



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 15, 2017 – 02:07 am GMT

PDB ID : 3P99  
Title : Sterol 14alpha-demethylase (CYP51) from Trypanosoma brucei in complex with delta7-14alpha-methylene-cyclopropyl-dihydrolanosterol  
Authors : Lepesheva, G.I.; Hargrove, T.Y.; Waterman, M.R.; Wawrzak, Z.  
Deposited on : 2010-10-16  
Resolution : 3.00 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

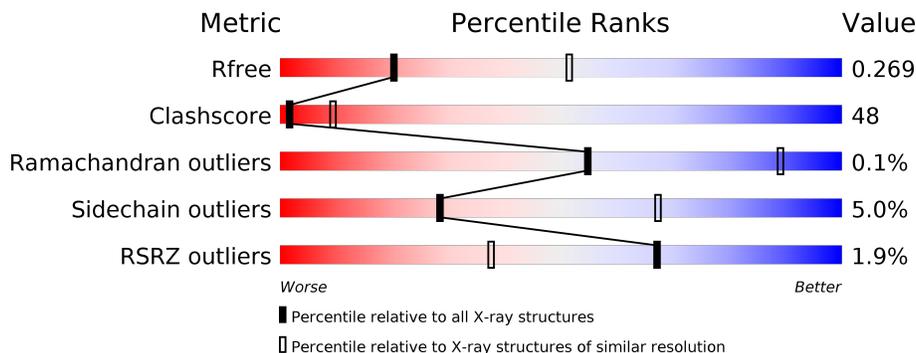
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.00 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	1692 (3.00-3.00)
Clashscore	112137	2037 (3.00-3.00)
Ramachandran outliers	110173	1973 (3.00-3.00)
Sidechain outliers	110143	1976 (3.00-3.00)
RSRZ outliers	101464	1716 (3.00-3.00)

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	453	
1	B	453	
1	C	453	
1	D	453	

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 crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	LNP	A	490	-	-	X	-
3	LNP	B	490	-	-	X	X
3	LNP	C	490	-	-	X	-
3	LNP	D	490	-	-	X	X

## 2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 14555 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 Sterol 14-alpha-demethylase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	448	3557	2271	621	638	27	0	0	0
1	B	448	3557	2271	621	638	27	0	0	0
1	C	444	3526	2254	615	630	27	0	0	0
1	D	448	3557	2271	621	638	27	0	0	0

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	29	GLY	PRO	ENGINEERED MUTATION	UNP Q385E8
A	30	LYS	THR	ENGINEERED MUTATION	UNP Q385E8
A	31	LEU	ASP	ENGINEERED MUTATION	UNP Q385E8
B	29	GLY	PRO	ENGINEERED MUTATION	UNP Q385E8
B	30	LYS	THR	ENGINEERED MUTATION	UNP Q385E8
B	31	LEU	ASP	ENGINEERED MUTATION	UNP Q385E8
C	29	GLY	PRO	ENGINEERED MUTATION	UNP Q385E8
C	30	LYS	THR	ENGINEERED MUTATION	UNP Q385E8
C	31	LEU	ASP	ENGINEERED MUTATION	UNP Q385E8
D	29	GLY	PRO	ENGINEERED MUTATION	UNP Q385E8
D	30	LYS	THR	ENGINEERED MUTATION	UNP Q385E8
D	31	LEU	ASP	ENGINEERED MUTATION	UNP Q385E8

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

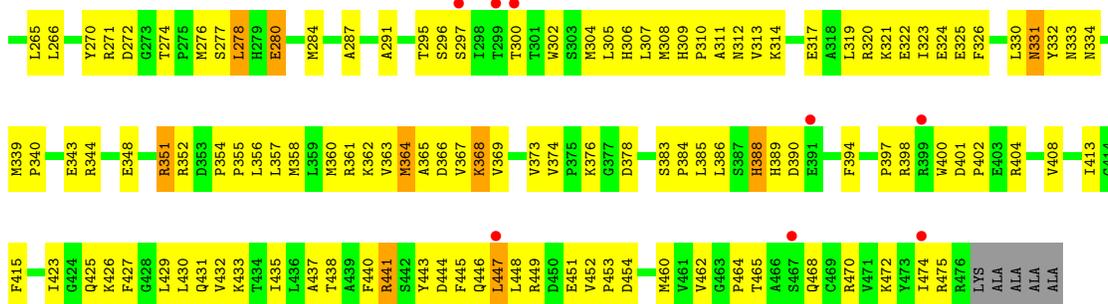


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			34	33	1		
3	B	1	Total	C	O	0	0
			34	33	1		
3	C	1	Total	C	O	0	0
			34	33	1		
3	D	1	Total	C	O	0	0
			34	33	1		

