



# Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 09:17 PM GMT

PDB ID : 1OAF  
Title : ASCOBATE PEROXIDASE FROM SOYBEAN CYTOSOL IN COMPLEX  
WITH ASCORBATE  
Authors : Sharp, K.H.; Raven, E.L.; Moody, P.C.E.  
Deposited on : 2003-01-13  
Resolution : 1.40 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.  
We welcome your comments at [validation@mail.wwpdb.org](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) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
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) : trunk26865

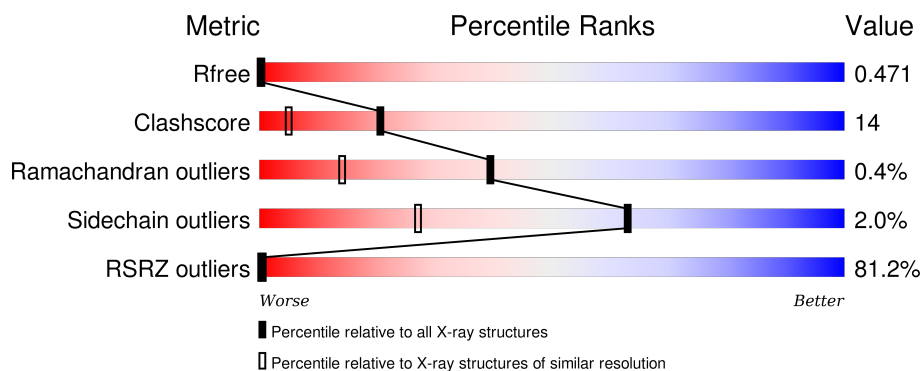
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.40 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))
$R_{free}$	91344	1199 (1.40-1.40)
Clashscore	102246	1295 (1.40-1.40)
Ramachandran outliers	100387	1259 (1.40-1.40)
Sidechain outliers	100360	1258 (1.40-1.40)
RSRZ outliers	91569	1198 (1.40-1.40)

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	261	

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
3	NA	A	1252	-	-	-	X

## 2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 2472 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 ASCORBATE PEROXIDASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	250	Total	C	N	O	S	0	0	0
			1911	1220	323	365	3			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	SER	MET	EXPRESSION TAG	UNP Q43758

- Molecule 2 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula:  $C_{34}H_{32}FeN_4O_4$ ).

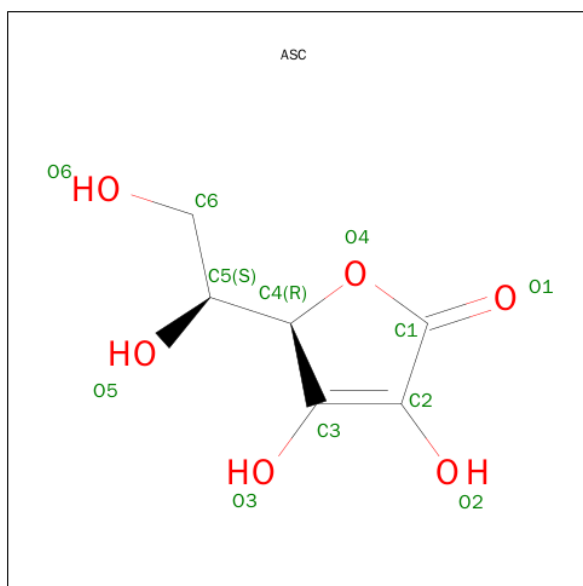


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		

- Molecule 3 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total Na 1 1	0	0

- Molecule 4 is ASCORBIC ACID (three-letter code: ASC) (formula:  $C_6H_8O_6$ ).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O 12 6 6	0	0

