



Full wwPDB X-ray Structure Validation Report ⓘ

May 17, 2020 – 06:08 am BST

PDB ID : 1K2R
Title : Structure of rat brain nNOS heme domain complexed with NG-nitro-L-arginine
Authors : Li, H.; Martasek, P.; Masters, B.S.S.; Poulos, T.L.; Raman, C.S.
Deposited on : 2001-09-28
Resolution : 2.15 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

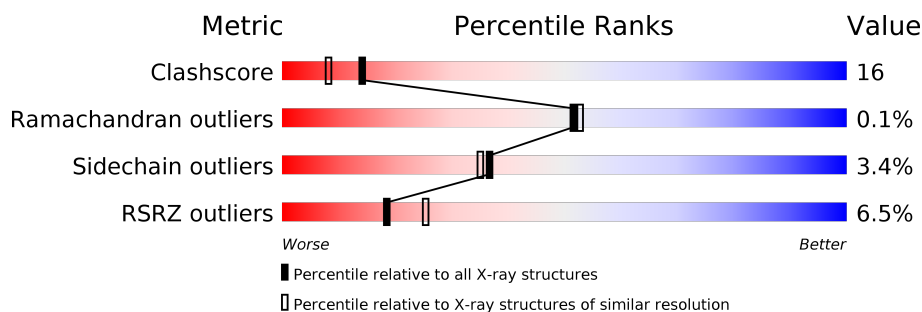
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.15 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))
Clashscore	141614	1585 (2.16-2.16)
Ramachandran outliers	138981	1560 (2.16-2.16)
Sidechain outliers	138945	1559 (2.16-2.16)
RSRZ outliers	127900	1456 (2.16-2.16)

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	419	<div> <div>9%</div> <div>65%</div> <div>30%</div> <div>..</div> </div>
1	B	419	<div> <div>4%</div> <div>67%</div> <div>29%</div> <div>..</div> </div>

2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 7206 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 nitric-oxide synthase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	407	Total	C	N	O	S	0	0	0
			3313	2121	566	605	21			
1	B	410	Total	C	N	O	S	0	0	0
			3341	2138	573	609	21			

- Molecule 2 is ACETATE ION (three-letter code: ACT) (formula: $C_2H_3O_2$).



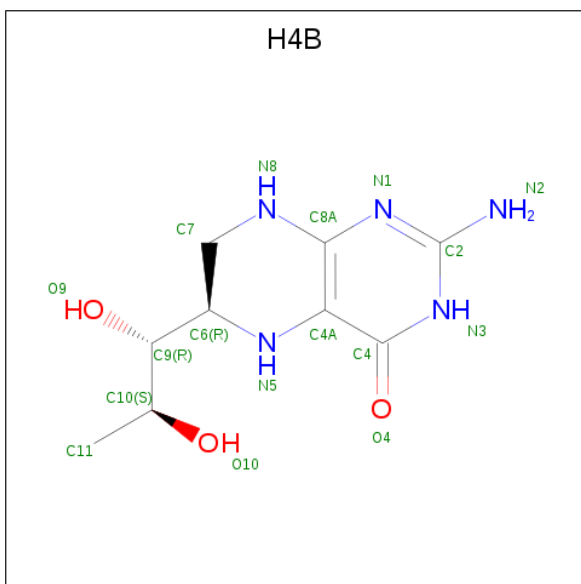
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			4	2	2		
2	B	1	Total	C	O	0	0
			4	2	2		

- Molecule 3 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula: $C_{34}H_{32}FeN_4O_4$).



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

- Molecule 4 is 5,6,7,8-TETRAHYDROBIOPTERIN (three-letter code: H4B) (formula: $\text{C}_9\text{H}_{15}\text{N}_5\text{O}_3$).



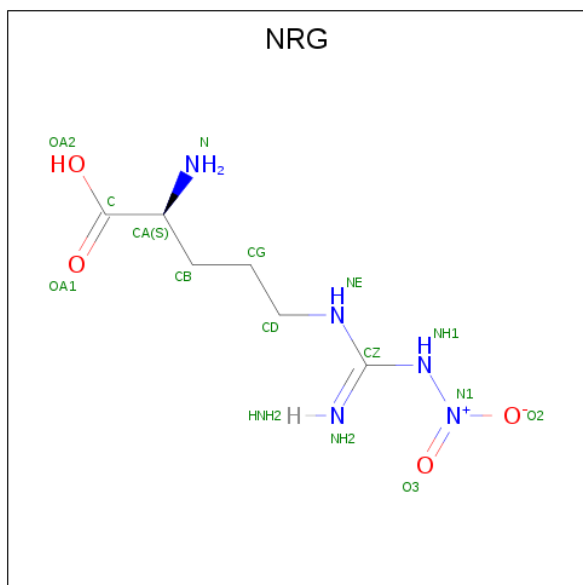
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			17	9	5	3		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	B	1	Total	C	N	O	0	0
			17	9	5	3		

- Molecule 5 is N-OMEGA-NITRO-L-ARGININE (three-letter code: NRG) (formula: $C_6H_{13}N_5O_4$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	N	O	0	0
			15	6	5	4		
5	B	1	Total	C	N	O	0	0
			15	6	5	4		

- Molecule 6 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	B	1	Total	Zn	0	0
			1	1		

