



# wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 31, 2016 – 06:57 PM GMT

PDB ID : 1D7W  
Title : CRYSTAL STRUCTURE OF HUMAN MYELOPEROXIDASE ISOFORM C  
COMPLEXED WITH CYANIDE AND BROMIDE AT PH 4.0  
Authors : Fiedler, T.J.; Fenna, R.E.  
Deposited on : 1999-10-20  
Resolution : 1.90 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 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : **NOT EXECUTED**  
EDS : **NOT EXECUTED**  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

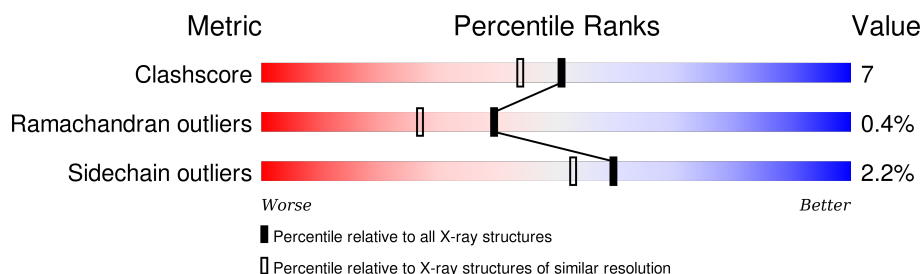
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.90 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))
Clashscore	102246	5398 (1.90-1.90)
Ramachandran outliers	100387	5338 (1.90-1.90)
Sidechain outliers	100360	5339 (1.90-1.90)

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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	104	
1	B	104	
2	C	466	
2	D	466	

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
8	ACT	C	1606	-	-	X	-

## 2 Entry composition

There are 11 unique types of molecules in this entry. The entry contains 10319 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 MYELOPEROXIDASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	104	Total	C	N	O	S	0	0	0
			838	529	148	156	5			
1	B	104	Total	C	N	O	S	0	0	0
			838	529	148	156	5			

- Molecule 2 is a protein called MYELOPEROXIDASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	466	Total	C	N	O	S	0	0	0
			3733	2351	687	668	27			
2	D	466	Total	C	N	O	S	0	0	0
			3733	2351	687	668	27			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	150	CSO	CYS	MODIFIED RESIDUE	UNP P05164
D	150	CSO	CYS	MODIFIED RESIDUE	UNP P05164

- Molecule 3 is SUGAR (N-ACETYL-D-GLUCOSAMINE) (three-letter code: NAG) (formula:  $C_8H_{15}NO_6$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	C	1	Total	C	N	O	0	0
			14	8	1	5		
3	C	1	Total	C	N	O	0	0
			14	8	1	5		
3	D	1	Total	C	N	O	0	0
			14	8	1	5		
3	D	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 4 is a polymer of unknown type called SUGAR (6-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	C	6	Total	C	N	O	0	0
			71	40	2	29		
4	D	6	Total	C	N	O	0	0
			71	40	2	29		

- Molecule 5 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	D	1	Total	Ca	0	0
			1	1		
5	C	1	Total	Ca	0	0
			1	1		

- Molecule 6 is BROMIDE ION (three-letter code: BR) (formula: Br).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	B	1	Total	Br	0	0
			1	1		
6	A	1	Total	Br	0	0
			1	1		
6	D	3	Total	Br	0	0
			3	3		
6	C	3	Total	Br	0	0
			3	3		

