



Full wwPDB X-ray Structure Validation Report ⓘ

May 15, 2020 – 05:54 pm BST

PDB ID : 4QWT
Title : Anaerobic crystal structure of delta413-417:GS LOX in complex with arachidonate
Authors : Neau, D.B.; Newcomer, M.E.
Deposited on : 2014-07-17
Resolution : 2.00 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 following versions of software and data (see [references ⓘ](#)) 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

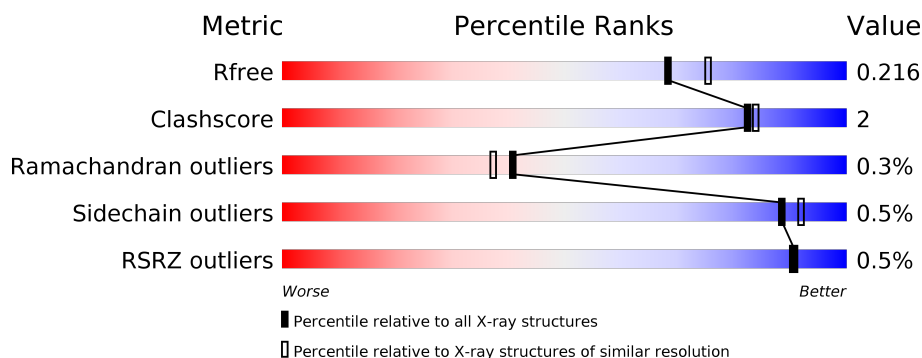
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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}	130704	8085 (2.00-2.00)
Clashscore	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)
RSRZ outliers	127900	7900 (2.00-2.00)

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 ≥ 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	696	<div> <div style="width: 91%;"></div> <div style="width: 7%;"></div> <div style="width: 2%;"></div> </div> <div>91% 7% •</div>
1	B	696	<div> <div style="width: 91%;"></div> <div style="width: 7%;"></div> <div style="width: 2%;"></div> </div> <div>91% 7% •</div>
1	C	696	<div> <div style="width: 93%;"></div> <div style="width: 5%;"></div> <div style="width: 2%;"></div> </div> <div>93% 5% •</div>
1	D	696	<div> <div style="width: 92%;"></div> <div style="width: 6%;"></div> <div style="width: 2%;"></div> </div> <div>92% 6% •</div>

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 23850 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 Allene oxide synthase-lipoxygenase protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	681	Total	C	N	O	S	0	17	0
			5510	3527	926	1044	13			
1	B	679	Total	C	N	O	S	0	10	0
			5345	3411	904	1017	13			
1	C	684	Total	C	N	O	S	0	14	0
			5503	3515	927	1048	13			
1	D	681	Total	C	N	O	S	0	13	0
			5455	3489	919	1034	13			

There are 52 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	MET	-	EXPRESSION TAG	UNP O16025
A	-1	HIS	-	EXPRESSION TAG	UNP O16025
A	0	HIS	-	EXPRESSION TAG	UNP O16025
A	1	HIS	-	EXPRESSION TAG	UNP O16025
A	2	HIS	-	EXPRESSION TAG	UNP O16025
A	3	HIS	-	EXPRESSION TAG	UNP O16025
A	?	-	TRP	DELETION	UNP O16025
A	?	-	PHE	DELETION	UNP O16025
A	?	-	HIS	DELETION	UNP O16025
A	43	GLY	ASN	ENGINEERED MUTATION	UNP O16025
A	44	SER	ASP	ENGINEERED MUTATION	UNP O16025
A	409	ILE	VAL	CONFLICT	UNP O16025
A	590	ILE	VAL	CONFLICT	UNP O16025
B	-2	MET	-	EXPRESSION TAG	UNP O16025
B	-1	HIS	-	EXPRESSION TAG	UNP O16025
B	0	HIS	-	EXPRESSION TAG	UNP O16025
B	1	HIS	-	EXPRESSION TAG	UNP O16025
B	2	HIS	-	EXPRESSION TAG	UNP O16025
B	3	HIS	-	EXPRESSION TAG	UNP O16025
B	?	-	TRP	DELETION	UNP O16025
B	?	-	PHE	DELETION	UNP O16025

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Chain	Residue	Modelled	Actual	Comment	Reference
B	?	-	HIS	DELETION	UNP O16025
B	43	GLY	ASN	ENGINEERED MUTATION	UNP O16025
B	44	SER	ASP	ENGINEERED MUTATION	UNP O16025
B	409	ILE	VAL	CONFLICT	UNP O16025
B	590	ILE	VAL	CONFLICT	UNP O16025
C	-2	MET	-	EXPRESSION TAG	UNP O16025
C	-1	HIS	-	EXPRESSION TAG	UNP O16025
C	0	HIS	-	EXPRESSION TAG	UNP O16025
C	1	HIS	-	EXPRESSION TAG	UNP O16025
C	2	HIS	-	EXPRESSION TAG	UNP O16025
C	3	HIS	-	EXPRESSION TAG	UNP O16025
C	?	-	TRP	DELETION	UNP O16025
C	?	-	PHE	DELETION	UNP O16025
C	?	-	HIS	DELETION	UNP O16025
C	43	GLY	ASN	ENGINEERED MUTATION	UNP O16025
C	44	SER	ASP	ENGINEERED MUTATION	UNP O16025
C	409	ILE	VAL	CONFLICT	UNP O16025
C	590	ILE	VAL	CONFLICT	UNP O16025
D	-2	MET	-	EXPRESSION TAG	UNP O16025
D	-1	HIS	-	EXPRESSION TAG	UNP O16025
D	0	HIS	-	EXPRESSION TAG	UNP O16025
D	1	HIS	-	EXPRESSION TAG	UNP O16025
D	2	HIS	-	EXPRESSION TAG	UNP O16025
D	3	HIS	-	EXPRESSION TAG	UNP O16025
D	?	-	TRP	DELETION	UNP O16025
D	?	-	PHE	DELETION	UNP O16025
D	?	-	HIS	DELETION	UNP O16025
D	43	GLY	ASN	ENGINEERED MUTATION	UNP O16025
D	44	SER	ASP	ENGINEERED MUTATION	UNP O16025
D	409	ILE	VAL	CONFLICT	UNP O16025
D	590	ILE	VAL	CONFLICT	UNP O16025

