O 117	0	0



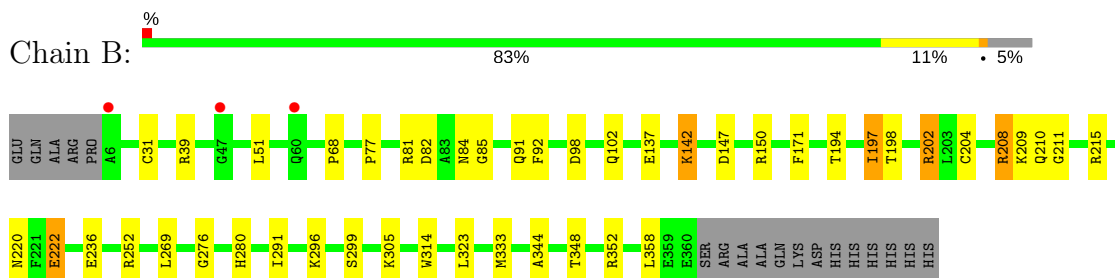
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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.

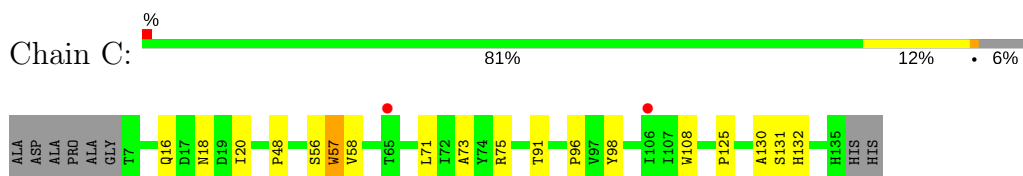
- Molecule 1: Methylamine utilization protein MauG



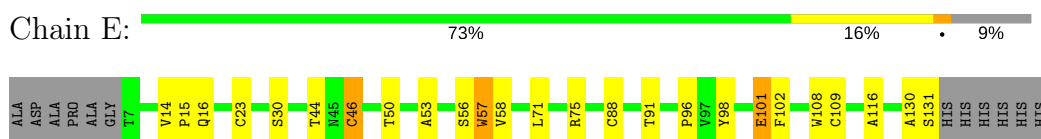
- Molecule 1: Methylamine utilization protein MauG



- Molecule 2: Methylamine dehydrogenase light chain

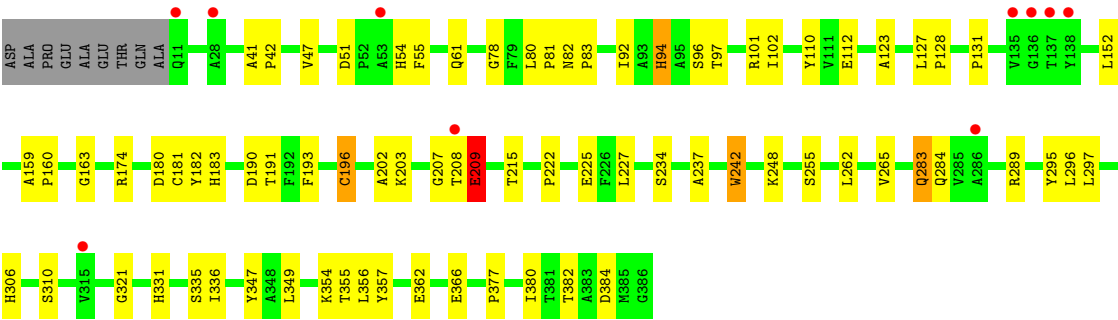


- Molecule 2: Methylamine dehydrogenase light chain

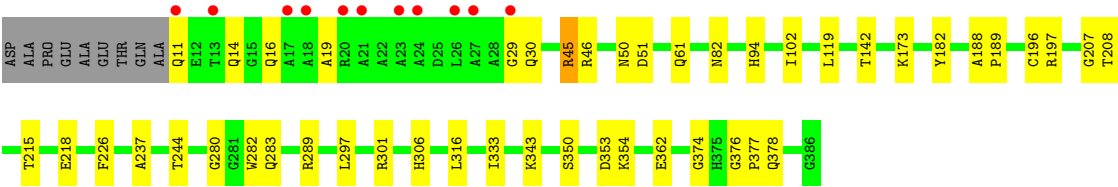
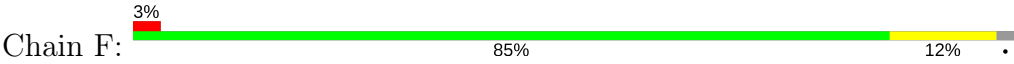


