



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 12:54 PM GMT

PDB ID : 3S7S
Title : Crystal structure of human placental aromatase complexed with breast cancer drug exemestane
Authors : Ghosh, D.
Deposited on : 2011-05-26
Resolution : 3.21 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
A user guide is available at
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

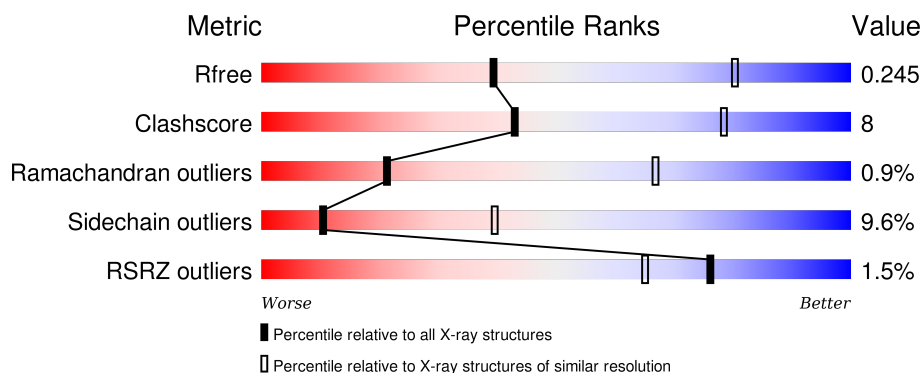
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.21 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	1095 (3.26-3.18)
Clashscore	102246	1046 (3.24-3.20)
Ramachandran outliers	100387	1026 (3.24-3.20)
Sidechain outliers	100360	1025 (3.24-3.20)
RSRZ outliers	91569	1100 (3.26-3.18)

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 ≥ 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	503	<div> <div></div> <div>66%</div> <div>20%</div> <div>•</div> <div>10%</div> </div>

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 3733 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 Cytochrome P450 19A1.

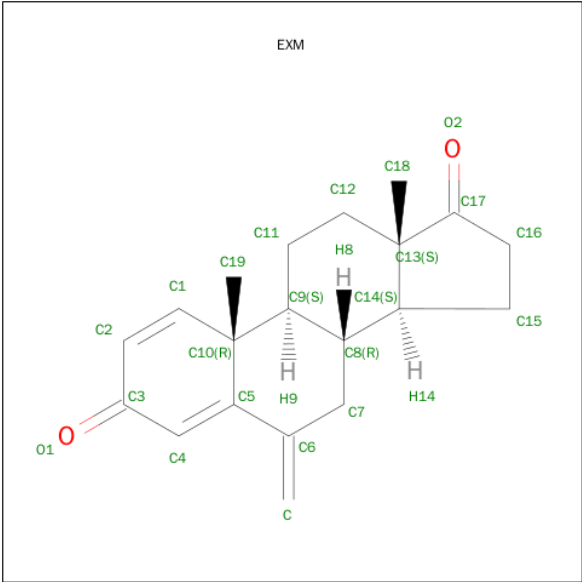
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	452	Total	C	N	O	S	0	1	0
			3668	2367	620	651	30			

- 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 (8ALPHA,10ALPHA,13ALPHA)-6-METHYLIDENEANDROSTA-1,4-DIENE-3,17-DIONE (three-letter code: EXM) (formula: $C_{20}H_{24}O_2$).

