



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 08:49 PM UTC

PDB ID : 4KVK / pdb_00004kvk
Title : Crystal structure of Oryza sativa fatty acid alpha-dioxygenase
Authors : Zhu, G.; Koszelak-Rosenblum, M.; Malkowski, M.G.
Deposited on : 2013-05-22
Resolution : 1.98 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 ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

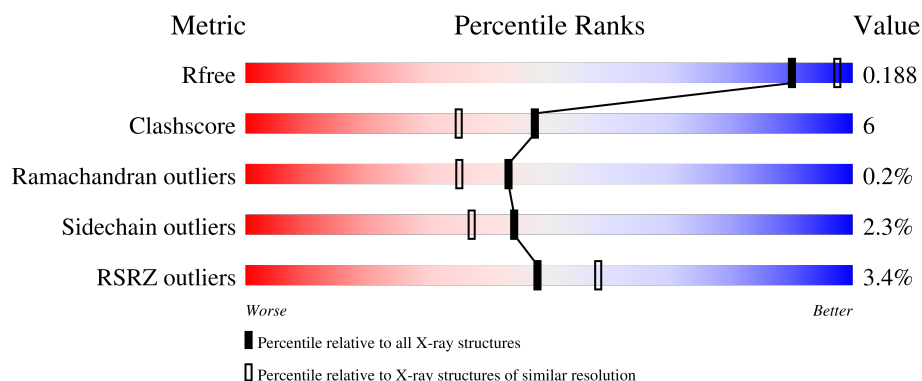
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

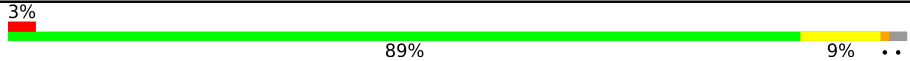
The reported resolution of this entry is 1.98 Å.

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}	180053	1506 (1.98-1.98)
Clashscore	190562	1534 (1.98-1.98)
Ramachandran outliers	187476	1518 (1.98-1.98)
Sidechain outliers	187428	1518 (1.98-1.98)
RSRZ outliers	180081	1506 (1.98-1.98)

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 of 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 $\leq 5\%$. 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	621	

2 Entry composition

There are 11 unique types of molecules in this entry. The entry contains 5676 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 Fatty acid alpha-oxidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	611	5030	3207	865	938	20	0	19	0

There are 12 discrepancies between the modelled and reference sequences:

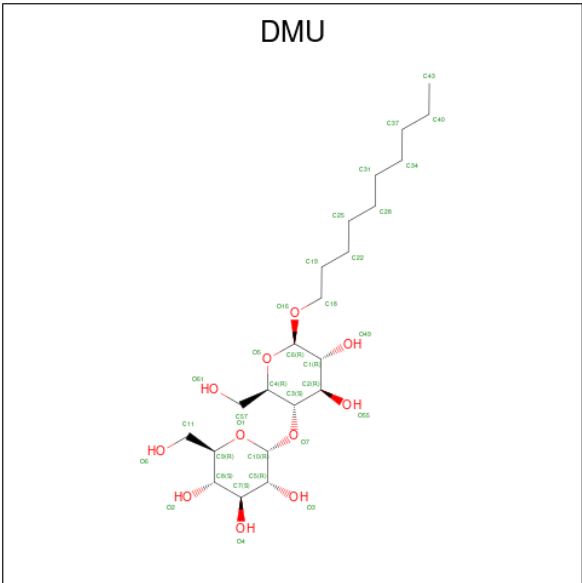
Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	MET	-	expression tag	UNP Q9M5J1
A	-1	ARG	-	expression tag	UNP Q9M5J1
A	0	GLY	-	expression tag	UNP Q9M5J1
A	1	SER	-	expression tag	UNP Q9M5J1
A	2	HIS	-	expression tag	UNP Q9M5J1
A	3	HIS	-	expression tag	UNP Q9M5J1
A	4	HIS	-	expression tag	UNP Q9M5J1
A	5	HIS	-	expression tag	UNP Q9M5J1
A	6	HIS	-	expression tag	UNP Q9M5J1
A	7	HIS	-	expression tag	UNP Q9M5J1
A	8	GLY	-	expression tag	UNP Q9M5J1
A	9	SER	-	expression tag	UNP Q9M5J1

- Molecule 2 is PROTOPORPHYRIN IX CONTAINING FE (CCD ID: 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 DECYL-BETA-D-MALTOPYRANOSIDE (CCD ID: DMU) (formula: $C_{22}H_{42}O_{11}$).