- Molecule 7 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



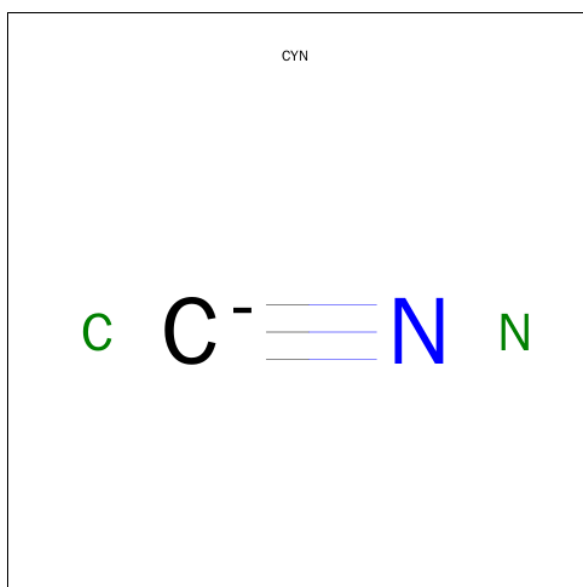
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	1	Total	O	S	0	0
			5	4	1		
7	C	1	Total	O	S	0	0
			5	4	1		
7	C	1	Total	O	S	0	0
			5	4	1		
7	B	1	Total	O	S	0	0
			5	4	1		
7	D	1	Total	O	S	0	0
			5	4	1		

- Molecule 8 is ACETATE ION (three-letter code: ACT) (formula: C<sub>2</sub>H<sub>3</sub>O<sub>2</sub>).



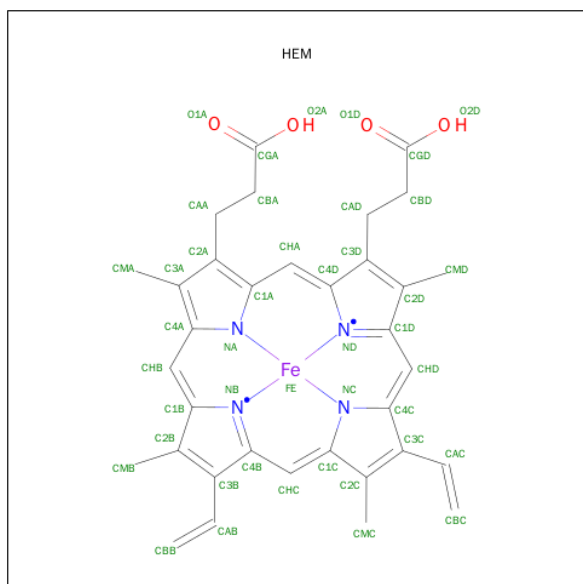
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	C	1	Total	C	O	0	0
			4	2	2		
8	C	1	Total	C	O	0	0
			4	2	2		
8	C	1	Total	C	O	0	0
			4	2	2		
8	B	1	Total	C	O	0	0
			4	2	2		
8	C	1	Total	C	O	0	0
			4	2	2		
8	C	1	Total	C	O	0	0
			4	2	2		
8	D	1	Total	C	O	0	0
			4	2	2		
8	D	1	Total	C	O	0	0
			4	2	2		
8	D	1	Total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

- Molecule 9 is CYANIDE ION (three-letter code: CYN) (formula: CN).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
9	A	1	Total	C	N	0	0
			2	1	1		
9	B	1	Total	C	N	0	0
			2	1	1		

- Molecule 10 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula:  $C_{34}H_{32}FeN_4O_4$ ).



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

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

- Molecule 11 is water.

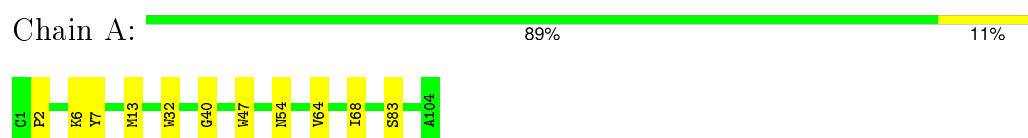
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
11	A	96	Total	O	0	0
			96	96		
11	B	98	Total	O	0	0
			98	98		
11	C	314	Total	O	0	0
			314	314		
11	D	298	Total	O	0	0
			298	298		

### 3 Residue-property plots

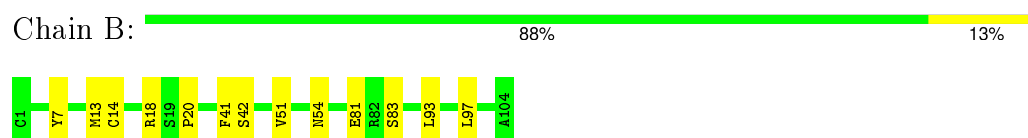
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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.

