



Full wwPDB X-ray Structure Validation Report ⓘ

May 19, 2020 – 10:27 am BST

PDB ID : 4L28
Title : Crystal structure of delta516-525 human cystathionine beta-synthase D444N mutant containing C-terminal 6xHis tag
Authors : Ereno, J.; Majtan, T.; Oyenarte, I.; Kraus, J.P.; Martinez, L.A.
Deposited on : 2013-06-04
Resolution : 2.63 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

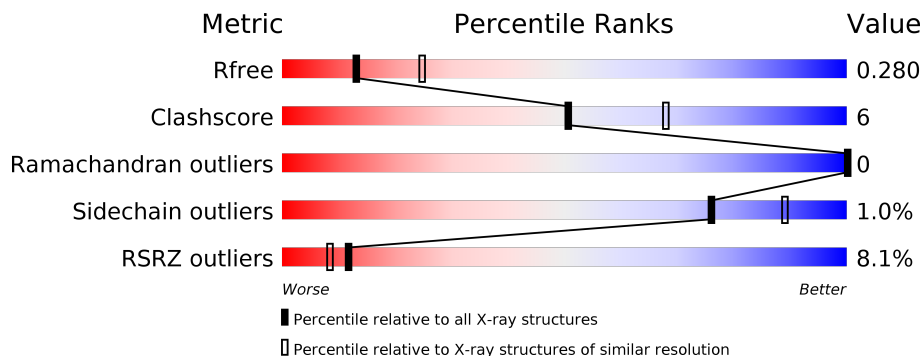
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.63 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	3797 (2.64-2.60)
Clashscore	141614	4168 (2.64-2.60)
Ramachandran outliers	138981	4093 (2.64-2.60)
Sidechain outliers	138945	4093 (2.64-2.60)
RSRZ outliers	127900	3731 (2.64-2.60)

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	558	 5% 76% 12% 12%
1	B	558	 9% 78% 11% 11%
1	C	558	 8% 76% 11% 12%
1	D	558	 7% 77% 11% 12%

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 15455 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 Cystathionine beta-synthase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	493	3803	2410	665	706	22	0	0	0
1	B	494	3813	2414	669	708	22	0	0	0
1	C	491	3791	2403	666	700	22	0	0	0
1	D	493	3816	2416	668	710	22	0	0	0

There are 36 discrepancies between the modelled and reference sequences:

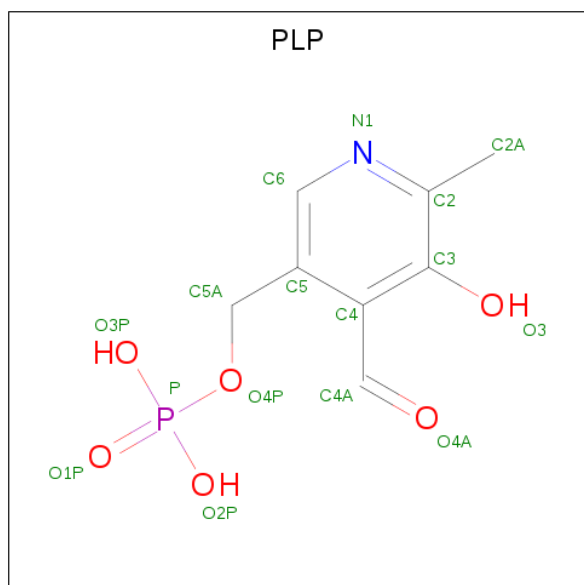
Chain	Residue	Modelled	Actual	Comment	Reference
A	444	ASN	ASP	ENGINEERED MUTATION	UNP P35520
A	552	LEU	-	EXPRESSION TAG	UNP P35520
A	553	GLU	-	EXPRESSION TAG	UNP P35520
A	554	HIS	-	EXPRESSION TAG	UNP P35520
A	555	HIS	-	EXPRESSION TAG	UNP P35520
A	556	HIS	-	EXPRESSION TAG	UNP P35520
A	557	HIS	-	EXPRESSION TAG	UNP P35520
A	558	HIS	-	EXPRESSION TAG	UNP P35520
A	559	HIS	-	EXPRESSION TAG	UNP P35520
B	444	ASN	ASP	ENGINEERED MUTATION	UNP P35520
B	552	LEU	-	EXPRESSION TAG	UNP P35520
B	553	GLU	-	EXPRESSION TAG	UNP P35520
B	554	HIS	-	EXPRESSION TAG	UNP P35520
B	555	HIS	-	EXPRESSION TAG	UNP P35520
B	556	HIS	-	EXPRESSION TAG	UNP P35520
B	557	HIS	-	EXPRESSION TAG	UNP P35520
B	558	HIS	-	EXPRESSION TAG	UNP P35520
B	559	HIS	-	EXPRESSION TAG	UNP P35520
C	444	ASN	ASP	ENGINEERED MUTATION	UNP P35520
C	552	LEU	-	EXPRESSION TAG	UNP P35520
C	553	GLU	-	EXPRESSION TAG	UNP P35520

