



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 5, 2026 – 08:07 AM JST

PDB ID : 5X23 / pdb_00005x23
Title : Crystal structure of CYP2C9 genetic variant A477T (*30) in complex with multiple losartan molecules
Authors : Maekawa, K.; Adachi, M.; Shah, M.B.
Deposited on : 2017-01-30
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 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	:	1.8.5 (274361), CSD as541be (2020)
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	:	9.0.015 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.50

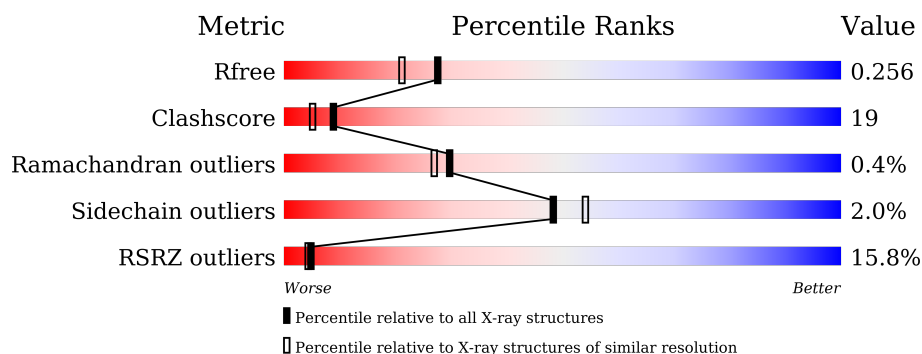
1 Overall quality at a glance

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}	180053	10052 (2.00-2.00)
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (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 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	476	15% 69% 24% ...

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	LSN	A	502	-	X	-	-
3	LSN	A	503	-	X	-	-

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	LSN	A	504[A]	-	X	X	X
3	LSN	A	504[B]	-	X	X	X

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 4026 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

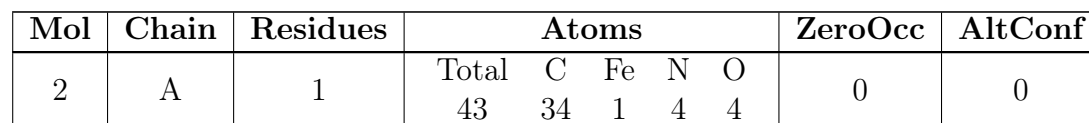
- Molecule 1 is a protein called Cytochrome P450 2C9.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	463	3660	2362	608	666	24	0	0	0

There are 11 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	19	MET	-	See Sequence details	UNP P11712
A	20	ALA	-	See Sequence details	UNP P11712
A	21	LYS	-	See Sequence details	UNP P11712
A	22	LYS	-	See Sequence details	UNP P11712
A	23	THR	-	See Sequence details	UNP P11712
A	477	THR	ALA	engineered mutation	UNP P11712
A	490	ILE	VAL	engineered mutation	UNP P11712
A	491	HIS	-	expression tag	UNP P11712
A	492	HIS	-	expression tag	UNP P11712
A	493	HIS	-	expression tag	UNP P11712
A	494	HIS	-	expression tag	UNP P11712

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



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- Chemical structure of LSN (Lansoprazole) is shown, featuring a benzimidazole core substituted with a 5-chloro-2-hydroxy-5-methyl-1H-benzimidazol-1-yl group and a 2-phenyl-1H-benzimidazol-1-yl group. The structure is labeled with atom identifiers: C1 through C22, N1 through N6, O, and Cl.

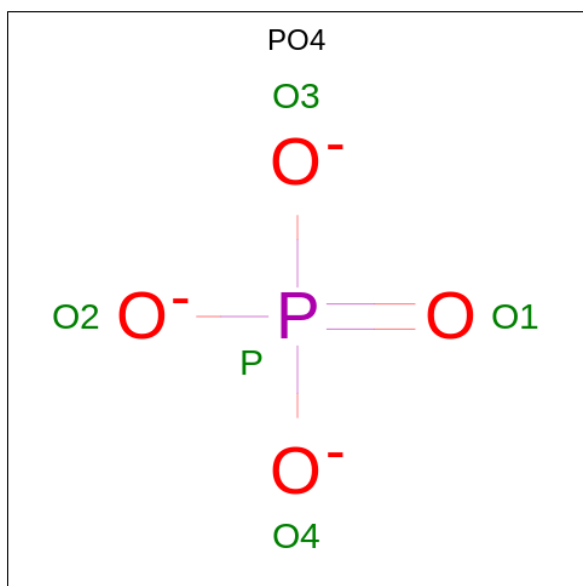
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total 30	C 22	Cl 1	N 6	O 1	0	0
3	A	1	Total 30	C 22	Cl 1	N 6	O 1	0	0



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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	Cl	N	O	
			60	44	2	12	2	
							0	1

- Molecule 4 is PHOSPHATE ION (CCD ID: PO4) (formula: O₄P).



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

- Molecule 5 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total K		
			1 1	0	0

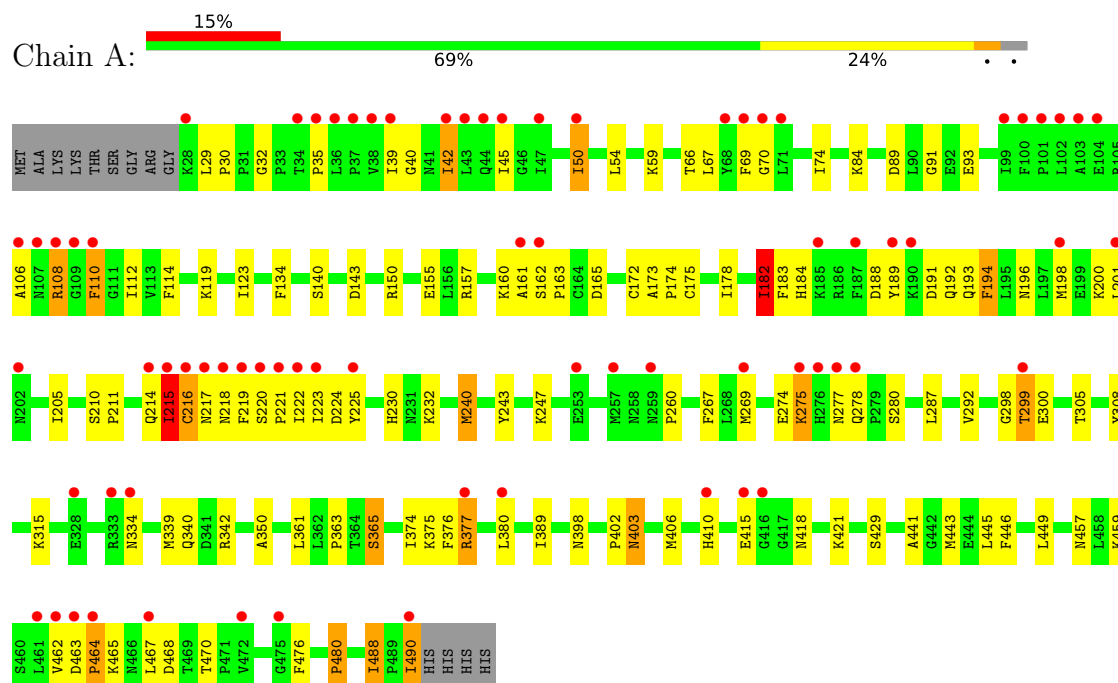
- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	197	Total O		
			197 197	0	0

3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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: Cytochrome P450 2C9



4 Data and refinement statistics

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	74.95Å 142.27Å 161.83Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	45.51 – 2.00 45.51 – 2.00	Depositor EDS
% Data completeness (in resolution range)	99.1 (45.51-2.00) 99.1 (45.51-2.00)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.39 (at 2.00Å)	Xtriage
Refinement program	REFMAC 5.5.0072	Depositor
R, R_{free}	0.217 , 0.253 0.236 , 0.256	Depositor DCC
R_{free} test set	2964 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	35.5	Xtriage
Anisotropy	0.100	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 49.0	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	0.95	EDS
Total number of atoms	4026	wwPDB-VP
Average B, all atoms (Å ²)	49.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.27% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: LSN, K, HEM, PO4

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	1.63	9/3750 (0.2%)	1.25	38/5084 (0.7%)

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	305	THR	CA-C	6.90	1.61	1.52
1	A	350	ALA	N-CA	-6.46	1.38	1.46
1	A	365	SER	C-O	-5.88	1.18	1.24
1	A	445	LEU	C-O	-5.58	1.17	1.24
1	A	74	ILE	C-O	-5.33	1.18	1.24
1	A	449	LEU	C-O	-5.20	1.18	1.24
1	A	441	ALA	C-O	-5.13	1.18	1.24
1	A	110	PHE	CA-C	5.11	1.59	1.52
1	A	446	PHE	C-O	-5.02	1.18	1.24