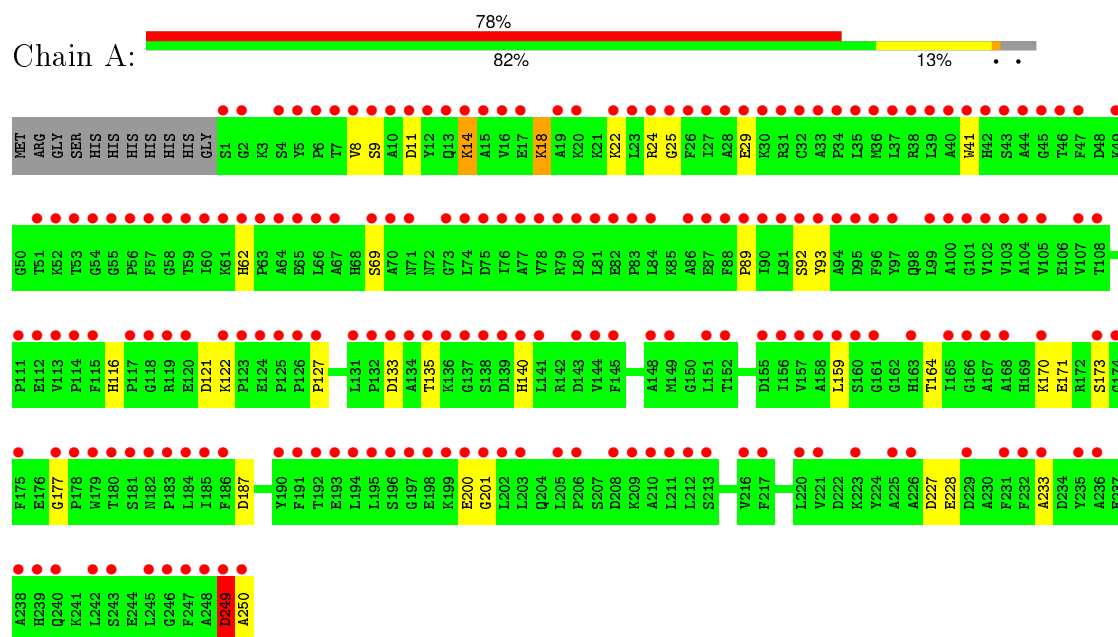
- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	505	Total O 505 505	0	0

### 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: ASCORBATE PEROXIDASE



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 42 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	81.33Å 81.33Å 74.88Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	57.74 – 1.40 31.38 – 1.38	Depositor EDS
% Data completeness (in resolution range)	99.0 (57.74-1.40) 95.2 (31.38-1.38)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.31 (at 1.38Å)	Xtriage
Refinement program	REFMAC	Depositor
R, $R_{free}$	0.161 , 0.196 0.472 , 0.471	Depositor DCC
$R_{free}$ test set	2451 reflections (5.36%)	DCC
Wilson B-factor (Å <sup>2</sup> )	15.1	Xtriage
Anisotropy	0.164	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.40 , 36.9	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 49346 reflections	Xtriage
$F_o, F_c$ correlation	0.77	EDS
Total number of atoms	2472	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	22.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 9.16% 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, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: ASC, HEM, NA

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	0.48	0/1962	0.76	2/2658 (0.1%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
1	A	227	ASP	CB-CG-OD2	5.27	123.04	118.30
1	A	249	ASP	CB-CG-OD2	5.09	122.88	118.30

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	1911	0	1871	56	3
2	A	43	0	30	1	0
3	A	1	0	0	0	0
4	A	12	0	6	0	0
5	A	505	0	0	48	6
All	All	2472	0	1907	56	9

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 14.