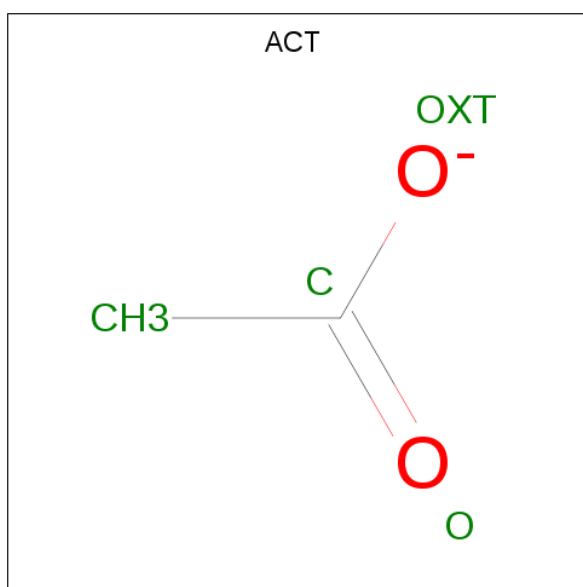
- Molecule 2 is FE (II) ION (three-letter code: FE2) (formula: Fe).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	B	1	Total Fe 1 1	0	0
2	A	1	Total Fe 1 1	0	0
2	D	1	Total Fe 1 1	0	0
2	C	1	Total Fe 1 1	0	0

- Molecule 3 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total 1	Ca 1	0	0
3	A	3	Total 3	Ca 3	0	0
3	D	1	Total 1	Ca 1	0	0
3	C	3	Total 3	Ca 3	0	0

- Molecule 4 is ACETATE ION (three-letter code: ACT) (formula: C₂H₃O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total 4	C 2	O 2	0	0
4	A	1	Total 4	C 2	O 2	0	0
4	A	1	Total 4	C 2	O 2	0	0
4	A	1	Total 4	C 2	O 2	0	0
4	A	1	Total 4	C 2	O 2	0	0
4	A	1	Total 4	C 2	O 2	0	0
4	A	1	Total 4	C 2	O 2	0	0

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			4	2	2		
4	A	1	Total	C	O	0	0
			4	2	2		
4	B	1	Total	C	O	0	0
			4	2	2		
4	B	1	Total	C	O	0	0
			4	2	2		
4	B	1	Total	C	O	0	0
			4	2	2		
4	B	1	Total	C	O	0	0
			4	2	2		
4	C	1	Total	C	O	0	0
			4	2	2		
4	C	1	Total	C	O	0	0
			4	2	2		
4	C	1	Total	C	O	0	0
			4	2	2		
4	C	1	Total	C	O	0	0
			4	2	2		
4	C	1	Total	C	O	0	0
			4	2	2		
4	C	1	Total	C	O	0	0
			4	2	2		
4	D	1	Total	C	O	0	0
			4	2	2		
4	D	1	Total	C	O	0	0
			4	2	2		
4	D	1	Total	C	O	0	0
			4	2	2		
4	D	1	Total	C	O	0	0
			4	2	2		
4	D	1	Total	C	O	0	0
			4	2	2		

- Molecule 5 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			6	3	3		
5	A	1	Total	C	O	0	0
			6	3	3		
5	A	1	Total	C	O	0	0
			6	3	3		
5	A	1	Total	C	O	0	0
			6	3	3		
5	B	1	Total	C	O	0	0
			6	3	3		
5	B	1	Total	C	O	0	0
			6	3	3		
5	B	1	Total	C	O	0	0
			6	3	3		
5	B	1	Total	C	O	0	0
			6	3	3		
5	C	1	Total	C	O	0	0
			6	3	3		
5	C	1	Total	C	O	0	0
			6	3	3		
5	C	1	Total	C	O	0	0
			6	3	3		
5	C	1	Total	C	O	0	0
			6	3	3		

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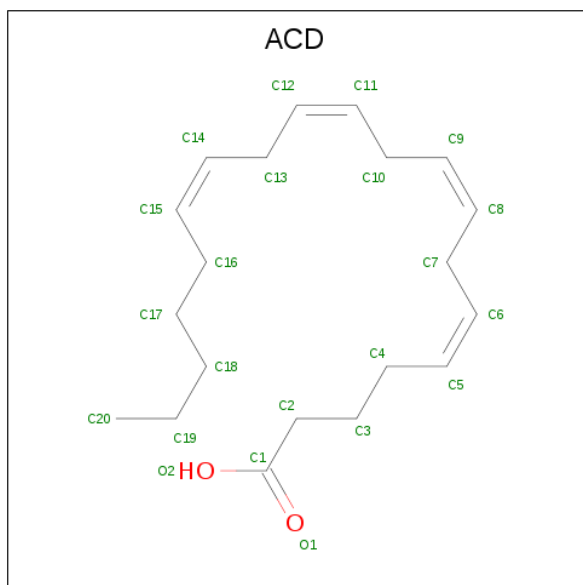
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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	C	1	Total	C	O	0	0
			6	3	3		
5	D	1	Total	C	O	0	0
			6	3	3		
5	D	1	Total	C	O	0	0
			6	3	3		

- Molecule 6 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	B	1	Total	Cl	0	0
			1	1		
6	A	2	Total	Cl	0	0
			2	2		
6	D	1	Total	Cl	0	0
			1	1		
6	C	2	Total	Cl	0	0
			2	2		

- Molecule 7 is ARACHIDONIC ACID (three-letter code: ACD) (formula: C₂₀H₃₂O₂).



