



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 13, 2017 – 04:42 pm GMT

PDB ID : 1Z1N  
Title : Crystal Structure of the sixteen heme cytochrome from *Desulfovibrio gigas*  
Authors : Santos-Silva, T.; Dias, J.M.; Romao, M.J.  
Deposited on : 2005-03-04  
Resolution : 2.10 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

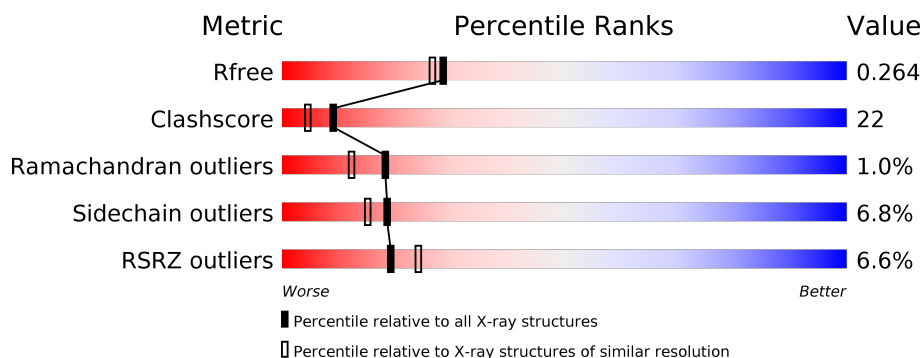
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.10 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	4243 (2.10-2.10)
Clashscore	112137	4788 (2.10-2.10)
Ramachandran outliers	110173	4740 (2.10-2.10)
Sidechain outliers	110143	4741 (2.10-2.10)
RSRZ outliers	101464	4275 (2.10-2.10)

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	X	560	<div> <div>6%</div> <div>68%</div> <div>21%</div> <div>•</div> <div>8%</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	NAG	X	900	X	-	-	-
5	GOL	X	803	-	-	X	-

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	GOL	X	804	-	-	-	X

## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 4998 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 sixteen heme cytochrome.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	X	516	Total	C	N	O	S	0	0	0
			3837	2355	703	739	40			

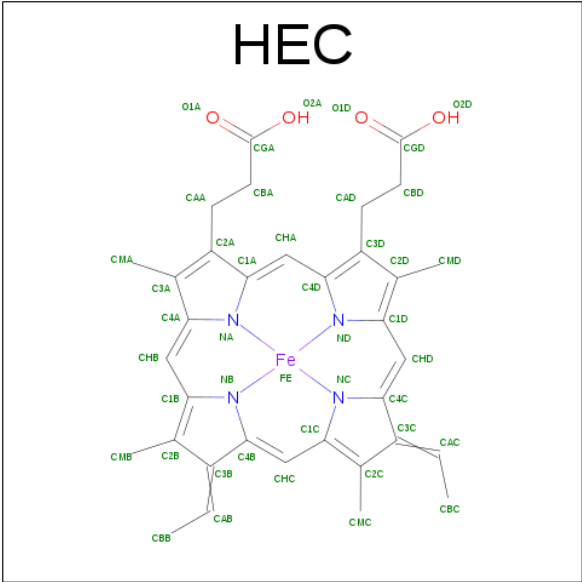
- Molecule 2 is a polymer of unknown type called SUGAR (N-ACETYL-D-GLUCOSAMINE).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	X	2	Total	C	N	O	0	0
			28	16	2	10		

- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	X	3	Total	Zn	0	0
			3	3		

- Molecule 4 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
4	X	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
4	X	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
4	X	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
4	X	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
4	X	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
4	X	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
4	X	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
4	X	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
4	X	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
4	X	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
4	X	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
4	X	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
4	X	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
4	X	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
4	X	1	Total 43	C 34	Fe 1	N 4	O 4	0	0

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	X	1	Total	C	Fe	N	O	
			43	34	1	4	4	
4	X	1	Total	C	Fe	N	O	
			43	34	1	4	4	