All (56) 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:135:THR:HG21	5:A:2363:HOH:O	1.40	1.18
1:A:200:GLU:OE1	5:A:2437:HOH:O	1.58	1.17
1:A:121:ASP:CB	5:A:2325:HOH:O	1.94	1.12
1:A:121:ASP:CG	5:A:2325:HOH:O	1.89	1.10
1:A:11:ASP:OD2	5:A:2071:HOH:O	1.66	1.10
1:A:121:ASP:OD2	5:A:2325:HOH:O	1.66	1.09
1:A:69:SER:HB2	5:A:2229:HOH:O	1.51	1.09
1:A:201:GLY:CA	5:A:2438:HOH:O	2.03	1.06
1:A:171:GLU:OE1	5:A:2397:HOH:O	1.82	0.98
1:A:93:TYR:CE1	5:A:2290:HOH:O	2.14	0.97
1:A:25:GLY:HA3	5:A:2115:HOH:O	1.65	0.97
1:A:249:ASP:OD1	5:A:2494:HOH:O	1.83	0.97
1:A:201:GLY:N	5:A:2438:HOH:O	1.96	0.96
1:A:201:GLY:HA2	5:A:2438:HOH:O	1.61	0.93
1:A:89:PRO:HB3	5:A:2145:HOH:O	1.71	0.91
1:A:69:SER:CB	5:A:2229:HOH:O	2.12	0.89
1:A:250:ALA:HB1	5:A:2496:HOH:O	1.71	0.88
1:A:133:ASP:H	1:A:140:HIS:HE1	1.20	0.87
1:A:116:HIS:NE2	5:A:2313:HOH:O	2.01	0.80
1:A:93:TYR:CZ	5:A:2290:HOH:O	2.34	0.78
1:A:93:TYR:OH	5:A:2290:HOH:O	2.03	0.77
1:A:171:GLU:HG3	5:A:2394:HOH:O	1.86	0.75
1:A:135:THR:HG23	5:A:2353:HOH:O	1.87	0.74
1:A:133:ASP:H	1:A:140:HIS:CE1	2.04	0.73
1:A:93:TYR:HE1	5:A:2290:HOH:O	1.60	0.71
1:A:200:GLU:CD	5:A:2437:HOH:O	2.15	0.68
1:A:177:GLY:HA2	5:A:2407:HOH:O	1.94	0.68
1:A:62:HIS:CD2	5:A:2210:HOH:O	2.47	0.68
1:A:11:ASP:HB2	5:A:2070:HOH:O	1.92	0.68
1:A:29:GLU:HG3	5:A:2123:HOH:O	1.93	0.67
1:A:62:HIS:HD2	5:A:2210:HOH:O	1.78	0.66
1:A:171:GLU:CG	5:A:2394:HOH:O	2.45	0.62
1:A:62:HIS:CD2	5:A:2211:HOH:O	2.53	0.62
1:A:121:ASP:HB2	5:A:2322:HOH:O	2.00	0.61
1:A:127:PRO:HA	5:A:2332:HOH:O	2.00	0.61
1:A:18:LYS:NZ	1:A:22:LYS:HG2	2.15	0.60
1:A:127:PRO:HB3	5:A:2332:HOH:O	2.01	0.60
1:A:233:ALA:HA	5:A:2475:HOH:O	2.05	0.57
1:A:24:ARG:CD	5:A:2108:HOH:O	2.53	0.56
1:A:133:ASP:N	1:A:140:HIS:HE1	1.97	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:170:LYS:HG2	5:A:2397:HOH:O	2.07	0.53
1:A:18:LYS:HZ2	1:A:22:LYS:HG2	1.74	0.52
1:A:11:ASP:CG	5:A:2071:HOH:O	2.29	0.52
1:A:92:SER:CB	5:A:2324:HOH:O	2.59	0.51
1:A:24:ARG:HD3	5:A:2108:HOH:O	2.09	0.51
1:A:116:HIS:CE1	5:A:2313:HOH:O	2.54	0.51
1:A:187:ASP:HB2	1:A:228:GLU:OE2	2.13	0.49
1:A:69:SER:HB3	5:A:2229:HOH:O	1.97	0.48
1:A:127:PRO:CA	5:A:2332:HOH:O	2.61	0.47
1:A:121:ASP:HB3	5:A:2325:HOH:O	1.87	0.46
1:A:177:GLY:CA	5:A:2407:HOH:O	2.60	0.45
1:A:159:LEU:HB3	2:A:1251:HEM:HMC3	1.97	0.45
1:A:14:LYS:HD3	1:A:14:LYS:O	2.19	0.42
1:A:127:PRO:CB	5:A:2332:HOH:O	2.65	0.42
1:A:121:ASP:HB2	5:A:2325:HOH:O	1.89	0.42
1:A:92:SER:HB2	5:A:2324:HOH:O	2.21	0.40

