Full wwPDB X-ray Structure Validation Report (i)

May 26, 2020 – 07:54 am BST

PDB ID	:	5JKV
Title	:	HUMAN PLACENTAL AROMATASE CYTOCHROME P450 (CYP19A1) AT 2.75 ANGSTROM WITH BOUND POLYETHYLENE GLYCOL
Authors	:	Ghosh, D.; Lo, J.; Egbuta, C.
Deposited on	:	2016-04-26
Resolution	:	2.75 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
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The following versions of software and data (see references (i)) were used in the production of this report:

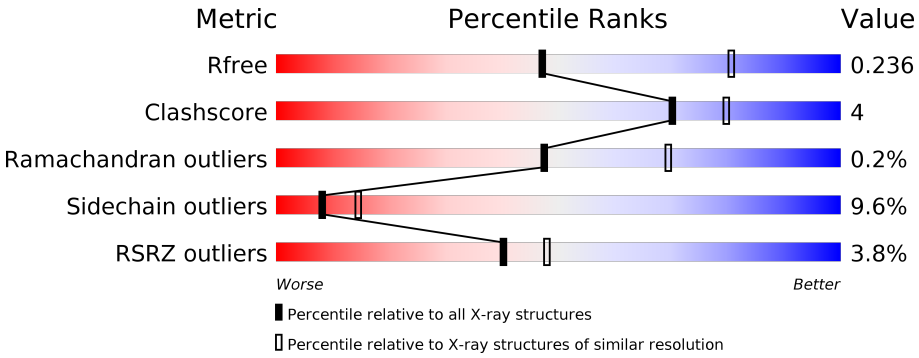
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

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 2.75 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}	130704	1235 (2.78-2.74)
Clashscore	141614	1277 (2.78-2.74)
Ramachandran outliers	138981	1257 (2.78-2.74)
Sidechain outliers	138945	1257 (2.78-2.74)
RSRZ outliers	127900	1207 (2.78-2.74)

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 respectively. 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 <=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	3% 76% 12% • 10%

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
4	1PE	A	603	-	-	-	X
5	PO4	A	606	-	-	-	X

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	PO4	A	607	-	-	-	X

2 Entry composition

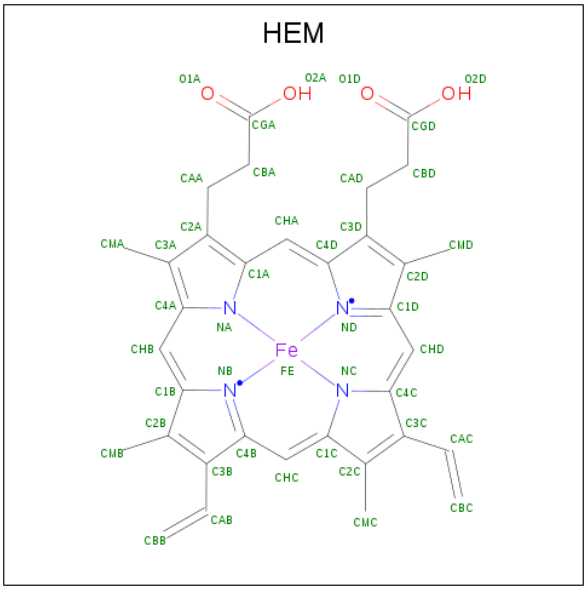
There are 6 unique types of molecules in this entry. The entry contains 3811 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Aromatase.

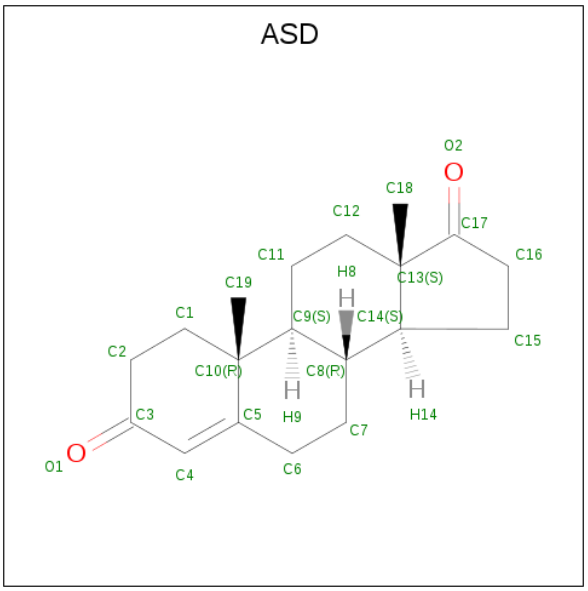
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	452	3668	2367	620	651	30	0	1	0