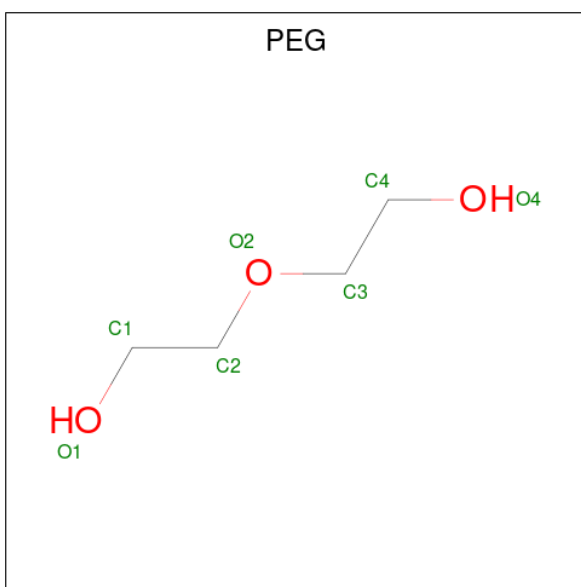
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			33	22	11		

- Molecule 4 is TETRAETHYLENE GLYCOL (CCD ID: PG4) (formula: $C_8H_{18}O_5$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			13	8	5		
4	A	1	Total	C	O	0	0
			13	8	5		
4	A	1	Total	C	O	0	0
			13	8	5		

- Molecule 5 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: $C_4H_{10}O_3$).



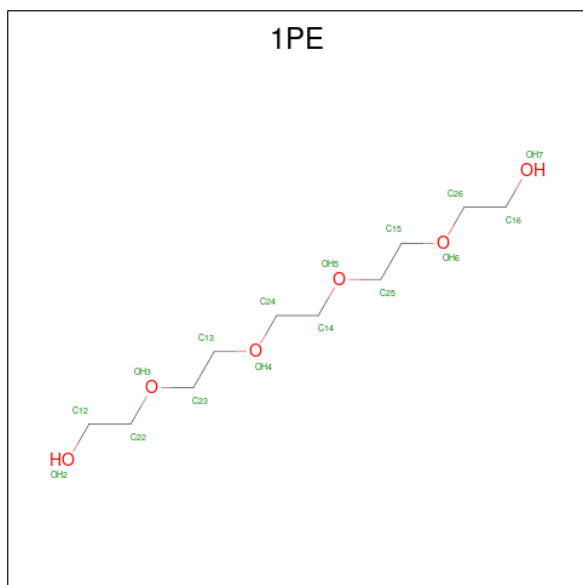
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			7	4	3		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			7	4	3		
5	A	1	Total	C	O	0	0
			7	4	3		
5	A	1	Total	C	O	0	0
			7	4	3		

- Molecule 6 is PENTAETHYLENE GLYCOL (CCD ID: 1PE) (formula: $C_{10}H_{22}O_6$).



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

- Molecule 7 is TRIETHYLENE GLYCOL (CCD ID: PGE) (formula: $C_6H_{14}O_4$).



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

- Molecule 8 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	1	Total	Ca	0	0
			1	1		

- Molecule 9 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	4	Total	Cl	0	0
			4	4		

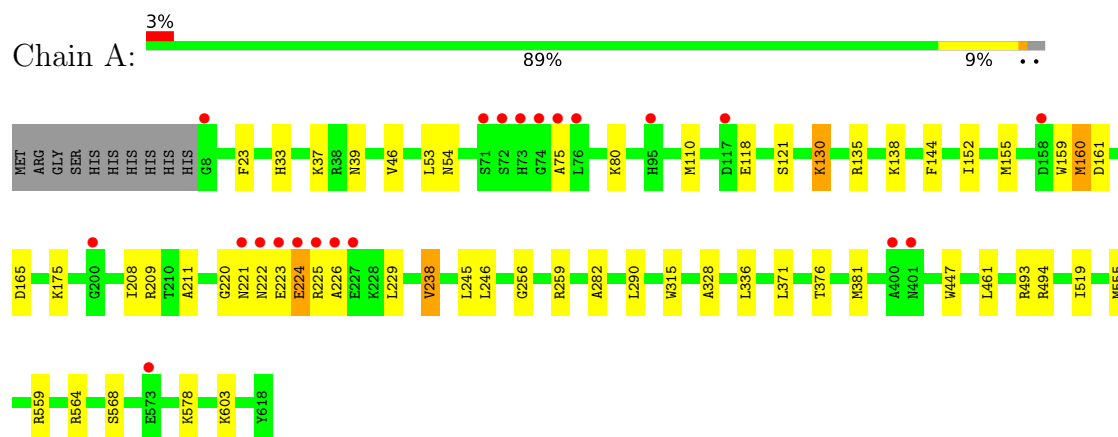
- Molecule 10 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	A	2	Total	Na	0	0
			2	2		

- Molecule 11 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
11	A	470	Total	O	0	0
			470	470		