All (9) 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:A:9:SER:OG	1:A:173:SER:O[6_565]	1.57	0.63
5:A:2101:HOH:O	5:A:2225:HOH:O[8_666]	1.62	0.58
5:A:2287:HOH:O	5:A:2406:HOH:O[6_565]	1.69	0.51
5:A:2144:HOH:O	5:A:2452:HOH:O[5_555]	1.71	0.49
1:A:122:LYS:O	1:A:200:GLU:CG[6_565]	2.14	0.06
1:A:8:VAL:CA	1:A:170:LYS:O[6_565]	2.15	0.05
5:A:2184:HOH:O	5:A:2288:HOH:O[6_465]	2.16	0.04
5:A:2061:HOH:O	5:A:2225:HOH:O[8_666]	2.17	0.03
5:A:2337:HOH:O	5:A:2337:HOH:O[8_665]	2.18	0.02

## 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	248/261 (95%)	243 (98%)	4 (2%)	1 (0%)	39 14

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	249	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	197/206 (96%)	193 (98%)	4 (2%)	63 27

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	14	LYS
1	A	18	LYS
1	A	41	TRP
1	A	164	THR

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

Mol	Chain	Res	Type
1	A	72	ASN
1	A	140	HIS

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 1 is monoatomic - leaving 2 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	$\# Z  > 2$
2	HEM	A	1251	1,5	30,50,50	2.32	8 (26%)	24,82,82	2.71	12 (50%)
4	ASC	A	1253	-	12,12,12	1.18	1 (8%)	17,17,17	1.02	1 (5%)

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	HEM	A	1251	1,5	-	0/10/54/54	0/0/8/8
4	ASC	A	1253	-	-	0/6/22/22	0/1/1/1

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1251	HEM	C3B-C4B	-7.67	1.45	1.51
2	A	1251	HEM	C3D-C4D	-6.45	1.43	1.51
2	A	1251	HEM	C2C-C1C	-4.06	1.44	1.52
2	A	1251	HEM	C2D-C1D	-2.57	1.43	1.51
2	A	1251	HEM	C2D-C3D	-2.31	1.47	1.54
2	A	1251	HEM	C2B-C1B	-2.16	1.44	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1251	HEM	FE-NC	2.10	2.04	1.95
2	A	1251	HEM	C1C-NC	2.37	1.38	1.36
4	A	1253	ASC	O4-C1	3.87	1.41	1.35

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1251	HEM	C3B-CAB-CBB	-3.60	118.93	124.46
2	A	1251	HEM	CAA-C2A-C1A	-3.39	123.33	127.01
2	A	1251	HEM	C3C-CAC-CBC	-3.05	119.78	124.46
2	A	1251	HEM	CAA-CBA-CGA	-2.73	107.75	112.75
2	A	1251	HEM	CMA-C3A-C4A	-2.33	124.52	128.36
4	A	1253	ASC	C5-C4-C3	-2.01	111.30	114.14
2	A	1251	HEM	CMD-C2D-C3D	2.54	125.59	114.35
2	A	1251	HEM	C2D-C3D-C4D	2.64	105.98	101.50
2	A	1251	HEM	C3B-C4B-CHC	2.91	127.26	123.16
2	A	1251	HEM	CAD-C3D-C4D	4.09	126.90	112.47
2	A	1251	HEM	CAD-C3D-C2D	4.84	127.12	113.22
2	A	1251	HEM	CMB-C2B-C3B	5.13	129.34	116.53
2	A	1251	HEM	CMC-C2C-C3C	5.34	129.86	116.53

There are no chirality outliers.