- Molecule 3: Methylamine dehydrogenase heavy chain





• Molecule 3: Methylamine dehydrogenase heavy chain



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	55.85Å 88.53Å 107.70Å 116.21° 91.83° 99.35°	Depositor
Resolution (Å)	47.86 – 2.52 43.28 – 2.52	Depositor EDS
% Data completeness (in resolution range)	96.9 (47.86-2.52) 81.6 (43.28-2.52)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.14 (at 2.51Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, $R_{free}$	0.174 , 0.243 0.187 , 0.255	Depositor DCC
$R_{free}$ test set	2992 reflections (5.31%)	DCC
Wilson B-factor (Å <sup>2</sup> )	43.3	Xtriage
Anisotropy	0.012	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.29 , 34.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	13939	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	52.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.86% 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: CSD, CA, HEC, EDO, 0AF, ACT

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	0.70	0/2799	0.78	5/3797 (0.1%)
1	B	0.77	0/2846	0.82	5/3858 (0.1%)
2	C	0.67	0/1007	0.74	0/1375
2	E	0.80	1/990 (0.1%)	0.80	0/1352
3	D	0.73	1/3009 (0.0%)	0.77	1/4100 (0.0%)
3	F	0.82	0/3006	0.81	1/4096 (0.0%)
All	All	0.75	2/13657 (0.0%)	0.79	12/18578 (0.1%)

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
2	C	0	2
2	E	0	3
All	All	0	5

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	196	CYS	CB-SG	-6.41	1.71	1.82
2	E	46	CYS	CB-SG	-5.76	1.72	1.81

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	208	ARG	NE-CZ-NH2	-9.75	115.42	120.30
1	A	208	ARG	NE-CZ-NH1	8.99	124.80	120.30
1	B	208	ARG	NE-CZ-NH1	-8.69	115.96	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	208	ARG	NE-CZ-NH2	8.26	124.43	120.30
1	B	352	ARG	NE-CZ-NH1	7.69	124.15	120.30

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	C	56	SER	Peptide
2	C	57	0AF	Mainchain
2	E	56	SER	Mainchain,Peptide
2	E	57	0AF	Mainchain

## 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	2744	0	2612	26	0
1	B	2788	0	2653	30	0
2	C	994	0	887	19	0
2	E	972	0	878	25	0
3	D	2929	0	2814	44	0
3	F	2926	0	2812	26	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
5	A	86	0	60	7	0
5	B	86	0	61	12	0
6	B	4	0	3	0	0
6	D	4	0	3	0	0
6	F	8	0	6	0	0
7	B	4	0	6	0	0
7	D	4	0	6	1	0
8	A	66	0	0	3	0
8	B	105	0	0	2	0
8	C	18	0	0	0	0
8	D	52	0	0	1	0
8	E	30	0	0	1	0
8	F	117	0	0	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	13939	0	12801	162	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 6.

The worst 5 of 162 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:57:0AF:HE3	2:C:108:TRP:CD1	1.30	1.66
2:E:57:0AF:HE3	2:E:108:TRP:CD1	1.20	1.63
2:E:57:0AF:CE3	2:E:108:TRP:CD1	1.98	1.47
2:C:57:0AF:CE3	2:C:108:TRP:CD1	2.05	1.39
2:E:57:0AF:CE3	2:E:108:TRP:HD1	1.32	1.30

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	352/373 (94%)	342 (97%)	10 (3%)	0	100	100
1	B	357/373 (96%)	346 (97%)	11 (3%)	0	100	100
2	C	126/137 (92%)	123 (98%)	3 (2%)	0	100	100
2	E	126/137 (92%)	120 (95%)	6 (5%)	0	100	100
3	D	375/385 (97%)	354 (94%)	16 (4%)	5 (1%)	14	24
3	F	375/385 (97%)	357 (95%)	16 (4%)	2 (0%)	32	52
All	All	1711/1790 (96%)	1642 (96%)	62 (4%)	7 (0%)	38	58