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

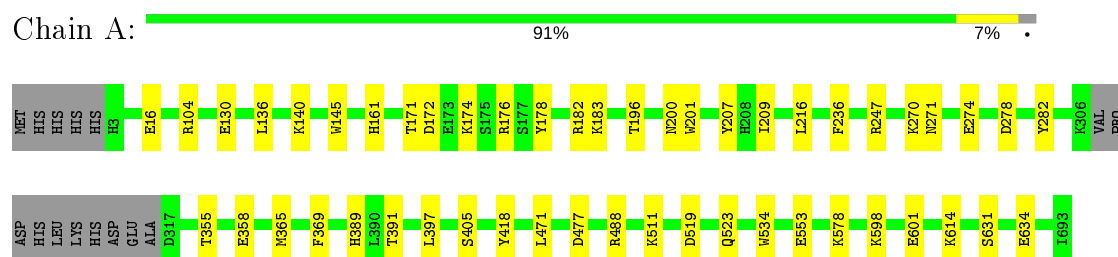
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	555	Total 555	O 555	0	0
8	B	356	Total 356	O 356	0	0
8	C	504	Total 504	O 504	0	0
8	D	380	Total 380	O 380	0	0

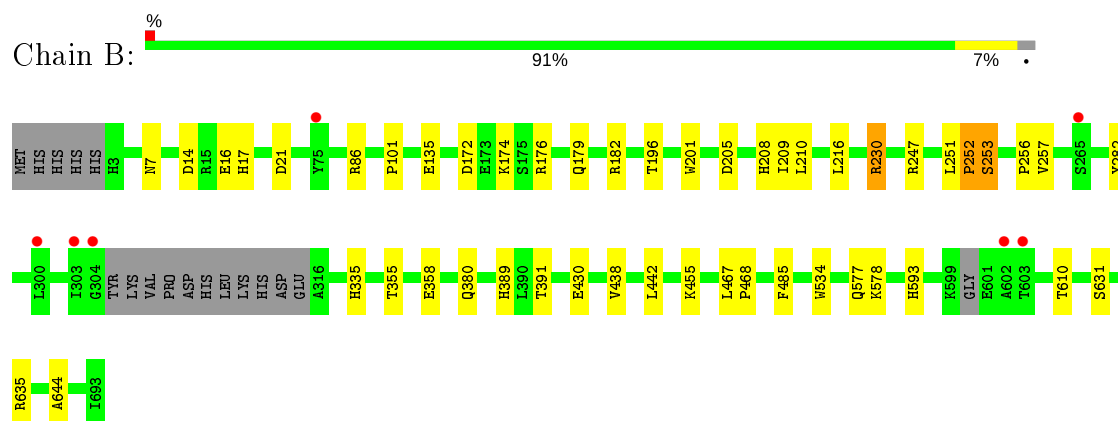
3 Residue-property plots [i](#)

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.

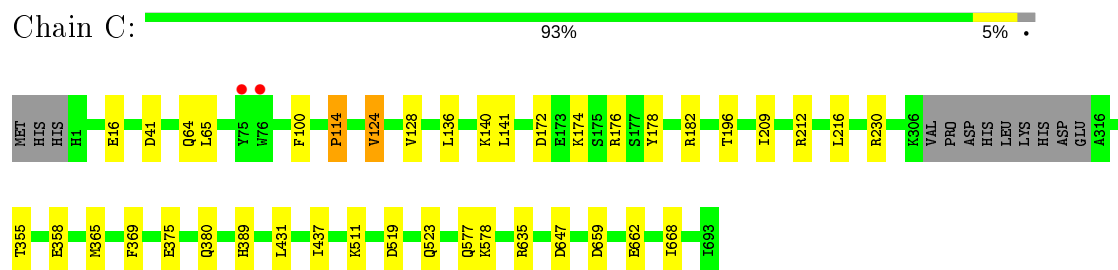
- Molecule 1: Allene oxide synthase-lipoxygenase protein



- Molecule 1: Allene oxide synthase-lipoxygenase protein

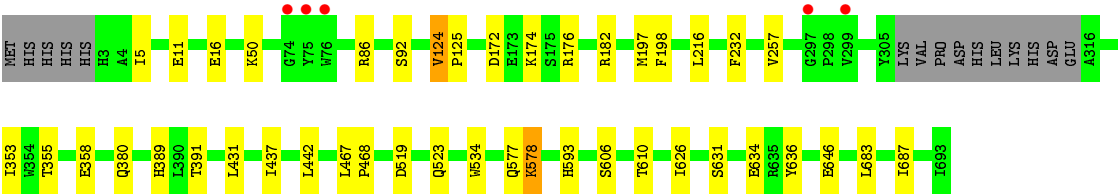


- Molecule 1: Allene oxide synthase-lipoxygenase protein



- Molecule 1: Allene oxide synthase-lipoxygenase protein





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	104.03Å 170.67Å 104.72Å 90.00° 95.36° 90.00°	Depositor
Resolution (Å)	48.42 – 2.00 49.94 – 2.00	Depositor EDS
% Data completeness (in resolution range)	99.5 (48.42-2.00) 92.5 (49.94-2.00)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	0.12	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.66 (at 2.00Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.9_1692)	Depositor
R, R_{free}	0.162 , 0.215 0.164 , 0.216	Depositor DCC
R_{free} test set	1988 reflections (0.82%)	wwPDB-VP
Wilson B-factor (Å ²)	24.0	Xtriage
Anisotropy	0.181	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 58.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.085 for l,-k,h	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	23850	wwPDB-VP
Average B, all atoms (Å ²)	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.89% 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: GOL, ACD, CA, CL, FE2, ACT

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	0.38	0/5713	0.50	0/7769
1	B	0.33	0/5517	0.48	0/7523
1	C	0.36	0/5691	0.49	1/7747 (0.0%)
1	D	0.34	0/5635	0.47	0/7671
All	All	0.36	0/22556	0.48	1/30710 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	65	LEU	CA-CB-CG	5.88	128.81	115.30

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	5510	0	5267	29	0
1	B	5345	0	4956	30	0
1	C	5503	0	5214	24	0
1	D	5455	0	5158	25	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	C	1	0	0	0	0
2	D	1	0	0	0	0
3	A	3	0	0	0	0
3	B	1	0	0	0	0
3	C	3	0	0	0	0
3	D	1	0	0	0	0
4	A	36	0	27	2	0
4	B	16	0	12	1	0
4	C	24	0	18	2	0
4	D	24	0	18	1	0
5	A	30	0	40	1	0
5	B	30	0	40	0	0
5	C	30	0	40	3	0
5	D	12	0	16	0	0
6	A	2	0	0	0	0
6	B	1	0	0	0	0
6	C	2	0	0	1	0
6	D	1	0	0	0	0
7	C	22	0	31	0	0
8	A	555	0	0	2	1
8	B	356	0	0	7	0
8	C	504	0	0	1	1
8	D	380	0	0	3	0
All	All	23850	0	20837	107	1

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 2.