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	A	1251	HEM	1	0

## 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, 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	250/261 (95%)	3.23	203 (81%) 0 0	10, 16, 27, 39	0

All (203) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	250	ALA	9.9
1	A	90	ILE	7.7
1	A	247	PHE	7.2
1	A	32	CYS	6.5
1	A	86	ALA	6.5
1	A	67	ALA	6.4
1	A	57	PHE	6.4
1	A	197	GLY	6.1
1	A	107	VAL	6.1
1	A	125	PRO	6.0
1	A	26	PHE	6.0
1	A	91	LEU	5.9
1	A	1	SER	5.9
1	A	7	THR	5.9
1	A	145	PHE	5.9
1	A	93	TYR	5.7
1	A	84	LEU	5.6
1	A	194	LEU	5.5
1	A	2	GLY	5.3
1	A	47	PHE	5.3
1	A	74	LEU	5.3
1	A	76	ILE	5.2
1	A	232	PHE	5.2
1	A	41	TRP	5.1
1	A	73	GLY	5.1
1	A	156	ILE	5.1
1	A	97	TYR	5.0

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Mol	Chain	Res	Type	RSRZ
1	A	205	LEU	4.9
1	A	96	PHE	4.9
1	A	203	LEU	4.9
1	A	37	LEU	4.9
1	A	174	GLY	4.8
1	A	105	VAL	4.8
1	A	66	LEU	4.8
1	A	196	SER	4.8
1	A	195	LEU	4.7
1	A	167	ALA	4.7
1	A	80	LEU	4.7
1	A	63	PRO	4.7
1	A	248	ALA	4.6
1	A	141	LEU	4.6
1	A	202	LEU	4.5
1	A	242	LEU	4.5
1	A	220	LEU	4.4
1	A	131	LEU	4.4
1	A	210	ALA	4.4
1	A	88	PHE	4.3
1	A	39	LEU	4.3
1	A	75	ASP	4.2
1	A	186	PHE	4.2
1	A	4	SER	4.2
1	A	134	ALA	4.2
1	A	78	VAL	4.1
1	A	54	GLY	4.1
1	A	17	GLU	4.1
1	A	83	PRO	4.1
1	A	15	ALA	4.1
1	A	16	VAL	4.0
1	A	64	ALA	4.0
1	A	179	TRP	4.0
1	A	198	GLU	4.0
1	A	30	LYS	4.0
1	A	113	VAL	3.9
1	A	25	GLY	3.9
1	A	201	GLY	3.9
1	A	62	HIS	3.9
1	A	249	ASP	3.9
1	A	94	ALA	3.8
1	A	245	LEU	3.8

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Mol	Chain	Res	Type	RSRZ
1	A	43	SER	3.8
1	A	8	VAL	3.8
1	A	165	ILE	3.8
1	A	236	ALA	3.8
1	A	103	VAL	3.8
1	A	133	ASP	3.7
1	A	12	TYR	3.7
1	A	132	PRO	3.7
1	A	40	ALA	3.7
1	A	44	ALA	3.7
1	A	35	LEU	3.7
1	A	58	GLY	3.7
1	A	226	ALA	3.7
1	A	235	TYR	3.7
1	A	60	ILE	3.6
1	A	157	VAL	3.6
1	A	217	PHE	3.6
1	A	151	LEU	3.6
1	A	100	ALA	3.6
1	A	6	PRO	3.6
1	A	65	GLU	3.6
1	A	108	THR	3.6
1	A	115	PHE	3.6
1	A	71	ASN	3.6
1	A	79	ARG	3.6
1	A	5	TYR	3.6
1	A	28	ALA	3.6
1	A	53	THR	3.5
1	A	175	PHE	3.5
1	A	231	PHE	3.5
1	A	216	VAL	3.5
1	A	29	GLU	3.5
1	A	159	LEU	3.5
1	A	212	LEU	3.4
1	A	102	VAL	3.4
1	A	213	SER	3.4
1	A	89	PRO	3.4
1	A	23	LEU	3.3
1	A	34	PRO	3.3
1	A	59	THR	3.3
1	A	61	LYS	3.3
1	A	183	PRO	3.2