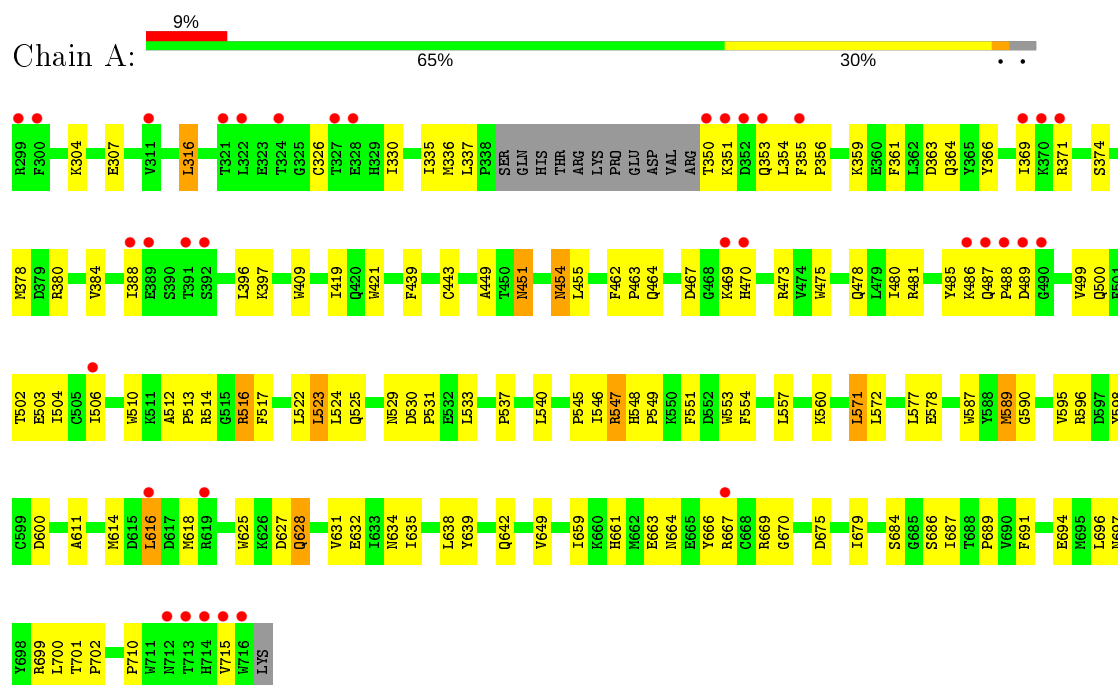
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	173	Total	O	0	0
			173	173		
7	B	220	Total	O	0	0
			220	220		

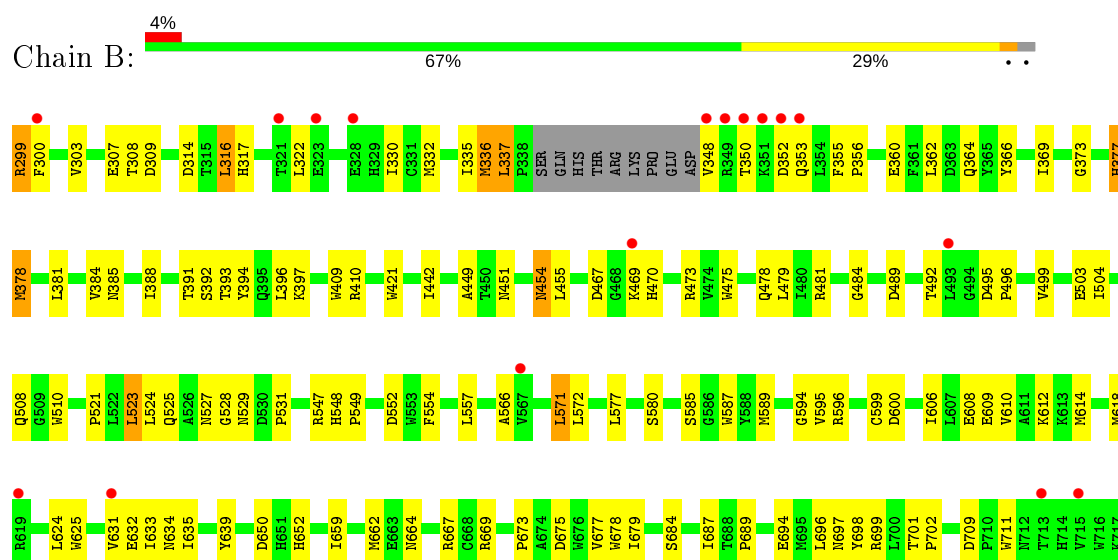
3 Residue-property plots

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: nitric-oxide synthase



• Molecule 1: nitric-oxide synthase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	51.65Å 110.49Å 164.74Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.50 – 2.15 29.50 – 2.14	Depositor EDS
% Data completeness (in resolution range)	98.3 (29.50-2.15) 87.1 (29.50-2.14)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	0.10	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.50 (at 2.14Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.228 , 0.270 0.216 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	25.7	Xtriage
Anisotropy	0.855	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 58.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	7206	wwPDB-VP
Average B, all atoms (Å ²)	42.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.46% 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: HEM, ZN, NRG, H4B, 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	0.34	0/3406	0.62	2/4621 (0.0%)
1	B	0.34	0/3434	0.62	1/4656 (0.0%)
All	All	0.34	0/6840	0.62	3/9277 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	326	CYS	CA-CB-SG	6.48	125.67	114.00
1	A	589	MET	N-CA-C	-5.21	96.93	111.00
1	B	589	MET	N-CA-C	-5.19	96.99	111.00

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	3313	0	3221	110	0
1	B	3341	0	3256	107	0
2	A	4	0	3	0	0
2	B	4	0	3	0	0
3	A	43	0	30	0	0
3	B	43	0	30	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	17	0	15	0	0
4	B	17	0	15	1	0
5	A	15	0	11	0	0
5	B	15	0	11	0	0
6	B	1	0	0	0	0
7	A	173	0	0	5	0
7	B	220	0	0	7	0
All	All	7206	0	6595	209	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 16.