All (107) 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:B:86:ARG:NH2	8:B:1140:HOH:O	2.13	0.81
1:C:216:LEU:HB3	1:C:578:LYS:HD2	1.68	0.74
1:D:16[A]:GLU:OE1	1:D:176:ARG:NH2	2.24	0.70
1:B:182:ARG:NH2	1:B:430:GLU:OE2	2.24	0.70
1:A:477:ASP:OD1	8:A:1326:HOH:O	2.08	0.69
1:B:380:GLN:NE2	1:B:577:GLN:OE1	2.22	0.69
1:B:7:ASN:ND2	8:B:974:HOH:O	2.26	0.68
1:D:380[A]:GLN:NE2	1:D:577:GLN:OE1	2.27	0.67
1:B:135:GLU:OE2	8:B:1067:HOH:O	2.12	0.67
1:A:130:GLU:OE1	8:A:1224:HOH:O	2.14	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:100:PHE:CE2	1:C:114:PRO:HB3	2.32	0.65
1:D:86:ARG:NH1	1:D:646:GLU:OE2	2.30	0.65
1:B:16[A]:GLU:OE1	1:B:176:ARG:NH2	2.30	0.64
1:A:200:ASN:O	5:A:716:GOL:O2	2.15	0.64
1:B:179:GLN:NE2	4:B:706:ACT:OXT	2.24	0.63
1:D:593:HIS:HB2	1:D:610:THR:HG22	1.80	0.63
1:B:216:LEU:HB3	1:B:578:LYS:HD2	1.82	0.61
1:C:659:ASP:OD1	5:C:716:GOL:O3	2.19	0.60
1:A:174[B]:LYS:HD3	1:A:631[B]:SER:HB2	1.85	0.59
1:A:270:LYS:NZ	1:A:278:ASP:OD2	2.28	0.59
1:D:5:ILE:HG12	1:D:92:SER:HB3	1.85	0.58
1:C:230:ARG:HH11	1:C:230:ARG:HG2	1.67	0.57
1:B:16[B]:GLU:OE2	1:B:176:ARG:NH2	2.27	0.57
1:D:216:LEU:HB3	1:D:578:LYS:HG3	1.86	0.56
1:B:17:HIS:ND1	8:B:828:HOH:O	2.17	0.56
1:D:11[B]:GLU:HG2	1:D:50:LYS:HE3	1.88	0.56
1:C:174:LYS:O	1:C:174:LYS:HD3	2.05	0.56
1:D:174:LYS:HD3	1:D:631:SER:HB2	1.88	0.55
1:A:171:THR:N	1:A:418[A]:TYR:OH	2.40	0.55
1:C:375:GLU:OE1	4:C:704:ACT:H1	2.07	0.54
1:B:252:PRO:O	1:B:253:SER:HB3	2.08	0.54
1:B:635:ARG:NH1	8:B:1142:HOH:O	2.42	0.53
1:A:236:PHE:CE1	4:A:704:ACT:H3	2.44	0.53
1:A:104:ARG:NH1	1:A:405[A]:SER:OG	2.42	0.52
1:B:174:LYS:HD3	1:B:631[B]:SER:HB2	1.92	0.52
1:B:201:TRP:HH2	1:B:210:LEU:HD11	1.75	0.51
1:A:355:THR:O	1:A:358:GLU:HG2	2.09	0.51
1:B:16[A]:GLU:HG2	1:B:17:HIS:CD2	2.46	0.51
1:C:647[B]:ASP:OD2	6:C:712:CL:CL	2.66	0.51
1:D:182:ARG:HD2	1:D:626:ILE:HD13	1.93	0.51
1:B:593:HIS:HB2	1:B:610:THR:HG23	1.93	0.51
1:B:174:LYS:HD3	1:B:631[A]:SER:HB2	1.93	0.50
1:D:232:PHE:CD1	4:D:701:ACT:H3	2.46	0.50
1:C:41:ASP:OD1	5:C:710:GOL:H11	2.11	0.50
1:B:455:LYS:NZ	8:B:939:HOH:O	2.43	0.49
1:D:16[B]:GLU:OE1	8:D:1178:HOH:O	2.20	0.49
1:A:201:TRP:HZ3	1:A:207:TYR:CE1	2.32	0.48
1:A:178:TYR:CZ	1:A:182[A]:ARG:HD2	2.49	0.47
1:B:205:ASP:HA	1:B:208:HIS:HD2	1.79	0.47
1:D:355:THR:O	1:D:358:GLU:HG2	2.13	0.47
1:C:124:VAL:HG13	1:C:128:VAL:HB	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:161:HIS:ND1	4:A:705:ACT:H3	2.30	0.47
1:B:21:ASP:OD1	8:B:1128:HOH:O	2.20	0.47
1:D:257:VAL:HG22	1:D:353:ILE:HD13	1.97	0.47
1:C:380:GLN:NE2	1:C:577:GLN:OE1	2.31	0.47
1:A:145:TRP:CE3	1:A:397:LEU:HD23	2.50	0.46
1:C:355:THR:O	1:C:358:GLU:HG2	2.15	0.46
1:C:662:GLU:OE1	5:C:716:GOL:O2	2.28	0.46
1:B:247:ARG:HA	1:B:282:TYR:CD2	2.51	0.46
1:A:271[A]:ASN:OD1	1:A:274:GLU:HG3	2.16	0.46
1:B:467:LEU:HB3	1:B:468:PRO:HD3	1.96	0.46
1:D:16[B]:GLU:OE2	1:D:176:ARG:NH2	2.28	0.45
1:A:196:THR:O	1:A:614:LYS:NZ	2.43	0.45
1:C:519:ASP:O	1:C:523:GLN:HG2	2.16	0.45
1:C:196:THR:HG22	1:C:209:ILE:HD13	1.97	0.45
1:C:178:TYR:CZ	1:C:182:ARG:HD2	2.52	0.45
1:A:553[A]:GLU:CD	1:A:553[A]:GLU:H	2.21	0.45
1:D:606:SER:O	1:D:610:THR:HG23	2.16	0.45
1:A:216:LEU:HB3	1:A:578:LYS:HG3	2.00	0.44
1:B:251:LEU:HD12	1:B:251:LEU:H	1.83	0.44
1:C:365:MET:HG3	1:C:369:PHE:CE2	2.52	0.44
1:D:431:LEU:HD12	1:D:437:ILE:HB	2.00	0.44
1:A:247:ARG:HA	1:A:282:TYR:CD2	2.53	0.44
1:A:391:THR:HB	1:A:534:TRP:CZ2	2.52	0.43
1:D:634[B]:GLU:OE2	8:D:818:HOH:O	2.09	0.43
1:B:391:THR:HB	1:B:534:TRP:CZ2	2.53	0.43
1:D:467:LEU:HB3	1:D:468:PRO:HD3	1.99	0.43
1:C:511:LYS:HA	1:C:511:LYS:HD3	1.76	0.43
1:A:471:LEU:HD13	1:A:488:ARG:HG3	2.01	0.43
1:C:431:LEU:HD12	1:C:437:ILE:HB	2.01	0.43
1:A:16:GLU:OE1	1:A:176:ARG:NH2	2.45	0.42
1:C:635:ARG:NH1	8:C:1281:HOH:O	2.52	0.42
1:A:136:LEU:O	1:A:140:LYS:HG2	2.18	0.42
1:A:519:ASP:O	1:A:523:GLN:HG2	2.20	0.42
1:D:124:VAL:HG22	1:D:125:PRO:HD2	2.02	0.42
1:D:634[B]:GLU:HG2	1:D:636:TYR:CZ	2.54	0.42
1:B:196:THR:HG22	1:B:209:ILE:HD13	2.00	0.42
1:B:209:ILE:HD12	1:C:212:ARG:CZ	2.50	0.42
1:A:365:MET:HG3	1:A:369:PHE:CE2	2.56	0.41
1:B:438:VAL:HG13	1:B:442:LEU:HD12	2.01	0.41
1:C:64:GLN:O	1:C:114:PRO:HG3	2.20	0.41
1:D:519:ASP:O	1:D:523:GLN:HG2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:511:LYS:HA	1:A:511:LYS:HD3	1.74	0.41
1:C:136:LEU:O	1:C:140:LYS:HG2	2.20	0.41
1:B:230:ARG:HG3	1:B:335:HIS:HB3	2.02	0.41
1:C:668:ILE:HG13	4:C:718:ACT:H3	2.02	0.41
1:A:209:ILE:HD12	1:A:209:ILE:HA	1.84	0.41
1:D:683:LEU:O	1:D:687:ILE:HG13	2.21	0.41
1:B:101:PRO:HB2	1:B:644:ALA:HB1	2.03	0.41
1:D:197:MET:HG2	1:D:198:PHE:CE1	2.56	0.41
1:A:183:LYS:HE2	1:A:183:LYS:HB3	1.86	0.41
1:C:16[B]:GLU:CD	1:C:176:ARG:HH22	2.24	0.41
1:D:197:MET:HA	8:D:930:HOH:O	2.21	0.41
1:B:355:THR:O	1:B:358:GLU:HG2	2.21	0.40
1:A:174[A]:LYS:NZ	1:A:634[A]:GLU:OE1	2.40	0.40
1:A:598:LYS:HE2	1:A:601:GLU:OE2	2.21	0.40
1:D:391:THR:HB	1:D:534:TRP:CZ2	2.57	0.40