All (38) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	42	ILE	N-CA-C	8.62	119.41	110.36
1	A	112	ILE	CB-CA-C	-8.12	103.82	111.05
1	A	457	ASN	N-CA-C	-7.49	98.02	109.85
1	A	29	LEU	CA-C-N	-7.23	114.46	119.66
1	A	29	LEU	C-N-CA	-7.23	114.46	119.66
1	A	188	ASP	N-CA-C	-7.17	99.67	110.28
1	A	91	GLY	N-CA-C	7.16	121.30	112.64
1	A	278	GLN	C-N-CD	7.07	136.15	120.60
1	A	361	LEU	N-CA-C	6.62	119.32	111.71
1	A	488	ILE	N-CA-C	6.53	114.01	107.55
1	A	299	THR	N-CA-C	6.36	121.70	113.88
1	A	216	CYS	N-CA-C	6.25	118.89	111.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	398	ASN	N-CA-C	6.22	120.47	113.01
1	A	165	ASP	N-CA-C	-5.79	98.10	108.47
1	A	30	PRO	O-C-N	5.78	123.87	121.15
1	A	377	ARG	N-CA-C	-5.76	98.35	108.08
1	A	108	ARG	N-CA-C	5.71	120.98	112.94
1	A	222	ILE	N-CA-C	5.70	118.66	112.96
1	A	480	PRO	CA-C-N	-5.60	114.98	120.52
1	A	480	PRO	C-N-CA	-5.60	114.98	120.52
1	A	377	ARG	CB-CA-C	-5.47	110.28	116.63
1	A	32	GLY	CA-C-N	-5.47	114.13	119.76
1	A	32	GLY	C-N-CA	-5.47	114.13	119.76
1	A	470	THR	CA-C-N	-5.46	114.33	119.85
1	A	470	THR	C-N-CA	-5.46	114.33	119.85
1	A	182	ILE	N-CA-C	5.40	116.48	111.45
1	A	30	PRO	CA-C-N	-5.40	115.03	120.21
1	A	30	PRO	C-N-CA	-5.40	115.03	120.21
1	A	215	ILE	N-CA-C	5.34	120.45	109.34
1	A	194	PHE	N-CA-C	-5.34	104.88	111.40
1	A	488	ILE	O-C-N	5.24	124.67	121.37
1	A	342	ARG	N-CA-C	5.16	116.90	111.28
1	A	403	ASN	CA-C-N	-5.14	114.31	119.56
1	A	403	ASN	C-N-CA	-5.14	114.31	119.56
1	A	275	LYS	N-CA-C	-5.13	99.87	110.80
1	A	70	GLY	N-CA-C	-5.07	101.53	110.86
1	A	210	SER	CA-C-N	-5.07	114.39	119.56
1	A	210	SER	C-N-CA	-5.07	114.39	119.56

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3660	0	3632	126	0
2	A	43	0	30	2	0
3	A	120	0	0	36	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	5	0	0	1	0
5	A	1	0	0	0	0
6	A	197	0	0	15	0
All	All	4026	0	3662	139	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 19.

All (139) 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:219:PHE:O	1:A:221:PRO:HD3	1.45	1.13
3:A:504[A]:LSN:C16	3:A:504[A]:LSN:C10	2.31	1.07
3:A:504[A]:LSN:C10	3:A:504[A]:LSN:C15	2.32	1.06
3:A:504[B]:LSN:C19	3:A:504[B]:LSN:C10	2.35	1.04
3:A:504[B]:LSN:N1	3:A:504[B]:LSN:C14	2.21	1.04
1:A:155:GLU:HG3	1:A:189:TYR:HD1	1.21	1.03
3:A:504[A]:LSN:N1	3:A:504[A]:LSN:C14	2.23	1.01
1:A:155:GLU:HG3	1:A:189:TYR:CD1	1.95	1.00
1:A:218:ASN:ND2	3:A:504[A]:LSN:CL	2.37	0.94
1:A:410:HIS:HB2	6:A:776:HOH:O	1.70	0.90
1:A:39:ILE:O	1:A:42:ILE:HG13	1.73	0.88
3:A:504[B]:LSN:C10	3:A:504[B]:LSN:C18	2.49	0.88
1:A:374:ILE:O	1:A:380:LEU:HD12	1.80	0.81
1:A:108:ARG:NE	3:A:502:LSN:O	2.15	0.80
1:A:108:ARG:O	1:A:114:PHE:HB2	1.84	0.77
1:A:211:PRO:HA	1:A:214:GLN:HG2	1.65	0.77
1:A:274:GLU:OE1	1:A:280:SER:OG	2.02	0.76
1:A:59:LYS:O	6:A:602:HOH:O	2.04	0.76
1:A:218:ASN:CG	3:A:504[A]:LSN:CL	2.65	0.76
1:A:476:PHE:HZ	3:A:504[B]:LSN:C16	1.99	0.76
1:A:201:LEU:HD12	3:A:502:LSN:C20	2.17	0.75
1:A:69:PHE:CZ	1:A:219:PHE:CE1	2.75	0.74
1:A:365:SER:O	3:A:504[B]:LSN:N1	2.21	0.73
1:A:267:PHE:CG	1:A:287:LEU:HD13	2.22	0.73
3:A:504[B]:LSN:C14	3:A:504[B]:LSN:C1	2.67	0.73
1:A:365:SER:O	3:A:504[A]:LSN:N1	2.22	0.72
1:A:172:CYS:SG	1:A:198:MET:HE1	2.28	0.72
3:A:504[A]:LSN:C14	3:A:504[A]:LSN:C1	2.69	0.71
1:A:84:LYS:NZ	1:A:89:ASP:OD1	2.24	0.71
1:A:215:ILE:HG22	1:A:216:CYS:N	2.05	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:69:PHE:CE1	1:A:219:PHE:HE1	2.09	0.70
1:A:232:LYS:HD2	3:A:503:LSN:CL	2.29	0.69
1:A:476:PHE:CZ	3:A:504[B]:LSN:C16	2.75	0.69
1:A:220:SER:OG	1:A:223:ILE:O	2.04	0.69
1:A:476:PHE:O	3:A:504[A]:LSN:N4	2.26	0.68
1:A:340:GLN:HG2	6:A:634:HOH:O	1.94	0.68
1:A:69:PHE:CZ	1:A:219:PHE:CD1	2.83	0.66
1:A:224:ASP:OD2	6:A:604:HOH:O	2.14	0.66
1:A:476:PHE:O	3:A:504[B]:LSN:N4	2.29	0.66
1:A:110:PHE:HA	1:A:119:LYS:HE2	1.78	0.66
1:A:205:ILE:HG21	1:A:300:GLU:HG2	1.77	0.65
1:A:374:ILE:HG13	1:A:375:LYS:N	2.11	0.65
1:A:201:LEU:CD1	3:A:502:LSN:C20	2.74	0.65
1:A:315:LYS:HD3	1:A:467:LEU:HD12	1.80	0.64
1:A:240:MET:HE3	3:A:502:LSN:C22	2.29	0.63
1:A:315:LYS:HD3	1:A:467:LEU:CD1	2.29	0.63
1:A:150:ARG:NH2	6:A:601:HOH:O	2.02	0.63
1:A:415:GLU:HG2	4:A:505:PO4:O4	1.99	0.62
1:A:418:ASN:ND2	6:A:603:HOH:O	2.05	0.62
1:A:274:GLU:O	1:A:275:LYS:C	2.39	0.62
1:A:35:PRO:HB2	1:A:40:GLY:HA2	1.80	0.62
1:A:219:PHE:O	1:A:221:PRO:CD	2.37	0.61
1:A:143:ASP:HB2	6:A:619:HOH:O	1.99	0.61
1:A:363:PRO:HD2	3:A:504[B]:LSN:N3	2.16	0.60
1:A:224:ASP:OD2	1:A:230:HIS:HD2	1.84	0.60
1:A:69:PHE:CZ	3:A:504[B]:LSN:CL	2.93	0.59
1:A:162:SER:O	1:A:163:PRO:C	2.45	0.59
1:A:224:ASP:CG	1:A:230:HIS:HD2	2.11	0.59
1:A:363:PRO:HD2	3:A:504[A]:LSN:N3	2.17	0.58
1:A:476:PHE:HZ	3:A:504[A]:LSN:C19	2.15	0.58
1:A:150:ARG:NE	6:A:601:HOH:O	2.29	0.58
1:A:183:PHE:O	1:A:184:HIS:HB3	2.05	0.56
1:A:106:ALA:HB3	1:A:108:ARG:HD2	1.87	0.56
1:A:69:PHE:CZ	1:A:219:PHE:HE1	2.17	0.56
1:A:108:ARG:HG2	3:A:502:LSN:C16	2.36	0.55
1:A:196:ASN:O	1:A:200:LYS:HG2	2.06	0.55
1:A:467:LEU:HD12	1:A:467:LEU:O	2.07	0.54
1:A:476:PHE:CZ	3:A:504[A]:LSN:C19	2.91	0.54
3:A:504[A]:LSN:C16	3:A:504[A]:LSN:C11	2.86	0.53
1:A:240:MET:HG2	1:A:292:VAL:HG22	1.90	0.53
1:A:108:ARG:NH2	1:A:114:PHE:CE1	2.77	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:490:ILE:HG22	1:A:490:ILE:O	2.09	0.53
1:A:173:ALA:HB3	1:A:174:PRO:HD3	1.91	0.52
1:A:376:PHE:O	1:A:377:ARG:HB2	2.09	0.52
1:A:402:PRO:O	1:A:403:ASN:HB2	2.10	0.51
3:A:504[A]:LSN:C22	6:A:792:HOH:O	2.58	0.51
1:A:463:ASP:OD1	1:A:464:PRO:HD2	2.10	0.51
1:A:223:ILE:HG13	1:A:225:TYR:CE2	2.46	0.51
1:A:155:GLU:HG3	1:A:189:TYR:CE1	2.44	0.51
1:A:224:ASP:OD1	1:A:230:HIS:CD2	2.64	0.51
3:A:504[B]:LSN:C19	3:A:504[B]:LSN:C11	2.89	0.51
1:A:45:ILE:HG23	1:A:45:ILE:O	2.11	0.50
1:A:406:MET:HE2	1:A:406:MET:HA	1.93	0.50
1:A:463:ASP:O	1:A:465:LYS:N	2.44	0.50
1:A:157:ARG:HH11	1:A:157:ARG:HG2	1.76	0.50
1:A:150:ARG:NH2	6:A:614:HOH:O	2.43	0.50
1:A:108:ARG:NH2	3:A:502:LSN:N1	2.59	0.49
1:A:334:ASN:N	6:A:607:HOH:O	2.28	0.49
1:A:274:GLU:O	1:A:277:ASN:HB3	2.13	0.49
1:A:315:LYS:HB2	1:A:467:LEU:HD11	1.94	0.49
1:A:315:LYS:CD	1:A:467:LEU:HD11	2.44	0.48
1:A:462:VAL:HG23	1:A:463:ASP:N	2.28	0.47
1:A:160:LYS:O	1:A:161:ALA:HB3	2.14	0.47
1:A:194:PHE:CZ	1:A:198:MET:SD	3.08	0.47
1:A:308:TYR:CD1	1:A:480:PRO:HB3	2.50	0.46
1:A:476:PHE:HB3	3:A:504[A]:LSN:N4	2.30	0.46
1:A:192:GLN:O	1:A:192:GLN:HG3	2.16	0.46
1:A:274:GLU:C	1:A:275:LYS:O	2.55	0.46
1:A:211:PRO:HA	1:A:214:GLN:CG	2.42	0.46
1:A:108:ARG:HH21	1:A:114:PHE:HE1	1.63	0.45
1:A:194:PHE:CE2	1:A:198:MET:SD	3.09	0.45
2:A:501:HEM:HBB2	2:A:501:HEM:HMB2	1.97	0.45
1:A:230:HIS:HB3	6:A:626:HOH:O	2.16	0.45
1:A:298:GLY:HA2	2:A:501:HEM:C2C	2.52	0.45
1:A:175:CYS:HA	1:A:299:THR:HG22	1.98	0.45
1:A:157:ARG:HH11	1:A:157:ARG:CG	2.30	0.45
1:A:184:HIS:O	1:A:184:HIS:CG	2.69	0.45
1:A:467:LEU:HD12	1:A:467:LEU:C	2.41	0.45
1:A:93:GLU:HG2	1:A:374:ILE:HD13	1.98	0.45
1:A:69:PHE:CE1	1:A:219:PHE:CE1	2.96	0.45
1:A:205:ILE:CG2	1:A:300:GLU:HG2	2.47	0.45
1:A:66:THR:HG22	1:A:67:LEU:N	2.32	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:69:PHE:CZ	1:A:219:PHE:HD1	2.34	0.44
1:A:201:LEU:O	1:A:205:ILE:HG12	2.17	0.44
1:A:459:LYS:HB2	1:A:488:ILE:CD1	2.47	0.44
1:A:223:ILE:HG13	1:A:225:TYR:HE2	1.83	0.44
1:A:260:PRO:HB3	1:A:269:MET:SD	2.58	0.43
1:A:315:LYS:HD3	1:A:467:LEU:HD11	2.00	0.43
1:A:243:TYR:OH	1:A:247:LYS:HE2	2.17	0.43
1:A:175:CYS:HA	1:A:299:THR:CG2	2.49	0.42
1:A:50:ILE:O	1:A:54:LEU:HG	2.20	0.42
1:A:220:SER:OG	1:A:223:ILE:HG13	2.18	0.42
1:A:178:ILE:O	1:A:182:ILE:HG13	2.20	0.42
1:A:468:ASP:N	6:A:605:HOH:O	2.27	0.42
1:A:217:ASN:HB3	6:A:648:HOH:O	2.20	0.42
1:A:232:LYS:HD2	3:A:503:LSN:C17	2.50	0.42
1:A:243:TYR:CZ	1:A:247:LYS:NZ	2.83	0.42
1:A:463:ASP:C	1:A:465:LYS:N	2.78	0.42
1:A:488:ILE:HG21	6:A:773:HOH:O	2.20	0.42
1:A:108:ARG:NH2	1:A:114:PHE:CZ	2.88	0.41
1:A:191:ASP:OD1	1:A:193:GLN:HG2	2.21	0.41
1:A:315:LYS:CD	1:A:467:LEU:CD1	2.95	0.41
1:A:339:MET:SD	1:A:443:MET:HG2	2.60	0.41
1:A:201:LEU:HD12	1:A:201:LEU:HA	1.87	0.41
1:A:476:PHE:HB3	3:A:504[B]:LSN:N4	2.34	0.41
1:A:240:MET:CE	3:A:502:LSN:C22	2.96	0.40
1:A:267:PHE:CD1	1:A:287:LEU:HD13	2.56	0.40
3:A:503:LSN:C12	3:A:503:LSN:C20	3.00	0.40
1:A:134:PHE:CE1	1:A:140:SER:HB3	2.57	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	461/476 (97%)	434 (94%)	25 (5%)	2 (0%)	30 27