All (209) 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:523:LEU:HD22	1:A:531:PRO:HB2	1.33	1.10
1:B:523:LEU:HD22	1:B:531:PRO:HB2	1.36	1.08
1:B:373:GLY:H	1:B:377:HIS:HD2	1.07	0.96
1:B:373:GLY:H	1:B:377:HIS:CD2	1.92	0.88
1:B:478:GLN:HB2	1:B:481:ARG:HG3	1.58	0.85
1:A:549:PRO:HG3	1:A:639:TYR:CG	2.14	0.83
1:B:489:ASP:HB2	7:B:2947:HOH:O	1.79	0.81
1:B:614:MET:HE3	1:B:632:GLU:HG3	1.64	0.80
1:A:396:LEU:HD13	1:A:577:LEU:HD12	1.65	0.77
1:B:587:TRP:H	3:B:750:HEM:HAB	1.52	0.73
1:A:478:GLN:HB2	1:A:481:ARG:HG3	1.71	0.72
1:A:337:LEU:HD12	1:A:337:LEU:O	1.89	0.72
1:B:470:HIS:HB3	1:B:527:ASN:ND2	2.05	0.72
1:B:299:ARG:HG3	1:B:300:PHE:N	2.05	0.71
1:A:537:PRO:HD2	1:A:540:LEU:HD12	1.74	0.69
1:A:545:PRO:HG2	1:A:547:ARG:NH1	2.10	0.66
1:B:350:THR:HB	1:B:352:ASP:OD1	1.93	0.66
1:A:616:LEU:HD13	1:A:625:TRP:HB2	1.77	0.66
1:B:610:VAL:HG21	1:B:633:ILE:HD11	1.78	0.66
1:A:554:PHE:O	1:A:557:LEU:HD13	1.94	0.66
1:B:451:ASN:HB3	1:B:454:ASN:O	1.97	0.64
1:A:366:TYR:HA	1:A:369:ILE:HG12	1.81	0.63
1:B:360:GLU:O	1:B:364:GLN:HG3	1.99	0.63
1:B:475:TRP:HB2	1:B:523:LEU:HB3	1.79	0.63
1:B:549:PRO:HG3	1:B:639:TYR:CG	2.33	0.63
1:B:523:LEU:CD2	1:B:531:PRO:HB2	2.23	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:330:ILE:HD11	1:B:317:HIS:CD2	2.34	0.62
1:A:553:TRP:CZ3	1:A:557:LEU:HD11	2.34	0.62
1:A:696:LEU:HD22	1:B:330:ILE:HD11	1.82	0.62
1:B:499:VAL:O	1:B:503:GLU:HG3	2.00	0.61
1:B:332:MET:HB3	1:B:335:ILE:HG13	1.82	0.61
1:B:566:ALA:HB2	1:B:585:SER:HB3	1.84	0.60
1:B:336:MET:HE2	1:B:678:TRP:HZ2	1.67	0.60
1:A:571:LEU:HD12	1:A:572:LEU:N	2.17	0.60
1:A:635:ILE:CD1	1:B:624:LEU:HB2	2.31	0.60
1:A:350:THR:HB	1:A:353:GLN:HG3	1.83	0.60
1:A:316:LEU:HD11	1:A:669:ARG:HD3	1.84	0.60
1:A:335:ILE:HD13	1:B:694:GLU:HB3	1.83	0.60
1:B:373:GLY:N	1:B:377:HIS:HD2	1.90	0.60
1:B:388:ILE:O	1:B:392:SER:N	2.33	0.59
1:A:537:PRO:HB2	1:A:540:LEU:HG	1.85	0.59
1:B:299:ARG:HH11	1:B:299:ARG:HG2	1.67	0.59
1:A:627:ASP:O	1:A:631:VAL:HG23	2.02	0.58
1:B:396:LEU:HG	1:B:577:LEU:HD12	1.85	0.58
1:B:631:VAL:O	1:B:635:ILE:HG12	2.02	0.58
1:A:694:GLU:HB3	1:B:335:ILE:HD13	1.86	0.58
1:A:473:ARG:NH2	1:A:710:PRO:HD3	2.18	0.58
1:A:635:ILE:HD11	1:B:624:LEU:HB2	1.84	0.57
1:A:485:TYR:HE2	1:A:512:ALA:HB1	1.69	0.57
1:A:304:LYS:O	1:A:694:GLU:HG3	2.03	0.57
1:A:684:SER:HB3	1:A:687:ILE:CG1	2.33	0.57
1:B:632:GLU:O	1:B:635:ILE:HB	2.05	0.57
1:A:684:SER:HB3	1:A:687:ILE:HG12	1.86	0.57
1:B:684:SER:HB3	1:B:687:ILE:HD11	1.86	0.56
1:B:355:PHE:CE1	1:B:385:ASN:HB2	2.41	0.56
1:B:610:VAL:O	1:B:614:MET:HG3	2.06	0.56
1:A:659:ILE:HG13	1:A:689:PRO:HB2	1.88	0.56
1:B:525:GLN:HG3	1:B:529:ASN:O	2.05	0.56
1:A:611:ALA:HB1	1:A:616:LEU:HD11	1.88	0.55
1:B:571:LEU:HD12	1:B:572:LEU:N	2.21	0.55
1:A:525:GLN:HG3	1:A:529:ASN:O	2.06	0.55
1:A:664:ASN:ND2	7:A:1993:HOH:O	2.40	0.55
1:B:299:ARG:HG3	1:B:300:PHE:H	1.71	0.55
1:B:337:LEU:HD12	1:B:337:LEU:O	2.05	0.55
1:A:307:GLU:HG3	7:B:2954:HOH:O	2.05	0.54
1:A:554:PHE:HA	1:A:557:LEU:HD13	1.90	0.54
1:A:361:PHE:O	1:A:364:GLN:HB3	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:478:GLN:HB2	1:A:481:ARG:CG	2.37	0.54
1:A:330:ILE:HD11	1:B:317:HIS:HD2	1.71	0.54
1:A:638:LEU:O	1:A:642:GLN:HG3	2.09	0.53
1:A:675:ASP:O	1:A:679:ILE:HG12	2.08	0.53
1:A:485:TYR:CE2	1:A:512:ALA:HB1	2.44	0.53
1:B:352:ASP:OD1	1:B:353:GLN:N	2.41	0.53
1:A:631:VAL:O	1:A:635:ILE:HG12	2.09	0.53
1:B:557:LEU:HD23	1:B:609:GLU:OE2	2.09	0.53
1:A:355:PHE:N	1:A:356:PRO:HD2	2.24	0.53
1:A:510:TRP:HB2	1:A:533:LEU:HD13	1.91	0.53
1:B:391:THR:O	1:B:392:SER:HB2	2.09	0.53
1:B:442:ILE:HG23	1:B:479:LEU:HD13	1.90	0.52
1:B:308:THR:O	1:B:309:ASP:HB2	2.09	0.52
1:B:684:SER:HB3	1:B:687:ILE:CG1	2.40	0.52
1:B:322:LEU:HB3	1:B:699:ARG:HH21	1.75	0.52
1:A:502:THR:O	1:A:506:ILE:HG13	2.10	0.52
1:A:396:LEU:HD13	1:A:577:LEU:CD1	2.38	0.51
1:A:571:LEU:HD11	1:A:578:GLU:HB3	1.93	0.51
1:A:715:VAL:O	1:A:715:VAL:HG23	2.11	0.51
1:A:684:SER:HB3	1:A:687:ILE:HD11	1.93	0.51
1:A:701:THR:HA	1:A:702:PRO:C	2.31	0.51
1:A:316:LEU:HD11	1:A:669:ARG:CD	2.41	0.51
1:A:487:GLN:HB3	1:A:488:PRO:HD2	1.93	0.51
1:A:396:LEU:CD1	1:A:577:LEU:HD12	2.39	0.50
1:A:522:LEU:O	1:A:533:LEU:HA	2.11	0.50
1:A:384:VAL:O	1:A:388:ILE:HG13	2.11	0.50
1:A:353:GLN:O	1:A:356:PRO:HG2	2.12	0.50
1:B:299:ARG:NH1	1:B:299:ARG:HG2	2.26	0.50
1:B:664:ASN:HA	1:B:667:ARG:HD2	1.93	0.49
1:A:545:PRO:HG2	1:A:547:ARG:HH11	1.76	0.49
1:A:589:MET:HA	1:A:649:VAL:O	2.12	0.49
1:B:314:ASP:OD1	1:B:317:HIS:ND1	2.42	0.49
1:A:659:ILE:O	1:A:663:GLU:HG3	2.13	0.49
1:B:332:MET:HB3	1:B:335:ILE:CG1	2.42	0.49
1:B:322:LEU:HB2	1:B:699:ARG:HE	1.77	0.49
1:B:388:ILE:HA	1:B:393:THR:O	2.13	0.49
1:B:484:GLY:HA3	1:B:495:ASP:O	2.12	0.49
1:A:666:TYR:O	1:A:670:GLY:HA2	2.13	0.48
1:A:553:TRP:HZ3	1:A:557:LEU:HD11	1.74	0.48