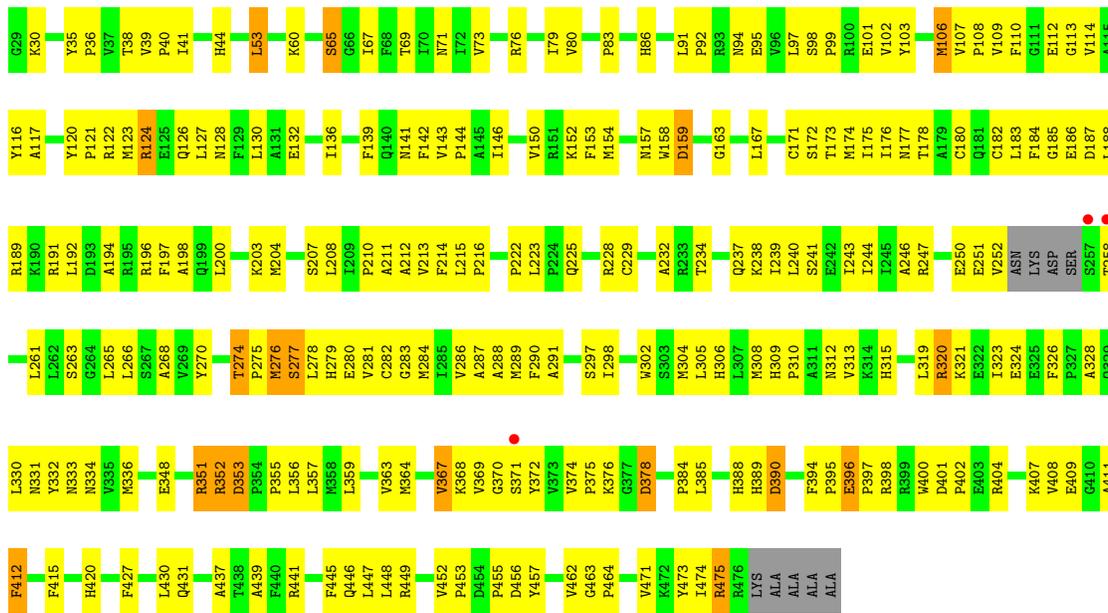
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	14	Total	O	0	0
			14	14		
4	B	13	Total	O	0	0
			13	13		
4	C	12	Total	O	0	0
			12	12		
4	D	11	Total	O	0	0
			11	11		