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



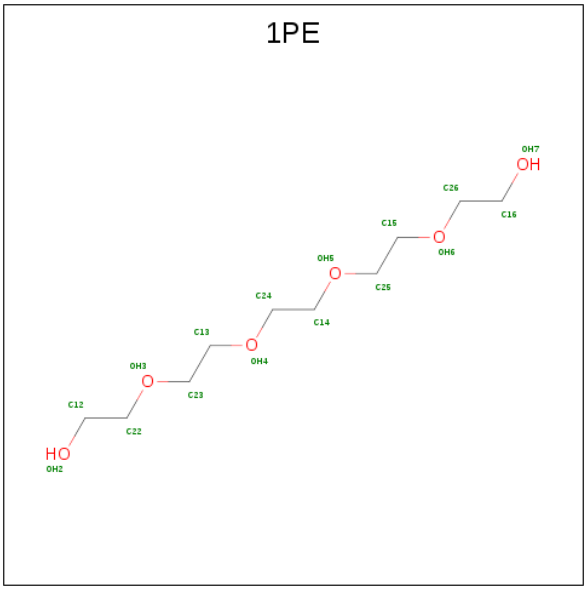
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	Fe	N	O		
2	A	1	43	34	1	4	4	0	0

- Molecule 3 is 4-ANDROSTENE-3-17-DIONE (three-letter code: ASD) (formula: $C_{19}H_{26}O_2$).



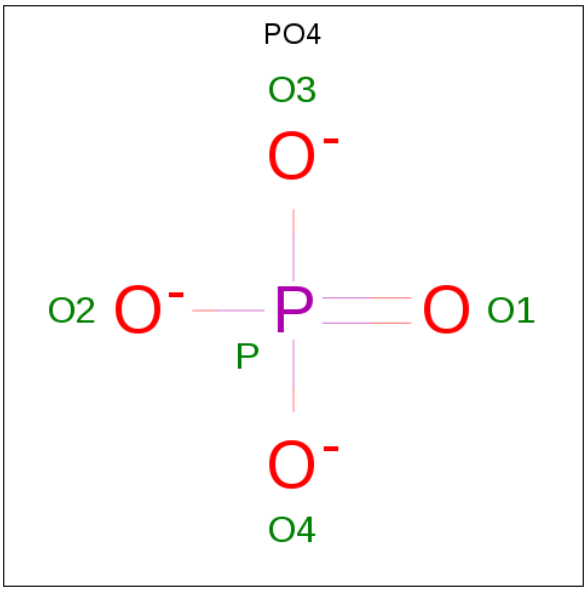
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C O 21 19 2	0	0

- Molecule 4 is PENTAETHYLENE GLYCOL (three-letter code: 1PE) (formula: $C_{10}H_{22}O_6$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O 16 10 6	0	0

- Molecule 5 is PHOSPHATE ION (three-letter code: PO4) (formula: O_4P).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total O P 5 4 1	0	0
5	A	1	Total O P 5 4 1	0	0
5	A	1	Total O P 5 4 1	0	0
5	A	1	Total O P 5 4 1	0	0

- Molecule 6 is water.