Note EDS was not executed.

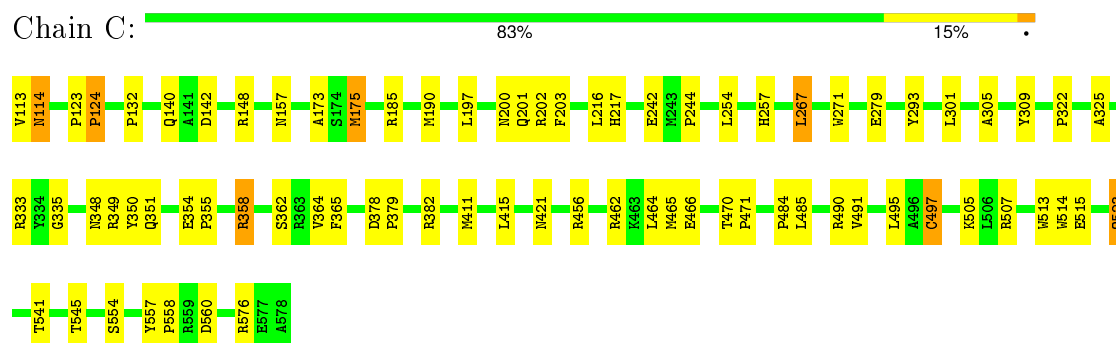
#### • Molecule 1: MYELOPEROXIDASE



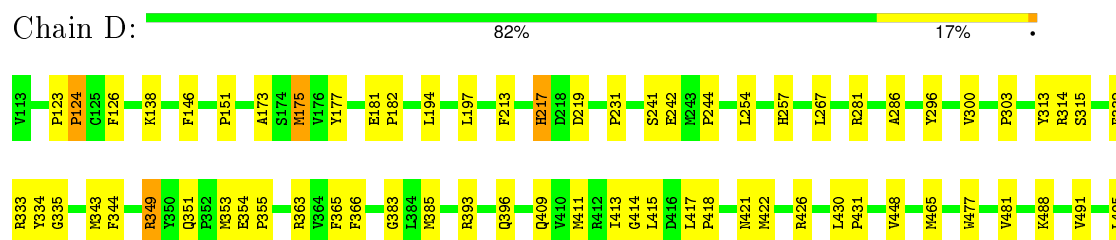
#### • Molecule 1: MYELOPEROXIDASE



#### • Molecule 2: MYELOPEROXIDASE



#### • Molecule 2: MYELOPEROXIDASE



R504
W514 E515
W522 Q523
L533 P534 R535
W548 W549
S554 N555
D560 F561 Y562
A569
R576 E577 A578

## 4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section will therefore be incomplete.

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	111.34Å 63.32Å 92.26Å 90.00° 97.41° 90.00°	Depositor
Resolution (Å)	30.00 – 1.90	Depositor
% Data completeness (in resolution range)	87.9 (30.00-1.90)	Depositor
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
Refinement program	X-PLOR 3.851	Depositor
R, $R_{free}$	0.215 , 0.270	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	10319	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	13.0	wwPDB-VP

## 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: CSO, BMA, NAG, SO4, CA, FUC, BR, ACT, HEM, CYN, MAN

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	0.69	0/863	0.72	0/1174
1	B	0.66	0/863	0.72	0/1174
2	C	0.67	0/3811	0.66	0/5168
2	D	0.65	0/3811	0.64	0/5168
All	All	0.66	0/9348	0.66	0/12684