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	429	SER
1	A	464	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	406/430 (94%)	398 (98%)	8 (2%)	48 54

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	50	ILE
1	A	123	ILE
1	A	182	ILE
1	A	215	ILE
1	A	240	MET
1	A	389	ILE
1	A	421	LYS
1	A	490	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	217	ASN
1	A	231	ASN
1	A	418	ASN
1	A	466	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 7 ligands modelled in this entry, 1 is monoatomic - leaving 6 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	LSN	A	504[A]	-	32,33,33	5.38	22 (68%)	39,45,45	3.14	16 (41%)
2	HEM	A	501	1,6	50,50,50	1.97	17 (34%)	66,82,82	1.65	14 (21%)
4	PO4	A	505	-	4,4,4	1.71	0	6,6,6	0.66	0
3	LSN	A	503	-	32,33,33	5.15	23 (71%)	39,45,45	2.61	15 (38%)
3	LSN	A	504[B]	-	32,33,33	5.39	22 (68%)	39,45,45	2.71	16 (41%)
3	LSN	A	502	-	32,33,33	5.07	24 (75%)	39,45,45	3.10	17 (43%)

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
3	LSN	A	504[A]	-	-	11/18/18/18	0/4/4/4
2	HEM	A	501	1,6	-	2/14/54/54	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	LSN	A	503	-	-	7/18/18/18	0/4/4/4
3	LSN	A	504[B]	-	-	13/18/18/18	0/4/4/4
3	LSN	A	502	-	-	7/18/18/18	0/4/4/4