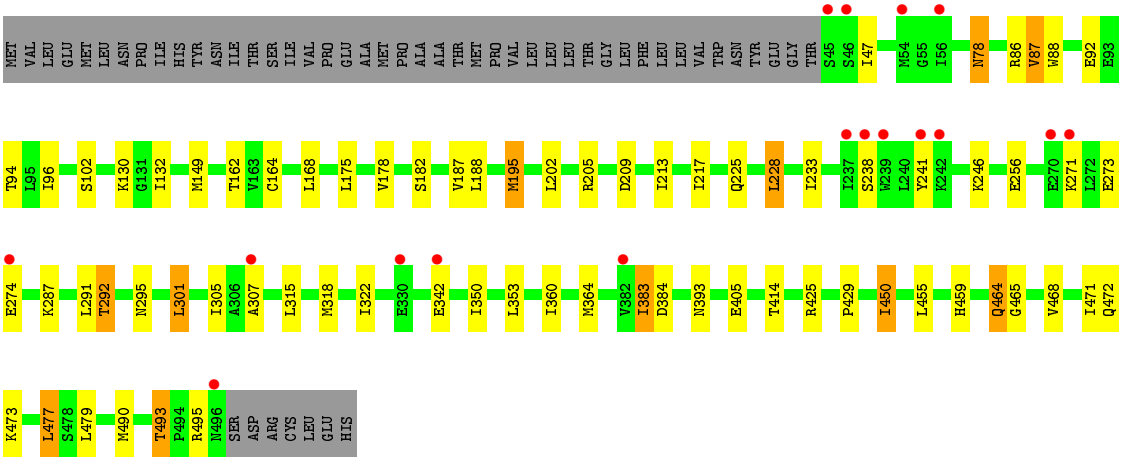
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	43	Total O 43 43	0	0

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: Aromatase

Chain A:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α, β, γ	140.22Å 140.22Å 119.27Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	121.43 – 2.75 37.78 – 2.75	Depositor EDS
% Data completeness (in resolution range)	99.1 (121.43-2.75) 99.2 (37.78-2.75)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.43 (at 2.77Å)	Xtriage
Refinement program	REFMAC 5.8.0131	Depositor
R, R_{free}	0.214 , 0.236 0.214 , 0.236	Depositor DCC
R_{free} test set	1753 reflections (4.95%)	wwPDB-VP
Wilson B-factor (Å^2)	68.2	Xtriage
Anisotropy	0.015	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 41.7	EDS
L-test for twinning[2]	$< \|L\| > = 0.51$, $< L^2 > = 0.34$	Xtriage
Estimated twinning fraction	0.018 for -h,-k,l	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	3811	wwPDB-VP
Average B, all atoms (Å^2)	71.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.55% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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: HEM, PO4, 1PE, ASD

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	0.42	0/3748	0.66	2/5050 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	301	LEU	CA-CB-CG	7.71	133.04	115.30
1	A	228	LEU	CA-CB-CG	5.11	127.05	115.30

There are no chirality outliers.

There are no planarity outliers.

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	A	3668	0	3741	25	0
2	A	43	0	30	1	0
3	A	21	0	26	1	0
4	A	16	0	22	3	0
5	A	20	0	0	1	0
6	A	43	0	0	0	0
All	All	3811	0	3819	27	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 4.

All (27) 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:149:MET:HE3	4:A:603:1PE:H121	1.73	0.70
1:A:225:GLN:HG3	1:A:477:LEU:HB2	1.79	0.65
1:A:459[B]:HIS:HB2	1:A:493:THR:HG23	1.83	0.60
1:A:217:ILE:HG12	1:A:305:ILE:HG22	1.84	0.58
1:A:477:LEU:HD22	3:A:602:ASD:H151	1.87	0.57
1:A:187:VAL:HG21	1:A:490:MET:HE3	1.87	0.57
1:A:292:THR:HG22	1:A:295:ASN:H	1.73	0.53
1:A:195:MET:HG3	1:A:307:ALA:HB1	1.89	0.53
1:A:132:ILE:HD11	2:A:601:HEM:HMD3	1.94	0.50
1:A:315:LEU:HD23	1:A:318:MET:HE2	1.94	0.50
1:A:350:ILE:HA	1:A:353:LEU:HD12	1.95	0.48
1:A:364:MET:HE1	1:A:429:PRO:HB2	1.95	0.48
1:A:168:LEU:HD22	1:A:450:ILE:HB	1.96	0.47
4:A:603:1PE:H231	5:A:607:PO4:O2	2.14	0.47
1:A:318:MET:HE3	1:A:360:ILE:HG12	1.96	0.46
1:A:94:THR:HB	1:A:393:ASN:HB2	1.99	0.45
1:A:315:LEU:HD22	1:A:450:ILE:HD11	1.99	0.45
1:A:102:SER:HA	1:A:383:ILE:HD11	2.00	0.44
4:A:603:1PE:H151	4:A:603:1PE:OH7	2.17	0.43
1:A:87:VAL:CG1	1:A:88:TRP:N	2.83	0.42
1:A:322:ILE:HD13	1:A:455:LEU:HD11	2.02	0.42
1:A:78:ASN:HA	1:A:78:ASN:HD22	1.65	0.41
1:A:209:ASP:O	1:A:213:ILE:HG12	2.21	0.41
1:A:238:SER:HA	1:A:241:TYR:CE1	2.56	0.41
1:A:468:VAL:HA	1:A:471:ILE:HD12	2.03	0.41
1:A:130:LYS:O	1:A:295:ASN:OD1	2.39	0.41
1:A:464:GLN:HB3	1:A:465:GLY:H	1.62	0.40