All (1) 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)
8:A:1318:HOH:O	8:C:1275:HOH:O[2_556]	2.13	0.07

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	694/696 (100%)	670 (96%)	23 (3%)	1 (0%)	51 49
1	B	683/696 (98%)	659 (96%)	19 (3%)	5 (1%)	22 16
1	C	694/696 (100%)	671 (97%)	21 (3%)	2 (0%)	41 37
1	D	690/696 (99%)	669 (97%)	20 (3%)	1 (0%)	51 49

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	2761/2784 (99%)	2669 (97%)	83 (3%)	9 (0%)	41	37

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	253	SER
1	B	256	PRO
1	C	389	HIS
1	B	257	VAL
1	B	389	HIS
1	A	389	HIS
1	B	252	PRO
1	D	389	HIS
1	C	114	PRO

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	586/602 (97%)	585 (100%)	1 (0%)	93	95
1	B	545/602 (90%)	541 (99%)	4 (1%)	84	88
1	C	580/602 (96%)	577 (100%)	3 (0%)	88	92
1	D	569/602 (94%)	565 (99%)	4 (1%)	84	88
All	All	2280/2408 (95%)	2268 (100%)	12 (0%)	88	92

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	172	ASP
1	B	14	ASP
1	B	172	ASP
1	B	230	ARG
1	B	485	PHE
1	C	124	VAL

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Mol	Chain	Res	Type
1	C	141	LEU
1	C	172	ASP
1	D	124	VAL
1	D	172	ASP
1	D	442	LEU
1	D	578	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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](#)