All (108) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	503	LSN	C17-CL	-16.82	1.43	1.72
3	A	504[B]	LSN	C1-N4	9.68	1.45	1.32
3	A	504[A]	LSN	C1-N4	9.62	1.45	1.32
3	A	502	LSN	C1-N4	9.32	1.45	1.32
3	A	502	LSN	C9-C10	8.64	1.54	1.38
3	A	504[B]	LSN	C6-C7	7.95	1.52	1.40
3	A	504[A]	LSN	C6-C7	7.93	1.52	1.40
3	A	504[A]	LSN	C3-C2	7.88	1.52	1.39
3	A	504[B]	LSN	C3-C2	7.87	1.52	1.39
3	A	504[A]	LSN	C14-C13	7.78	1.52	1.38
3	A	504[A]	LSN	C9-C10	7.77	1.52	1.38
3	A	504[B]	LSN	C9-C10	7.75	1.52	1.38
3	A	504[B]	LSN	C14-C13	7.73	1.52	1.38
3	A	502	LSN	C3-C2	7.63	1.52	1.39
3	A	502	LSN	C9-C8	7.43	1.55	1.39
3	A	503	LSN	C9-C10	7.41	1.52	1.38
3	A	504[A]	LSN	C18-N6	7.33	1.45	1.32
3	A	504[B]	LSN	C2-C7	7.32	1.52	1.40
3	A	504[A]	LSN	C2-C7	7.31	1.52	1.40
3	A	504[B]	LSN	C17-N6	7.29	1.47	1.36
3	A	504[A]	LSN	C17-N6	7.28	1.47	1.36
3	A	504[B]	LSN	C18-N6	7.28	1.45	1.32
3	A	502	LSN	C1-N1	7.23	1.45	1.35
3	A	502	LSN	C2-C7	7.20	1.51	1.40
3	A	504[A]	LSN	C1-N1	7.13	1.45	1.35
3	A	504[B]	LSN	C1-N1	7.11	1.45	1.35
3	A	502	LSN	C10-C11	6.85	1.53	1.38
3	A	504[A]	LSN	C5-C6	6.83	1.53	1.38
3	A	504[B]	LSN	C4-C3	6.80	1.53	1.38
3	A	504[A]	LSN	C4-C3	6.78	1.53	1.38
3	A	504[B]	LSN	C5-C6	6.77	1.53	1.38
3	A	504[A]	LSN	C10-C11	6.51	1.52	1.38
3	A	504[B]	LSN	C10-C11	6.45	1.52	1.38
3	A	503	LSN	C14-C13	6.44	1.50	1.38
3	A	504[B]	LSN	C13-C11	6.44	1.52	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	504[A]	LSN	C13-C11	6.43	1.52	1.38
3	A	504[B]	LSN	C9-C8	6.41	1.53	1.39
3	A	504[A]	LSN	C9-C8	6.40	1.53	1.39
3	A	504[A]	LSN	C14-C8	6.40	1.53	1.39
3	A	504[B]	LSN	C14-C8	6.37	1.52	1.39
3	A	502	LSN	C18-N6	6.36	1.43	1.32
3	A	503	LSN	C1-N4	6.36	1.41	1.32
3	A	502	LSN	C18-N5	6.35	1.47	1.37
3	A	503	LSN	C18-N6	6.25	1.43	1.32
3	A	502	LSN	C6-C7	6.25	1.49	1.40
3	A	502	LSN	C17-N6	6.10	1.45	1.36
3	A	502	LSN	C4-C3	6.10	1.51	1.38
3	A	503	LSN	C3-C2	6.03	1.49	1.39
3	A	503	LSN	C17-N6	5.97	1.45	1.36
3	A	504[B]	LSN	C4-C5	5.87	1.53	1.38
3	A	504[A]	LSN	C4-C5	5.87	1.53	1.38
3	A	502	LSN	C14-C8	5.86	1.51	1.39
3	A	502	LSN	C14-C13	5.60	1.48	1.38
3	A	503	LSN	C13-C11	5.60	1.50	1.38
3	A	502	LSN	C5-C6	5.60	1.50	1.38
3	A	503	LSN	C9-C8	5.51	1.51	1.39
2	A	501	HEM	C1B-NB	-5.51	1.30	1.40
3	A	503	LSN	C4-C3	5.49	1.50	1.38
3	A	503	LSN	C10-C11	5.44	1.50	1.38
3	A	503	LSN	C5-C6	5.39	1.50	1.38
3	A	503	LSN	C6-C7	5.32	1.48	1.40
3	A	504[B]	LSN	C17-CL	5.30	1.81	1.72
3	A	502	LSN	C13-C11	5.15	1.50	1.38
3	A	502	LSN	C4-C5	5.09	1.51	1.38
3	A	503	LSN	C14-C8	4.94	1.49	1.39
3	A	503	LSN	C2-C7	4.92	1.48	1.40
3	A	504[A]	LSN	C17-CL	4.84	1.81	1.72
3	A	503	LSN	C4-C5	4.67	1.50	1.38
3	A	504[B]	LSN	C18-N5	4.57	1.44	1.37
3	A	504[A]	LSN	C18-N5	4.47	1.44	1.37
3	A	503	LSN	C1-N1	4.40	1.41	1.35
2	A	501	HEM	C4D-ND	-4.01	1.33	1.40
3	A	502	LSN	C12-N5	-3.91	1.41	1.47
2	A	501	HEM	C1C-C2C	-3.87	1.37	1.45
3	A	503	LSN	N3-N4	-3.60	1.28	1.33
2	A	501	HEM	FE-NB	3.54	2.05	1.94
2	A	501	HEM	C4B-NB	-3.53	1.31	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	504[A]	LSN	C15-N5	3.44	1.46	1.38
3	A	504[B]	LSN	C15-N5	3.43	1.46	1.38
2	A	501	HEM	FE-NC	3.40	2.06	1.95
3	A	504[B]	LSN	C16-C15	3.23	1.54	1.49
2	A	501	HEM	C1D-ND	-3.18	1.32	1.38
3	A	504[A]	LSN	C16-C15	3.16	1.54	1.49
3	A	503	LSN	C18-N5	3.07	1.42	1.37
2	A	501	HEM	C1C-NC	-3.00	1.33	1.39
3	A	503	LSN	C15-N5	2.99	1.45	1.38
2	A	501	HEM	FE-ND	-2.80	1.86	1.94
2	A	501	HEM	C4C-NC	-2.70	1.34	1.39
2	A	501	HEM	C4A-NA	-2.65	1.34	1.39
2	A	501	HEM	O2A-CGA	-2.63	1.21	1.30
3	A	502	LSN	N3-N2	2.62	1.35	1.31
3	A	502	LSN	C16-C15	2.56	1.53	1.49
3	A	504[A]	LSN	C19-C18	2.56	1.52	1.49
3	A	504[B]	LSN	C19-C18	2.46	1.52	1.49
3	A	503	LSN	N1-N2	-2.46	1.28	1.32
2	A	501	HEM	C3C-C4C	-2.44	1.41	1.46
3	A	502	LSN	C19-C18	2.34	1.52	1.49
3	A	502	LSN	C17-CL	2.26	1.76	1.72
3	A	504[B]	LSN	C2-C1	2.25	1.53	1.47
2	A	501	HEM	C3D-C2D	-2.24	1.31	1.36
3	A	503	LSN	C16-C15	2.24	1.52	1.49
2	A	501	HEM	C2A-C3A	-2.23	1.32	1.38
3	A	504[A]	LSN	C2-C1	2.23	1.53	1.47
2	A	501	HEM	O2D-CGD	-2.21	1.23	1.30
3	A	502	LSN	C7-C8	2.18	1.53	1.49
2	A	501	HEM	C1A-C2A	-2.14	1.40	1.44
3	A	502	LSN	C2-C1	2.02	1.52	1.47
3	A	503	LSN	C12-N5	-2.01	1.44	1.47

All (78) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	504[A]	LSN	CL-C17-N6	11.40	135.30	120.58
3	A	504[B]	LSN	C17-N6-C18	7.04	110.50	104.59
3	A	502	LSN	C11-C12-N5	-6.98	102.29	113.15
3	A	504[A]	LSN	C17-N6-C18	6.94	110.42	104.59
3	A	503	LSN	C1-N1-N2	-6.88	100.38	105.64
3	A	502	LSN	C12-C11-C13	-6.63	108.30	120.77
3	A	502	LSN	C15-N5-C18	6.53	111.92	107.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	502	LSN	C12-N5-C15	-6.45	118.09	125.12
3	A	502	LSN	C1-N1-N2	-6.36	100.78	105.64
3	A	503	LSN	C17-N6-C18	5.43	109.15	104.59
3	A	504[B]	LSN	CL-C17-N6	5.41	127.56	120.58
3	A	504[A]	LSN	C1-N1-N2	-5.24	101.64	105.64
3	A	503	LSN	C11-C12-N5	5.23	121.29	113.15
3	A	504[A]	LSN	C11-C12-N5	-5.23	105.00	113.15
3	A	504[B]	LSN	C1-N1-N2	-5.22	101.65	105.64
3	A	504[B]	LSN	C11-C12-N5	-5.20	105.05	113.15
3	A	504[B]	LSN	N4-C1-N1	-5.13	109.60	112.27
3	A	504[A]	LSN	N4-C1-N1	-5.10	109.61	112.27
2	A	501	HEM	CHC-C4B-NB	5.00	129.85	124.42
3	A	503	LSN	C12-C11-C13	-4.40	112.49	120.77
3	A	503	LSN	C12-N5-C15	4.36	129.87	125.12
3	A	503	LSN	N3-N2-N1	4.29	113.51	106.85
3	A	504[A]	LSN	N3-N2-N1	4.19	113.36	106.85
3	A	504[B]	LSN	N3-N2-N1	4.17	113.32	106.85
3	A	502	LSN	C13-C11-C10	4.11	124.62	118.17
2	A	501	HEM	C1B-NB-C4B	4.09	109.30	105.07
3	A	503	LSN	C12-N5-C18	-4.06	120.41	126.57
2	A	501	HEM	CHA-C4D-ND	3.97	129.27	124.37
3	A	504[B]	LSN	C13-C11-C10	3.96	124.40	118.17
3	A	504[A]	LSN	C13-C11-C10	3.95	124.38	118.17
3	A	502	LSN	C14-C8-C7	-3.93	114.55	120.91
3	A	502	LSN	C1-N4-N3	-3.75	97.43	101.92
3	A	502	LSN	C14-C13-C11	-3.53	116.17	121.03
3	A	502	LSN	C19-C18-N5	3.52	129.41	123.76
2	A	501	HEM	CHD-C1D-ND	3.49	128.21	124.42
3	A	503	LSN	C14-C8-C7	-3.38	115.43	120.91
3	A	502	LSN	N5-C18-N6	-3.23	107.89	111.76
3	A	502	LSN	C10-C9-C8	-3.22	116.50	121.13
3	A	504[B]	LSN	N5-C18-N6	-3.20	107.92	111.76
3	A	504[B]	LSN	C6-C7-C2	3.17	121.62	118.03
2	A	501	HEM	CHA-C4D-C3D	-3.16	119.39	125.33
3	A	504[A]	LSN	C14-C8-C9	3.16	123.89	117.59
2	A	501	HEM	C4C-NC-C1C	3.15	108.44	105.35
3	A	504[A]	LSN	N5-C18-N6	-3.15	107.98	111.76
3	A	504[A]	LSN	C6-C7-C2	3.14	121.59	118.03
3	A	502	LSN	C19-C18-N6	-3.14	119.86	125.34
3	A	503	LSN	C9-C10-C11	-3.14	116.71	121.03
3	A	504[B]	LSN	C14-C8-C9	3.13	123.83	117.59
3	A	503	LSN	C13-C11-C10	2.99	122.87	118.17