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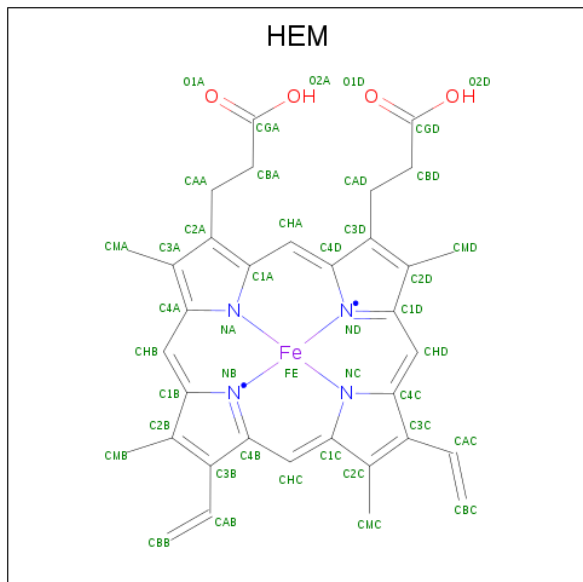
Chain	Residue	Modelled	Actual	Comment	Reference
C	554	HIS	-	EXPRESSION TAG	UNP P35520
C	555	HIS	-	EXPRESSION TAG	UNP P35520
C	556	HIS	-	EXPRESSION TAG	UNP P35520
C	557	HIS	-	EXPRESSION TAG	UNP P35520
C	558	HIS	-	EXPRESSION TAG	UNP P35520
C	559	HIS	-	EXPRESSION TAG	UNP P35520
D	444	ASN	ASP	ENGINEERED MUTATION	UNP P35520
D	552	LEU	-	EXPRESSION TAG	UNP P35520
D	553	GLU	-	EXPRESSION TAG	UNP P35520
D	554	HIS	-	EXPRESSION TAG	UNP P35520
D	555	HIS	-	EXPRESSION TAG	UNP P35520
D	556	HIS	-	EXPRESSION TAG	UNP P35520
D	557	HIS	-	EXPRESSION TAG	UNP P35520
D	558	HIS	-	EXPRESSION TAG	UNP P35520
D	559	HIS	-	EXPRESSION TAG	UNP P35520

- Molecule 2 is PYRIDOXAL-5'-PHOSPHATE (three-letter code: PLP) (formula: C₈H₁₀NO₆P).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
2	A	1	Total	C	N	O	P	0	0
			15	8	1	5	1		
2	B	1	Total	C	N	O	P	0	0
			15	8	1	5	1		
2	C	1	Total	C	N	O	P	0	0
			15	8	1	5	1		
2	D	1	Total	C	N	O	P	0	0
			15	8	1	5	1		