Of 61 ligands modelled in this entry, 18 are monoatomic - leaving 43 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	$\# Z > 2$
5	GOL	B	707	-	5,5,5	0.32	0	5,5,5	0.22	0
4	ACT	A	707	-	1,3,3	1.51	0	0,3,3	0.00	-
4	ACT	C	707	-	1,3,3	1.10	0	0,3,3	0.00	-
5	GOL	C	711	-	5,5,5	0.40	0	5,5,5	0.39	0
5	GOL	A	712	-	5,5,5	0.28	0	5,5,5	0.30	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	GOL	D	706	-	5,5,5	0.42	0	5,5,5	0.46	0
5	GOL	A	709	-	5,5,5	0.37	0	5,5,5	0.59	0
5	GOL	A	711	-	5,5,5	0.37	0	5,5,5	0.55	0
7	ACD	C	715	-	18,21,21	0.31	0	17,21,21	0.49	0
5	GOL	B	708	-	5,5,5	0.31	0	5,5,5	0.34	0
5	GOL	C	716	-	5,5,5	0.38	0	5,5,5	0.72	0
4	ACT	D	701	-	1,3,3	0.24	0	0,3,3	0.00	-
4	ACT	C	704	-	1,3,3	0.13	0	0,3,3	0.00	-
4	ACT	A	717	-	1,3,3	1.14	0	0,3,3	0.00	-
4	ACT	A	708	-	1,3,3	1.17	0	0,3,3	0.00	-
5	GOL	C	710	-	5,5,5	0.33	0	5,5,5	0.42	0
5	GOL	A	710	-	5,5,5	0.38	0	5,5,5	0.30	0
4	ACT	A	718	-	1,3,3	1.88	0	0,3,3	0.00	-
4	ACT	D	704	-	1,3,3	1.20	0	0,3,3	0.00	-
4	ACT	C	706	-	1,3,3	1.52	0	0,3,3	0.00	-
4	ACT	C	708	-	1,3,3	0.93	0	0,3,3	0.00	-
4	ACT	B	705	-	1,3,3	0.82	0	0,3,3	0.00	-
4	ACT	C	705	-	1,3,3	1.61	0	0,3,3	0.00	-
5	GOL	B	712	-	5,5,5	0.33	0	5,5,5	0.53	0
5	GOL	C	717	-	5,5,5	0.45	0	5,5,5	0.41	0
5	GOL	C	709	-	5,5,5	0.39	0	5,5,5	0.38	0
5	GOL	B	711	-	5,5,5	0.30	0	5,5,5	0.52	0
4	ACT	B	703	-	1,3,3	1.05	0	0,3,3	0.00	-
4	ACT	D	710	-	1,3,3	1.44	0	0,3,3	0.00	-
5	GOL	B	710	-	5,5,5	0.34	0	5,5,5	0.94	0
4	ACT	C	718	-	1,3,3	1.35	0	0,3,3	0.00	-
4	ACT	A	706	-	1,3,3	1.06	0	0,3,3	0.00	-
4	ACT	B	704	-	1,3,3	1.54	0	0,3,3	0.00	-
4	ACT	D	709	-	1,3,3	1.07	0	0,3,3	0.00	-
4	ACT	A	720	-	1,3,3	0.43	0	0,3,3	0.00	-
5	GOL	A	716	-	5,5,5	0.37	0	5,5,5	0.60	0
4	ACT	D	705	-	1,3,3	1.31	0	0,3,3	0.00	-
4	ACT	A	705	-	1,3,3	1.11	0	0,3,3	0.00	-
4	ACT	D	711	-	1,3,3	1.44	0	0,3,3	0.00	-
4	ACT	A	704	-	1,3,3	0.27	0	0,3,3	0.00	-
4	ACT	B	706	-	1,3,3	1.28	0	0,3,3	0.00	-
4	ACT	A	719	-	1,3,3	1.44	0	0,3,3	0.00	-
5	GOL	D	708	-	5,5,5	0.49	0	5,5,5	0.18	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
5	GOL	B	707	-	-	0/4/4/4	-
5	GOL	C	710	-	-	2/4/4/4	-
7	ACD	C	715	-	-	8/17/19/19	-
5	GOL	A	710	-	-	0/4/4/4	-
5	GOL	B	710	-	-	2/4/4/4	-
5	GOL	C	709	-	-	0/4/4/4	-
5	GOL	C	711	-	-	0/4/4/4	-
5	GOL	A	716	-	-	3/4/4/4	-
5	GOL	A	711	-	-	1/4/4/4	-
5	GOL	C	716	-	-	2/4/4/4	-
5	GOL	A	712	-	-	2/4/4/4	-
5	GOL	B	712	-	-	4/4/4/4	-
5	GOL	B	708	-	-	4/4/4/4	-
5	GOL	A	709	-	-	1/4/4/4	-
5	GOL	C	717	-	-	0/4/4/4	-
5	GOL	D	706	-	-	2/4/4/4	-
5	GOL	B	711	-	-	2/4/4/4	-
5	GOL	D	708	-	-	4/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (37) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	712	GOL	O1-C1-C2-C3
7	C	715	ACD	C1-C2-C3-C4
5	B	708	GOL	C1-C2-C3-O3
5	B	712	GOL	O1-C1-C2-C3
5	B	711	GOL	O1-C1-C2-C3
5	A	716	GOL	O1-C1-C2-C3
5	D	708	GOL	O1-C1-C2-C3
5	D	708	GOL	O2-C2-C3-O3
5	C	716	GOL	O1-C1-C2-C3
5	C	710	GOL	C1-C2-C3-O3
5	B	712	GOL	C1-C2-C3-O3
5	B	710	GOL	O1-C1-C2-C3
5	D	708	GOL	C1-C2-C3-O3
5	A	712	GOL	O1-C1-C2-O2

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Mol	Chain	Res	Type	Atoms
5	C	716	GOL	O1-C1-C2-O2
5	B	712	GOL	O1-C1-C2-O2
5	B	711	GOL	O1-C1-C2-O2
5	A	716	GOL	O1-C1-C2-O2
5	B	708	GOL	O2-C2-C3-O3
5	D	708	GOL	O1-C1-C2-O2
7	C	715	ACD	C17-C18-C19-C20
7	C	715	ACD	C5-C6-C7-C8
7	C	715	ACD	C12-C13-C14-C15
5	A	716	GOL	O2-C2-C3-O3
5	D	706	GOL	C1-C2-C3-O3
5	A	711	GOL	O1-C1-C2-O2
5	C	710	GOL	O2-C2-C3-O3
7	C	715	ACD	C6-C7-C8-C9
7	C	715	ACD	C11-C10-C9-C8
7	C	715	ACD	C9-C10-C11-C12
5	A	709	GOL	O1-C1-C2-O2
5	B	708	GOL	O1-C1-C2-C3
5	B	712	GOL	O2-C2-C3-O3
5	B	710	GOL	O1-C1-C2-O2
7	C	715	ACD	C14-C15-C16-C17
5	B	708	GOL	O1-C1-C2-O2
5	D	706	GOL	O2-C2-C3-O3