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	451/503 (90%)	431 (96%)	19 (4%)	1 (0%)	47 69

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	384	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	407/452 (90%)	368 (90%)	39 (10%)	8 14

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

Mol	Chain	Res	Type
1	A	47	ILE
1	A	78	ASN
1	A	86	ARG
1	A	87	VAL
1	A	92	GLU
1	A	96	ILE
1	A	162	THR
1	A	164	CYS
1	A	175	LEU
1	A	178	VAL
1	A	182	SER
1	A	188	LEU
1	A	195	MET
1	A	202	LEU
1	A	205	ARG
1	A	228	LEU
1	A	233	ILE
1	A	246	LYS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	256	GLU
1	A	271	LYS
1	A	273	GLU
1	A	274	GLU
1	A	287	LYS
1	A	291	LEU
1	A	292	THR
1	A	301	LEU
1	A	342	GLU
1	A	383	ILE
1	A	405	GLU
1	A	414	THR
1	A	425	ARG
1	A	450	ILE
1	A	464	GLN
1	A	472	GLN
1	A	473	LYS
1	A	477	LEU
1	A	479	LEU
1	A	493	THR
1	A	495	ARG

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	78	ASN
1	A	180	ASN
1	A	393	ASN

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)

7 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	$\#\|Z\| > 2$
5	PO4	A	607	-	4,4,4	0.93	0	6,6,6	0.36	0
5	PO4	A	604	-	4,4,4	0.86	0	6,6,6	0.50	0
5	PO4	A	605	-	4,4,4	0.90	0	6,6,6	0.48	0
4	1PE	A	603	-	15,15,15	0.58	0	14,14,14	0.35	0
5	PO4	A	606	-	4,4,4	0.87	0	6,6,6	0.49	0
2	HEM	A	601	1	27,50,50	2.13	6 (22%)	17,82,82	1.46	3 (17%)
3	ASD	A	602	-	24,24,24	0.73	0	39,39,39	1.50	6 (15%)

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	1PE	A	603	-	-	10/13/13/13	-
3	ASD	A	602	-	-	-	0/4/4/4
2	HEM	A	601	1	-	0/6/54/54	-

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	601	HEM	C3D-C2D	5.22	1.53	1.37
2	A	601	HEM	C3B-C2B	-4.32	1.34	1.40
2	A	601	HEM	C3C-C2C	-3.91	1.34	1.40
2	A	601	HEM	C3B-CAB	3.73	1.55	1.47
2	A	601	HEM	C3C-CAC	3.62	1.55	1.47
2	A	601	HEM	CAA-C2A	2.38	1.55	1.52

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	A	602	ASD	C16-C17-C13	4.30	112.84	108.59
2	A	601	HEM	CBD-CAD-C3D	-3.29	106.41	112.48
2	A	601	HEM	CBA-CAA-C2A	-2.71	107.48	112.49
3	A	602	ASD	C6-C5-C4	-2.59	116.53	120.87
3	A	602	ASD	C15-C16-C17	-2.58	103.11	105.70
3	A	602	ASD	C18-C13-C14	2.40	116.53	112.98
2	A	601	HEM	C1D-C2D-C3D	-2.30	105.39	107.00
3	A	602	ASD	C15-C14-C13	2.18	106.03	104.08
3	A	602	ASD	C6-C5-C10	2.10	120.64	116.77

There are no chirality outliers.

