



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 14, 2020 – 03:08 pm GMT

PDB ID : 6TXL
Title : Crystal structure of thermotoga maritima E65A Ferritin
Deposited on : 2020-01-14
Resolution : 2.10 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report.

This report is produced by the wwPDB biocuration pipeline after annotation of the structure.

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 : 1.8.0 (224370), CSD as540be (2019)
Xtriage (Phenix) : 1.13
EDS : 2.7
buster-report : 1.1.7 (2018)
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)
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) : 2.7

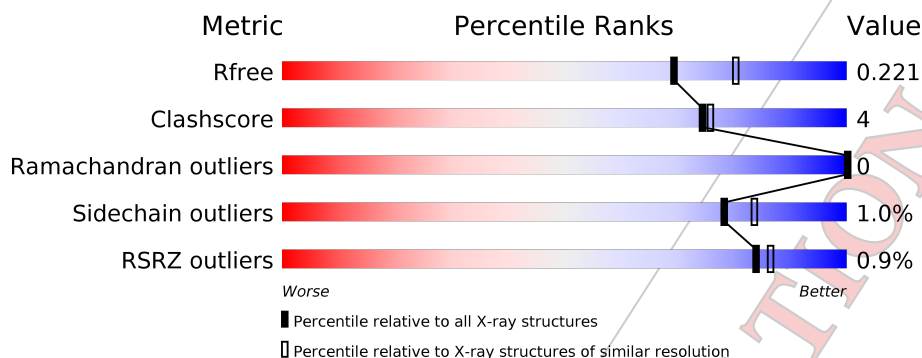
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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}	111664	4608 (2.10-2.10)
Clashscore	122126	5109 (2.10-2.10)
Ramachandran outliers	120053	5059 (2.10-2.10)
Sidechain outliers	120020	5060 (2.10-2.10)
RSRZ outliers	108989	4497 (2.10-2.10)

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	164	<div> <div>92%</div> <div>8%</div> </div>
1	B	164	<div> <div>93%</div> <div>7%</div> </div>
1	C	164	<div> <div>88%</div> <div>10%</div> </div>
1	D	164	<div> <div>93%</div> <div>7%</div> </div>
1	E	164	<div> <div>96%</div> <div>.</div> </div>
1	F	164	<div> <div>90%</div> <div>10%</div> </div>

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Mol	Chain	Length	Quality of chain
1	G	164	<div> <div></div> <div>92%</div> <div>8%</div> </div>
1	H	164	<div> <div></div> <div>85%</div> <div>15%</div> </div>

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
3	SO4	F	202	-	-	X	-

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 11921 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 Ferritin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	164	Total	C	N	O	S	0	2	0
			1379	882	225	266	6			
1	B	164	Total	C	N	O	S	0	7	0
			1413	905	233	269	6			
1	C	164	Total	C	N	O	S	0	4	0
			1391	890	226	269	6			
1	D	164	Total	C	N	O	S	0	3	0
			1387	888	229	264	6			
1	E	164	Total	C	N	O	S	0	5	0
			1396	894	229	267	6			
1	F	164	Total	C	N	O	S	0	3	0
			1385	886	226	267	6			
1	G	164	Total	C	N	O	S	0	2	0
			1382	884	227	265	6			
1	H	164	Total	C	N	O	S	0	6	0
			1404	899	233	266	6			

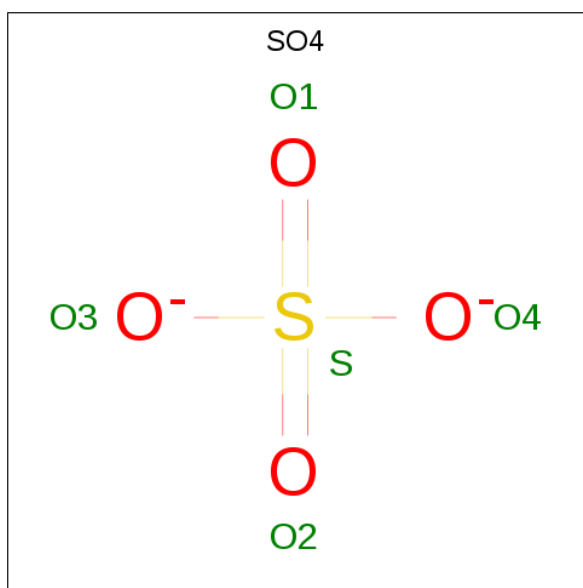
There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	65	GLN	GLU	engineered mutation	UNP Q9X0L2
B	65	GLN	GLU	engineered mutation	UNP Q9X0L2
C	65	GLN	GLU	engineered mutation	UNP Q9X0L2
D	65	GLN	GLU	engineered mutation	UNP Q9X0L2
E	65	GLN	GLU	engineered mutation	UNP Q9X0L2
F	65	GLN	GLU	engineered mutation	UNP Q9X0L2
G	65	GLN	GLU	engineered mutation	UNP Q9X0L2
H	65	GLN	GLU	engineered mutation	UNP Q9X0L2

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

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	G	1	Total Fe 1 1	0	0
2	D	1	Total Fe 1 1	0	0
2	E	1	Total Fe 1 1	0	0
2	H	1	Total Fe 1 1	0	0
2	B	1	Total Fe 1 1	0	0
2	C	1	Total Fe 1 1	0	0
2	A	1	Total Fe 1 1	0	0
2	F	1	Total Fe 1 1	0	0

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



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

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	C	1	Total	O	S	0	0
			5	4	1		
3	C	1	Total	O	S	0	0
			5	4	1		
3	C	1	Total	O	S	0	0
			5	4	1		
3	D	1	Total	O	S	0	0
			5	4	1		
3	D	1	Total	O	S	0	0
			5	4	1		
3	D	1	Total	O	S	0	0
			5	4	1		
3	D	1	Total	O	S	0	0
			5	4	1		
3	E	1	Total	O	S	0	0
			5	4	1		
3	E	1	Total	O	S	0	0
			5	4	1		
3	F	1	Total	O	S	0	0
			5	4	1		
3	F	1	Total	O	S	0	0
			5	4	1		
3	G	1	Total	O	S	0	0
			5	4	1		
3	G	1	Total	O	S	0	0
			5	4	1		
3	G	1	Total	O	S	0	0
			5	4	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	H	1	Total	O	S	0	0
			5	4	1		
3	H	1	Total	O	S	0	0
			5	4	1		