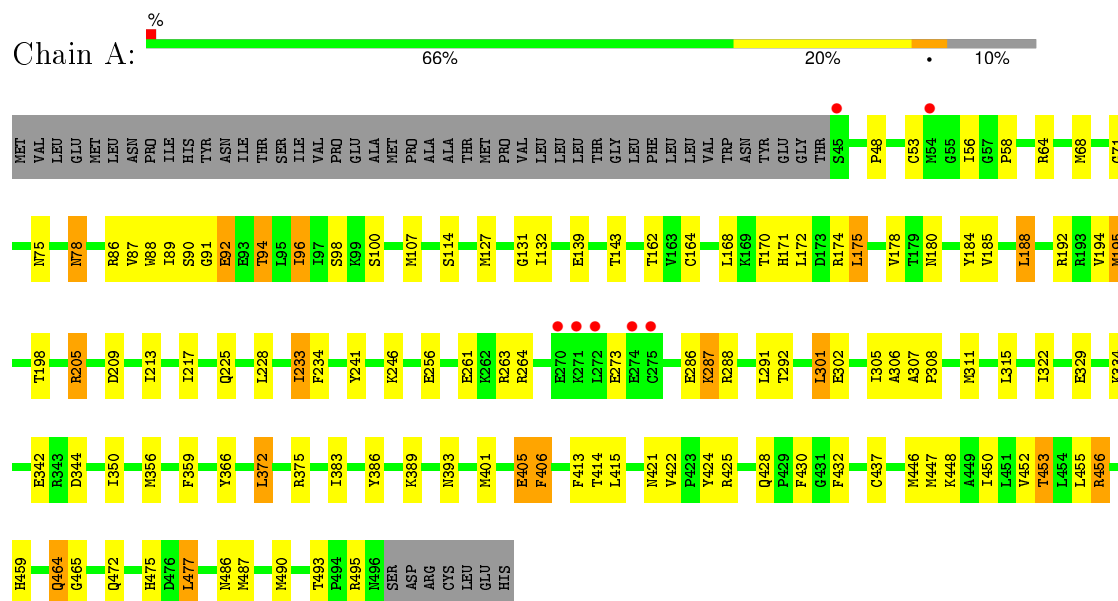


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			22	20	2		

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: Cytochrome P450 19A1



4 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α , β , γ	140.63Å 140.63Å 119.02Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	121.79 – 3.21 46.03 – 3.21	Depositor EDS
% Data completeness (in resolution range)	99.3 (121.79-3.21) 99.4 (46.03-3.21)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.37 (at 3.19Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.221 , 0.256 0.211 , 0.245	Depositor DCC
R_{free} test set	1147 reflections (5.37%)	DCC
Wilson B-factor (Å ²)	96.9	Xtriage
Anisotropy	0.145	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 48.7	EDS
Estimated twinning fraction	0.025 for -h,-k,l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	1 of 22501 reflections (0.004%)	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	3733	wwPDB-VP
Average B, all atoms (Å ²)	95.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.39% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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: HEM, EXM

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	0.43	0/3748	0.59	1/5050 (0.0%)

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	A	0	1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	301	LEU	CA-CB-CG	7.25	131.98	115.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	131	GLY	Peptide

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	3668	0	3741	60	0
2	A	43	0	30	3	0
3	A	22	0	24	2	0
All	All	3733	0	3795	62	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 8.