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	838	0	798	10	0
1	B	838	0	798	10	0
2	C	3733	0	3725	55	0
2	D	3733	0	3725	53	0
3	C	28	0	26	1	0
3	D	28	0	26	0	0
4	C	71	0	61	0	0
4	D	71	0	61	2	0
5	C	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	D	1	0	0	0	0
6	A	1	0	0	0	0
6	B	1	0	0	0	0
6	C	3	0	0	0	0
6	D	3	0	0	0	0
7	A	5	0	0	0	0
7	B	5	0	0	0	0
7	C	10	0	0	0	0
7	D	5	0	0	1	0
8	A	4	0	3	0	0
8	B	8	0	6	0	0
8	C	20	0	15	3	0
8	D	16	0	12	2	0
9	A	2	0	0	0	0
9	B	2	0	0	0	0
10	A	43	0	30	4	0
10	B	43	0	30	3	0
11	A	96	0	0	2	0
11	B	98	0	0	5	0
11	C	314	0	0	9	0
11	D	298	0	0	9	0
All	All	10319	0	9316	129	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 7.

The worst 5 of 129 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:A:6:LYS:O	11:A:726(A):HOH:O	1.75	1.02
2:D:411:MET:HE2	2:D:415:LEU:HD21	1.61	0.83
1:A:64:VAL:HG13	1:A:68:ILE:HD12	1.65	0.78
2:D:349:ARG:HG3	2:D:351:GLN:HG2	1.67	0.76
2:C:514:TRP:CE2	2:C:515:GLU:HG3	2.21	0.76

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	102/104 (98%)	98 (96%)	4 (4%)	0	100	100
1	B	102/104 (98%)	98 (96%)	4 (4%)	0	100	100
2	C	463/466 (99%)	448 (97%)	13 (3%)	2 (0%)	39	27
2	D	463/466 (99%)	448 (97%)	13 (3%)	2 (0%)	39	27
All	All	1130/1140 (99%)	1092 (97%)	34 (3%)	4 (0%)	39	27

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	C	114	ASN
2	C	142	ASP
2	D	555	ASN
2	D	219	ASP

### 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	90/90 (100%)	88 (98%)	2 (2%)	60	53
1	B	90/90 (100%)	89 (99%)	1 (1%)	80	79
2	C	410/410 (100%)	399 (97%)	11 (3%)	52	43
2	D	410/410 (100%)	402 (98%)	8 (2%)	63	57
All	All	1000/1000 (100%)	978 (98%)	22 (2%)	60	53

5 of 22 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	C	470	THR
2	C	558	PRO
2	D	353	MET
2	C	497	CYS
2	C	523	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 10 such sidechains are listed below:

Mol	Chain	Res	Type
2	C	201	GLN
2	C	348	ASN
2	D	204	GLN
2	C	200	ASN
1	B	54	ASN

### 5.3.3 RNA ⓘ

There are no RNA molecules 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	CSO	C	150	2	3,6,7	0.76	0	1,6,8	1.79	0
2	CSO	D	150	2	3,6,7	0.87	0	1,6,8	1.62	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.



Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	CSO	C	150	2	-	0/1/5/7	0/0/0/0
2	CSO	D	150	2	-	0/1/5/7	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.

No monomer is involved in short contacts.

## 5.5 Carbohydrates [i](#)

12 carbohydrates 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	$\# Z  > 2$
4	NAG	C	1640	2,4	14,14,15	0.75	0	15,19,21	1.02	1 (6%)
4	NAG	C	1641	4	14,14,15	0.63	0	15,19,21	1.04	1 (6%)
4	BMA	C	1642	4	11,11,12	0.51	0	14,15,17	0.79	0
4	MAN	C	1643	4	11,11,12	0.52	0	14,15,17	0.86	1 (7%)
4	MAN	C	1644	4	11,11,12	0.78	0	14,15,17	0.62	0
4	FUC	C	1645	4	10,10,11	0.75	1 (10%)	14,14,16	0.59	0
4	NAG	D	2640	2,4	14,14,15	0.66	0	15,19,21	1.09	1 (6%)
4	NAG	D	2641	4	14,14,15	0.81	1 (7%)	15,19,21	0.99	2 (13%)
4	BMA	D	2642	4	11,11,12	0.49	0	14,15,17	0.68	0
4	MAN	D	2643	4	11,11,12	0.57	0	14,15,17	0.77	0
4	MAN	D	2644	4	11,11,12	0.95	0	14,15,17	0.66	0
4	FUC	D	2645	4	10,10,11	0.60	0	14,14,16	0.89	1 (7%)