1:A:596:ARG:O	1:A:600:ASP:HB2	2.14	0.48
1:A:628:GLN:NE2	1:B:632:GLU:OE2	2.47	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:594:GLY:HA3	1:B:634:ASN:ND2	2.29	0.47
1:B:554:PHE:HB3	7:B:2971:HOH:O	2.14	0.47
1:B:610:VAL:HG21	1:B:633:ILE:CD1	2.44	0.47
1:A:595:VAL:HG23	1:A:634:ASN:HD21	1.79	0.47
1:A:475:TRP:HB2	1:A:523:LEU:HB3	1.97	0.47
1:A:499:VAL:O	1:A:503:GLU:HG3	2.15	0.47
1:B:650:ASP:OD2	1:B:652:HIS:HB2	2.15	0.47
1:B:504:ILE:O	1:B:508:GLN:HG2	2.15	0.47
1:B:393:THR:HG23	1:B:394:TYR:N	2.30	0.47
1:B:303:VAL:HG13	1:B:694:GLU:HB2	1.97	0.46
1:B:596:ARG:O	1:B:600:ASP:HB2	2.16	0.46
1:A:684:SER:HB3	1:A:687:ILE:CD1	2.46	0.46
1:B:397:LYS:HD2	7:B:2899:HOH:O	2.15	0.46
1:A:686:SER:HA	1:A:691:PHE:CG	2.51	0.46
1:A:510:TRP:HB2	1:A:533:LEU:CD1	2.46	0.46
1:A:467:ASP:OD1	1:A:470:HIS:ND1	2.45	0.45
1:A:664:ASN:OD1	1:A:667:ARG:NH2	2.49	0.45
1:B:510:TRP:CE2	1:B:521:PRO:HD3	2.52	0.45
1:B:348:VAL:O	1:B:348:VAL:HG13	2.17	0.45
1:B:352:ASP:OD1	1:B:353:GLN:HG3	2.16	0.45
1:B:492:THR:HG21	1:B:496:PRO:HA	1.99	0.45
1:A:451:ASN:HB3	1:A:454:ASN:O	2.16	0.45
1:B:366:TYR:HA	1:B:369:ILE:HG12	1.99	0.45
1:A:409:TRP:CE3	1:A:421:TRP:HA	2.51	0.45
1:B:355:PHE:N	1:B:356:PRO:HD2	2.31	0.45
1:A:548:HIS:ND1	1:A:549:PRO:HD2	2.32	0.45
1:A:487:GLN:HB3	1:A:488:PRO:CD	2.47	0.45
1:A:517:PHE:HB2	1:A:560:LYS:HE2	1.99	0.45
1:A:549:PRO:HG3	1:A:639:TYR:CD2	2.49	0.45
1:B:675:ASP:O	1:B:679:ILE:HG12	2.16	0.45
1:B:316:LEU:HB3	1:B:698:TYR:OH	2.17	0.45
1:B:701:THR:HA	1:B:702:PRO:C	2.37	0.45
1:A:378:MET:HE2	1:A:378:MET:HA	1.98	0.44
1:A:467:ASP:OD2	1:A:469:LYS:HB2	2.16	0.44
1:B:524:LEU:O	1:B:531:PRO:HA	2.17	0.44
1:B:571:LEU:HD13	1:B:580:SER:HA	1.99	0.44
1:B:684:SER:HB3	1:B:687:ILE:CD1	2.47	0.44
1:A:614:MET:HE3	1:A:632:GLU:HG3	1.99	0.44
1:B:664:ASN:O	1:B:667:ARG:HG2	2.18	0.44
1:A:590:GLY:HA3	7:A:1898:HOH:O	2.18	0.44
1:B:608:GLU:O	1:B:612:LYS:HG3	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:464:GLN:HG2	7:A:1975:HOH:O	2.18	0.44
1:B:709:ASP:HB3	1:B:711:TRP:CE2	2.52	0.44
1:A:516:ARG:HG2	1:A:517:PHE:CE1	2.52	0.44
1:B:362:LEU:HD11	1:B:384:VAL:HG21	2.00	0.44
1:A:475:TRP:HA	1:A:710:PRO:HG3	1.99	0.44
1:A:455:LEU:HD12	1:A:587:TRP:HB3	2.00	0.44
1:B:378:MET:CE	1:B:381:LEU:HD12	2.47	0.44
1:B:409:TRP:CE3	1:B:421:TRP:HA	2.53	0.44
1:A:551:PHE:HB3	1:A:553:TRP:NE1	2.33	0.43
1:A:513:PRO:O	1:A:514:ARG:HB2	2.18	0.43
1:A:359:LYS:HG2	1:A:363:ASP:OD2	2.19	0.43
1:A:524:LEU:O	1:A:531:PRO:HA	2.19	0.43
1:A:330:ILE:CD1	1:B:317:HIS:CD2	3.01	0.43
1:B:554:PHE:O	1:B:557:LEU:HB2	2.18	0.43
1:A:614:MET:CE	1:A:632:GLU:HG3	2.49	0.42
1:B:396:LEU:HG	1:B:577:LEU:CD1	2.48	0.42
1:A:462:PHE:HB3	1:A:463:PRO:CD	2.49	0.42
1:B:470:HIS:HA	1:B:528:GLY:HA3	2.02	0.42
1:A:486:LYS:HG3	7:A:1941:HOH:O	2.18	0.42
1:B:481:ARG:HB2	7:B:2867:HOH:O	2.20	0.42
1:B:659:ILE:HG13	1:B:689:PRO:HB2	2.01	0.42
1:A:419:ILE:O	1:A:419:ILE:HG12	2.20	0.42
1:A:548:HIS:HA	1:A:549:PRO:HD3	1.90	0.42
1:B:467:ASP:OD2	1:B:469:LYS:HB2	2.18	0.42
1:A:350:THR:HG22	1:A:351:LYS:N	2.35	0.42
1:B:673:PRO:HA	1:B:696:LEU:O	2.19	0.42
1:B:336:MET:HE2	1:B:678:TRP:CZ2	2.52	0.42
1:B:595:VAL:HG23	1:B:634:ASN:HD21	1.85	0.42
1:A:449:ALA:O	1:A:455:LEU:HA	2.20	0.42
3:B:750:HEM:CMC	3:B:750:HEM:HBC2	2.49	0.42
1:A:371:ARG:HG3	1:A:371:ARG:HH11	1.85	0.41
1:B:393:THR:O	1:B:394:TYR:HB3	2.20	0.41
1:B:548:HIS:ND1	1:B:549:PRO:HD2	2.35	0.41
1:B:548:HIS:NE2	1:B:632:GLU:OE1	2.53	0.41
1:A:618:MET:HA	1:A:625:TRP:CD1	2.55	0.41
1:B:595:VAL:O	1:B:599:CYS:HB2	2.20	0.41
1:A:455:LEU:HD12	1:A:587:TRP:CB	2.49	0.41
1:A:553:TRP:CE3	1:A:557:LEU:HD11	2.54	0.41
1:A:380:ARG:NH1	1:A:397:LYS:HE3	2.35	0.41
1:A:439:PHE:CZ	1:A:443:CYS:SG	3.14	0.41
1:B:307:GLU:HG3	7:B:2893:HOH:O	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:480:ILE:HA	7:A:1944:HOH:O	2.20	0.41
1:A:546:ILE:HG13	1:A:598:TYR:OH	2.20	0.41
1:B:606:ILE:HD11	1:B:633:ILE:HD13	2.02	0.41
1:A:557:LEU:N	1:A:557:LEU:HD12	2.35	0.41
1:B:677:VAL:CG1	4:B:2760:H4B:H71	2.51	0.41
1:A:419:ILE:HB	1:A:661:HIS:HB2	2.03	0.41
1:A:699:ARG:O	1:A:700:LEU:HD23	2.21	0.41
1:A:616:LEU:O	1:A:616:LEU:HD12	2.21	0.41
1:B:473:ARG:HD3	1:B:580:SER:HB2	2.03	0.41
1:B:632:GLU:HA	1:B:635:ILE:HG13	2.03	0.41
1:B:350:THR:HG22	1:B:352:ASP:H	1.85	0.40
1:A:500:GLN:O	1:A:504:ILE:HG13	2.21	0.40
1:A:618:MET:HG2	1:A:625:TRP:CD2	2.56	0.40
1:B:449:ALA:O	1:B:455:LEU:HA	2.22	0.40
1:B:410:ARG:CZ	1:B:669:ARG:HD2	2.51	0.40
1:B:662:MET:HE3	7:B:2932:HOH:O	2.20	0.40
1:A:350:THR:O	1:A:354:LEU:N	2.38	0.40
1:B:618:MET:HG2	1:B:625:TRP:CD2	2.57	0.40
1:B:667:ARG:HE	1:B:667:ARG:HB3	1.74	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	403/419 (96%)	375 (93%)	27 (7%)	1 (0%)	47	46
1	B	406/419 (97%)	383 (94%)	23 (6%)	0	100	100
All	All	809/838 (96%)	758 (94%)	50 (6%)	1 (0%)	51	53