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Mol	Chain	Res	Type	RSRZ
1	A	246	GLY	3.2
1	A	144	VAL	3.2
1	A	19	ALA	3.1
1	A	166	GLY	3.1
1	A	136	LYS	3.1
1	A	33	ALA	3.1
1	A	199	LYS	3.1
1	A	69	SER	3.1
1	A	177	GLY	3.1
1	A	99	LEU	3.0
1	A	184	LEU	3.0
1	A	243	SER	3.0
1	A	221	VAL	3.0
1	A	152	THR	3.0
1	A	149	MET	3.0
1	A	14	LYS	2.9
1	A	10	ALA	2.9
1	A	70	ALA	2.9
1	A	193	GLU	2.9
1	A	124	GLU	2.9
1	A	82	GLU	2.9
1	A	111	PRO	2.9
1	A	123	PRO	2.9
1	A	120	GLU	2.8
1	A	137	GLY	2.8
1	A	127	PRO	2.8
1	A	229	ASP	2.8
1	A	170	LYS	2.8
1	A	208	ASP	2.8
1	A	160	SER	2.8
1	A	158	ALA	2.8
1	A	51	THR	2.8
1	A	13	GLN	2.8
1	A	49	LYS	2.8
1	A	27	ILE	2.7
1	A	191	PHE	2.7
1	A	192	THR	2.7
1	A	233	ALA	2.7
1	A	126	PRO	2.7
1	A	55	GLY	2.7
1	A	42	HIS	2.7
1	A	112	GLU	2.7

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Mol	Chain	Res	Type	RSRZ
1	A	117	PRO	2.7
1	A	238	ALA	2.7
1	A	81	LEU	2.7
1	A	122	LYS	2.7
1	A	211	LEU	2.6
1	A	223	LYS	2.6
1	A	240	GLN	2.6
1	A	101	GLY	2.6
1	A	209	LYS	2.6
1	A	190	TYR	2.6
1	A	31	ARG	2.6
1	A	135	THR	2.6
1	A	56	PRO	2.5
1	A	92	SER	2.5
1	A	45	GLY	2.5
1	A	87	GLU	2.5
1	A	200	GLU	2.5
1	A	9	SER	2.4
1	A	239	HIS	2.4
1	A	178	PRO	2.4
1	A	182	ASN	2.4
1	A	46	THR	2.4
1	A	114	PRO	2.4
1	A	181	SER	2.4
1	A	118	GLY	2.4
1	A	185	ILE	2.4
1	A	163	HIS	2.3
1	A	104	ALA	2.3
1	A	155	ASP	2.3
1	A	225	ALA	2.3
1	A	180	THR	2.3
1	A	143	ASP	2.3
1	A	36	MET	2.2
1	A	140	HIS	2.2
1	A	77	ALA	2.2
1	A	22	LYS	2.2
1	A	139	ASP	2.2
1	A	161	GLY	2.2
1	A	20	LYS	2.2
1	A	38	ARG	2.1
1	A	138	SER	2.1
1	A	95	ASP	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	148	ALA	2.1
1	A	52	LYS	2.1
1	A	119	ARG	2.1
1	A	173	SER	2.1
1	A	24	ARG	2.0
1	A	168	ALA	2.0
1	A	206	PRO	2.0
1	A	11	ASP	2.0

## 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](#)

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
3	NA	A	1252	1/1	0.89	0.44	9.45	14,14,14,14	0
2	HEM	A	1251	43/43	0.79	0.23	0.27	9,11,14,15	0
4	ASC	A	1253	12/12	0.58	0.21	-0.65	14,17,24,27	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.