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	D	209	GLU
3	F	218	GLU
3	D	102	ILE
3	D	180	ASP
3	D	283	GLN

### 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	276/291 (95%)	264 (96%)	12 (4%)	33	57
1	B	281/291 (97%)	269 (96%)	12 (4%)	33	57
2	C	108/112 (96%)	105 (97%)	3 (3%)	49	75
2	E	108/112 (96%)	103 (95%)	5 (5%)	31	53
3	D	305/310 (98%)	297 (97%)	8 (3%)	51	77
3	F	305/310 (98%)	298 (98%)	7 (2%)	56	80
All	All	1383/1426 (97%)	1336 (97%)	47 (3%)	44	68

5 of 47 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	269	LEU
2	C	132	HIS
3	F	45	ARG
1	B	358	LEU
3	D	92	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 17 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	163	GLN
1	B	210	GLN
3	D	284	GLN
1	B	91	GLN

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Mol	Chain	Res	Type
3	D	331	HIS

### 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	CSD	A	107	1,5	4,7,8	0.93	0	2,8,10	2.39	1 (50%)
1	CSD	B	107	1,5	4,7,8	1.26	0	2,8,10	2.98	1 (50%)
2	0AF	C	57	2	14,16,17	1.30	2 (14%)	12,22,24	1.97	4 (33%)
2	0AF	E	57	2	14,16,17	1.24	1 (7%)	12,22,24	1.82	4 (33%)

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	CSD	A	107	1,5	-	1/2/6/8	0/0/0/0
1	CSD	B	107	1,5	-	1/2/6/8	0/0/0/0
2	0AF	C	57	2	-	0/3/6/8	0/2/2/2
2	0AF	E	57	2	-	0/3/6/8	0/2/2/2

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	57	0AF	CZ2-CE2	-2.49	1.39	1.42
2	C	57	0AF	CZ3-CE3	2.14	1.41	1.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	57	0AF	CZ3-CE3	2.16	1.41	1.36

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	57	0AF	CB-CG-CD1	-3.59	123.53	127.97
2	E	57	0AF	CB-CG-CD1	-3.25	123.95	127.97
2	C	57	0AF	CZ3-CH2-CZ2	-2.95	116.42	120.29
2	E	57	0AF	CZ3-CH2-CZ2	-2.76	116.67	120.29
2	C	57	0AF	O-C-CA	-2.65	117.69	125.02

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	B	107	CSD	CA-CB-SG-OD1
1	A	107	CSD	CA-CB-SG-OD1

There are no ring outliers.

2 monomers are involved in 15 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	57	0AF	8	0
2	E	57	0AF	7	0

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 12 ligands modelled in this entry, 2 are monoatomic - leaving 10 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	28,50,50	2.24	5 (17%)	16,82,82	2.04	3 (18%)
5	HEC	A	403	1	28,50,50	2.29	3 (10%)	16,82,82	1.97	4 (25%)
5	HEC	B	402	1	28,50,50	2.32	5 (17%)	16,82,82	2.10	4 (25%)
6	ACT	B	403	-	1,3,3	1.33	0	0,3,3	0.00	-
5	HEC	B	404	1	28,50,50	2.17	10 (35%)	16,82,82	2.70	7 (43%)
7	EDO	B	405	-	3,3,3	0.72	0	2,2,2	0.10	0
6	ACT	D	401	-	1,3,3	2.42	1 (100%)	0,3,3	0.00	-
7	EDO	D	402	-	3,3,3	0.56	0	2,2,2	0.04	0
6	ACT	F	401	-	1,3,3	1.71	0	0,3,3	0.00	-
6	ACT	F	402	-	1,3,3	2.21	1 (100%)	0,3,3	0.00	-