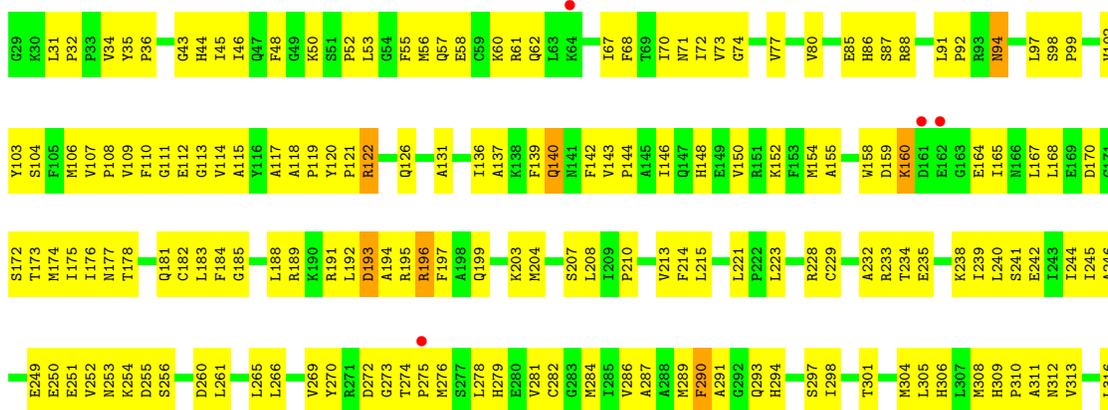




• Molecule 1: Sterol 14-alpha-demethylase



• Molecule 1: Sterol 14-alpha-demethylase



F394	L319	L330	L350	Y363	I379	R475	R476
P397	R320	I331	I351	K364	I380	LYS	ALA
R398	K321	Y332	R352	A365	A381	ALA	ALA
R399	E322	I333	D353	D366	C382	ALA	ALA
R404	I323	N334	P354	V367	S383	ALA	ALA
D405	E324	V335	P355	V367	P384	ALA	ALA
I411	F326	M336	L356	K368	L385	ALA	ALA
I423	P327	M339	L357	Y369	L386	ALA	ALA
G424	L429	I350	K358	G370	S387	H388	H389
F427	Q431	I351	L359	S371	Y372		
L429	V432	L352	R360	V373	V374		
L430		L353		P375	P376		
Q431		L354		K376			
V432		L355					
I435		L356					
L436		L357					
A437		L358					
F445		L359					
L448		R360					
E451		Y363					
V452		K364					
P453		A365					
D454		D366					
P455		V367					
Y457		K368					
H458		Y369					
T459		G370					
M460		S371					
V461		V372					
P464		V373					
Q468		P375					
C469		K376					
R470							
V471							
K472							
R475							
LYS							
ALA							
ALA							
ALA							
ALA							
ALA							
S387							
H388							
H389							

## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	59.61Å 80.57Å 115.80Å 107.93° 102.43° 99.57°	Depositor
Resolution (Å)	29.39 – 3.00 29.39 – 3.00	Depositor EDS
% Data completeness (in resolution range)	97.8 (29.39-3.00) 86.1 (29.39-3.00)	Depositor EDS
$R_{merge}$	0.10	Depositor
$R_{sym}$	0.07	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.91 (at 3.00Å)	Xtrriage
Refinement program	REFMAC 5.5.0109	Depositor
R, $R_{free}$	0.223 , 0.271 0.221 , 0.269	Depositor DCC
$R_{free}$ test set	1894 reflections (5.25%)	DCC
Wilson B-factor (Å <sup>2</sup> )	79.9	Xtrriage
Anisotropy	0.030	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.28 , 58.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.30$	Xtrriage
Estimated twinning fraction	0.015 for -h,-k,h+k+l	Xtrriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	14555	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	84.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 36.48 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 4.9656e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<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 [i](#)

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

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

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	0.47	0/3639	0.48	0/4922
1	B	0.41	0/3639	0.48	0/4922
1	C	0.56	0/3607	0.52	0/4878
1	D	0.46	0/3639	0.46	0/4922
All	All	0.48	0/14524	0.49	0/19644

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	3557	0	3594	339	0
1	B	3557	0	3594	313	0
1	C	3526	0	3565	327	0
1	D	3557	0	3594	372	0
2	A	43	0	30	9	0
2	B	43	0	30	7	0
2	C	43	0	30	5	0
2	D	43	0	30	6	0
3	A	34	0	54	27	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	34	0	54	36	0
3	C	34	0	54	59	0
3	D	34	0	54	45	0
4	A	14	0	0	6	0
4	B	13	0	0	6	0
4	C	12	0	0	9	0
4	D	11	0	0	5	0
All	All	14555	0	14683	1394	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 48.

The worst 5 of 1394 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:364:MET:CE	1:A:364:MET:HA	1.54	1.34
1:A:64:LYS:N	1:A:64:LYS:HE3	1.42	1.32
1:D:284:MET:HG2	3:D:490:LNP:CBE	1.61	1.29
1:C:291:ALA:HB2	3:C:490:LNP:CAP	1.66	1.26
1:A:143:VAL:HG23	1:A:144:PRO:CD	1.64	1.25

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	446/453 (98%)	425 (95%)	21 (5%)	0	100 100
1	B	446/453 (98%)	415 (93%)	30 (7%)	1 (0%)	51 86
1	C	440/453 (97%)	421 (96%)	18 (4%)	1 (0%)	51 86
1	D	446/453 (98%)	419 (94%)	27 (6%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	1778/1812 (98%)	1680 (94%)	96 (5%)	2 (0%)	55 89

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	211	ALA
1	B	340	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	A	390/391 (100%)	373 (96%)	17 (4%)	33 72
1	B	390/391 (100%)	369 (95%)	21 (5%)	26 64
1	C	386/391 (99%)	363 (94%)	23 (6%)	22 60
1	D	390/391 (100%)	373 (96%)	17 (4%)	33 72
All	All	1556/1564 (100%)	1478 (95%)	78 (5%)	28 67

5 of 78 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	388	HIS
1	C	159	ASP
1	D	325	GLU
1	B	441	ARG
1	C	53	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 42 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	44	HIS
1	C	334	ASN
1	D	388	HIS