All (10) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	603	1PE	OH4-C13-C23-OH3
4	A	603	1PE	OH5-C14-C24-OH4
4	A	603	1PE	C15-C25-OH5-C14
4	A	603	1PE	C14-C24-OH4-C13
4	A	603	1PE	C16-C26-OH6-C15
4	A	603	1PE	C13-C23-OH3-C22
4	A	603	1PE	C24-C14-OH5-C25
4	A	603	1PE	C12-C22-OH3-C23
4	A	603	1PE	OH6-C15-C25-OH5
4	A	603	1PE	C23-C13-OH4-C24

There are no ring outliers.

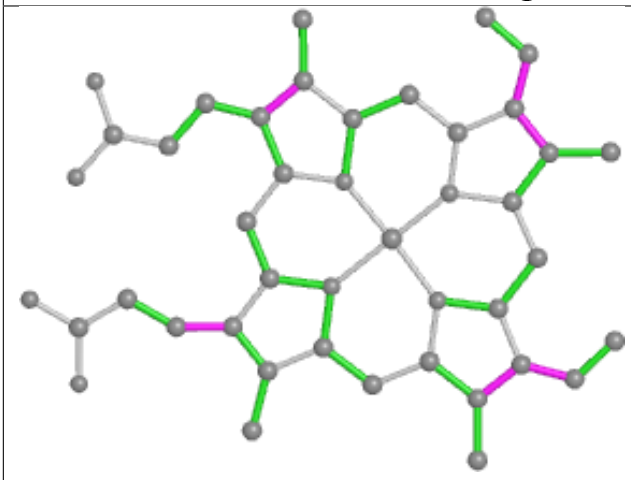
4 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	607	PO4	1	0
4	A	603	1PE	3	0
2	A	601	HEM	1	0
3	A	602	ASD	1	0

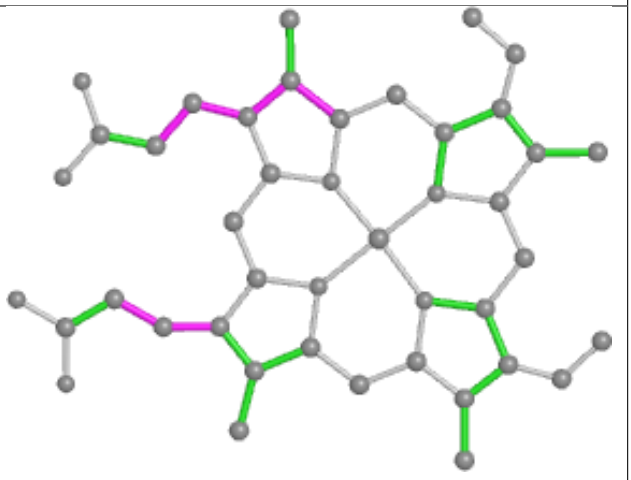
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and