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	NAG	C	1640	2,4	-	0/6/23/26	0/1/1/1
4	NAG	C	1641	4	-	0/6/23/26	0/1/1/1
4	BMA	C	1642	4	-	0/2/19/22	0/1/1/1
4	MAN	C	1643	4	-	0/2/19/22	0/1/1/1
4	MAN	C	1644	4	-	0/2/19/22	0/1/1/1
4	FUC	C	1645	4	-	0/0/17/20	0/1/1/1
4	NAG	D	2640	2,4	-	0/6/23/26	0/1/1/1
4	NAG	D	2641	4	-	0/6/23/26	0/1/1/1
4	BMA	D	2642	4	-	0/2/19/22	0/1/1/1
4	MAN	D	2643	4	-	0/2/19/22	0/1/1/1
4	MAN	D	2644	4	-	0/2/19/22	0/1/1/1
4	FUC	D	2645	4	-	0/0/17/20	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	C	1645	FUC	C2-C3	2.06	1.55	1.52
4	D	2641	NAG	C1-C2	2.09	1.55	1.52

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	C	1641	NAG	C2-N2-C7	-3.02	119.16	123.04
4	D	2641	NAG	C4-C3-C2	-2.37	107.54	111.23
4	C	1640	NAG	C2-N2-C7	-2.37	120.00	123.04
4	D	2640	NAG	C2-N2-C7	-2.27	120.12	123.04
4	D	2641	NAG	C2-N2-C7	-2.20	120.21	123.04

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	D	2640	NAG	1	0
4	D	2644	MAN	1	0