- Molecule 1: Fatty acid alpha-oxidase



4 Data and refinement statistics

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	72.46Å 128.58Å 188.74Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	106.27 – 1.98 106.27 – 1.98	Depositor EDS
% Data completeness (in resolution range)	99.9 (106.27-1.98) 99.9 (106.27-1.98)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.35 (at 1.98Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.166 , 0.192 (Not available) , 0.188	Depositor DCC
R_{free} test set	3133 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å ²)	31.9	Xtriage
Anisotropy	0.041	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 36.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	5676	wwPDB-VP
Average B, all atoms (Å ²)	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.21% 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, 0.333 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: NA, PEG, DMU, PG4, PGE, CA, CL, 1PE, HEM

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	0.53	1/5188 (0.0%)	0.76	0/7013

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	46	VAL	CA-CB	5.86	1.57	1.54

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	5030	0	4978	53	0
2	A	43	0	30	1	0
3	A	33	0	42	4	0
4	A	39	0	54	5	0
5	A	28	0	40	0	0
6	A	16	0	22	4	0
7	A	10	0	14	2	0
8	A	1	0	0	0	0
9	A	4	0	0	0	0
10	A	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
11	A	470	0	0	3	0
All	All	5676	0	5180	58	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 6.

All (58) 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:221[B]:ASN:ND2	1:A:225[B]:ARG:CB	1.71	1.31
1:A:221[B]:ASN:ND2	1:A:225[B]:ARG:HB2	1.14	1.05
1:A:224[A]:GLU:O	1:A:224[A]:GLU:OE1	1.77	1.01
1:A:494:ARG:HA	7:A:706:PGE:H42	1.63	0.80
1:A:223[A]:GLU:HA	1:A:223[A]:GLU:OE2	1.82	0.78
1:A:224[A]:GLU:OE1	1:A:224[A]:GLU:CA	2.29	0.78
1:A:221[B]:ASN:HD22	1:A:225[B]:ARG:HB2	1.45	0.77
1:A:224[A]:GLU:OE1	1:A:224[A]:GLU:C	2.28	0.75
1:A:238[A]:VAL:HG13	1:A:246:LEU:HD12	1.69	0.72
1:A:224[A]:GLU:OE1	1:A:224[A]:GLU:HA	1.90	0.71
1:A:23:PHE:HB3	3:A:702:DMU:H11	1.73	0.70
1:A:224[B]:GLU:HG3	1:A:225[B]:ARG:HD2	1.74	0.70
1:A:221[B]:ASN:HD22	1:A:221[B]:ASN:N	1.90	0.68
1:A:238[A]:VAL:CG1	1:A:246:LEU:HD12	2.23	0.67
1:A:224[A]:GLU:O	1:A:224[A]:GLU:CD	2.37	0.67
1:A:221[B]:ASN:ND2	1:A:222[B]:ASN:H	1.92	0.67
1:A:381:MET:HB2	2:A:701:HEM:HAC	1.76	0.65
1:A:224[B]:GLU:HG3	1:A:225[B]:ARG:HH21	1.63	0.62
1:A:118[B]:GLU:HG3	1:A:121[B]:SER:HB3	1.82	0.61
3:A:702:DMU:H13	4:A:709:PG4:O1	2.03	0.58
6:A:705:1PE:H161	11:A:832:HOH:O	2.02	0.58
1:A:225[A]:ARG:O	1:A:229:LEU:HG	2.04	0.58
1:A:161:ASP:OD2	1:A:259:ARG:HD3	2.03	0.58
1:A:221[B]:ASN:ND2	1:A:221[B]:ASN:N	2.52	0.57
3:A:702:DMU:H35	3:A:702:DMU:H30	1.87	0.56
1:A:224[B]:GLU:OE1	1:A:225[B]:ARG:NH2	2.39	0.56
1:A:54:ASN:HB2	4:A:703:PG4:H41	1.89	0.55
1:A:155:MET:HB3	1:A:159:TRP:CZ2	2.41	0.55
1:A:222[B]:ASN:OD1	1:A:225[B]:ARG:HG2	2.08	0.54
3:A:702:DMU:H4	4:A:709:PG4:H61	1.90	0.53
1:A:555:MET:O	1:A:559:ARG:HG3	2.10	0.52
1:A:222[A]:ASN:ND2	1:A:223[A]:GLU:N	2.58	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:224[A]:GLU:C	1:A:224[A]:GLU:CD	2.79	0.51
1:A:39:ASN:HD21	6:A:705:1PE:H151	1.78	0.49
1:A:564:ARG:HG3	1:A:568[B]:SER:OG	2.13	0.49
1:A:33:HIS:CD2	1:A:37:LYS:HD2	2.48	0.47
1:A:221[B]:ASN:CG	1:A:222[B]:ASN:H	2.22	0.46
1:A:221[B]:ASN:ND2	1:A:222[B]:ASN:N	2.62	0.45
1:A:39:ASN:ND2	6:A:705:1PE:H151	2.31	0.45
1:A:224[B]:GLU:CG	1:A:225[B]:ARG:HH21	2.29	0.45
1:A:225[A]:ARG:O	1:A:226[A]:ALA:C	2.60	0.44
1:A:135[A]:ARG:HG3	1:A:447:TRP:HB3	2.00	0.44
6:A:705:1PE:H142	6:A:705:1PE:H152	1.77	0.44
1:A:208:ILE:CD1	1:A:461:LEU:HD21	2.48	0.43
1:A:328:ALA:HB1	4:A:703:PG4:H71	2.00	0.43
1:A:152:ILE:HB	1:A:315:TRP:CZ2	2.54	0.42
1:A:160:MET:HE2	1:A:376:THR:OG1	2.19	0.42
1:A:175:LYS:HG3	11:A:1243:HOH:O	2.20	0.42
1:A:224[B]:GLU:HG3	1:A:225[B]:ARG:N	2.34	0.42
1:A:211:ALA:HB1	1:A:371:LEU:HG	2.01	0.42
1:A:220:GLY:HA2	1:A:256:GLY:HA2	2.01	0.41
1:A:130:LYS:HB2	1:A:519:ILE:HD11	2.03	0.41
1:A:282:ALA:HB1	1:A:578:LYS:HE3	2.02	0.41
1:A:493:ARG:HB3	7:A:706:PGE:H62	2.03	0.41
1:A:53:LEU:HB3	4:A:703:PG4:H72	2.03	0.41
1:A:559:ARG:HD3	11:A:801:HOH:O	2.20	0.41
1:A:209:ARG:HA	1:A:221[C]:ASN:HD21	1.85	0.40