any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

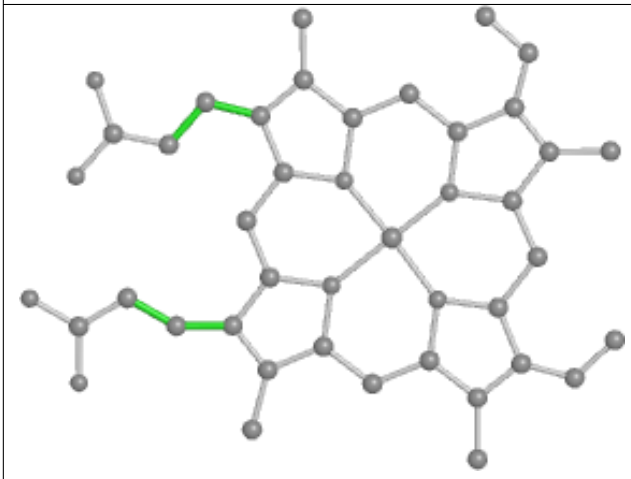
Ligand HEM A 601



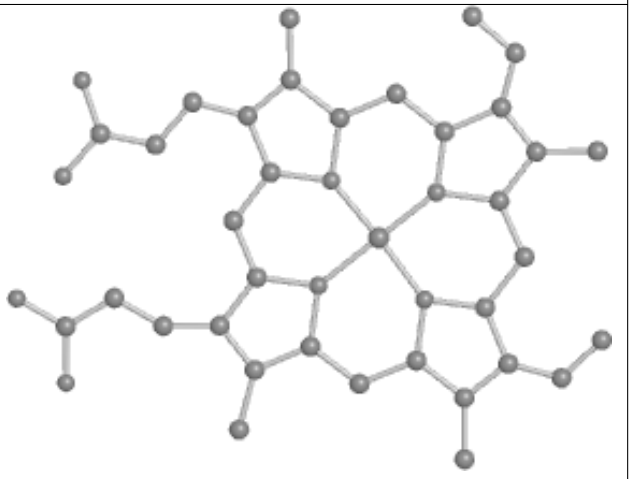
Bond lengths



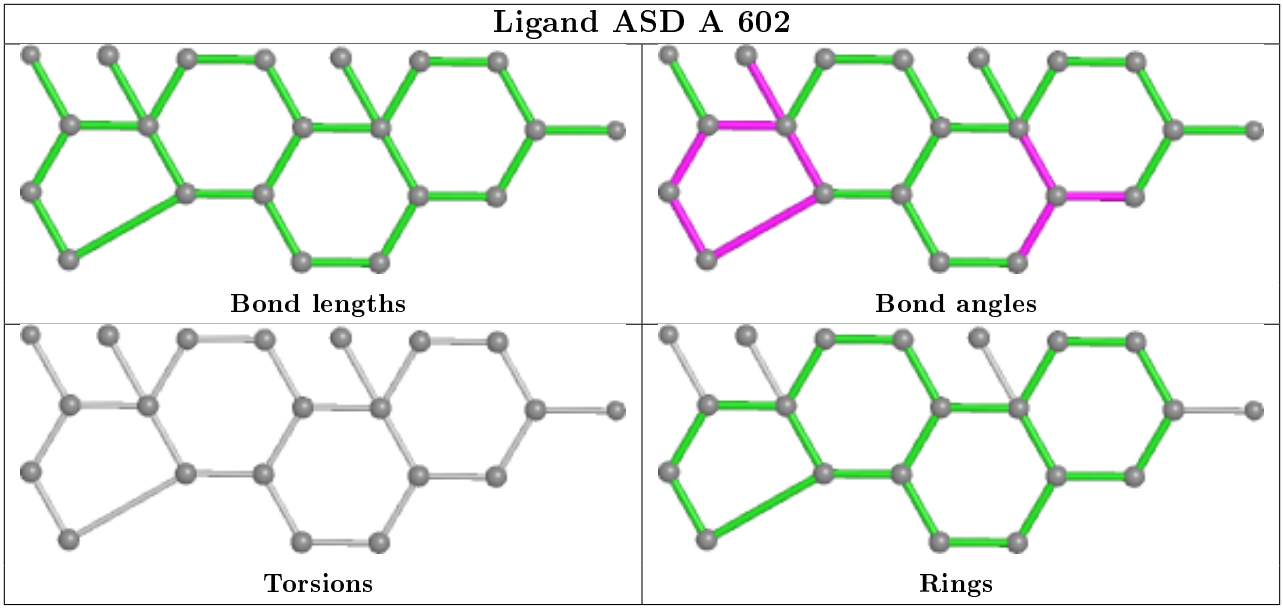
Bond angles



Torsions



Rings



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^{th} 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%)	0.14	17 (3%) 40 48	51, 68, 102, 142	0

All (17) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	239	TRP	6.3
1	A	45	SER	5.6
1	A	496	ASN	4.8
1	A	54	MET	3.8
1	A	270	GLU	3.2
1	A	382	VAL	3.1
1	A	238	SER	3.1
1	A	46	SER	3.0
1	A	342	GLU	3.0
1	A	271	LYS	2.9
1	A	241	TYR	2.9
1	A	56	ILE	2.8
1	A	237	ILE	2.8
1	A	274	GLU	2.7
1	A	330	GLU	2.6
1	A	307	ALA	2.2
1	A	242	LYS	2.1

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

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

6.3 Carbohydrates

There are no carbohydrates in this entry.