- Molecule 4 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



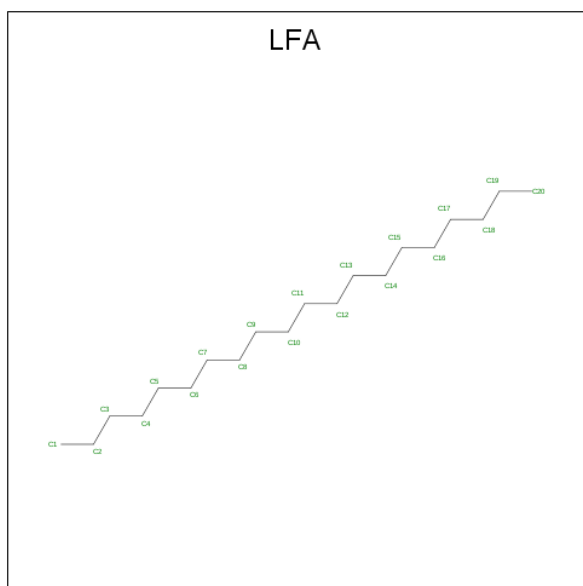
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			6	3	3		
4	A	1	Total	C	O	0	0
			6	3	3		
4	A	1	Total	C	O	0	0
			6	3	3		
4	B	1	Total	C	O	0	0
			6	3	3		
4	B	1	Total	C	O	0	0
			6	3	3		
4	C	1	Total	C	O	0	0
			6	3	3		
4	C	1	Total	C	O	0	0
			6	3	3		
4	D	1	Total	C	O	0	0
			6	3	3		
4	D	1	Total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

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	E	1	Total	C	O	0	0
			6	3	3		
4	F	1	Total	C	O	0	0
			6	3	3		
4	G	1	Total	C	O	0	0
			6	3	3		
4	G	1	Total	C	O	0	0
			6	3	3		
4	H	1	Total	C	O	0	0
			6	3	3		
4	H	1	Total	C	O	0	0
			6	3	3		

- Molecule 5 is EICOSANE (three-letter code: LFA) (formula: $C_{20}H_{42}$).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	1	Total	C	0	0
			20	20		
5	C	1	Total	C	0	0
			20	20		
5	E	1	Total	C	0	0
			20	20		
5	H	1	Total	C	0	0
			20	20		

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	89	Total	O	0	0
			89	89		
6	B	91	Total	O	0	0
			91	91		
6	C	48	Total	O	0	0
			48	48		
6	D	68	Total	O	0	0
			68	68		
6	E	74	Total	O	0	0
			74	74		
6	F	56	Total	O	0	0
			56	56		
6	G	31	Total	O	0	0
			31	31		
6	H	14	Total	O	0	0
			14	14		

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.

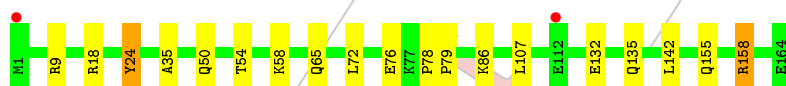
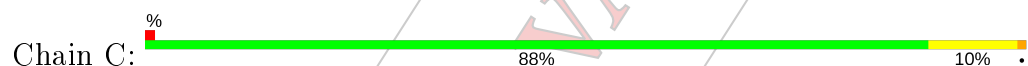
- Molecule 1: Ferritin



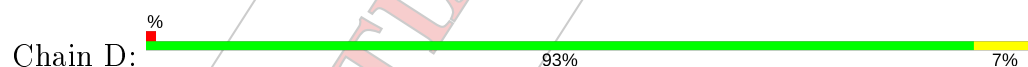
- Molecule 1: Ferritin



- Molecule 1: Ferritin



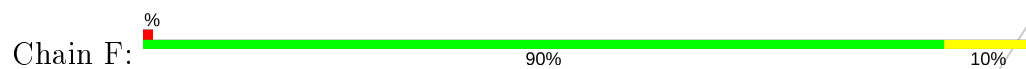
- Molecule 1: Ferritin



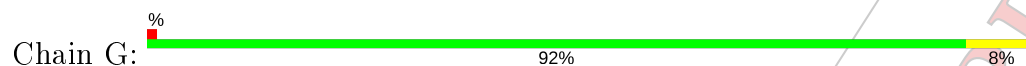
- Molecule 1: Ferritin



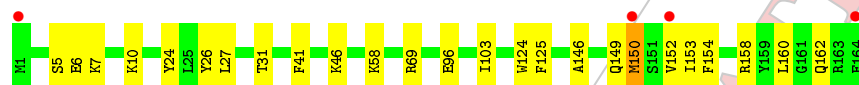
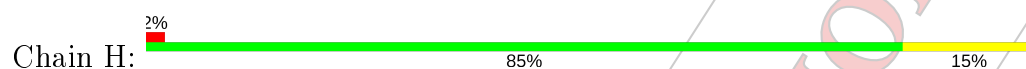
- Molecule 1: Ferritin



• Molecule 1: Ferritin



• Molecule 1: Ferritin



4 Data and refinement statistics

Property	Value	Source
Space group	H 3 2	Depositor
Cell constants a, b, c, α , β , γ	176.22Å 176.22Å 355.05Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	26.88 – 2.10 49.12 – 2.10	Depositor EDS
% Data completeness (in resolution range)	99.8 (26.88-2.10) 88.5 (49.12-2.10)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.32 (at 2.10Å)	Xtriage
Refinement program	PHENIX 1.15.1 3469	Depositor
R, R_{free}	0.193 , 0.222 0.194 , 0.221	Depositor DCC
R_{free} test set	2100 reflections (1.70%)	wwPDB-VP
Wilson B-factor (Å ²)	38.2	Xtriage
Anisotropy	0.166	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 64.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	11921	wwPDB-VP
Average B, all atoms (Å ²)	66.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.48% of the height of the origin peak. No significant pseudotranslation is detected.*

¹ Intensities estimated from amplitudes.

² Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, LFA, FE, SO4

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	0.35	0/1414	0.44	0/1900
1	B	0.37	0/1460	0.45	0/1959
1	C	0.33	0/1431	0.45	0/1920
1	D	0.34	0/1425	0.43	0/1913
1	E	0.32	0/1440	0.43	0/1933
1	F	0.33	0/1423	0.42	0/1912
1	G	0.30	0/1414	0.43	0/1899
1	H	0.39	1/1451 (0.1%)	0.55	2/1947 (0.1%)
All	All	0.34	1/11458 (0.0%)	0.45	2/15383 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	H	150	MET	CB-CG	6.62	1.72	1.51

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	H	150	MET	CA-CB-CG	-6.99	101.41	113.30
1	H	149	GLN	C-N-CA	-6.03	106.63	121.70

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	1379	0	1335	10	0
1	B	1413	0	1387	10	0
1	C	1391	0	1349	11	0
1	D	1387	0	1355	12	0
1	E	1396	0	1366	5	0
1	F	1385	0	1343	13	0
1	G	1382	0	1340	14	0
1	H	1404	0	1381	17	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
2	E	1	0	0	0	0
2	F	1	0	0	0	0
2	G	1	0	0	0	0
2	H	1	0	0	0	0
3	A	25	0	0	2	0
3	B	30	0	0	0	0
3	C	15	0	0	0	0
3	D	20	0	0	0	0
3	E	10	0	0	0	0
3	F	10	0	0	3	0
3	G	15	0	0	1	0
3	H	10	0	0	1	0
4	A	18	0	24	0	0
4	B	12	0	16	0	0
4	C	12	0	16	0	0
4	D	12	0	16	1	0
4	E	6	0	8	0	0
4	F	6	0	8	1	0
4	G	12	0	16	3	0
4	H	12	0	16	2	0
5	B	20	0	42	1	0
5	C	20	0	42	1	0
5	E	20	0	42	0	0
5	H	20	0	42	1	0
6	A	89	0	0	1	0
6	B	91	0	0	1	0
6	C	48	0	0	1	0
6	D	68	0	0	2	0
6	E	74	0	0	1	0
6	F	56	0	0	7	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	G	31	0	0	0	0
6	H	14	0	0	1	0
All	All	11921	0	11144	80	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 (80) 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:F:131[A]:GLU:OE2	6:F:301:HOH:O	1.97	0.81
1:D:66[B]:ARG:NH2	1:D:115:ASP:OD1	2.20	0.74
1:D:66[B]:ARG:HH21	1:D:117:ALA:HB3	1.55	0.71
1:H:46:LYS:HB3	5:H:205:LFA:H22	1.74	0.69
1:A:57:MET:HG3	5:B:207:LFA:H32	1.74	0.68
1:F:18:ARG:NH2	6:F:304:HOH:O	2.29	0.66
1:H:69[B]:ARG:NH1	6:H:301:HOH:O	2.25	0.64
3:F:202:SO4:O2	6:F:302:HOH:O	2.11	0.64
1:A:28:SER:HB2	1:B:72:LEU:HD12	1.81	0.63
1:B:50[A]:GLN:NE2	6:B:301:HOH:O	2.33	0.61
1:C:72:LEU:HD12	1:D:28:SER:HB2	1.83	0.60
1:G:75:ILE:HD11	1:H:24:TYR:CZ	2.35	0.60
1:B:141:ASP:OD2	1:B:145:LYS:NZ	2.35	0.59
1:D:50[A]:GLN:OE1	6:D:301:HOH:O	2.18	0.57
1:C:65:GLN:NE2	1:E:131[A]:GLU:OE2	2.33	0.54
1:G:158:ARG:HG3	1:G:158:ARG:HH11	1.73	0.54
1:D:3:VAL:O	1:D:66[B]:ARG:NH1	2.41	0.54
1:H:150:MET:HG2	1:H:153:ILE:HB	1.90	0.53
1:F:98:PHE:CZ	4:F:203:GOL:H12	2.43	0.53
1:F:132:GLU:O	1:F:135:GLN:HG2	2.10	0.52
1:G:98:PHE:HZ	4:G:203:GOL:H32	1.74	0.52
1:C:155:GLN:O	1:C:158:ARG:HG3	2.10	0.51
1:E:72:LEU:HD12	1:F:28:SER:HB2	1.93	0.51
3:F:202:SO4:O4	6:F:303:HOH:O	2.16	0.51
1:H:5:SER:HB2	4:H:204:GOL:H32	1.93	0.51
1:C:142:LEU:HD22	1:H:154:PHE:CZ	2.46	0.50
1:D:3:VAL:HG23	1:D:66[B]:ARG:HD2	1.95	0.49
1:F:1:MET:N	6:F:305:HOH:O	2.45	0.48
1:A:35:ALA:HB2	1:B:69[B]:ARG:HG3	1.96	0.48
1:F:80:SER:N	3:F:204:SO4:O4	2.38	0.48