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	374	SER

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	363/375 (97%)	350 (96%)	13 (4%)	35	33
1	B	366/375 (98%)	354 (97%)	12 (3%)	38	37
All	All	729/750 (97%)	704 (97%)	25 (3%)	37	35

All (25) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	316	LEU
1	A	336	MET
1	A	451	ASN
1	A	454	ASN
1	A	489	ASP
1	A	516	ARG
1	A	523	LEU
1	A	530	ASP
1	A	547	ARG
1	A	571	LEU
1	A	616	LEU
1	A	628	GLN
1	A	697	ASN
1	B	299	ARG
1	B	316	LEU
1	B	336	MET
1	B	337	LEU
1	B	377	HIS
1	B	378	MET
1	B	454	ASN
1	B	523	LEU
1	B	547	ARG
1	B	552	ASP

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Mol	Chain	Res	Type
1	B	571	LEU
1	B	697	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	329	HIS
1	A	353	GLN
1	A	364	GLN
1	A	451	ASN
1	A	454	ASN
1	A	628	GLN
1	A	634	ASN
1	A	697	ASN
1	A	712	ASN
1	A	714	HIS
1	B	377	HIS
1	B	425	GLN
1	B	451	ASN
1	B	454	ASN
1	B	527	ASN
1	B	634	ASN
1	B	697	ASN
1	B	712	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 carbohydrates in this entry.