## 5.6 Ligand geometry ⓘ

Of 35 ligands modelled in this entry, 10 are monoatomic - leaving 25 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
7	SO4	A	1602	-	4,4,4	0.20	0	6,6,6	0.20	0
9	CYN	A	1844	10	0,1,1	0.00	-	0,0,0	0.00	-
8	ACT	A	2608	-	1,3,3	3.97	1 (100%)	0,3,3	0.00	-
10	HEM	A	605	1,9,2	30,50,50	2.60	9 (30%)	24,82,82	2.04	6 (25%)
8	ACT	B	1608	-	1,3,3	4.14	1 (100%)	0,3,3	0.00	-
7	SO4	B	2602	-	4,4,4	0.20	0	6,6,6	0.05	0
8	ACT	B	2611	-	1,3,3	3.18	1 (100%)	0,3,3	0.00	-
9	CYN	B	2844	10	0,1,1	0.00	-	0,0,0	0.00	-
10	HEM	B	605	1,9,2	30,50,50	2.70	8 (26%)	24,82,82	2.06	6 (25%)
7	SO4	C	1603	-	4,4,4	0.23	0	6,6,6	0.07	0
8	ACT	C	1604	-	1,3,3	1.81	0	0,3,3	0.00	-
8	ACT	C	1606	-	1,3,3	1.01	0	0,3,3	0.00	-
8	ACT	C	1607	-	1,3,3	3.43	1 (100%)	0,3,3	0.00	-
8	ACT	C	1609	-	1,3,3	1.87	0	0,3,3	0.00	-
7	SO4	C	1610	-	4,4,4	0.11	0	6,6,6	0.16	0
8	ACT	C	1612	-	1,3,3	3.27	1 (100%)	0,3,3	0.00	-
3	NAG	C	1620	2	14,14,15	0.44	0	15,19,21	1.06	2 (13%)
3	NAG	C	1630	2	14,14,15	0.81	0	15,19,21	0.78	0
8	ACT	D	2604	-	1,3,3	2.72	1 (100%)	0,3,3	0.00	-
8	ACT	D	2606	-	1,3,3	2.46	1 (100%)	0,3,3	0.00	-
8	ACT	D	2607	-	1,3,3	2.42	1 (100%)	0,3,3	0.00	-
8	ACT	D	2609	-	1,3,3	2.09	1 (100%)	0,3,3	0.00	-
7	SO4	D	2610	-	4,4,4	0.10	0	6,6,6	0.09	0
3	NAG	D	2620	2	14,14,15	0.60	0	15,19,21	0.93	0
3	NAG	D	2630	2	14,14,15	0.65	0	15,19,21	0.94	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
7	SO4	A	1602	-	-	0/0/0/0	0/0/0/0
9	CYN	A	1844	10	-	0/0/0/0	0/0/0/0
8	ACT	A	2608	-	-	0/0/0/0	0/0/0/0
10	HEM	A	605	1,9,2	-	0/10/54/54	0/0/8/8
8	ACT	B	1608	-	-	0/0/0/0	0/0/0/0
7	SO4	B	2602	-	-	0/0/0/0	0/0/0/0
8	ACT	B	2611	-	-	0/0/0/0	0/0/0/0
9	CYN	B	2844	10	-	0/0/0/0	0/0/0/0
10	HEM	B	605	1,9,2	-	0/10/54/54	0/0/8/8
7	SO4	C	1603	-	-	0/0/0/0	0/0/0/0
8	ACT	C	1604	-	-	0/0/0/0	0/0/0/0
8	ACT	C	1606	-	-	0/0/0/0	0/0/0/0
8	ACT	C	1607	-	-	0/0/0/0	0/0/0/0
8	ACT	C	1609	-	-	0/0/0/0	0/0/0/0
7	SO4	C	1610	-	-	0/0/0/0	0/0/0/0
8	ACT	C	1612	-	-	0/0/0/0	0/0/0/0
3	NAG	C	1620	2	-	0/6/23/26	0/1/1/1
3	NAG	C	1630	2	-	0/6/23/26	0/1/1/1
8	ACT	D	2604	-	-	0/0/0/0	0/0/0/0
8	ACT	D	2606	-	-	0/0/0/0	0/0/0/0
8	ACT	D	2607	-	-	0/0/0/0	0/0/0/0
8	ACT	D	2609	-	-	0/0/0/0	0/0/0/0
7	SO4	D	2610	-	-	0/0/0/0	0/0/0/0
3	NAG	D	2620	2	-	0/6/23/26	0/1/1/1
3	NAG	D	2630	2	-	0/6/23/26	0/1/1/1

The worst 5 of 26 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
10	B	605	HEM	C3B-C4B	-6.37	1.46	1.51
10	A	605	HEM	C2D-C3D	-5.98	1.36	1.54
10	B	605	HEM	C3C-CAC	-5.96	1.40	1.51
10	A	605	HEM	C3B-C4B	-5.94	1.46	1.51
10	B	605	HEM	C2D-C3D	-5.93	1.36	1.54

The worst 5 of 14 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	1620	NAG	C2-N2-C7	-2.20	120.22	123.04
3	C	1620	NAG	C1-O5-C5	2.12	114.93	112.25
10	A	605	HEM	C2D-C3D-C4D	2.50	105.74	101.50

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Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
10	B	605	HEM	C2D-C3D-C4D	2.68	106.05	101.50
10	B	605	HEM	CMD-C2D-C3D	2.88	127.08	114.35

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

8 monomers are involved in 14 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
10	A	605	HEM	4	0
10	B	605	HEM	3	0
8	C	1606	ACT	2	0
8	C	1609	ACT	1	0
3	C	1620	NAG	1	0
8	D	2604	ACT	1	0
8	D	2609	ACT	1	0
7	D	2610	SO4	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 ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

EDS was not executed - this section will therefore be empty.

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

EDS was not executed - this section will therefore be empty.

### 6.3 Carbohydrates ⓘ

EDS was not executed - this section will therefore be empty.

### 6.4 Ligands ⓘ

EDS was not executed - this section will therefore be empty.

### 6.5 Other polymers ⓘ

EDS was not executed - this section will therefore be empty.