1:C:50[B]:GLN:NE2	5:C:204:LFA:H182	2.29	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:38:PHE:CE2	1:A:85:ILE:HD11	2.49	0.47
1:C:18:ARG:NH2	6:C:302:HOH:O	2.47	0.47
1:G:98:PHE:CZ	4:G:203:GOL:H12	2.50	0.47
3:A:208:SO4:O2	6:A:301:HOH:O	2.20	0.47
1:C:35:ALA:HB2	1:D:69:ARG:HG3	1.97	0.47
1:E:55:HIS:HE1	6:E:311:HOH:O	1.98	0.46
1:A:81:ASN:OD1	1:B:69[B]:ARG:NH2	2.46	0.46
1:E:15:GLN:HB2	1:E:106:ILE:HD11	1.96	0.46
1:G:35:ALA:HB2	1:H:69[A]:ARG:HG3	1.97	0.46
1:D:18:ARG:NH1	4:D:203:GOL:O2	2.45	0.46
1:H:6:GLU:H	4:H:204:GOL:H11	1.80	0.46
1:A:72:LEU:HD12	1:B:28:SER:HB2	1.98	0.46
1:G:10:LYS:C	1:G:10:LYS:HD3	2.37	0.45
1:C:132:GLU:O	1:C:135[A]:GLN:HG2	2.16	0.45
1:F:15:GLN:HB2	1:F:106:ILE:HD11	2.00	0.44
1:H:158:ARG:O	1:H:162:GLN:HG2	2.17	0.44
1:D:18:ARG:NH2	6:D:305:HOH:O	2.51	0.44
1:H:146:ALA:HA	1:H:152:VAL:HG11	1.98	0.44
1:A:15:GLN:HB2	1:A:106:ILE:HD11	2.00	0.44
1:F:38:PHE:HB3	1:F:41:PHE:HD2	1.83	0.43
1:G:80:SER:N	3:G:205:SO4:O1	2.40	0.43
1:H:27:LEU:O	1:H:31:THR:HG23	2.19	0.43
1:B:66:ARG:HD2	1:B:66:ARG:HA	1.82	0.43
1:G:66:ARG:HA	1:G:66:ARG:HD2	1.82	0.43
1:H:41:PHE:CD1	1:H:160:LEU:HD12	2.54	0.43
1:F:66:ARG:HA	1:F:66:ARG:HD2	1.92	0.43
1:G:35:ALA:HB2	1:H:69[B]:ARG:HG3	2.00	0.43
1:A:80:SER:N	3:A:206:SO4:O3	2.47	0.43
1:D:141:ASP:OD1	1:D:145:LYS:NZ	2.51	0.42
1:C:54:THR:O	1:C:58:LYS:HG3	2.18	0.42
1:G:38:PHE:CE2	1:G:85:ILE:HD11	2.55	0.42
1:G:7:LYS:HB2	1:G:7:LYS:HE2	1.80	0.42
1:H:26:TYR:OH	1:H:96:GLU:OE2	2.29	0.42
1:F:58:LYS:HD3	6:F:355:HOH:O	2.19	0.42
1:G:84:GLY:HA3	4:G:202:GOL:H12	1.99	0.42
1:C:24:TYR:CZ	1:D:75:ILE:HD11	2.55	0.42
1:B:132:GLU:O	1:B:135[B]:GLN:HG2	2.19	0.41
1:H:58:LYS:HE2	1:H:124:TRP:CZ3	2.56	0.41
1:D:66[A]:ARG:HD2	1:D:66[A]:ARG:HA	1.93	0.41
1:G:60:TYR:CE2	1:H:31:THR:HG22	2.56	0.41
1:H:103:ILE:HD13	1:H:125:PHE:HB3	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:78:PRO:C	1:C:79:PRO:N	2.73	0.41
1:A:27:LEU:HG	1:B:72:LEU:HD11	2.03	0.40
1:B:15:GLN:HB2	1:B:106:ILE:HD11	2.03	0.40
1:F:119:VAL:HG13	6:F:353:HOH:O	2.21	0.40
1:E:28:SER:HB2	1:F:72:LEU:HD12	2.04	0.40
1:A:66:ARG:HA	1:A:66:ARG:HD2	1.94	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	164/164 (100%)	164 (100%)	0	0	100	100
1	B	169/164 (103%)	169 (100%)	0	0	100	100
1	C	164/164 (100%)	163 (99%)	1 (1%)	0	100	100
1	D	165/164 (101%)	164 (99%)	1 (1%)	0	100	100
1	E	167/164 (102%)	167 (100%)	0	0	100	100
1	F	165/164 (101%)	164 (99%)	1 (1%)	0	100	100
1	G	164/164 (100%)	163 (99%)	1 (1%)	0	100	100
1	H	168/164 (102%)	167 (99%)	1 (1%)	0	100	100
All	All	1326/1312 (101%)	1321 (100%)	5 (0%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	146/144 (101%)	145 (99%)	1 (1%)	85	89
1	B	151/144 (105%)	147 (97%)	4 (3%)	49	53
1	C	148/144 (103%)	141 (95%)	7 (5%)	29	27
1	D	147/144 (102%)	146 (99%)	1 (1%)	85	89
1	E	149/144 (104%)	149 (100%)	0	100	100
1	F	147/144 (102%)	147 (100%)	0	100	100
1	G	146/144 (101%)	146 (100%)	0	100	100
1	H	150/144 (104%)	147 (98%)	3 (2%)	58	63
All	All	1184/1152 (103%)	1168 (99%)	16 (1%)	78	76