All (62) 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:315:LEU:HD22	1:A:450:ILE:HD11	1.45	0.96
1:A:225:GLN:HG3	1:A:477:LEU:HB2	1.48	0.93
1:A:94:THR:HB	1:A:393:ASN:HB2	1.59	0.83
1:A:100:SER:HB3	1:A:405:GLU:OE1	1.87	0.74
1:A:477:LEU:HD22	3:A:601:EXM:H115	1.72	0.70
1:A:315:LEU:HD21	1:A:447:MET:HG2	1.73	0.69
2:A:600:HEM:HMC1	2:A:600:HEM:HBC2	1.76	0.68
1:A:170:THR:HG23	1:A:174:ARG:HH21	1.65	0.61
1:A:307:ALA:HB3	1:A:308:PRO:HD3	1.82	0.60
1:A:87:VAL:CG1	1:A:88:TRP:N	2.65	0.60
1:A:389:LYS:H	1:A:389:LYS:HD2	1.67	0.60
1:A:168:LEU:HD23	1:A:453:THR:HB	1.83	0.59
1:A:71:GLY:HA2	1:A:372:LEU:HD21	1.82	0.59
1:A:359:PHE:HA	1:A:415:LEU:HD21	1.84	0.59
1:A:89:ILE:H	1:A:94:THR:CG2	2.16	0.58
1:A:185:VAL:HG22	1:A:490:MET:O	2.04	0.58
1:A:58:PRO:HA	1:A:88:TRP:HB2	1.86	0.57
1:A:263:ARG:NH2	1:A:286:GLU:OE1	2.38	0.56
2:A:600:HEM:CMC	2:A:600:HEM:HBC2	2.36	0.55
1:A:172:LEU:O	1:A:175:LEU:HD22	2.06	0.55
1:A:78:ASN:CG	1:A:96:ILE:HD11	2.28	0.54
1:A:311:MET:HE1	1:A:446:MET:HB2	1.89	0.54
1:A:322:ILE:HD13	1:A:455:LEU:HD11	1.89	0.53
1:A:87:VAL:HG12	1:A:88:TRP:N	2.24	0.51
1:A:217:ILE:HG12	1:A:305:ILE:HG22	1.92	0.51
1:A:234:PHE:CE2	1:A:241:TYR:HB3	2.46	0.50
1:A:406:PHE:CE2	1:A:422:VAL:HG12	2.47	0.50
1:A:315:LEU:CD2	1:A:450:ILE:HD11	2.29	0.50
1:A:188:LEU:O	1:A:192:ARG:HG3	2.11	0.49
1:A:452:VAL:O	1:A:456:ARG:HB2	2.12	0.49
1:A:459[B]:HIS:CE1	1:A:495:ARG:HG3	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:356:MET:HE1	1:A:452:VAL:HG23	1.94	0.48
1:A:127:MET:HG2	1:A:302:GLU:OE2	2.13	0.48
1:A:366:TYR:CD2	1:A:413:PHE:HB2	2.49	0.48
1:A:75:ASN:HD22	1:A:475:HIS:HE1	1.60	0.48
1:A:64:ARG:O	1:A:68:MET:HB2	2.13	0.48
1:A:455:LEU:O	1:A:495:ARG:NH1	2.47	0.47
1:A:195:MET:HA	1:A:195:MET:CE	2.44	0.47
1:A:464:GLN:HB3	1:A:465:GLY:H	1.51	0.47
1:A:430:PHE:HB3	1:A:437:CYS:HB3	1.97	0.46
1:A:356:MET:CE	1:A:452:VAL:HG23	2.46	0.46
1:A:171:HIS:CG	1:A:194:VAL:HG12	2.51	0.46
1:A:132:ILE:HD11	2:A:600:HEM:HMD3	1.99	0.45
1:A:107:MET:HE1	1:A:428:GLN:HG3	1.98	0.45
1:A:261:GLU:OE1	1:A:264:ARG:NH1	2.49	0.45
1:A:233:ILE:HG13	1:A:233:ILE:H	1.46	0.45
1:A:180:ASN:HB2	1:A:184:TYR:HB2	1.97	0.45
1:A:486:ASN:O	1:A:487:MET:HB2	2.15	0.45
1:A:114:SER:O	1:A:375:ARG:HA	2.17	0.45
1:A:92:GLU:HG3	1:A:393:ASN:OD1	2.17	0.45
1:A:306:ALA:HA	3:A:601:EXM:O1	2.17	0.44
1:A:53:CYS:HB3	1:A:56:ILE:HB	2.01	0.43
1:A:415:LEU:HD23	1:A:415:LEU:HA	1.84	0.43
1:A:356:MET:HE3	1:A:448:LYS:O	2.19	0.42
1:A:48:PRO:HD3	1:A:386:TYR:CE1	2.54	0.42
1:A:209:ASP:O	1:A:213:ILE:HG12	2.20	0.42
1:A:107:MET:HE3	1:A:432:PHE:HD2	1.85	0.42
1:A:139:GLU:O	1:A:143:THR:HG23	2.19	0.42
1:A:90:SER:HB3	1:A:91:GLY:H	1.70	0.42
1:A:48:PRO:HD3	1:A:386:TYR:HE1	1.85	0.41
1:A:98:SER:O	1:A:401:MET:HG3	2.20	0.41
1:A:287:LYS:HD3	1:A:287:LYS:HA	1.85	0.41

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	451/503 (90%)	409 (91%)	38 (8%)	4 (1%)	21	67

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	288	ARG
1	A	406	PHE
1	A	421	ASN
1	A	205	ARG

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	407/452 (90%)	368 (90%)	39 (10%)	10	39