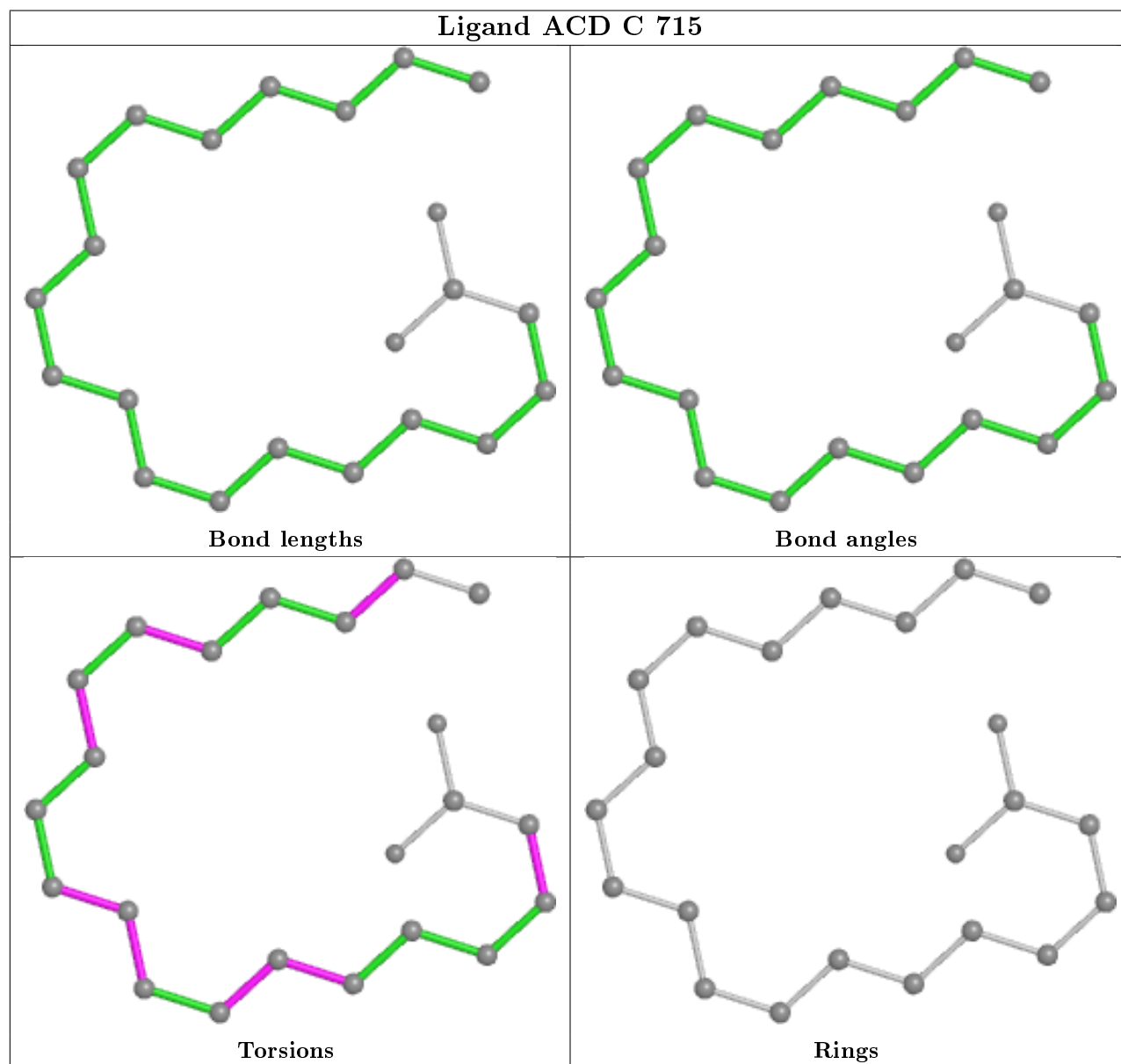
There are no ring outliers.

9 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	C	716	GOL	2	0
4	D	701	ACT	1	0
4	C	704	ACT	1	0
5	C	710	GOL	1	0
4	C	718	ACT	1	0
5	A	716	GOL	1	0
4	A	705	ACT	1	0
4	A	704	ACT	1	0
4	B	706	ACT	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 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 ⓘ

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, 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	681/696 (97%)	-0.61	0 100 100	17, 24, 34, 48	115 (16%)
1	B	679/696 (97%)	-0.47	7 (1%) 82 81	19, 31, 56, 70	132 (19%)
1	C	684/696 (98%)	-0.57	2 (0%) 94 93	18, 25, 37, 52	129 (18%)
1	D	681/696 (97%)	-0.57	5 (0%) 87 87	18, 30, 44, 53	165 (24%)
All	All	2725/2784 (97%)	-0.55	14 (0%) 91 90	17, 27, 44, 70	541 (19%)

All (14) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	75	TYR	4.7
1	C	75	TYR	4.0
1	C	76	TRP	3.0
1	B	265	SER	2.6
1	B	300	LEU	2.5
1	B	303	ILE	2.4
1	D	297	GLY	2.3
1	D	76	TRP	2.3
1	B	602	ALA	2.2
1	D	74	GLY	2.1
1	B	75	TYR	2.1
1	B	603	THR	2.1
1	D	299	VAL	2.1
1	B	304	GLY	2.0