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	111	SER
1	B	69[A]	ARG
1	B	69[B]	ARG
1	B	131[A]	GLU
1	B	131[B]	GLU
1	C	9	ARG
1	C	24	TYR
1	C	76[A]	GLU
1	C	76[B]	GLU
1	C	86	LYS
1	C	107	LEU
1	C	158	ARG
1	D	9	ARG
1	H	7	LYS
1	H	10[A]	LYS
1	H	10[B]	LYS

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

5.3.3 RNA ⓘ

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 54 ligands modelled in this entry, 8 are monoatomic - leaving 46 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	$\# Z > 2$
3	SO4	A	202	-	4,4,4	0.18	0	6,6,6	0.16	0
4	GOL	A	203	-	5,5,5	1.00	0	5,5,5	0.99	0
4	GOL	A	204	-	5,5,5	0.91	0	5,5,5	0.97	0
4	GOL	A	205	-	5,5,5	1.00	0	5,5,5	0.97	0
3	SO4	A	206	-	4,4,4	0.18	0	6,6,6	0.07	0
3	SO4	A	207	-	4,4,4	0.17	0	6,6,6	0.13	0
3	SO4	A	208	-	4,4,4	0.12	0	6,6,6	0.14	0
3	SO4	A	209	-	4,4,4	0.16	0	6,6,6	0.15	0
3	SO4	B	202	-	4,4,4	0.16	0	6,6,6	0.05	0
3	SO4	B	203	-	4,4,4	0.13	0	6,6,6	0.14	0
4	GOL	B	204	-	5,5,5	1.09	0	5,5,5	0.87	0
3	SO4	B	205	-	4,4,4	0.17	0	6,6,6	0.23	0
4	GOL	B	206	-	5,5,5	1.05	0	5,5,5	0.90	0
5	LFA	B	207	-	19,19,19	0.11	0	18,18,18	0.30	0
3	SO4	B	208	-	4,4,4	0.19	0	6,6,6	0.09	0
3	SO4	B	209	-	4,4,4	0.12	0	6,6,6	0.13	0
3	SO4	B	210	-	4,4,4	0.16	0	6,6,6	0.09	0
4	GOL	C	202	-	5,5,5	0.97	0	5,5,5	0.86	0
4	GOL	C	203	-	5,5,5	0.81	0	5,5,5	1.03	0
5	LFA	C	204	-	19,19,19	0.11	0	18,18,18	0.27	0
3	SO4	C	205	-	4,4,4	0.18	0	6,6,6	0.09	0
3	SO4	C	206	-	4,4,4	0.17	0	6,6,6	0.06	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	SO4	C	207	-	4,4,4	0.17	0	6,6,6	0.04	0
3	SO4	D	202	-	4,4,4	0.17	0	6,6,6	0.14	0
4	GOL	D	203	-	5,5,5	1.05	0	5,5,5	0.88	0
4	GOL	D	204	-	5,5,5	1.02	0	5,5,5	0.82	0
3	SO4	D	205	-	4,4,4	0.15	0	6,6,6	0.11	0
3	SO4	D	206	-	4,4,4	0.17	0	6,6,6	0.14	0
3	SO4	D	207	-	4,4,4	0.19	0	6,6,6	0.05	0
3	SO4	E	202	-	4,4,4	0.19	0	6,6,6	0.11	0
4	GOL	E	203	-	5,5,5	0.92	0	5,5,5	1.01	0
5	LFA	E	204	-	19,19,19	0.08	0	18,18,18	0.18	0
3	SO4	E	205	-	4,4,4	0.18	0	6,6,6	0.10	0
3	SO4	F	202	-	4,4,4	0.16	0	6,6,6	0.09	0
4	GOL	F	203	-	5,5,5	1.05	0	5,5,5	0.94	0
3	SO4	F	204	-	4,4,4	0.18	0	6,6,6	0.11	0
4	GOL	G	202	-	5,5,5	0.92	0	5,5,5	1.01	0
4	GOL	G	203	-	5,5,5	1.01	0	5,5,5	0.89	0
3	SO4	G	204	-	4,4,4	0.20	0	6,6,6	0.07	0
3	SO4	G	205	-	4,4,4	0.15	0	6,6,6	0.06	0
3	SO4	G	206	-	4,4,4	0.17	0	6,6,6	0.09	0
3	SO4	H	202	-	4,4,4	0.16	0	6,6,6	0.10	0
4	GOL	H	203	-	5,5,5	1.00	0	5,5,5	0.92	0
4	GOL	H	204	-	5,5,5	0.98	0	5,5,5	0.83	0
5	LFA	H	205	-	19,19,19	0.08	0	18,18,18	0.15	0
3	SO4	H	206	-	4,4,4	0.15	0	6,6,6	0.07	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	GOL	A	203	-	-	4/4/4/4	-
4	GOL	A	204	-	-	2/4/4/4	-
4	GOL	A	205	-	-	1/4/4/4	-
4	GOL	B	204	-	-	1/4/4/4	-
4	GOL	B	206	-	-	2/4/4/4	-
5	LFA	B	207	-	-	2/17/17/17	-
4	GOL	C	202	-	-	2/4/4/4	-
4	GOL	C	203	-	-	2/4/4/4	-
5	LFA	C	204	-	-	1/17/17/17	-
4	GOL	D	203	-	-	1/4/4/4	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	GOL	D	204	-	-	4/4/4/4	-
4	GOL	E	203	-	-	2/4/4/4	-
5	LFA	E	204	-	-	2/17/17/17	-
4	GOL	F	203	-	-	2/4/4/4	-
4	GOL	G	202	-	-	2/4/4/4	-
4	GOL	G	203	-	-	0/4/4/4	-
4	GOL	H	203	-	-	0/4/4/4	-
4	GOL	H	204	-	-	3/4/4/4	-
5	LFA	H	205	-	-	4/17/17/17	-

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
4	E	203	GOL	O1-C1-C2-C3
4	F	203	GOL	C1-C2-C3-O3
4	B	206	GOL	C1-C2-C3-O3
4	G	202	GOL	O1-C1-C2-C3
4	H	204	GOL	C1-C2-C3-O3
4	A	203	GOL	O1-C1-C2-C3
4	A	203	GOL	C1-C2-C3-O3
4	C	202	GOL	O1-C1-C2-C3
4	D	204	GOL	C1-C2-C3-O3
4	C	203	GOL	O1-C1-C2-C3
4	D	204	GOL	O1-C1-C2-C3
4	B	206	GOL	O2-C2-C3-O3
4	A	203	GOL	O1-C1-C2-O2
5	C	204	LFA	C11-C10-C9-C8
4	F	203	GOL	O2-C2-C3-O3
4	G	202	GOL	O1-C1-C2-O2
4	H	204	GOL	O2-C2-C3-O3
4	A	203	GOL	O2-C2-C3-O3
4	C	202	GOL	O1-C1-C2-O2
4	B	204	GOL	O1-C1-C2-C3
4	H	204	GOL	O1-C1-C2-C3
5	E	204	LFA	C10-C11-C12-C13
5	H	205	LFA	C13-C14-C15-C16