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	629/621 (101%)	606 (96%)	22 (4%)	1 (0%)	43	35

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	75	ALA

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	545/535 (102%)	531 (97%)	14 (3%)	40	32

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	80	LYS
1	A	110	MET
1	A	130	LYS
1	A	144	PHE
1	A	160	MET
1	A	165	ASP
1	A	224[A]	GLU
1	A	224[B]	GLU
1	A	238[A]	VAL
1	A	238[B]	VAL
1	A	245	LEU
1	A	290	LEU
1	A	336	LEU
1	A	603	LYS

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

Mol	Chain	Res	Type
1	A	397	GLN
1	A	581	GLN
1	A	594	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 18 ligands modelled in this entry, 7 are monoatomic - leaving 11 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	PG4	A	703	-	12,12,12	0.50	0	11,11,11	0.21	0
6	1PE	A	705	10	15,15,15	0.51	0	14,14,14	0.42	0
5	PEG	A	711	-	6,6,6	0.46	0	5,5,5	0.29	0
2	HEM	A	701	1	50,50,50	1.95	11 (22%)	67,82,82	1.42	7 (10%)
3	DMU	A	702	-	34,34,34	0.65	0	45,45,45	1.06	2 (4%)
5	PEG	A	710	-	6,6,6	0.41	0	5,5,5	0.36	0
4	PG4	A	709	-	12,12,12	0.46	0	11,11,11	0.26	0
4	PG4	A	707	10	12,12,12	0.46	0	11,11,11	0.30	0
5	PEG	A	708	-	6,6,6	0.51	0	5,5,5	0.30	0
5	PEG	A	704	-	6,6,6	0.45	0	5,5,5	0.24	0
7	PGE	A	706	-	9,9,9	0.47	0	8,8,8	0.37	0

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	PG4	A	703	-	-	6/10/10/10	-
6	1PE	A	705	10	-	8/13/13/13	-
5	PEG	A	711	-	-	3/4/4/4	-
2	HEM	A	701	1	-	4/14/54/54	-
3	DMU	A	702	-	-	7/19/59/59	0/2/2/2
5	PEG	A	710	-	-	4/4/4/4	-
4	PG4	A	709	-	-	6/10/10/10	-
4	PG4	A	707	10	-	1/10/10/10	-
5	PEG	A	708	-	-	1/4/4/4	-
5	PEG	A	704	-	-	2/4/4/4	-
7	PGE	A	706	-	-	3/7/7/7	-

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	701	HEM	C3D-C2D	7.36	1.52	1.36
2	A	701	HEM	FE-NB	5.11	2.10	1.94
2	A	701	HEM	FE-ND	5.05	2.10	1.94
2	A	701	HEM	FE-NC	3.33	2.06	1.95
2	A	701	HEM	FE-NA	3.27	2.06	1.95
2	A	701	HEM	CAB-C3B	2.82	1.54	1.47
2	A	701	HEM	CMC-C2C	2.63	1.56	1.50
2	A	701	HEM	CAC-C3C	2.56	1.54	1.47
2	A	701	HEM	CMD-C2D	2.55	1.56	1.50
2	A	701	HEM	CMB-C2B	2.29	1.55	1.50
2	A	701	HEM	CMA-C3A	2.22	1.55	1.50