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Mol	Chain	Res	Type
1	C	157	ASN
1	C	315	HIS

### 5.3.3 RNA [i](#)

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](#)

8 ligands 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	HEM	A	482	1	28,50,50	2.26	6 (21%)	17,82,82	1.42	3 (17%)
3	LNP	A	490	-	35,38,38	1.04	2 (5%)	54,62,62	2.07	12 (22%)
2	HEM	B	482	1	28,50,50	2.25	6 (21%)	17,82,82	1.47	3 (17%)
3	LNP	B	490	-	35,38,38	1.09	2 (5%)	54,62,62	1.71	12 (22%)
2	HEM	C	482	1	28,50,50	2.24	6 (21%)	17,82,82	1.38	2 (11%)
3	LNP	C	490	-	35,38,38	1.12	2 (5%)	54,62,62	1.84	12 (22%)
2	HEM	D	482	1	28,50,50	2.24	6 (21%)	17,82,82	1.40	3 (17%)
3	LNP	D	490	-	35,38,38	1.23	5 (14%)	54,62,62	1.80	11 (20%)

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	482	1	-	0/6/54/54	0/0/8/8
3	LNP	A	490	-	-	0/10/89/89	0/4/5/5
2	HEM	B	482	1	-	0/6/54/54	0/0/8/8
3	LNP	B	490	-	-	0/10/89/89	0/4/5/5
2	HEM	C	482	1	-	0/6/54/54	0/0/8/8
3	LNP	C	490	-	-	0/10/89/89	0/4/5/5
2	HEM	D	482	1	-	0/6/54/54	0/0/8/8
3	LNP	D	490	-	-	0/10/89/89	0/4/5/5

The worst 5 of 35 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	482	HEM	C3C-C2C	-4.98	1.33	1.40
2	D	482	HEM	C3C-C2C	-4.98	1.33	1.40
2	C	482	HEM	C3C-C2C	-4.89	1.33	1.40
2	A	482	HEM	C3B-C2B	-4.81	1.34	1.40
2	A	482	HEM	C3C-C2C	-4.72	1.34	1.40

The worst 5 of 58 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	490	LNP	CAN-CAH-CAG	-5.41	111.53	117.15
3	C	490	LNP	CAE-CAQ-CAV	-4.91	112.73	119.26
3	A	490	LNP	CAE-CAQ-CAV	-4.88	112.77	119.26
3	B	490	LNP	CAE-CAQ-CAV	-4.87	112.78	119.26
3	D	490	LNP	CAN-CAH-CAG	-4.38	112.59	117.15

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

8 monomers are involved in 190 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	482	HEM	9	0
3	A	490	LNP	27	0
2	B	482	HEM	7	0
3	B	490	LNP	36	0
2	C	482	HEM	5	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	490	LNP	59	0
2	D	482	HEM	6	0
3	D	490	LNP	45	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	448/453 (98%)	-0.13	12 (2%) 55 26	27, 80, 104, 123	0
1	B	448/453 (98%)	-0.15	15 (3%) 47 21	50, 90, 133, 166	0
1	C	444/453 (98%)	-0.28	3 (0%) 87 67	44, 73, 100, 131	0
1	D	448/453 (98%)	-0.23	4 (0%) 84 61	41, 86, 138, 209	0
All	All	1788/1812 (98%)	-0.20	34 (1%) 67 37	27, 81, 124, 209	0

The worst 5 of 34 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	65	SER	5.0
1	B	163	GLY	4.8
1	B	164	GLU	4.4
1	A	161	ASP	4.3
1	A	393	ALA	4.1

### 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(Å <sup>2</sup> )	Q<0.9
3	LNP	D	490	34/34	0.85	0.42	3.04	56,64,75,77	34
3	LNP	B	490	34/34	0.90	0.40	2.39	54,66,71,72	34
3	LNP	C	490	34/34	0.85	0.30	0.89	53,75,80,82	0
3	LNP	A	490	34/34	0.91	0.28	0.46	62,70,76,78	0
2	HEM	D	482	43/43	0.97	0.25	0.42	32,41,50,57	0
2	HEM	C	482	43/43	0.96	0.26	0.33	35,43,50,55	0
2	HEM	A	482	43/43	0.95	0.24	-0.08	37,50,57,60	0
2	HEM	B	482	43/43	0.97	0.19	-0.71	40,48,55,61	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.