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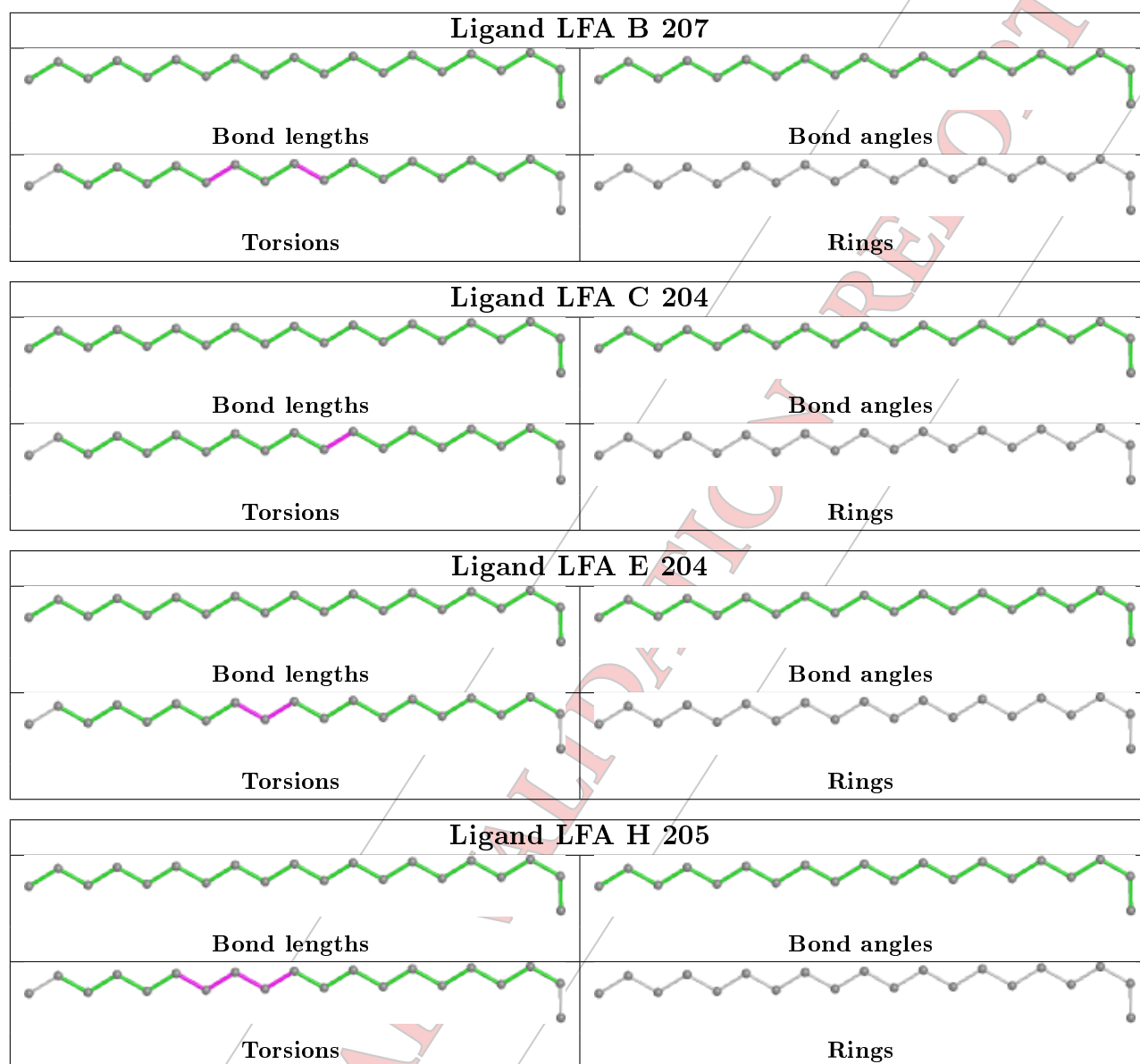
Mol	Chain	Res	Type	Atoms
5	B	207	LFA	C9-C10-C11-C12
4	C	203	GOL	O1-C1-C2-O2
5	B	207	LFA	C12-C13-C14-C15
5	H	205	LFA	C11-C12-C13-C14
5	E	204	LFA	C11-C12-C13-C14
4	E	203	GOL	O1-C1-C2-O2
4	A	204	GOL	O2-C2-C3-O3
4	D	204	GOL	O1-C1-C2-O2
5	H	205	LFA	C12-C13-C14-C15
5	H	205	LFA	C10-C11-C12-C13
4	D	204	GOL	O2-C2-C3-O3
4	D	203	GOL	O2-C2-C3-O3
4	A	204	GOL	C1-C2-C3-O3
4	A	205	GOL	O2-C2-C3-O3

There are no ring outliers.

8 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	207	LFA	1	0
5	C	204	LFA	1	0
4	D	203	GOL	1	0
4	F	203	GOL	1	0
4	G	202	GOL	1	0
4	G	203	GOL	2	0
4	H	204	GOL	2	0
5	H	205	LFA	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 [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	C	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	C	78:PRO	C	79:PRO	N	2.73

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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	164/164 (100%)	-0.31	1 (0%) 89 91	46, 56, 73, 113	0
1	B	164/164 (100%)	-0.37	0 100 100	45, 54, 79, 114	0
1	C	164/164 (100%)	-0.25	2 (1%) 79 82	52, 64, 88, 111	0
1	D	164/164 (100%)	-0.29	1 (0%) 89 91	50, 61, 79, 115	0
1	E	164/164 (100%)	-0.35	1 (0%) 89 91	49, 60, 76, 116	0
1	F	164/164 (100%)	-0.25	2 (1%) 79 82	50, 64, 91, 105	0
1	G	164/164 (100%)	-0.20	1 (0%) 89 91	58, 69, 92, 122	0
1	H	164/164 (100%)	-0.03	4 (2%) 59 64	63, 74, 111, 131	0
All	All	1312/1312 (100%)	-0.26	12 (0%) 84 86	45, 63, 90, 131	0

All (12) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	H	150	MET	4.3
1	C	1	MET	3.2
1	A	1	MET	3.0
1	D	164	GLU	2.8
1	G	1	MET	2.7
1	H	164	GLU	2.6
1	F	154	PHE	2.5
1	H	152	VAL	2.4
1	E	1	MET	2.3
1	F	158	ARG	2.3
1	H	1	MET	2.2
1	C	112[A]	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. 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	GOL	G	203	6/6	0.57	0.25	105,106,107,107	0
4	GOL	H	203	6/6	0.60	0.29	99,101,102,104	0
4	GOL	D	203	6/6	0.62	0.26	104,105,105,106	0
4	GOL	C	203	6/6	0.63	0.28	95,97,97,100	0
4	GOL	C	202	6/6	0.63	0.21	94,95,96,97	0
4	GOL	B	206	6/6	0.69	0.17	87,88,88,88	0
3	SO4	A	209	5/5	0.73	0.25	89,90,90,91	5
4	GOL	H	204	6/6	0.73	0.31	105,105,105,105	0
4	GOL	A	205	6/6	0.74	0.28	92,93,93,94	0
3	SO4	D	207	5/5	0.74	0.29	111,111,112,112	5
3	SO4	A	202	5/5	0.74	0.19	121,121,121,122	0
3	SO4	D	206	5/5	0.74	0.34	82,83,83,84	5
4	GOL	A	203	6/6	0.78	0.19	89,90,90,91	0
3	SO4	G	206	5/5	0.81	0.20	118,118,118,119	5
3	SO4	A	208	5/5	0.82	0.27	80,80,81,82	5
5	LFA	C	204	20/20	0.82	0.22	62,66,75,76	0
3	SO4	G	205	5/5	0.82	0.38	106,106,106,106	5
3	SO4	H	202	5/5	0.82	0.15	117,117,117,117	5
3	SO4	D	202	5/5	0.82	0.15	126,127,127,127	0
3	SO4	B	208	5/5	0.83	0.34	71,71,71,71	5
3	SO4	C	207	5/5	0.84	0.37	115,115,116,116	5
5	LFA	H	205	20/20	0.84	0.16	69,73,83,84	0
4	GOL	F	203	6/6	0.84	0.22	92,92,93,93	0
3	SO4	E	202	5/5	0.85	0.17	92,92,93,93	5
3	SO4	H	206	5/5	0.86	0.32	102,102,102,102	5
3	SO4	F	204	5/5	0.86	0.17	88,88,89,89	5
3	SO4	B	203	5/5	0.86	0.16	101,102,102,102	0