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	701	HEM	C4D-ND-C1D	5.59	111.83	105.21
2	A	701	HEM	C1B-NB-C4B	3.04	108.81	105.21
2	A	701	HEM	CMD-C2D-C1D	3.01	129.73	125.03
2	A	701	HEM	C4C-C3C-C2C	2.64	109.10	106.81
2	A	701	HEM	C3B-C4B-NB	-2.46	107.70	109.47
3	A	702	DMU	C57-C4-C3	-2.44	106.53	113.38
2	A	701	HEM	CAA-CBA-CGA	-2.12	108.03	113.67
3	A	702	DMU	O1-C9-C11	2.06	111.53	106.44
2	A	701	HEM	CHA-C4D-ND	2.04	126.89	124.37

There are no chirality outliers.

All (45) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	702	DMU	O6-C11-C9-O1
3	A	702	DMU	O6-C11-C9-C8
4	A	709	PG4	O2-C3-C4-O3
6	A	705	1PE	OH5-C14-C24-OH4
6	A	705	1PE	C15-C25-OH5-C14
5	A	711	PEG	O1-C1-C2-O2
4	A	703	PG4	O3-C5-C6-O4
5	A	704	PEG	O1-C1-C2-O2
5	A	708	PEG	O2-C3-C4-O4
7	A	706	PGE	O3-C5-C6-O4
3	A	702	DMU	C19-C22-C25-C28
5	A	710	PEG	O1-C1-C2-O2
3	A	702	DMU	C18-C19-C22-C25
4	A	703	PG4	O4-C7-C8-O5
4	A	703	PG4	O2-C3-C4-O3
7	A	706	PGE	O2-C3-C4-O3
4	A	709	PG4	C1-C2-O2-C3
2	A	701	HEM	C2C-C3C-CAC-CBC
4	A	709	PG4	C3-C4-O3-C5
4	A	703	PG4	C6-C5-O3-C4
2	A	701	HEM	C4C-C3C-CAC-CBC
5	A	711	PEG	C4-C3-O2-C2
6	A	705	1PE	C16-C26-OH6-C15
6	A	705	1PE	C13-C23-OH3-C22
4	A	709	PG4	C6-C5-O3-C4
3	A	702	DMU	C34-C37-C40-C43
6	A	705	1PE	C24-C14-OH5-C25
7	A	706	PGE	C3-C4-O3-C5
3	A	702	DMU	C31-C34-C37-C40
5	A	711	PEG	O2-C3-C4-O4
6	A	705	1PE	OH7-C16-C26-OH6
5	A	710	PEG	C1-C2-O2-C3
6	A	705	1PE	C14-C24-OH4-C13
5	A	710	PEG	C4-C3-O2-C2
6	A	705	1PE	OH6-C15-C25-OH5
5	A	710	PEG	O2-C3-C4-O4
4	A	709	PG4	C4-C3-O2-C2
3	A	702	DMU	O16-C18-C19-C22
2	A	701	HEM	CAA-CBA-CGA-O2A
5	A	704	PEG	O2-C3-C4-O4
2	A	701	HEM	CAA-CBA-CGA-O1A
4	A	703	PG4	C1-C2-O2-C3