- Molecule 5 is GLYCEROL (three-letter code: GOL) (formula:  $C_3H_8O_3$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	X	1	Total	C	O		
			6	3	3		
5	X	1	Total	C	O		
			6	3	3		
5	X	1	Total	C	O		
			6	3	3		
5	X	1	Total	C	O		
			6	3	3		
5	X	1	Total	C	O		
			6	3	3		

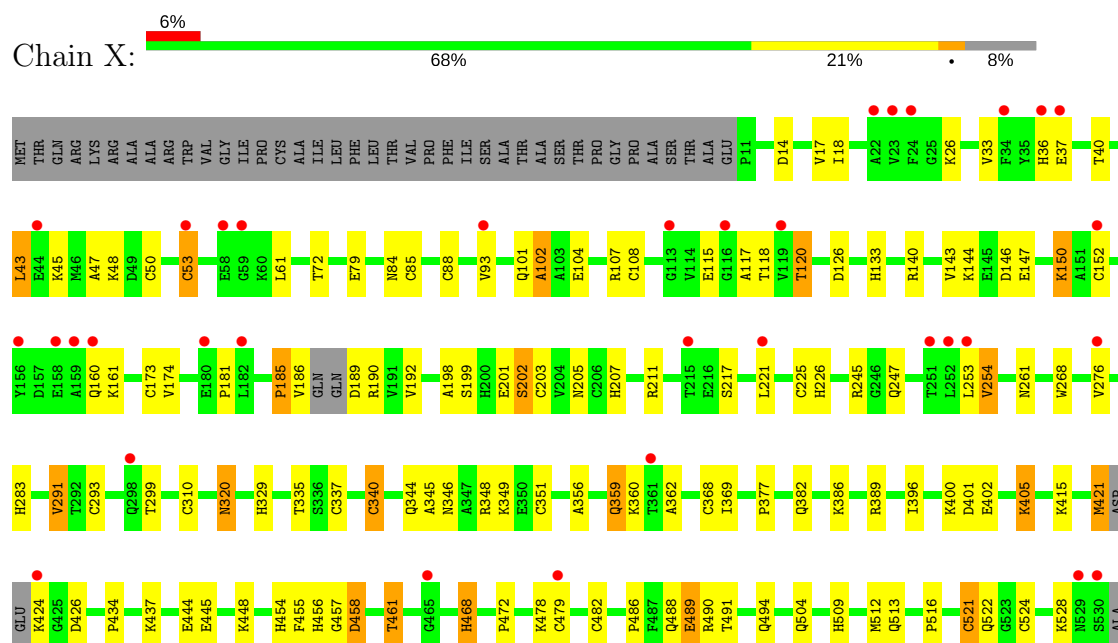
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	X	412	Total	O		
			412	412		

### 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: sixteen heme cytochrome



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	88.89Å 90.80Å 83.93Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	25.00 – 2.10 24.81 – 2.10	Depositor EDS
% Data completeness (in resolution range)	98.2 (25.00-2.10) 98.2 (24.81-2.10)	Depositor EDS
$R_{merge}$	0.04	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.46 (at 2.10Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, $R_{free}$	0.194 , 0.260 0.204 , 0.264	Depositor DCC
$R_{free}$ test set	1978 reflections (5.26%)	DCC
Wilson B-factor (Å <sup>2</sup> )	44.3	Xtriage
Anisotropy	0.057	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 56.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	0.025 for k,h,-l	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	4998	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	54.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.19% 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: GOL, ZN, NAA, NAG, HEC

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	X	1.00	6/3925 (0.2%)	0.98	8/5326 (0.2%)

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
1	X	0	1
2	X	1	0
All	All	1	1

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	X	479	CYS	CB-SG	6.77	1.93	1.82
1	X	276	VAL	CB-CG2	6.29	1.66	1.52
1	X	53	CYS	CB-SG	-5.78	1.72	1.81
1	X	340	CYS	CB-SG	5.38	1.91	1.82
1	X	455	PHE	CE1-CZ	5.08	1.47	1.37