6.4 Ligands

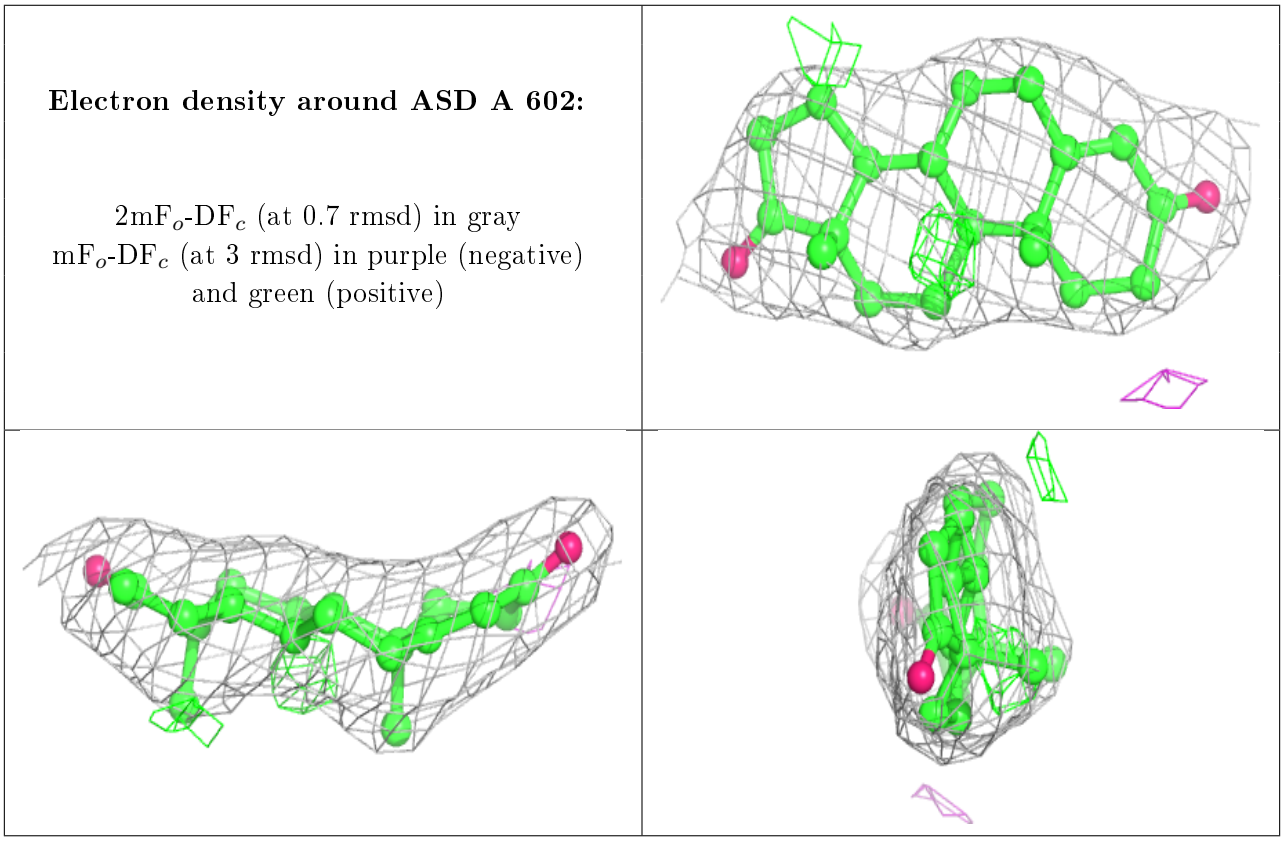
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
4	1PE	A	603	16/16	0.54	0.46	97,109,114,114	0
5	PO4	A	607	5/5	0.56	0.47	100,100,100,100	5
5	PO4	A	606	5/5	0.76	0.47	105,105,106,106	5
5	PO4	A	604	5/5	0.92	0.19	120,120,120,120	0
5	PO4	A	605	5/5	0.95	0.13	103,103,103,103	0
3	ASD	A	602	21/21	0.97	0.29	48,49,51,51	0
2	HEM	A	601	43/43	0.99	0.24	44,46,51,53	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