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	-	0/6/54/54	0/0/8/8
5	HEC	A	403	1	-	0/6/54/54	0/0/8/8
5	HEC	B	402	1	-	0/6/54/54	0/0/8/8
6	ACT	B	403	-	-	0/0/0/0	0/0/0/0
5	HEC	B	404	1	-	0/6/54/54	0/0/8/8
7	EDO	B	405	-	-	0/1/1/1	0/0/0/0
6	ACT	D	401	-	-	0/0/0/0	0/0/0/0
7	EDO	D	402	-	-	0/1/1/1	0/0/0/0
6	ACT	F	401	-	-	0/0/0/0	0/0/0/0
6	ACT	F	402	-	-	0/0/0/0	0/0/0/0

The worst 5 of 25 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	403	HEC	C3B-C2B	-7.42	1.32	1.40
5	A	402	HEC	C3C-C2C	-6.31	1.34	1.40
5	B	402	HEC	C3B-C2B	-6.22	1.34	1.40
5	B	402	HEC	C3C-C2C	-5.79	1.34	1.40
5	A	403	HEC	C3C-C2C	-5.73	1.34	1.40

The worst 5 of 18 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	B	404	HEC	CBD-CAD-C3D	-6.38	100.28	112.48

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	403	HEC	CBD-CAD-C3D	-5.61	101.76	112.48
5	A	402	HEC	CBD-CAD-C3D	-5.51	101.96	112.48
5	B	402	HEC	CBD-CAD-C3D	-5.09	102.75	112.48
5	B	404	HEC	C1D-C2D-C3D	-4.85	103.62	107.00

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5 monomers are involved in 20 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	402	HEC	3	0
5	A	403	HEC	4	0
5	B	402	HEC	4	0
5	B	404	HEC	8	0
7	D	402	EDO	1	0

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

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

There are no chain breaks in this entry.

## 6 Fit of model and data [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

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	353/373 (94%)	-0.32	5 (1%) 75 77	36, 53, 80, 96	0
1	B	354/373 (94%)	-0.33	3 (0%) 86 87	30, 48, 79, 96	0
2	C	128/137 (93%)	0.04	2 (1%) 72 74	37, 53, 87, 115	1 (0%)
2	E	124/137 (90%)	-0.12	0 100 100	35, 44, 65, 85	0
3	D	376/385 (97%)	-0.02	10 (2%) 55 58	34, 61, 85, 98	0
3	F	376/385 (97%)	-0.18	11 (2%) 52 55	33, 44, 70, 92	2 (0%)
All	All	1711/1790 (95%)	-0.19	31 (1%) 69 71	30, 51, 80, 115	3 (0%)

The worst 5 of 31 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	6	ALA	7.8
3	F	17	ALA	4.4
3	F	13	THR	3.5
3	F	23	ALA	3.5
3	F	11	GLN	3.4

### 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. 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	RSCC	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
2	OAF	E	57	15/16	0.95	0.17	-	44,47,51,56	0
1	CSD	B	107	8/9	0.99	0.09	-	49,52,54,54	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
2	OAF	C	57	15/16	0.95	0.20	-	56,59,62,65	0
1	CSD	A	107	8/9	0.98	0.09	-	52,54,55,56	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. 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	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
6	ACT	B	403	4/4	0.93	0.18	2.13	67,67,67,67	0
7	EDO	D	402	4/4	0.90	0.15	0.69	63,64,64,65	0
5	HEC	A	402	43/43	0.97	0.13	0.46	38,44,49,50	0
5	HEC	A	403	43/43	0.98	0.12	0.15	34,43,45,45	0
5	HEC	B	404	43/43	0.99	0.12	-0.15	18,27,34,37	0
7	EDO	B	405	4/4	0.93	0.13	-0.21	50,51,51,52	0
4	CA	A	401	1/1	0.91	0.11	-0.26	41,41,41,41	0
4	CA	B	401	1/1	0.97	0.10	-0.27	38,38,38,38	0
5	HEC	B	402	43/43	0.98	0.12	-0.40	29,40,45,49	0
6	ACT	D	401	4/4	0.95	0.10	-	62,62,63,63	0
6	ACT	F	401	4/4	0.95	0.16	-	51,51,51,52	0
6	ACT	F	402	4/4	0.86	0.29	-	71,71,72,72	0

### 6.5 Other polymers [i](#)

There are no such residues in this entry.