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

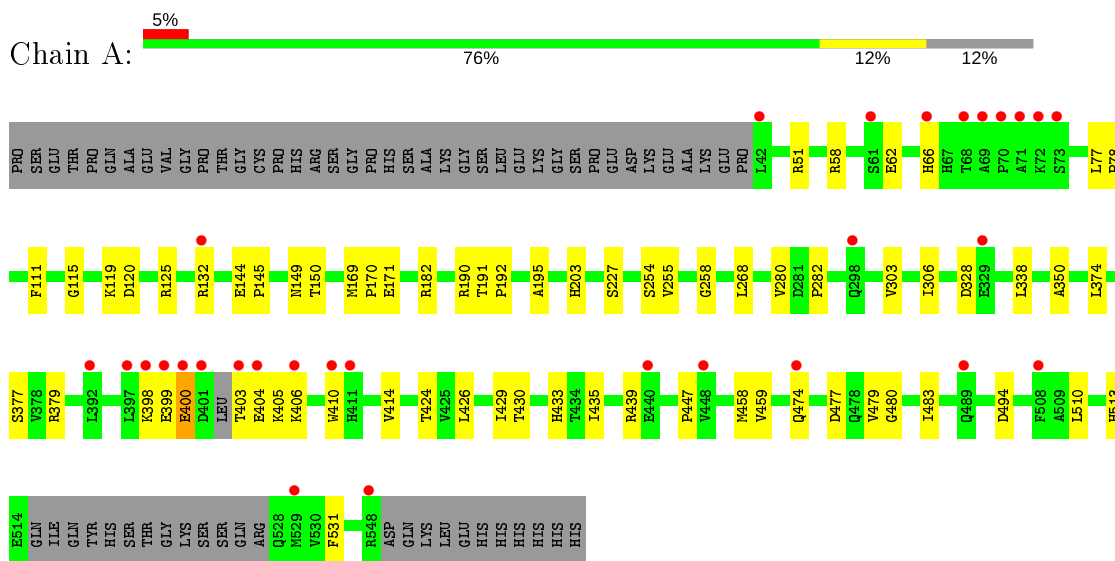


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
			Total	C	Fe	N			O
3	A	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
3	B	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
3	C	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
3	D	1	Total 43	C 34	Fe 1	N 4	O 4	0	0

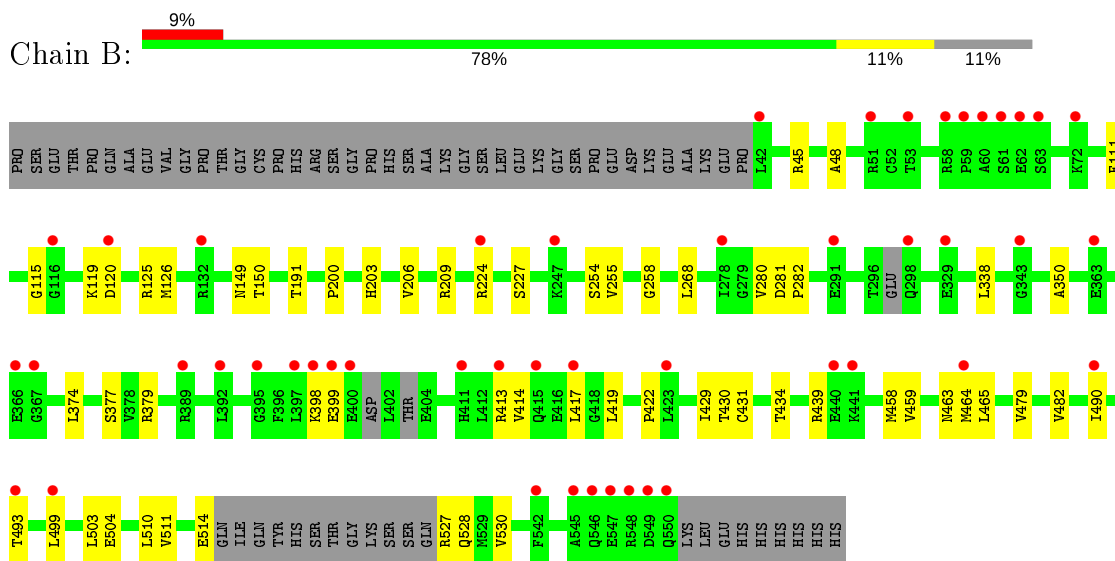
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: Cystathionine beta-synthase



- Molecule 1: Cystathionine beta-synthase



- Molecule 1: Cystathionine beta-synthase

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	109.48Å 131.07Å 207.06Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.39 – 2.63 49.41 – 2.63	Depositor EDS
% Data completeness (in resolution range)	98.1 (48.39-2.63) 98.3 (49.41-2.63)	Depositor EDS
R_{merge}	0.36	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.07 (at 2.61Å)	Xtrriage
Refinement program	PHENIX (phenix.refine: 1.8.1_1168)	Depositor
R, R_{free}	0.256 , 0.281 0.257 , 0.280	Depositor DCC
R_{free} test set	4431 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	58.8	Xtrriage
Anisotropy	0.415	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 54.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	15455	wwPDB-VP
Average B, all atoms (Å ²)	88.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 49.62 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to $7.2651e-05$. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: HEM, PLP

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	0.60	0/3874	0.52	0/5245
1	B	0.60	0/3882	0.52	0/5253
1	C	0.60	0/3860	0.52	0/5222
1	D	0.62	0/3886	0.53	0/5258
All	All	0.61	0/15502	0.52	0/20978

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3803	0	3855	41	0
1	B	3813	0	3859	42	0
1	C	3791	0	3852	49	0
1	D	3816	0	3871	43	0
2	A	15	0	6	2	0
2	B	15	0	6	2	0
2	C	15	0	6	2	0
2	D	15	0	6	2	0
3	A	43	0	30	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	43	0	30	1	0
3	C	43	0	30	2	0
3	D	43	0	30	2	0
All	All	15455	0	15581	176	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 6.