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, 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
4	ACT	A	718	4/4	0.79	0.16	23,49,50,57	0
5	GOL	B	712	6/6	0.81	0.15	37,44,56,64	0
5	GOL	B	710	6/6	0.84	0.12	35,46,50,51	1
4	ACT	D	705	4/4	0.85	0.13	41,43,46,49	2
4	ACT	A	717	4/4	0.86	0.17	25,37,46,49	0
4	ACT	D	710	4/4	0.86	0.16	34,43,44,50	0
4	ACT	A	719	4/4	0.87	0.17	41,54,55,63	0
5	GOL	D	708	6/6	0.87	0.14	33,43,55,59	1
4	ACT	C	707	4/4	0.88	0.14	31,33,34,40	2
4	ACT	B	704	4/4	0.88	0.20	34,43,44,47	1
4	ACT	A	720	4/4	0.88	0.20	37,41,44,47	2
7	ACD	C	715	22/22	0.89	0.14	29,36,51,55	0
4	ACT	C	708	4/4	0.89	0.14	34,35,37,42	1
5	GOL	B	711	6/6	0.90	0.14	46,47,51,52	2
5	GOL	C	717	6/6	0.90	0.15	36,52,63,68	0
5	GOL	B	708	6/6	0.91	0.12	35,39,39,40	5
4	ACT	D	711	4/4	0.91	0.14	43,48,50,59	0
4	ACT	D	701	4/4	0.92	0.14	31,39,40,41	0
4	ACT	A	707	4/4	0.92	0.22	30,34,38,43	2
4	ACT	A	704	4/4	0.92	0.15	26,30,31,33	1
4	ACT	A	708	4/4	0.92	0.16	30,32,35,35	3
5	GOL	C	716	6/6	0.92	0.11	38,49,50,51	0
5	GOL	C	710	6/6	0.93	0.12	37,40,45,49	2
6	CL	A	714	1/1	0.93	0.06	35,35,35,35	1
6	CL	C	712	1/1	0.93	0.09	38,38,38,38	1
4	ACT	B	705	4/4	0.94	0.14	32,33,37,38	3
4	ACT	C	704	4/4	0.94	0.14	33,33,33,34	0
4	ACT	B	703	4/4	0.94	0.12	35,40,41,42	1
5	GOL	C	711	6/6	0.94	0.12	30,34,37,40	3
4	ACT	C	706	4/4	0.95	0.19	26,34,38,41	2
4	ACT	C	705	4/4	0.95	0.14	30,40,44,44	1
5	GOL	A	716	6/6	0.95	0.11	26,40,44,44	2

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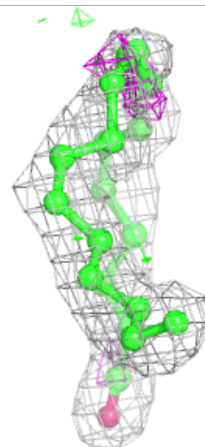
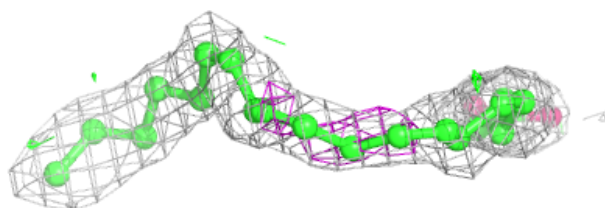
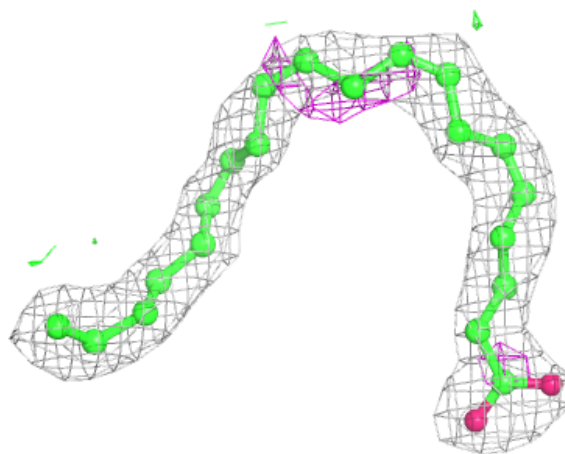
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
5	GOL	A	709	6/6	0.95	0.10	27,28,34,37	4
4	ACT	C	718	4/4	0.96	0.10	35,37,40,41	3
4	ACT	A	705	4/4	0.96	0.12	44,46,47,48	0
5	GOL	A	711	6/6	0.96	0.16	26,30,35,36	2
4	ACT	D	709	4/4	0.96	0.11	37,39,41,44	1
5	GOL	A	712	6/6	0.96	0.32	23,28,30,31	6
5	GOL	B	707	6/6	0.96	0.11	26,28,30,31	3
4	ACT	D	704	4/4	0.97	0.11	36,36,37,41	3
5	GOL	C	709	6/6	0.97	0.09	26,28,32,33	3
4	ACT	A	706	4/4	0.97	0.09	30,32,36,39	4
4	ACT	B	706	4/4	0.97	0.09	43,44,46,46	1
5	GOL	A	710	6/6	0.97	0.12	28,30,35,36	1
5	GOL	D	706	6/6	0.97	0.11	27,29,32,33	2
3	CA	C	714	1/1	0.99	0.06	23,23,23,23	0
6	CL	A	713	1/1	0.99	0.07	25,25,25,25	0
6	CL	D	707	1/1	0.99	0.10	29,29,29,29	0
3	CA	D	703	1/1	0.99	0.05	25,25,25,25	0
3	CA	B	702	1/1	1.00	0.04	25,25,25,25	0
3	CA	A	715	1/1	1.00	0.05	23,23,23,23	0
3	CA	A	703	1/1	1.00	0.04	24,24,24,24	0
3	CA	A	702	1/1	1.00	0.06	25,25,25,25	0
2	FE2	C	701	1/1	1.00	0.12	22,22,22,22	0
2	FE2	B	701	1/1	1.00	0.10	26,26,26,26	0
6	CL	C	713	1/1	1.00	0.06	26,26,26,26	0
6	CL	B	709	1/1	1.00	0.08	31,31,31,31	0
2	FE2	D	702	1/1	1.00	0.11	24,24,24,24	0
3	CA	C	702	1/1	1.00	0.06	26,26,26,26	0
2	FE2	A	701	1/1	1.00	0.11	22,22,22,22	0
3	CA	C	703	1/1	1.00	0.05	23,23,23,23	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 ACD C 715:

$2mF_o-DF_c$ (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.