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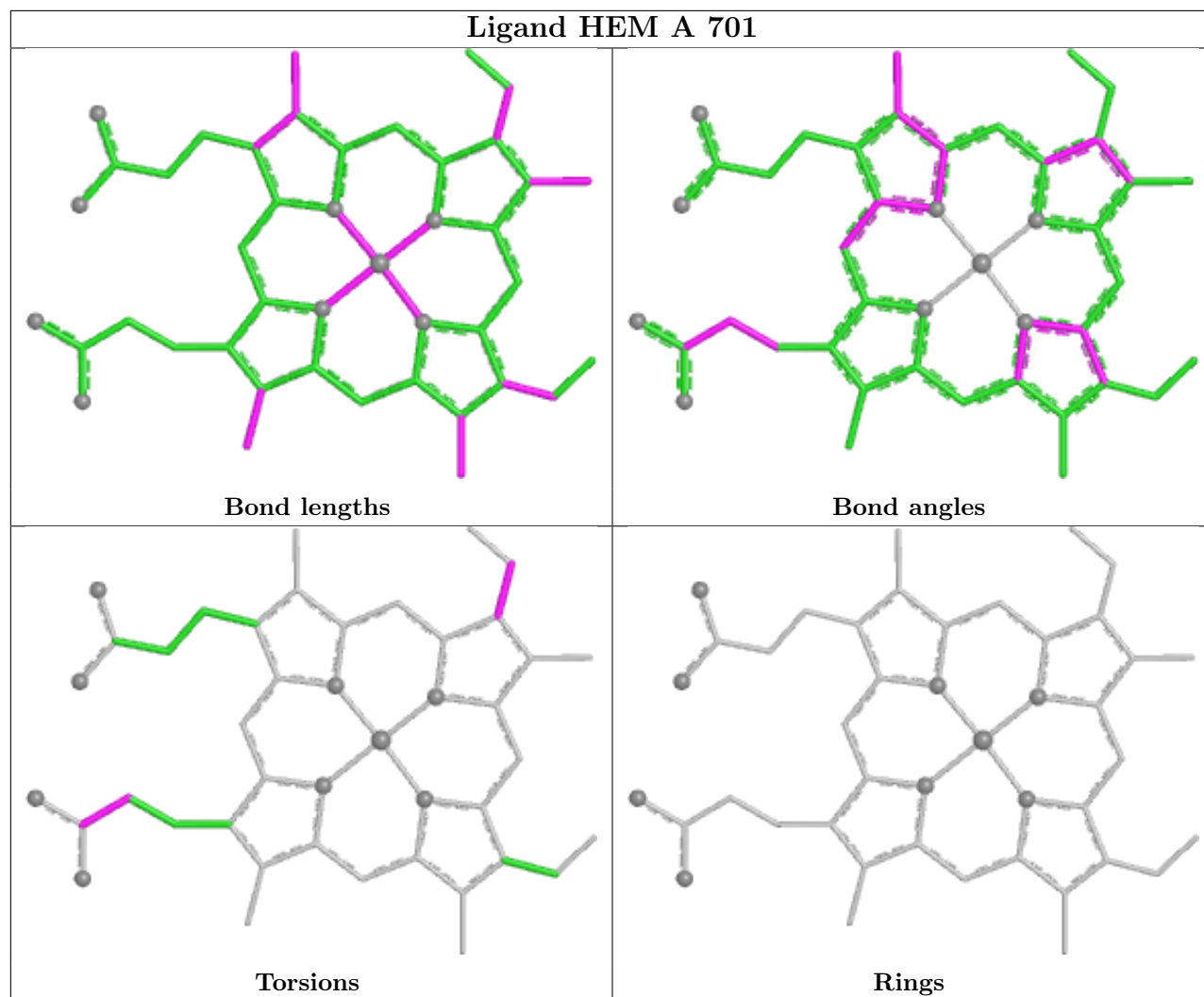
Mol	Chain	Res	Type	Atoms
4	A	703	PG4	C4-C3-O2-C2
4	A	709	PG4	O3-C5-C6-O4
4	A	707	PG4	C5-C6-O4-C7