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	503	LSN	C13-C14-C8	-2.97	116.86	121.13
3	A	503	LSN	C14-C8-C9	2.90	123.37	117.59
3	A	502	LSN	N3-N2-N1	2.89	111.34	106.85
3	A	502	LSN	C9-C10-C11	-2.86	117.10	121.03
3	A	504[A]	LSN	C15-N5-C18	2.73	109.37	107.54
3	A	504[B]	LSN	C15-N5-C18	2.70	109.35	107.54
3	A	504[B]	LSN	C2-C7-C8	-2.65	119.17	123.08
3	A	504[A]	LSN	C2-C7-C8	-2.60	119.25	123.08
2	A	501	HEM	C4B-C3B-C2B	-2.59	105.06	107.11
2	A	501	HEM	O2A-CGA-CBA	2.52	122.11	114.03
2	A	501	HEM	CHB-C1B-NB	2.51	127.47	124.37
2	A	501	HEM	O2A-CGA-O1A	-2.41	117.29	123.30
3	A	504[A]	LSN	C9-C10-C11	-2.40	117.72	121.03
3	A	504[B]	LSN	C9-C10-C11	-2.39	117.74	121.03
3	A	504[B]	LSN	C14-C13-C11	-2.39	117.74	121.03
3	A	503	LSN	C3-C2-C1	-2.38	114.32	118.33
3	A	504[A]	LSN	C14-C13-C11	-2.36	117.78	121.03
2	A	501	HEM	CAC-C3C-C4C	2.33	130.52	124.90
3	A	502	LSN	C2-C7-C8	-2.24	119.78	123.08
2	A	501	HEM	CHD-C1D-C2D	-2.16	121.61	124.98
2	A	501	HEM	O2D-CGD-O1D	-2.11	118.03	123.30
3	A	504[A]	LSN	C13-C14-C8	-2.11	118.10	121.13
3	A	504[B]	LSN	C10-C9-C8	-2.09	118.13	121.13
3	A	504[A]	LSN	C10-C9-C8	-2.09	118.13	121.13
3	A	502	LSN	C4-C3-C2	-2.07	115.91	119.81
3	A	504[B]	LSN	C13-C14-C8	-2.06	118.16	121.13
2	A	501	HEM	O2D-CGD-CBD	2.06	120.65	114.03
3	A	503	LSN	C12-C11-C10	2.05	124.63	120.77
3	A	503	LSN	C3-C2-C7	2.05	122.10	119.74

There are no chirality outliers.

All (40) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	503	LSN	C17-C15-C16-O
3	A	503	LSN	N5-C15-C16-O
3	A	503	LSN	N5-C18-C19-C20
3	A	504[A]	LSN	C17-C15-C16-O
3	A	504[B]	LSN	C17-C15-C16-O
3	A	504[B]	LSN	C18-C19-C20-C21
3	A	502	LSN	C2-C7-C8-C14
3	A	504[B]	LSN	C11-C12-N5-C15

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Mol	Chain	Res	Type	Atoms
3	A	502	LSN	C18-C19-C20-C21
3	A	504[B]	LSN	C2-C7-C8-C14
3	A	504[A]	LSN	C11-C12-N5-C18
3	A	504[A]	LSN	C11-C12-N5-C15
3	A	503	LSN	N6-C18-C19-C20
3	A	504[A]	LSN	C2-C7-C8-C14
3	A	504[B]	LSN	C6-C7-C8-C14
3	A	503	LSN	C19-C20-C21-C22
3	A	504[A]	LSN	C19-C20-C21-C22
3	A	504[B]	LSN	N6-C18-C19-C20
3	A	504[A]	LSN	C6-C7-C8-C14
3	A	504[B]	LSN	C6-C7-C8-C9
3	A	504[B]	LSN	C2-C7-C8-C9
3	A	504[B]	LSN	C11-C12-N5-C18
3	A	502	LSN	N6-C18-C19-C20
2	A	501	HEM	CAA-CBA-CGA-O2A
2	A	501	HEM	CAA-CBA-CGA-O1A
3	A	502	LSN	N4-C1-C2-C3
3	A	504[A]	LSN	C6-C7-C8-C9
3	A	504[A]	LSN	N5-C15-C16-O
3	A	504[B]	LSN	N5-C15-C16-O
3	A	502	LSN	C19-C20-C21-C22
3	A	504[A]	LSN	C2-C7-C8-C9
3	A	504[B]	LSN	C10-C11-C12-N5
3	A	502	LSN	C2-C7-C8-C9
3	A	504[A]	LSN	C10-C11-C12-N5
3	A	504[B]	LSN	C13-C11-C12-N5
3	A	504[B]	LSN	N5-C18-C19-C20
3	A	504[A]	LSN	C13-C11-C12-N5
3	A	502	LSN	N1-C1-C2-C7
3	A	503	LSN	N1-C1-C2-C7
3	A	503	LSN	N1-C1-C2-C3

There are no ring outliers.

6 monomers are involved in 39 short contacts:

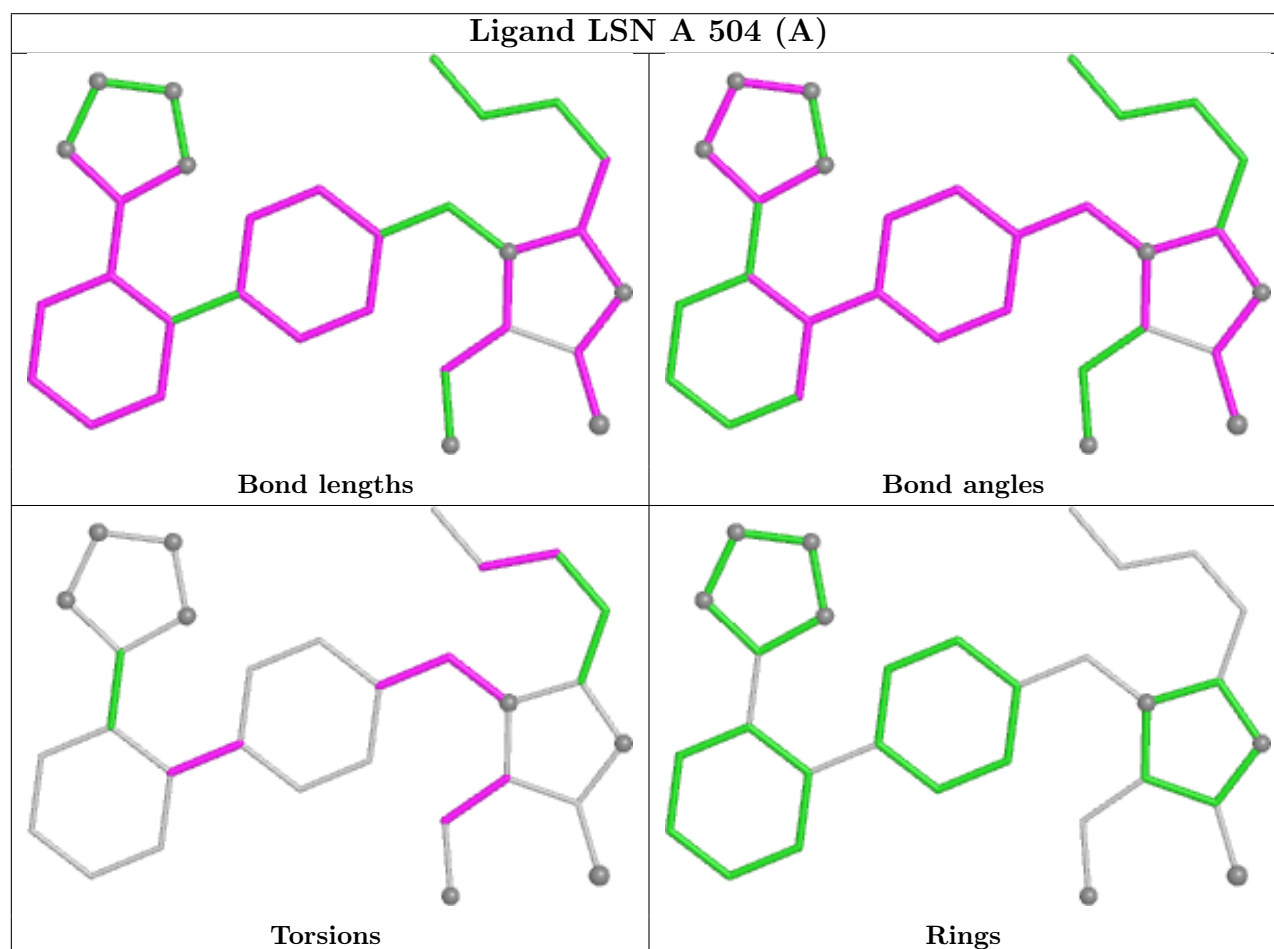
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	504[A]	LSN	14	0
2	A	501	HEM	2	0
4	A	505	PO4	1	0
3	A	503	LSN	3	0
3	A	504[B]	LSN	12	0