5.6 Ligand geometry

Of 9 ligands modelled in this entry, 1 is monoatomic - leaving 8 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	NRG	B	2775	-	6,14,14	0.82	0	6,17,17	0.80	0
3	HEM	A	750	1	27,50,50	1.56	6 (22%)	17,82,82	1.28	2 (11%)
3	HEM	B	750	1	27,50,50	1.77	6 (22%)	17,82,82	1.52	2 (11%)
2	ACT	B	2860	-	1,3,3	2.21	1 (100%)	0,3,3	0.00	-
5	NRG	A	1775	-	6,14,14	0.88	0	6,17,17	0.39	0
4	H4B	A	1760	-	16,18,18	2.24	3 (18%)	11,26,26	4.16	8 (72%)
2	ACT	A	1860	-	1,3,3	3.63	1 (100%)	0,3,3	0.00	-
4	H4B	B	2760	-	16,18,18	2.19	4 (25%)	11,26,26	4.25	9 (81%)

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	NRG	B	2775	-	-	0/8/15/15	-
3	HEM	A	750	1	-	0/6/54/54	-
3	HEM	B	750	1	-	0/6/54/54	-
5	NRG	A	1775	-	-	0/8/15/15	-
4	H4B	A	1760	-	-	0/8/17/17	0/2/2/2
4	H4B	B	2760	-	-	0/8/17/17	0/2/2/2

All (21) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	1760	H4B	C4-N3	5.87	1.43	1.33
4	B	2760	H4B	C4-N3	5.36	1.42	1.33
4	A	1760	H4B	C4A-N5	4.43	1.47	1.38
4	B	2760	H4B	C6-N5	4.15	1.54	1.45
3	B	750	HEM	C3B-C2B	-4.04	1.34	1.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	750	HEM	C3B-CAB	-4.01	1.39	1.47
4	B	2760	H4B	C4A-N5	4.01	1.46	1.38
4	A	1760	H4B	C6-N5	4.01	1.53	1.45
2	A	1860	ACT	CH3-C	3.63	1.53	1.48
3	B	750	HEM	C3C-CAC	-3.54	1.40	1.47
3	A	750	HEM	C3B-C2B	-3.53	1.35	1.40
3	A	750	HEM	C3C-CAC	-3.28	1.41	1.47
3	A	750	HEM	C3B-CAB	-3.06	1.41	1.47
3	B	750	HEM	C3C-C2C	-2.85	1.36	1.40
3	B	750	HEM	CAA-C2A	2.63	1.55	1.52
3	A	750	HEM	C1D-ND	2.37	1.41	1.36
2	B	2860	ACT	CH3-C	2.21	1.51	1.48
3	A	750	HEM	C1A-NA	2.19	1.40	1.36
3	A	750	HEM	CAA-C2A	2.10	1.55	1.52
4	B	2760	H4B	C7-N8	2.07	1.48	1.44
3	B	750	HEM	C1A-NA	2.02	1.40	1.36

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	2760	H4B	C4-C4A-C8A	9.30	122.83	114.57
4	A	1760	H4B	C4-C4A-C8A	8.77	122.36	114.57
4	A	1760	H4B	C4-N3-C2	5.65	124.91	115.93
4	B	2760	H4B	C4-N3-C2	5.53	124.71	115.93
4	A	1760	H4B	N3-C2-N1	-4.74	117.98	125.42
4	B	2760	H4B	N3-C2-N1	-4.54	118.30	125.42
4	A	1760	H4B	C4A-C4-N3	-3.74	113.39	124.01
4	A	1760	H4B	C2-N1-C8A	3.72	122.88	114.54
4	B	2760	H4B	C4A-C4-N3	-3.64	113.66	124.01
3	B	750	HEM	CBA-CAA-C2A	-3.58	105.89	112.49
4	B	2760	H4B	C2-N1-C8A	3.46	122.29	114.54
4	B	2760	H4B	N2-C2-N1	3.34	122.44	117.25
4	A	1760	H4B	N2-C2-N1	3.20	122.22	117.25
4	B	2760	H4B	C4-C4A-N5	-3.19	116.44	119.12
3	B	750	HEM	CBD-CAD-C3D	-3.12	106.73	112.48
4	A	1760	H4B	C4A-N5-C6	-3.05	112.87	121.16
4	B	2760	H4B	C4A-N5-C6	-3.00	112.98	121.16
3	A	750	HEM	CBA-CAA-C2A	-2.64	107.62	112.49
4	A	1760	H4B	C4-C4A-N5	-2.20	117.28	119.12
4	B	2760	H4B	O9-C9-C6	2.09	113.97	108.98
3	A	750	HEM	CBD-CAD-C3D	-2.01	108.78	112.48

There are no chirality outliers.

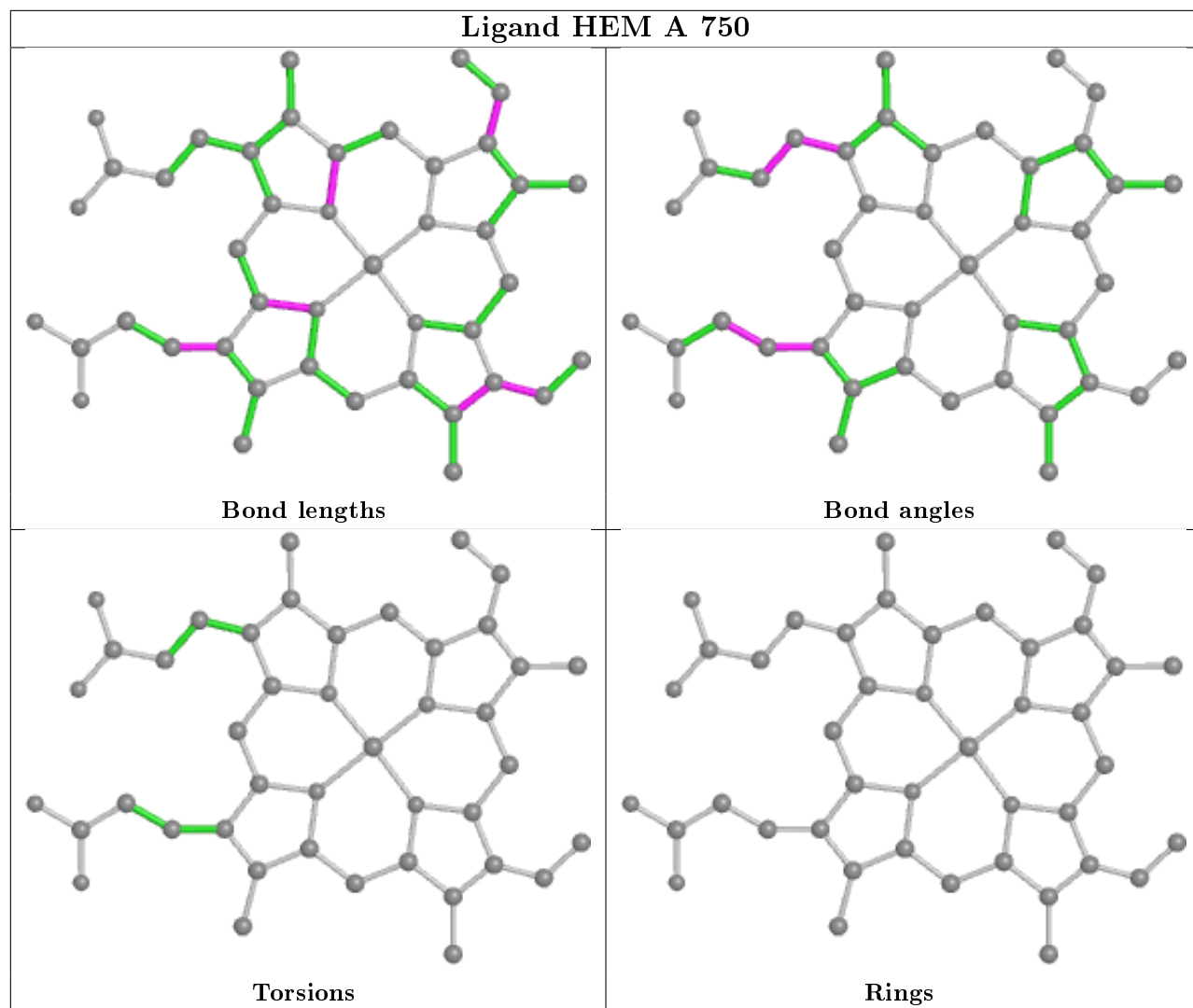
There are no torsion outliers.