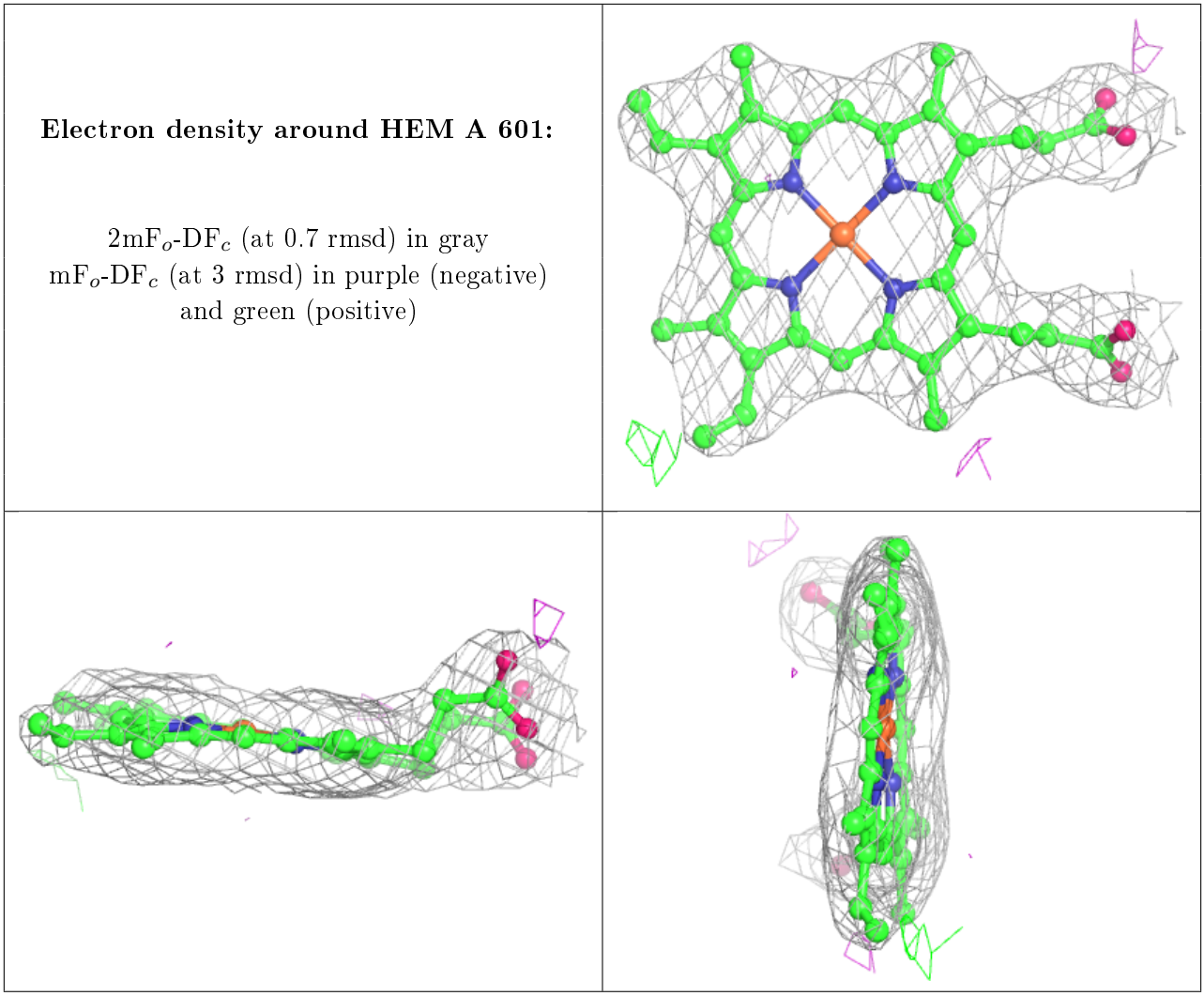
Electron density around ASD A 602:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)



Electron density around HEM A 601:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)



6.5 Other polymers

There are no such residues in this entry.