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	X	389	ARG	NE-CZ-NH2	-11.92	114.34	120.30
1	X	389	ARG	NE-CZ-NH1	10.31	125.45	120.30
1	X	448	LYS	CD-CE-NZ	-7.46	94.53	111.70
1	X	291	VAL	CG1-CB-CG2	7.42	122.77	110.90
1	X	291	VAL	CB-CA-C	-7.21	97.70	111.40

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	X	900	NAG	C1

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	X	424	LYS	Peptide

## 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	X	3837	0	3662	154	2
2	X	28	0	25	1	0
3	X	3	0	0	0	0
4	X	688	0	495	112	2
5	X	30	0	40	6	0
6	X	412	0	0	20	2
All	All	4998	0	4222	182	3

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 22.

The worst 5 of 182 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:X:50:CYS:SG	4:X:601:HEC:HAB	1.37	1.63
1:X:152:CYS:SG	4:X:604:HEC:HAC	1.54	1.44
1:X:524:CYS:SG	4:X:616:HEC:CAC	2.12	1.36
1:X:85:CYS:SG	4:X:602:HEC:CAB	2.14	1.35
1:X:88:CYS:SG	4:X:602:HEC:HAC	1.67	1.33

All (3) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:401:ASP:O	6:X:1234:HOH:O[3_546]	1.75	0.45
4:X:613:HEC:O2A	6:X:1304:HOH:O[3_556]	2.14	0.06
1:X:437:LYS:NZ	4:X:615:HEC:O2D[2_565]	2.15	0.05

## 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	X	510/560 (91%)	484 (95%)	21 (4%)	5 (1%)	18 12

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	X	102	ALA
1	X	160	GLN
1	X	150	LYS
1	X	161	LYS
1	X	185	PRO

### 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	X	410/450 (91%)	382 (93%)	28 (7%)	18 15

5 of 28 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	X	254	VAL
1	X	320	ASN
1	X	488	GLN
1	X	291	VAL
1	X	299	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 9 such sidechains are listed below:

Mol	Chain	Res	Type
1	X	346	ASN
1	X	513	GLN
1	X	382	GLN
1	X	320	ASN
1	X	359	GLN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates ⓘ

2 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	$\# Z  > 2$
2	NAG	X	900	1,2	14,14,15	0.76	1 (7%)	15,19,21	2.95	6 (40%)
2	NAA	X	901	2	14,14,15	0.85	1 (7%)	15,19,21	1.22	1 (6%)

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	NAG	X	900	1,2	1/1/5/7	0/6/23/26	0/1/1/1
2	NAA	X	901	2	-	0/6/23/26	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	X	900	NAG	C3-C2	2.25	1.57	1.52
2	X	901	NAA	C8-C7	2.61	1.56	1.50

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	X	900	NAG	C3-C4-C5	-4.74	101.87	110.22
2	X	900	NAG	C1-C2-N2	-2.70	105.88	110.49
2	X	900	NAG	O4-C4-C3	2.47	115.74	110.36
2	X	901	NAA	C3-C4-C5	2.83	115.21	110.22
2	X	900	NAG	O4-C4-C5	2.90	116.59	109.28