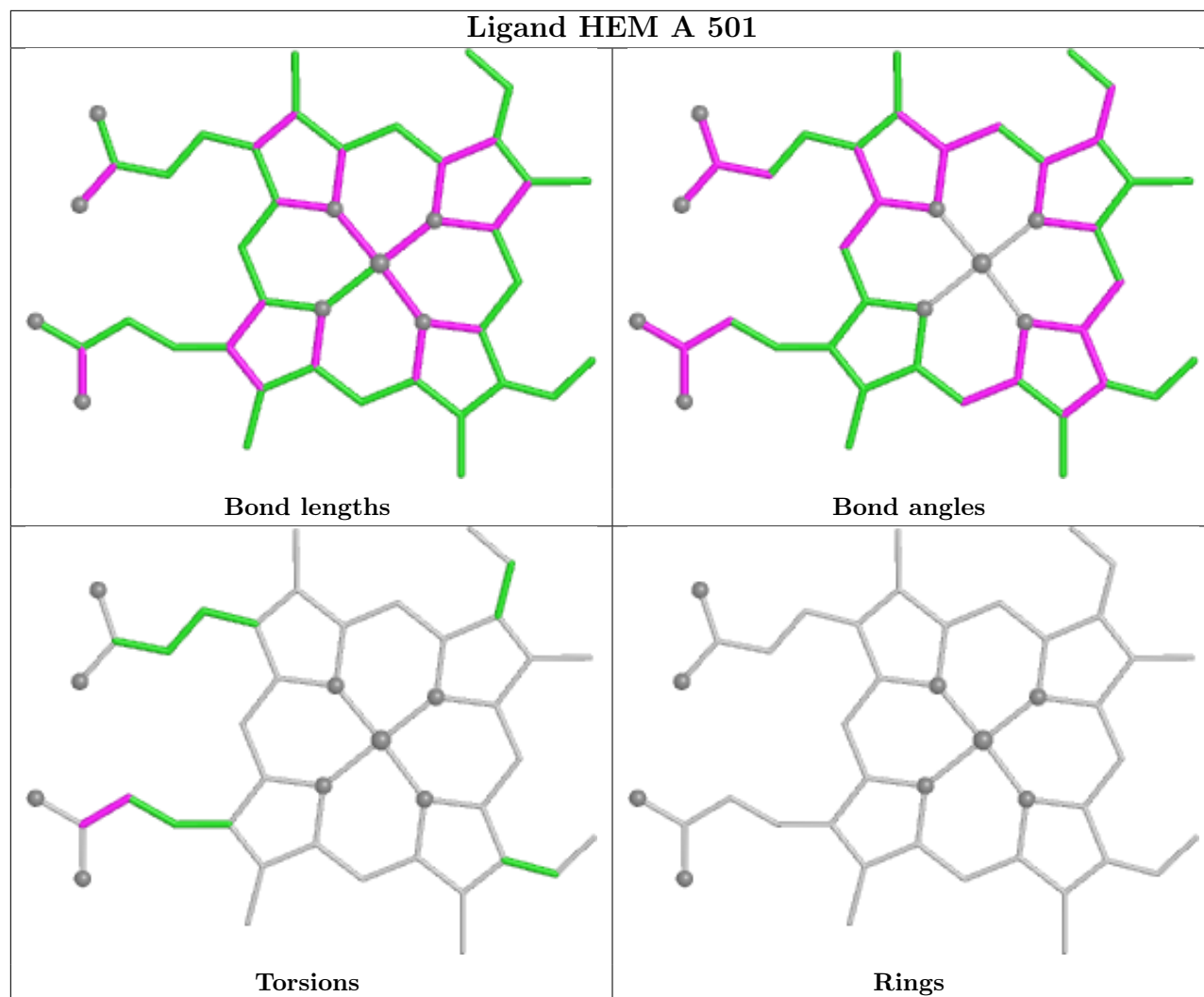
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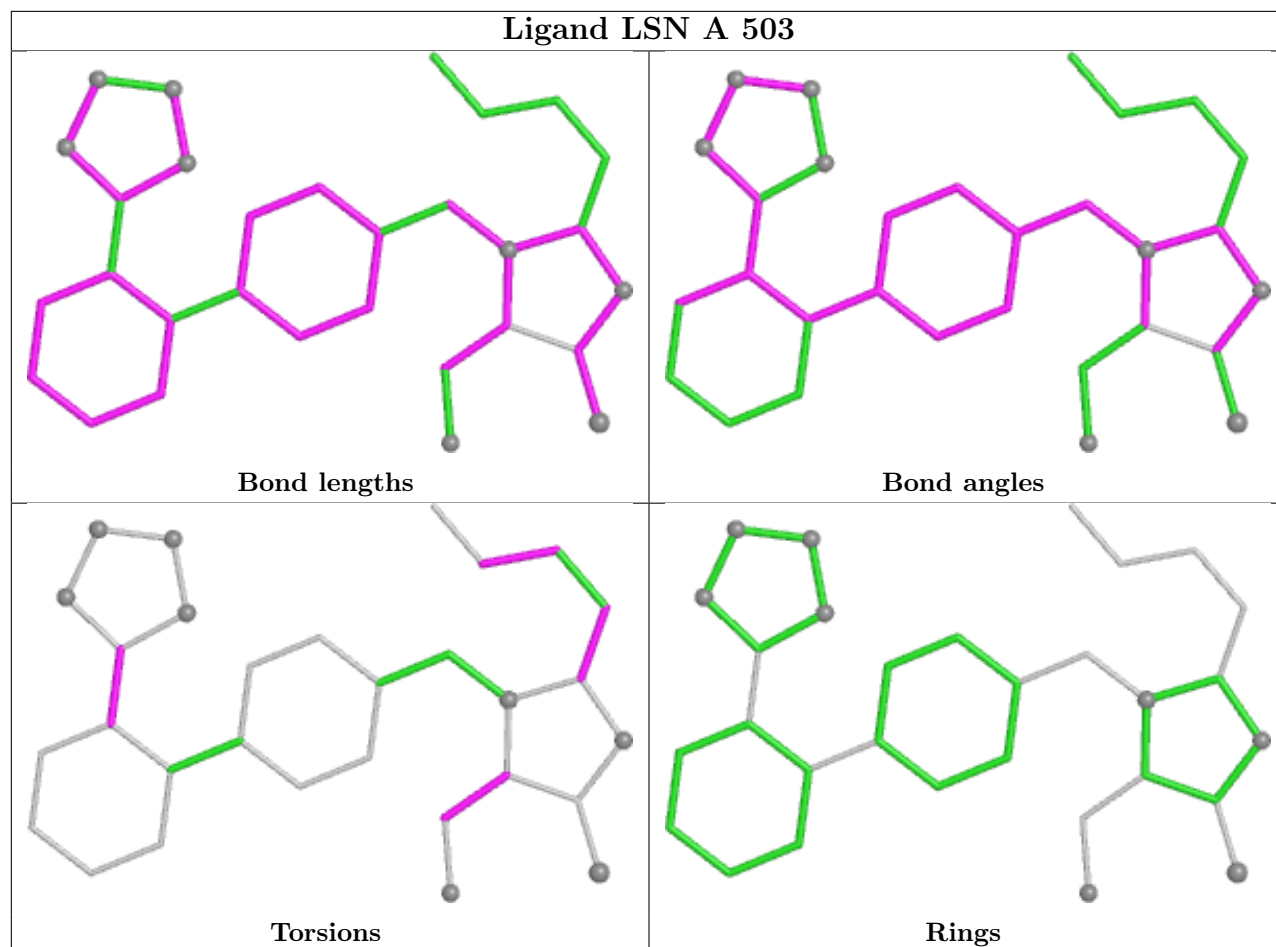
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	502	LSN	7	0

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.