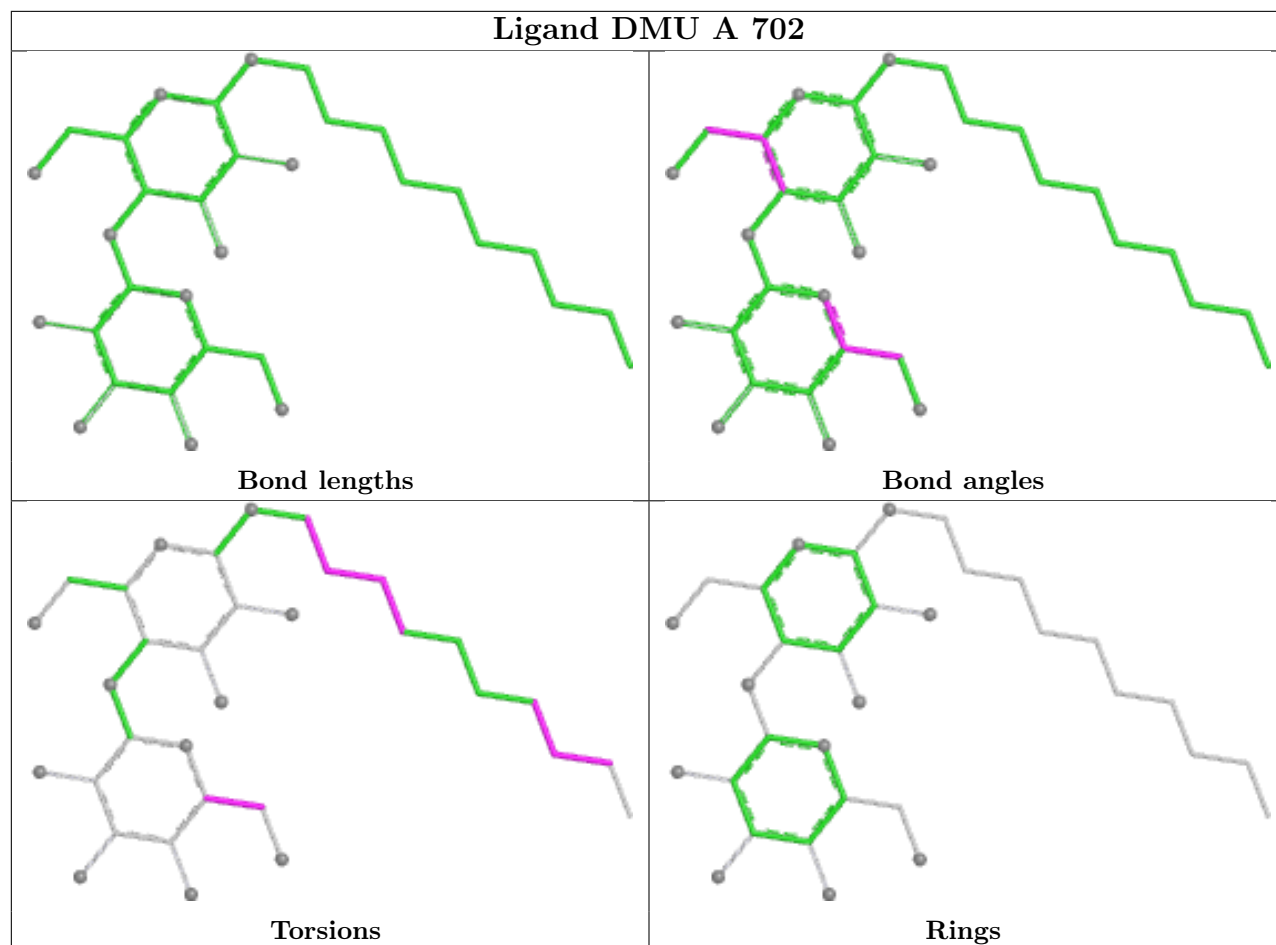
There are no ring outliers.

6 monomers are involved in 14 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	703	PG4	3	0
6	A	705	1PE	4	0
2	A	701	HEM	1	0
3	A	702	DMU	4	0
4	A	709	PG4	2	0
7	A	706	PGE	2	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 than 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.





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	611/621 (98%)	-0.03	21 (3%)	48	58	16, 31, 49, 81	19 (3%)

All (21) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	225[A]	ARG	8.3
1	A	75	ALA	5.1
1	A	74	GLY	5.0
1	A	224[A]	GLU	4.3
1	A	221[A]	ASN	4.3
1	A	73	HIS	4.0
1	A	226[A]	ALA	3.4
1	A	95	HIS	3.2
1	A	76	LEU	2.9
1	A	72	SER	2.8
1	A	401	ASN	2.7
1	A	400	ALA	2.7
1	A	227	GLU	2.6
1	A	71	SER	2.6
1	A	573	GLU	2.4
1	A	222[A]	ASN	2.4
1	A	8	GLY	2.3
1	A	117	ASP	2.1
1	A	200	GLY	2.1
1	A	223[A]	GLU	2.1
1	A	158	ASP	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 ⓘ

There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

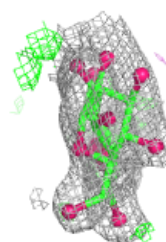
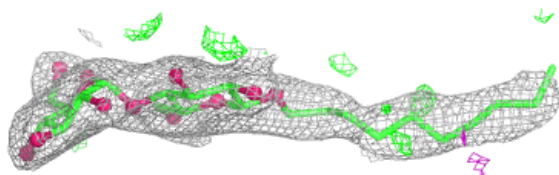
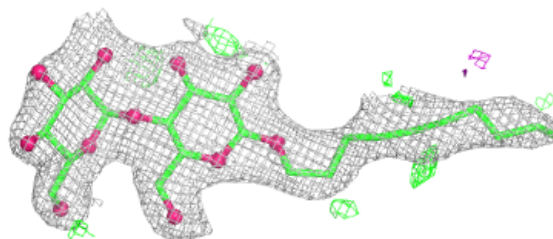
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