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	X	900	NAG	C1

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	X	900	NAG	1	0

## 5.6 Ligand geometry

Of 24 ligands modelled in this entry, 3 are monoatomic - leaving 21 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	HEC	X	601	1	28,50,50	1.85	5 (17%)	16,82,82	2.79	8 (50%)
4	HEC	X	602	1	28,50,50	2.42	9 (32%)	16,82,82	1.92	5 (31%)
4	HEC	X	603	1	28,50,50	2.10	4 (14%)	16,82,82	2.46	6 (37%)
4	HEC	X	604	1	28,50,50	2.06	6 (21%)	16,82,82	2.58	5 (31%)
4	HEC	X	605	1	28,50,50	1.98	4 (14%)	16,82,82	2.53	7 (43%)
4	HEC	X	606	1	28,50,50	2.24	6 (21%)	16,82,82	2.29	7 (43%)
4	HEC	X	607	1	28,50,50	2.05	4 (14%)	16,82,82	2.25	8 (50%)
4	HEC	X	608	1	28,50,50	2.17	6 (21%)	16,82,82	3.59	9 (56%)
4	HEC	X	609	1	28,50,50	1.89	5 (17%)	16,82,82	2.60	7 (43%)
4	HEC	X	610	1	28,50,50	2.24	11 (39%)	16,82,82	3.39	10 (62%)
4	HEC	X	611	1	28,50,50	1.67	6 (21%)	16,82,82	3.46	8 (50%)
4	HEC	X	612	1	28,50,50	1.81	7 (25%)	16,82,82	3.77	8 (50%)
4	HEC	X	613	1	28,50,50	2.43	10 (35%)	16,82,82	3.02	8 (50%)
4	HEC	X	614	1,5	28,50,50	2.98	13 (46%)	16,82,82	3.69	8 (50%)
4	HEC	X	615	1	28,50,50	1.82	7 (25%)	16,82,82	3.42	6 (37%)
4	HEC	X	616	1,3	28,50,50	2.38	10 (35%)	16,82,82	3.51	6 (37%)
5	GOL	X	801	-	5,5,5	0.45	0	5,5,5	0.30	0
5	GOL	X	802	-	5,5,5	0.31	0	5,5,5	0.34	0
5	GOL	X	803	4	5,5,5	0.62	0	5,5,5	0.45	0
5	GOL	X	804	-	5,5,5	0.40	0	5,5,5	0.50	0
5	GOL	X	805	-	5,5,5	0.64	0	5,5,5	1.90	2 (40%)

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	HEC	X	601	1	-	0/6/54/54	0/0/8/8
4	HEC	X	602	1	-	0/6/54/54	0/0/8/8
4	HEC	X	603	1	-	0/6/54/54	0/0/8/8
4	HEC	X	604	1	-	0/6/54/54	0/0/8/8
4	HEC	X	605	1	-	0/6/54/54	0/0/8/8
4	HEC	X	606	1	-	0/6/54/54	0/0/8/8
4	HEC	X	607	1	-	0/6/54/54	0/0/8/8

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	HEC	X	608	1	-	0/6/54/54	0/0/8/8
4	HEC	X	609	1	-	0/6/54/54	0/0/8/8
4	HEC	X	610	1	-	0/6/54/54	0/0/8/8
4	HEC	X	611	1	-	0/6/54/54	0/0/8/8
4	HEC	X	612	1	-	0/6/54/54	0/0/8/8
4	HEC	X	613	1	-	0/6/54/54	0/0/8/8
4	HEC	X	614	1,5	-	0/6/54/54	0/0/8/8
4	HEC	X	615	1	-	0/6/54/54	0/0/8/8
4	HEC	X	616	1,3	-	0/6/54/54	0/0/8/8
5	GOL	X	801	-	-	0/4/4/4	0/0/0/0
5	GOL	X	802	-	-	0/4/4/4	0/0/0/0
5	GOL	X	803	4	-	0/4/4/4	0/0/0/0
5	GOL	X	804	-	-	0/4/4/4	0/0/0/0
5	GOL	X	805	-	-	0/4/4/4	0/0/0/0

The worst 5 of 113 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	X	607	HEC	C3B-C2B	-6.82	1.33	1.40
4	X	602	HEC	C3B-C2B	-6.58	1.33	1.40
4	X	608	HEC	C3B-C2B	-6.30	1.34	1.40
4	X	614	HEC	C3C-C2C	-6.20	1.34	1.40
4	X	613	HEC	C3B-C2B	-5.97	1.34	1.40