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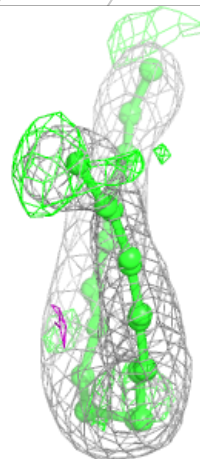
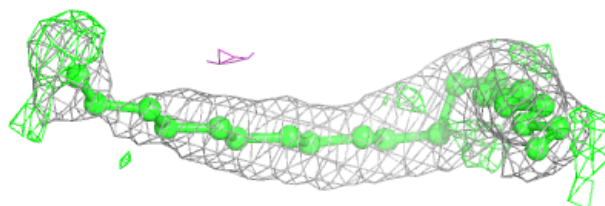
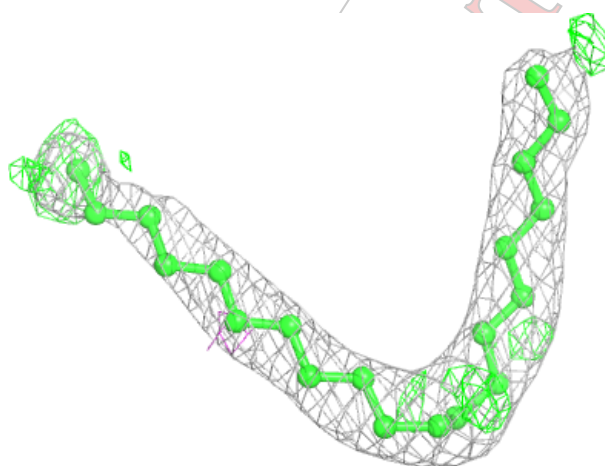
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	SO4	C	205	5/5	0.87	0.20	79,80,80,81	5
5	LFA	E	204	20/20	0.87	0.23	65,69,86,87	0
3	SO4	B	209	5/5	0.88	0.22	70,71,72,74	5
3	SO4	C	206	5/5	0.88	0.26	87,87,88,90	5
4	GOL	A	204	6/6	0.88	0.17	103,104,105,105	0
3	SO4	B	210	5/5	0.89	0.20	132,133,133,133	5
3	SO4	D	205	5/5	0.89	0.22	84,84,84,85	5
2	FE	E	201	1/1	0.90	0.08	48,48,48,48	1
3	SO4	E	205	5/5	0.90	0.24	100,100,100,100	5
3	SO4	A	207	5/5	0.90	0.15	87,87,88,89	5
2	FE	F	201	1/1	0.91	0.09	62,62,62,62	1
3	SO4	B	202	5/5	0.91	0.27	116,116,116,116	5
5	LFA	B	207	20/20	0.91	0.17	59,60,80,81	0
4	GOL	B	204	6/6	0.91	0.11	73,75,76,76	0
4	GOL	D	204	6/6	0.91	0.18	86,87,88,88	0
2	FE	A	201	1/1	0.92	0.06	113,113,113,113	1
4	GOL	G	202	6/6	0.93	0.09	86,86,87,87	0
3	SO4	G	204	5/5	0.93	0.13	86,86,86,86	5
3	SO4	F	202	5/5	0.93	0.09	99,100,100,100	5
3	SO4	A	206	5/5	0.93	0.19	67,68,68,68	5
2	FE	G	201	1/1	0.94	0.07	88,88,88,88	0
2	FE	B	201	1/1	0.95	0.10	50,50,50,50	1
4	GOL	E	203	6/6	0.95	0.09	84,86,86,87	0
2	FE	H	201	1/1	0.98	0.03	93,93,93,93	0
2	FE	C	201	1/1	0.98	0.13	58,58,58,58	1
2	FE	D	201	1/1	0.99	0.11	59,59,59,59	1
3	SO4	B	205	5/5	0.99	0.12	60,61,64,64	5

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 LFA C 204:

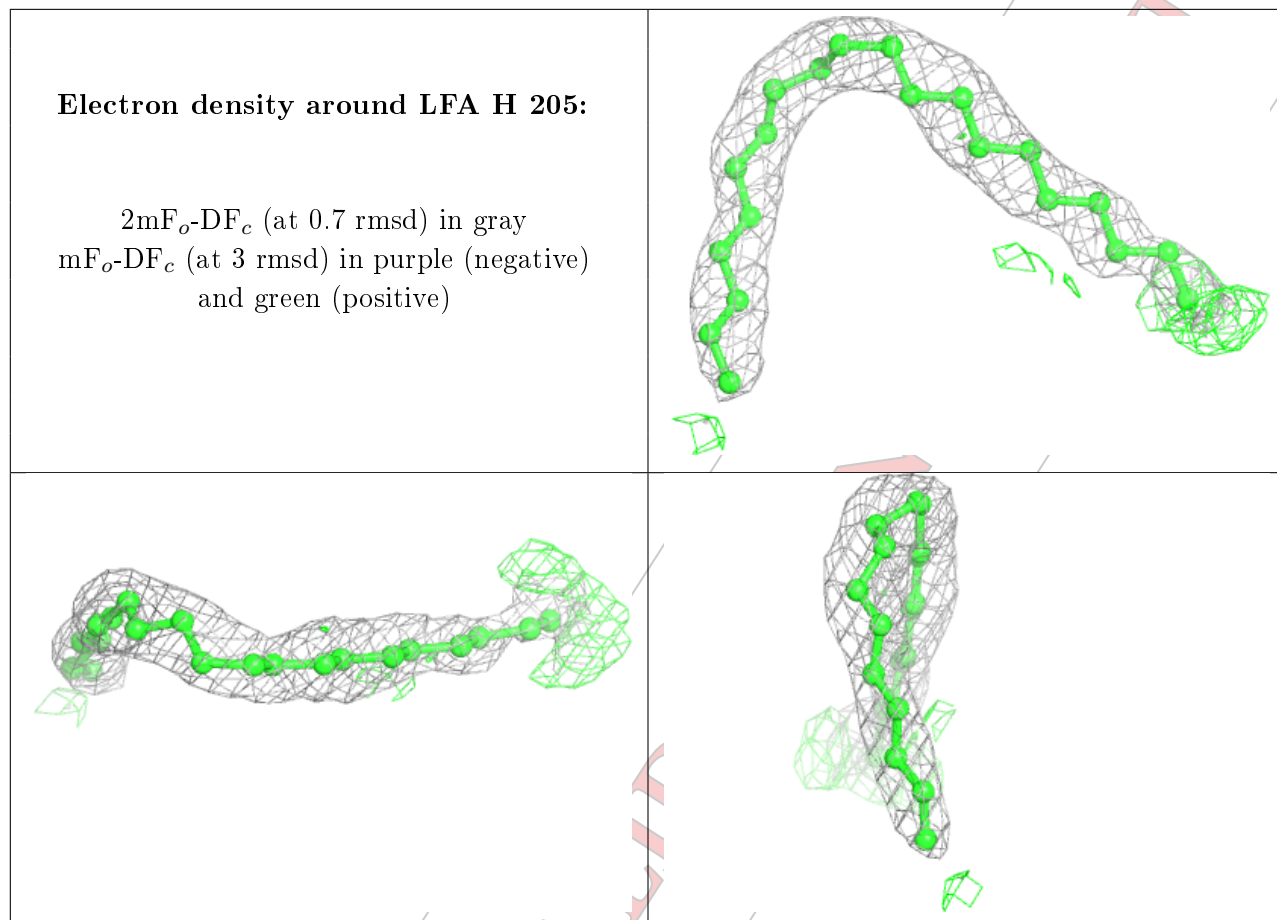
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



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Electron density around LFA H 205:

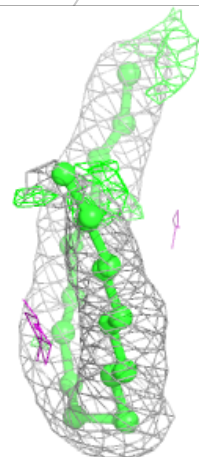
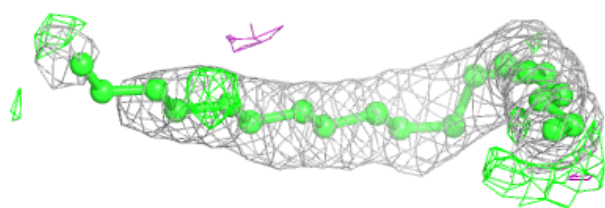
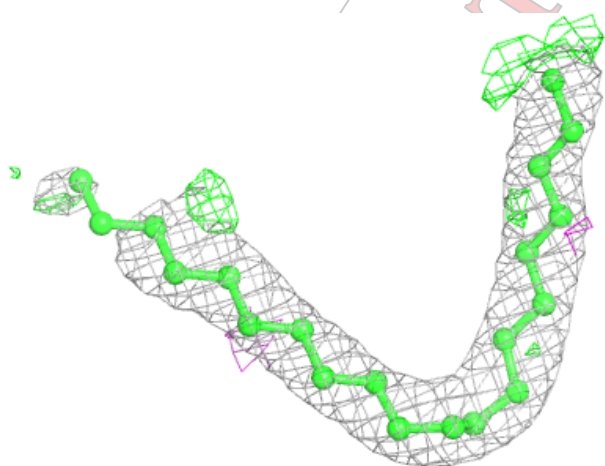
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



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Electron density around LFA E 204:

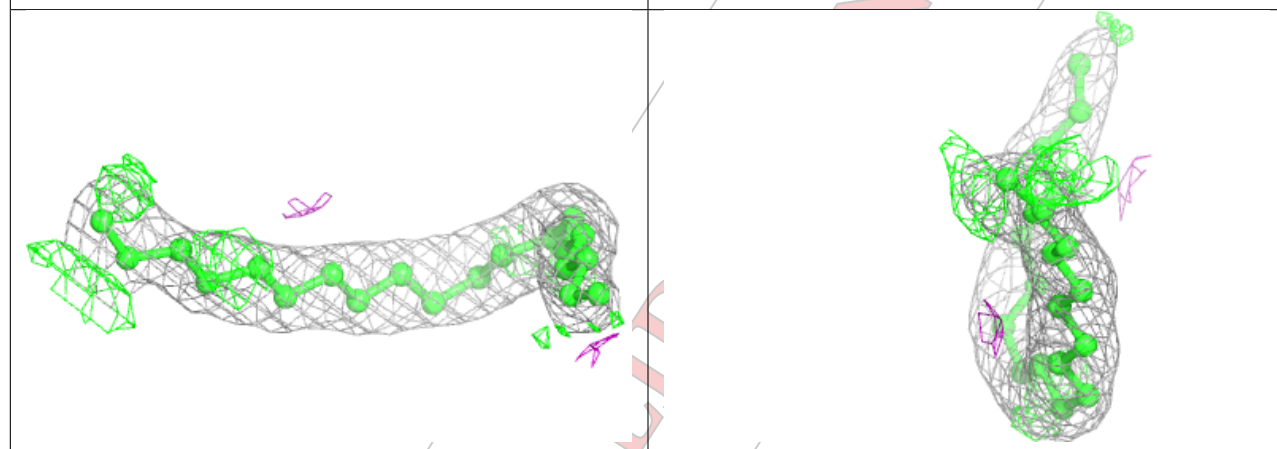
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



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Electron density around LFA B 207:

$2mF_o-DF_c$ (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.

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