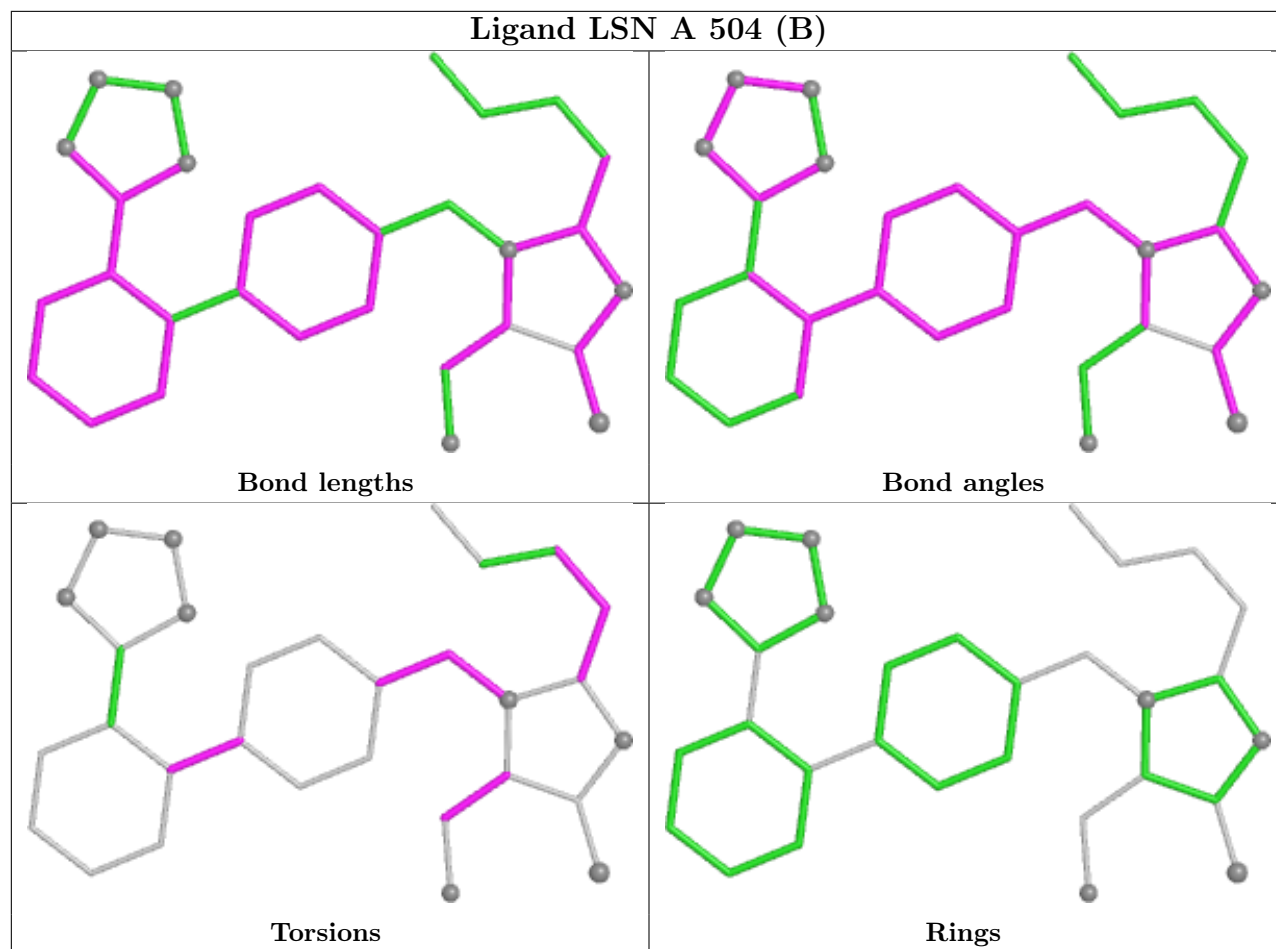


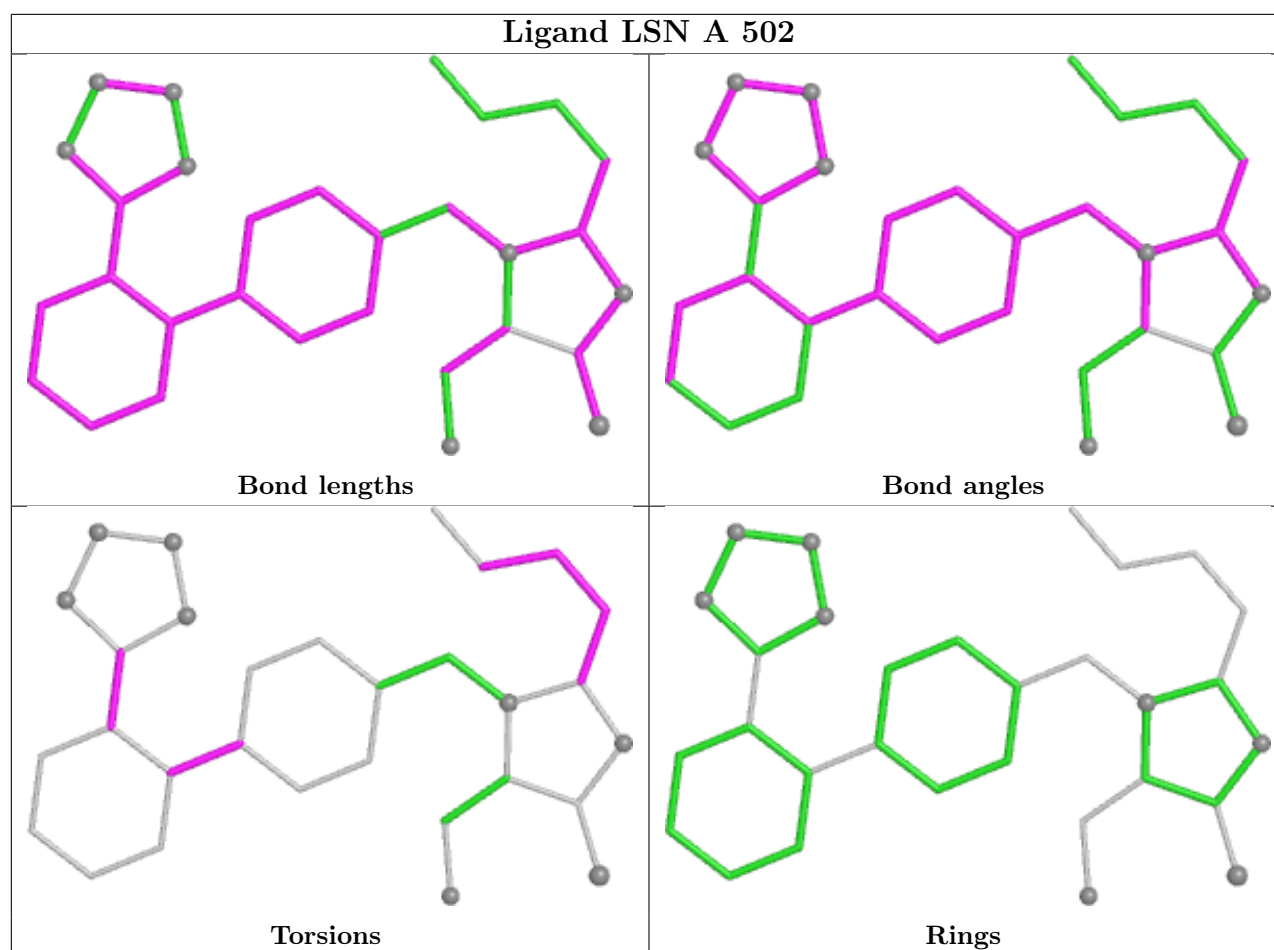


Ligand LSN A 503



Ligand LSN A 504 (B)





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 ⓘ

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	463/476 (97%)	0.82	73 (15%) 5 4	27, 47, 76, 88	0

All (73) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	100	PHE	6.6
1	A	222	ILE	5.3
1	A	45	ILE	4.6
1	A	43	LEU	4.6
1	A	275	LYS	4.6
1	A	71	LEU	4.5
1	A	223	ILE	4.1
1	A	47	ILE	4.0
1	A	216	CYS	3.8
1	A	467	LEU	3.8
1	A	299	THR	3.8
1	A	215	ILE	3.8
1	A	472	VAL	3.6
1	A	462	VAL	3.6
1	A	110	PHE	3.5
1	A	108	ARG	3.5
1	A	253	GLU	3.5
1	A	104	GLU	3.4
1	A	185	LYS	3.4
1	A	278	GLN	3.4
1	A	99	ILE	3.4
1	A	106	ALA	3.4
1	A	219	PHE	3.4
1	A	28	LYS	3.4
1	A	42	ILE	3.3
1	A	328	GLU	3.3
1	A	464	PRO	3.2

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Mol	Chain	Res	Type	RSRZ
1	A	490	ILE	3.1
1	A	68	TYR	3.1
1	A	109	GLY	3.1
1	A	101	PRO	3.1
1	A	257	MET	3.0
1	A	44	GLN	2.9
1	A	35	PRO	2.9
1	A	221	PRO	2.9
1	A	102	LEU	2.9
1	A	217	ASN	2.9
1	A	198	MET	2.8
1	A	461	LEU	2.8
1	A	70	GLY	2.8
1	A	201	LEU	2.8
1	A	69	PHE	2.7
1	A	333	ARG	2.7
1	A	218	ASN	2.7
1	A	225	TYR	2.7
1	A	190	LYS	2.7
1	A	277	ASN	2.6
1	A	380	LEU	2.6
1	A	39	ILE	2.6
1	A	202	ASN	2.5
1	A	463	ASP	2.5
1	A	189	TYR	2.5
1	A	415	GLU	2.5
1	A	276	HIS	2.5
1	A	475	GLY	2.5
1	A	103	ALA	2.4
1	A	37	PRO	2.4
1	A	38	VAL	2.4
1	A	161	ALA	2.4
1	A	334	ASN	2.4
1	A	214	GLN	2.3
1	A	410	HIS	2.3
1	A	50	ILE	2.3
1	A	220	SER	2.2
1	A	36	LEU	2.2
1	A	107	ASN	2.2
1	A	259	ASN	2.2
1	A	187	PHE	2.1
1	A	377	ARG	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	162	SER	2.1
1	A	269	MET	2.0
1	A	34	THR	2.0
1	A	416	GLY	2.0

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 oligosaccharides in this entry.

6.4 Ligands [i](#)

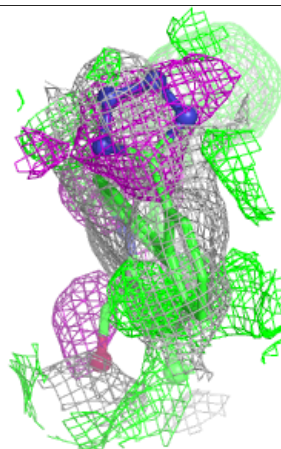
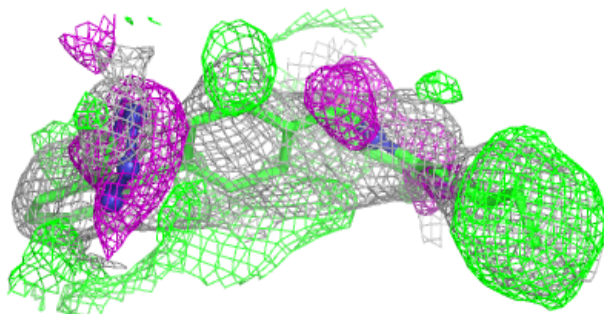
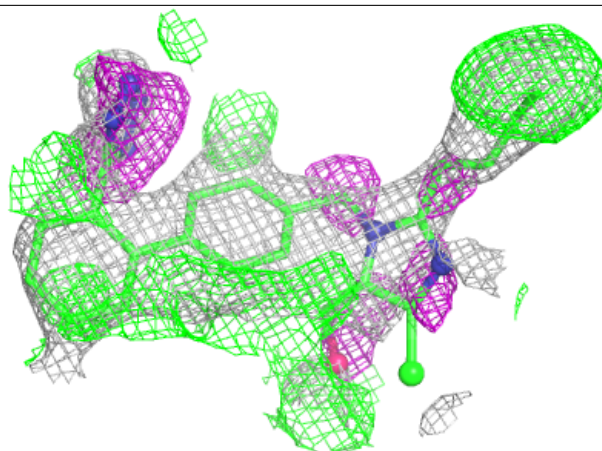
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	LSN	A	504[A]	30/30	0.27	0.45	19,51,96,140	30
3	LSN	A	504[B]	30/30	0.27	0.45	35,69,109,198	30
4	PO4	A	505	5/5	0.84	0.10	99,99,100,101	0
3	LSN	A	503	30/30	0.88	0.16	34,45,64,74	0
5	K	A	506	1/1	0.91	0.32	30,30,30,30	0
3	LSN	A	502	30/30	0.92	0.13	53,59,73,76	0
2	HEM	A	501	43/43	0.98	0.06	21,28,34,39	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.