The worst 5 of 118 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	X	611	HEC	CMC-C2C-C1C	-9.31	114.15	128.46
4	X	608	HEC	CMC-C2C-C1C	-9.03	114.58	128.46
4	X	612	HEC	CAD-CBD-CGD	-8.90	97.45	112.66
4	X	616	HEC	CMC-C2C-C1C	-8.41	115.54	128.46
4	X	615	HEC	CMC-C2C-C1C	-7.51	116.92	128.46

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

18 monomers are involved in 115 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	X	601	HEC	14	0
4	X	602	HEC	12	0

*Continued on next page...*

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	X	603	HEC	2	0
4	X	604	HEC	6	0
4	X	605	HEC	3	0
4	X	606	HEC	7	0
4	X	607	HEC	6	0
4	X	608	HEC	11	0
4	X	609	HEC	4	0
4	X	610	HEC	13	0
4	X	611	HEC	1	0
4	X	612	HEC	4	0
4	X	613	HEC	1	1
4	X	614	HEC	10	0
4	X	615	HEC	7	1
4	X	616	HEC	12	0
5	X	803	GOL	5	0
5	X	804	GOL	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	X	516/560 (92%)	0.35	34 (6%) 19 24	28, 55, 82, 91	0

The worst 5 of 34 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	X	530	SER	8.3
1	X	159	ALA	5.1
1	X	529	ASN	4.1
1	X	58	GLU	3.7
1	X	119	VAL	3.6

### 6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

### 6.3 Carbohydrates [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	NAG	X	900	14/15	0.81	0.26	-	75,79,86,86	0
2	NAA	X	901	14/15	0.86	0.37	-	89,91,94,94	0

## 6.4 Ligands ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q < 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
5	GOL	X	804	6/6	0.85	0.37	3.22	53,61,66,70	0
4	HEC	X	612	43/43	0.97	0.21	1.29	30,38,56,65	0
4	HEC	X	611	43/43	0.96	0.15	0.78	28,33,52,58	0
5	GOL	X	803	6/6	0.91	0.17	0.74	28,54,59,60	0
4	HEC	X	601	43/43	0.94	0.19	0.61	52,59,63,65	0
4	HEC	X	604	43/43	0.97	0.16	0.59	38,48,54,57	0
4	HEC	X	606	43/43	0.94	0.15	0.49	45,49,65,71	0
4	HEC	X	602	43/43	0.93	0.18	0.48	45,51,75,80	0
4	HEC	X	615	43/43	0.96	0.15	0.40	25,31,49,56	0
4	HEC	X	608	43/43	0.96	0.14	0.28	27,37,52,61	0
4	HEC	X	605	43/43	0.90	0.17	0.28	48,58,73,78	0
4	HEC	X	614	43/43	0.93	0.14	0.21	20,31,41,50	0
4	HEC	X	607	43/43	0.95	0.14	0.03	49,55,65,72	0
4	HEC	X	613	43/43	0.97	0.14	0.01	28,31,43,53	0
4	HEC	X	603	43/43	0.93	0.15	-0.28	58,73,75,77	0
4	HEC	X	609	43/43	0.95	0.12	-0.32	40,50,61,67	0
4	HEC	X	616	43/43	0.94	0.12	-0.34	29,38,50,64	0
4	HEC	X	610	43/43	0.97	0.10	-0.43	20,26,41,47	0
3	ZN	X	703	1/1	0.84	0.07	-2.01	69,69,69,69	0
3	ZN	X	701	1/1	0.99	0.08	-	42,42,42,42	0
5	GOL	X	805	6/6	0.88	0.17	-	57,62,66,73	0
3	ZN	X	702	1/1	0.85	0.11	-	72,72,72,72	0
5	GOL	X	802	6/6	0.81	0.17	-	62,69,71,73	0
5	GOL	X	801	6/6	0.85	0.29	-	86,88,89,90	0

## 6.5 Other polymers ⓘ

There are no such residues in this entry.