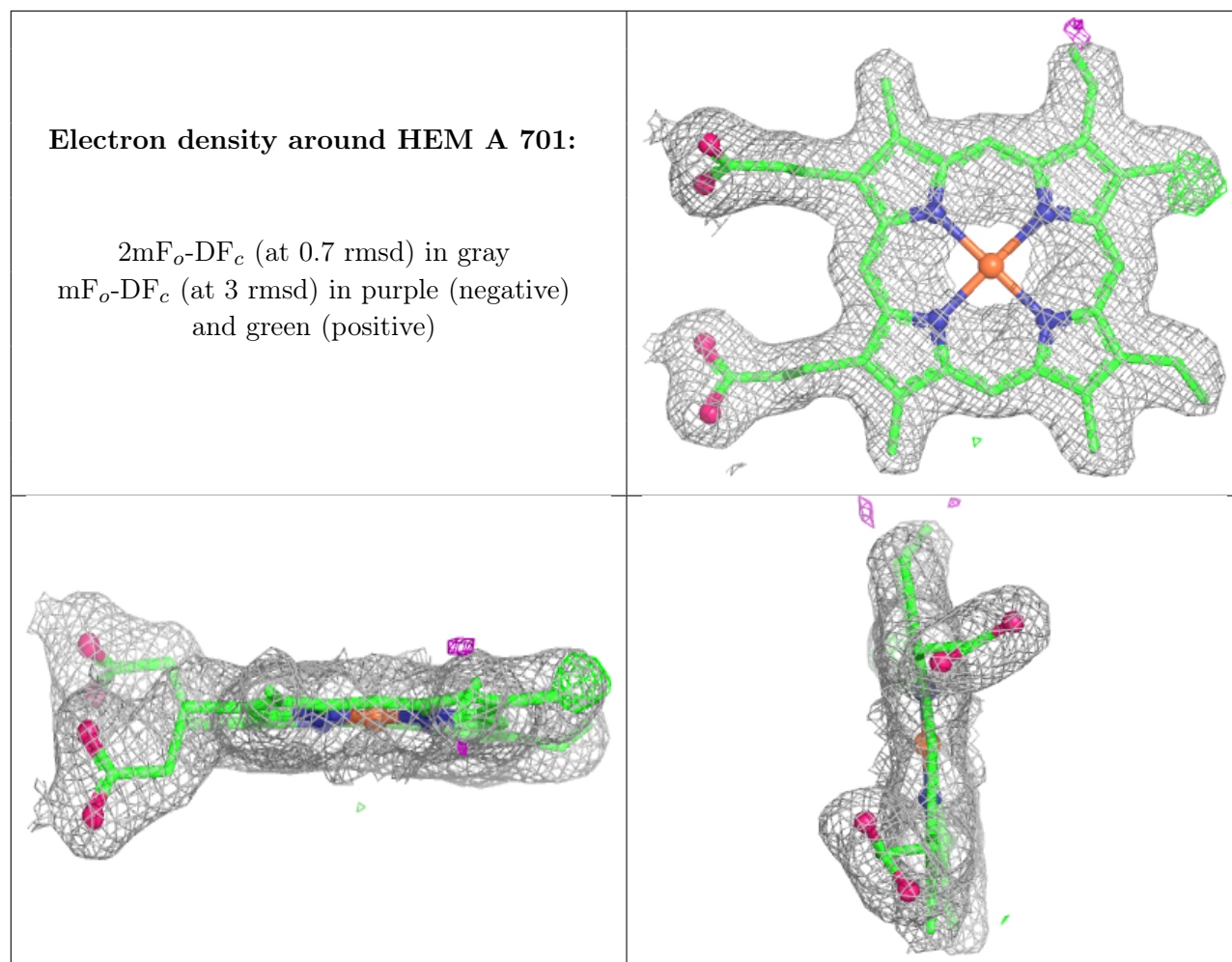
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
10	NA	A	718	1/1	0.69	0.20	54,54,54,54	0
5	PEG	A	708	7/7	0.83	0.18	54,57,57,59	0
5	PEG	A	711	7/7	0.85	0.16	74,76,77,77	0
3	DMU	A	702	33/33	0.87	0.13	50,58,71,73	0
5	PEG	A	710	7/7	0.87	0.18	64,66,68,69	0
5	PEG	A	704	7/7	0.88	0.16	49,51,55,56	0
6	1PE	A	705	16/16	0.89	0.14	36,45,49,50	0
4	PG4	A	703	13/13	0.89	0.18	54,57,60,62	0
10	NA	A	717	1/1	0.90	0.09	51,51,51,51	0
4	PG4	A	709	13/13	0.91	0.15	65,67,75,76	0
7	PGE	A	706	10/10	0.92	0.12	40,46,55,57	0
4	PG4	A	707	13/13	0.93	0.12	45,49,58,61	0
8	CA	A	712	1/1	0.96	0.12	58,58,58,58	0
2	HEM	A	701	43/43	0.98	0.06	21,27,32,36	0
9	CL	A	716	1/1	0.98	0.08	33,33,33,33	0
9	CL	A	713	1/1	0.99	0.03	30,30,30,30	0
9	CL	A	714	1/1	0.99	0.04	29,29,29,29	0
9	CL	A	715	1/1	0.99	0.07	41,41,41,41	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 DMU A 702:

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





6.5 Other polymers [i](#)

There are no such residues in this entry.