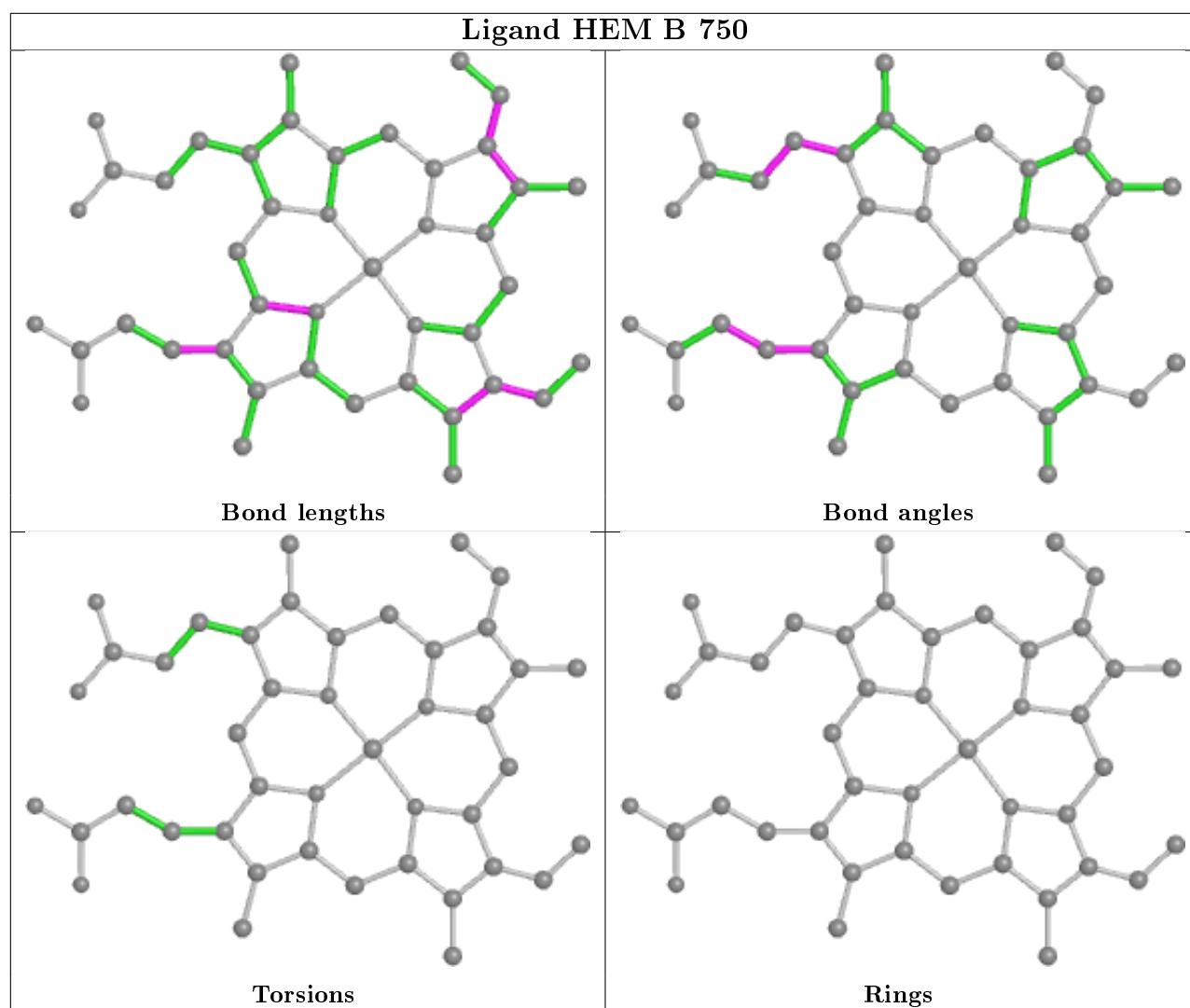
There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	750	HEM	2	0
4	B	2760	H4B	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](#)

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	407/419 (97%)	0.59	36 (8%) 10 14	21, 41, 75, 92	0
1	B	410/419 (97%)	0.30	17 (4%) 37 46	18, 37, 64, 95	0
All	All	817/838 (97%)	0.44	53 (6%) 18 25	18, 38, 72, 95	0

All (53) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	348	VAL	7.8
1	A	716	TRP	5.1
1	B	351	LYS	4.9
1	A	322	LEU	4.9
1	A	715	VAL	4.7
1	B	300	PHE	4.7
1	A	488	PRO	4.6
1	A	352	ASP	4.3
1	B	619	ARG	4.2
1	B	350	THR	4.1
1	A	469	LYS	3.7
1	A	299	ARG	3.6
1	A	712	ASN	3.6
1	A	486	LYS	3.5
1	A	324	THR	3.5
1	A	355	PHE	3.5
1	B	321	THR	3.5
1	A	351	LYS	3.4
1	A	619	ARG	3.4
1	A	350	THR	3.4
1	B	715	VAL	3.4
1	A	370	LYS	3.2
1	A	713	THR	3.2
1	A	353	GLN	3.1