All (39) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	78	ASN
1	A	86	ARG
1	A	92	GLU
1	A	94	THR
1	A	96	ILE
1	A	162	THR
1	A	164	CYS
1	A	175	LEU
1	A	178	VAL
1	A	188	LEU
1	A	195	MET
1	A	198	THR
1	A	205	ARG
1	A	228	LEU
1	A	233	ILE

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Mol	Chain	Res	Type
1	A	246	LYS
1	A	256	GLU
1	A	273	GLU
1	A	287	LYS
1	A	291	LEU
1	A	292	THR
1	A	301	LEU
1	A	329	GLU
1	A	334	LYS
1	A	342	GLU
1	A	344	ASP
1	A	350	ILE
1	A	372	LEU
1	A	383	ILE
1	A	405	GLU
1	A	414	THR
1	A	424	TYR
1	A	425	ARG
1	A	453	THR
1	A	456	ARG
1	A	464	GLN
1	A	472	GLN
1	A	477	LEU
1	A	493	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	75	ASN
1	A	78	ASN
1	A	109	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 ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

2 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	600	1	30,50,50	2.25	8 (26%)	24,82,82	2.39	9 (37%)
3	EXM	A	601	-	24,25,25	1.47	5 (20%)	34,41,41	1.50	5 (14%)

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	600	1	-	0/10/54/54	0/0/8/8
3	EXM	A	601	-	-	0/0/61/61	0/4/4/4

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	600	HEM	C3B-C4B	-7.94	1.44	1.51
2	A	600	HEM	C3D-C4D	-5.31	1.44	1.51
2	A	600	HEM	C2C-C1C	-3.69	1.45	1.52
3	A	601	EXM	C10-C1	-2.83	1.46	1.50
3	A	601	EXM	C2-C3	-2.81	1.39	1.45
3	A	601	EXM	C10-C9	-2.63	1.54	1.57
3	A	601	EXM	C4-C3	-2.32	1.39	1.45
2	A	600	HEM	C2D-C1D	-2.27	1.44	1.51
2	A	600	HEM	C2B-C1B	-2.02	1.45	1.51
2	A	600	HEM	C3C-CAC	2.18	1.55	1.51
2	A	600	HEM	C3B-CAB	2.18	1.55	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	600	HEM	FE-ND	2.64	2.11	1.97
3	A	601	EXM	C2-C1	3.47	1.39	1.33

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	600	HEM	CBD-CAD-C3D	-3.03	104.73	113.55
2	A	600	HEM	CBA-CAA-C2A	-2.96	107.23	112.53
3	A	601	EXM	C15-C16-C17	-2.64	102.90	105.65
3	A	601	EXM	O2-C17-C16	-2.52	122.49	125.71
3	A	601	EXM	C19-C10-C9	-2.30	110.28	111.73
2	A	600	HEM	C3C-CAC-CBC	-2.17	121.13	124.46
2	A	600	HEM	C2D-C3D-C4D	2.42	105.61	101.50
2	A	600	HEM	CMD-C2D-C3D	3.09	128.02	114.35
3	A	601	EXM	C2-C3-C4	3.24	120.64	117.12
3	A	601	EXM	C16-C17-C13	3.99	112.59	108.64
2	A	600	HEM	CMB-C2B-C3B	4.20	127.02	116.53
2	A	600	HEM	CAD-C3D-C4D	4.40	128.00	112.47
2	A	600	HEM	CAD-C3D-C2D	4.58	126.38	113.22
2	A	600	HEM	CMC-C2C-C3C	4.61	128.04	116.53

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	600	HEM	3	0
3	A	601	EXM	2	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, 95th 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 ²)	Q<0.9
1	A	452/503 (89%)	-0.09	7 (1%) 76 65	75, 95, 123, 133	0

All (7) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	270	GLU	4.8
1	A	45	SER	3.5
1	A	271	LYS	3.1
1	A	54	MET	2.5
1	A	272	LEU	2.3
1	A	275	CYS	2.2
1	A	274	GLU	2.1

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, 95th 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(\AA^2)	Q<0.9
3	EXM	A	601	22/22	0.98	0.23	-0.19	73,74,75,77	0
2	HEM	A	600	43/43	0.99	0.21	-0.43	54,59,66,67	0

6.5 Other polymers [i](#)

There are no such residues in this entry.