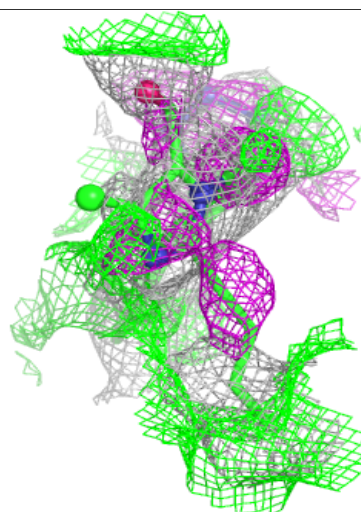
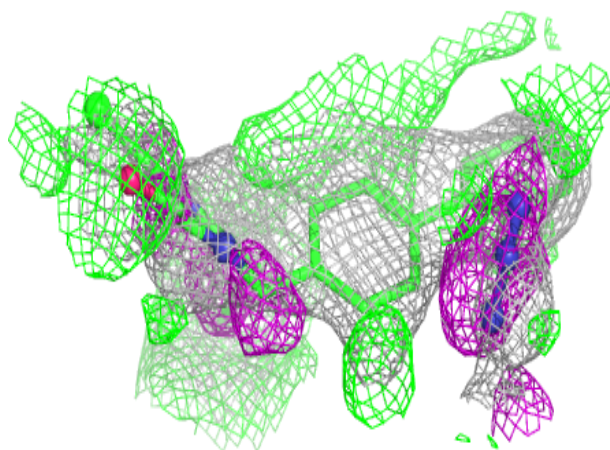
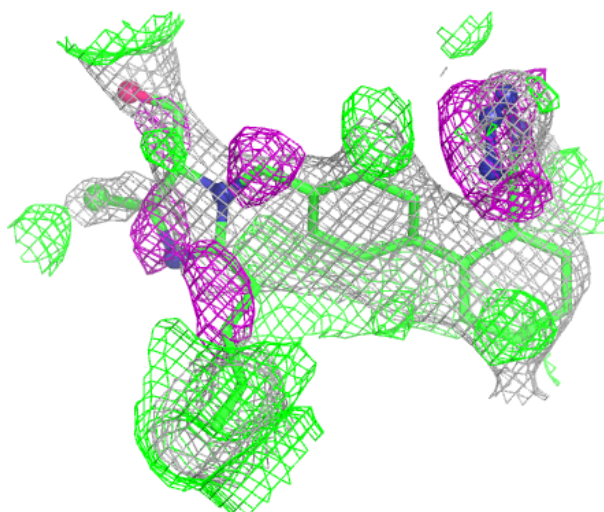
Electron density around LSN A 504 (A):

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



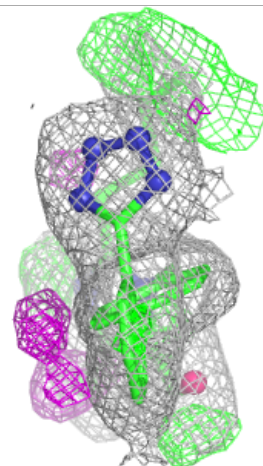
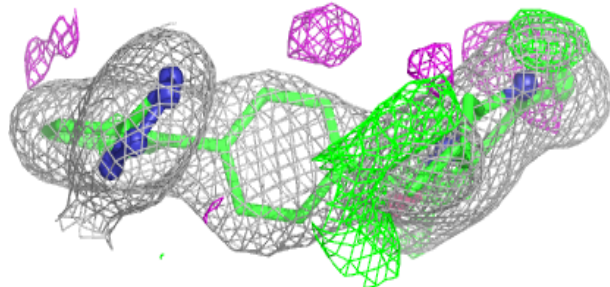
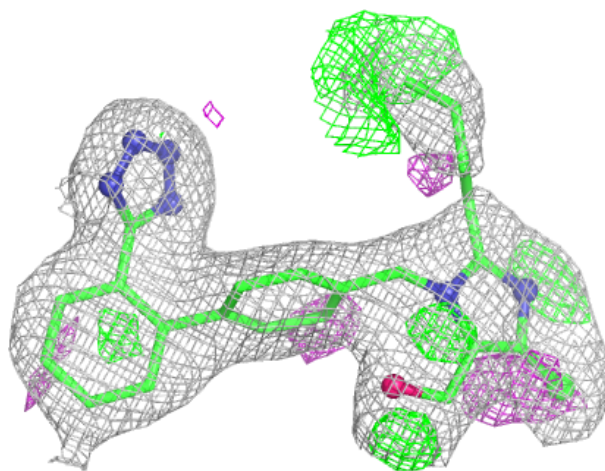
Electron density around LSN A 504 (B):

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



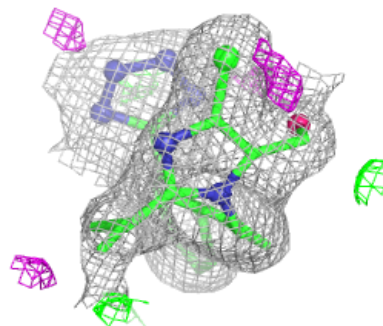
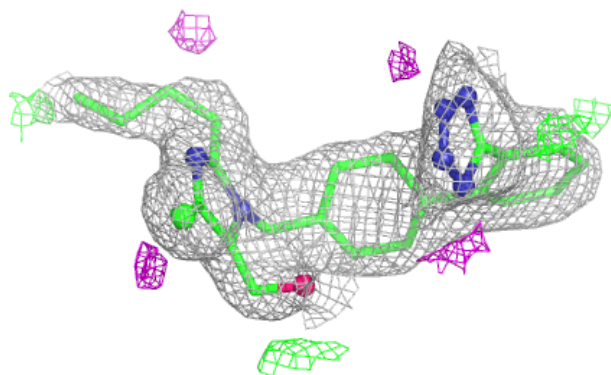
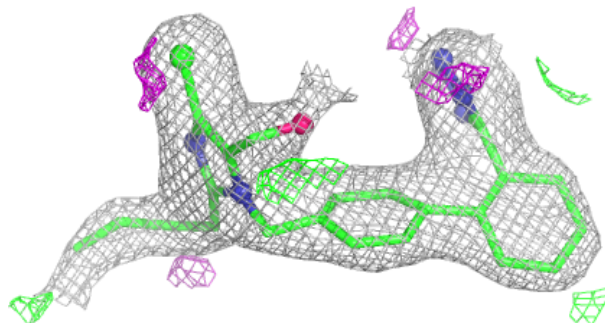
Electron density around LSN A 503:

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



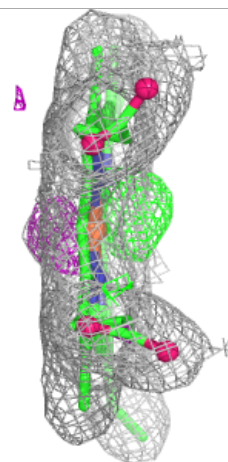
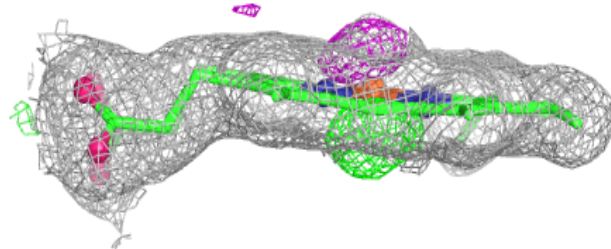
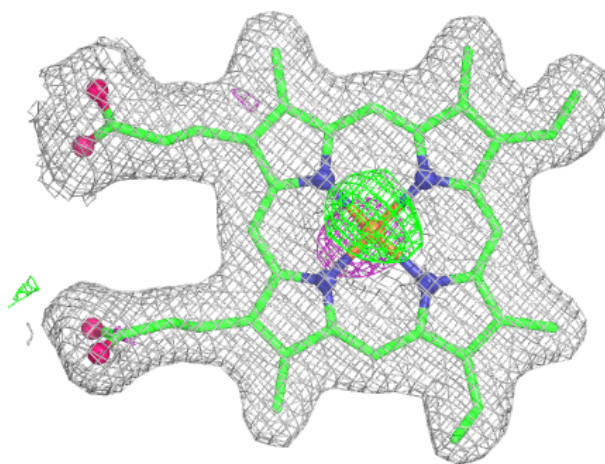
Electron density around LSN A 502:

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



Electron density around HEM A 501:

$2mF_o-DF_c$ (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.