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Mol	Chain	Res	Type	RSRZ
1	B	352	ASP	3.1
1	A	321	THR	3.1
1	A	489	ASP	2.9
1	A	388	ILE	2.9
1	A	300	PHE	2.9
1	A	392	SER	2.8
1	A	389	GLU	2.7
1	B	349	ARG	2.6
1	A	311	VAL	2.6
1	A	470	HIS	2.6
1	A	714	HIS	2.4
1	A	327	THR	2.4
1	A	487	GLN	2.4
1	B	567	VAL	2.3
1	B	353	GLN	2.3
1	B	328	GLU	2.3
1	B	493	LEU	2.3
1	A	371	ARG	2.3
1	A	328	GLU	2.2
1	B	713	THR	2.2
1	A	667	ARG	2.2
1	B	631	VAL	2.2
1	B	323	GLU	2.2
1	A	369	ILE	2.1
1	A	506	ILE	2.1
1	A	490	GLY	2.1
1	B	469	LYS	2.1
1	A	616	LEU	2.1
1	A	391	THR	2.1

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

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

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands

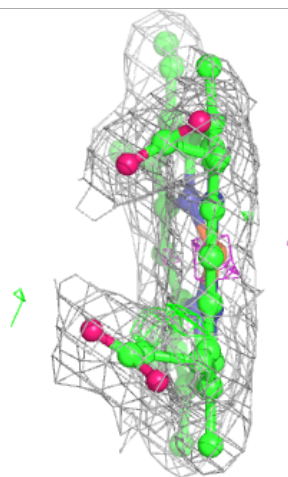
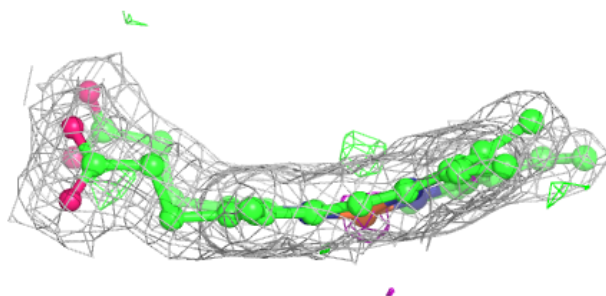
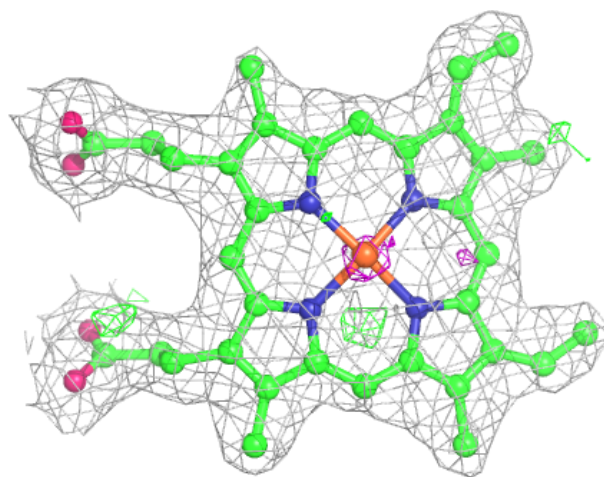
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
5	NRG	B	2775	15/15	0.93	0.18	15,24,33,35	0
2	ACT	A	1860	4/4	0.93	0.15	46,46,49,51	0
4	H4B	A	1760	17/17	0.95	0.15	18,23,31,34	0
5	NRG	A	1775	15/15	0.95	0.17	20,25,29,32	0
3	HEM	A	750	43/43	0.96	0.17	18,26,29,31	0
4	H4B	B	2760	17/17	0.96	0.14	20,23,33,36	0
3	HEM	B	750	43/43	0.97	0.16	17,23,29,32	0
2	ACT	B	2860	4/4	0.99	0.08	25,31,31,34	0
6	ZN	B	900	1/1	0.99	0.08	37,37,37,37	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.

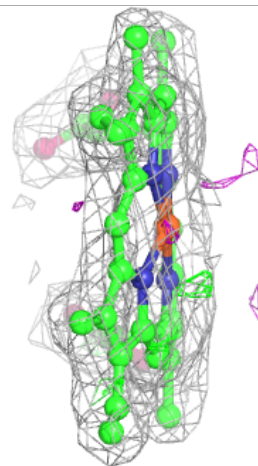
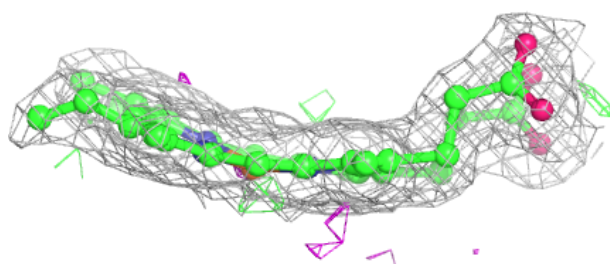
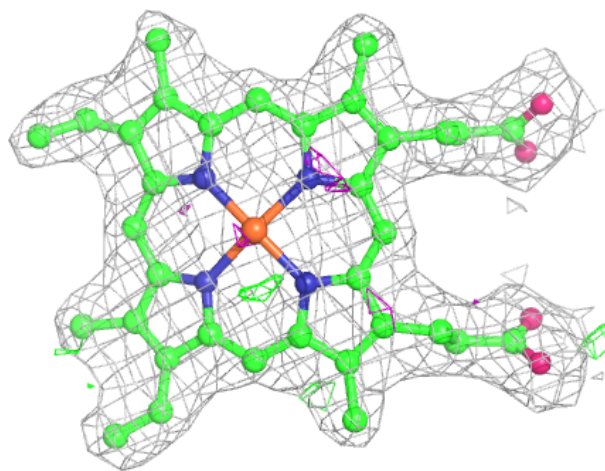
Electron density around HEM A 750:

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



Electron density around HEM B 750:

$2mF_o-DF_c$ (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.