All (176) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:48:ALA:HB3	1:B:224:ARG:HH12	1.19	1.07
1:A:403:THR:HA	1:A:406:LYS:HD2	1.43	0.99
1:D:513:HIS:HB2	1:D:531:PHE:HE2	1.45	0.80
1:B:431:CYS:HB3	1:B:464:MET:HE1	1.63	0.79
1:B:514:GLU:O	1:B:527:ARG:NH2	2.17	0.78
1:A:406:LYS:HD3	1:A:410:TRP:CE2	2.19	0.77
1:A:513:HIS:HB2	1:A:531:PHE:HE2	1.53	0.72
1:B:504:GLU:OE1	1:D:182:ARG:NH1	2.23	0.72
1:C:464:MET:SD	1:C:482:VAL:HG21	2.30	0.71
1:B:419:LEU:HD13	1:B:511:VAL:HG11	1.72	0.71
1:A:66:HIS:CE1	1:A:132:ARG:NH1	2.60	0.69
1:C:513:HIS:HB2	1:C:531:PHE:HE2	1.56	0.69
1:B:458:MET:HE1	1:B:510:LEU:HD21	1.75	0.69
1:B:48:ALA:HB3	1:B:224:ARG:NH1	2.01	0.68
1:A:66:HIS:CE1	1:A:132:ARG:HH12	2.12	0.68
1:D:350:ALA:HB1	1:D:374:LEU:HD22	1.77	0.66
1:A:182:ARG:NH1	1:C:504:GLU:OE1	2.29	0.65
1:C:513:HIS:HB2	1:C:531:PHE:CE2	2.34	0.63
1:B:48:ALA:CB	1:B:224:ARG:HH12	2.05	0.63
1:B:149:ASN:ND2	2:B:601:PLP:H2A1	2.15	0.62
1:D:149:ASN:ND2	2:D:601:PLP:H2A1	2.14	0.62
1:A:149:ASN:ND2	2:A:601:PLP:H2A1	2.14	0.61
3:B:602:HEM:HBB2	3:B:602:HEM:HMB1	1.82	0.61
1:B:439:ARG:HH21	1:B:465:LEU:HD21	1.65	0.61
1:D:430:THR:HG23	1:D:433:HIS:HB2	1.83	0.60
1:B:200:PRO:O	1:B:209:ARG:NH2	2.35	0.60
1:B:398:LYS:NZ	1:C:400:GLU:OE1	2.33	0.60
3:A:602:HEM:HMB1	3:A:602:HEM:HBB2	1.83	0.59
1:A:350:ALA:HB1	1:A:374:LEU:HD22	1.85	0.59
1:B:350:ALA:HB1	1:B:374:LEU:HD22	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:350:ALA:HB1	1:C:374:LEU:HD22	1.85	0.59
1:A:191:THR:HG21	1:A:203:HIS:HA	1.85	0.58
1:B:464:MET:SD	1:B:482:VAL:HG11	2.44	0.58
1:D:406:LYS:HD3	1:D:410:TRP:CE2	2.39	0.58
1:B:191:THR:HG21	1:B:203:HIS:HA	1.86	0.57
1:C:115:GLY:O	1:C:379:ARG:NH2	2.37	0.57
1:C:200:PRO:O	1:C:209:ARG:NH2	2.37	0.57
1:C:429:ILE:HD13	1:C:434:THR:HG22	1.86	0.57
3:D:602:HEM:HMB1	3:D:602:HEM:HBB2	1.85	0.57
1:A:254:SER:HA	1:A:280:VAL:HB	1.87	0.57
1:C:281:ASP:OD2	1:C:282:PRO:HD2	2.04	0.56
1:D:513:HIS:HB2	1:D:531:PHE:CE2	2.35	0.56
1:B:45:ARG:O	1:B:224:ARG:NH1	2.39	0.55
1:B:413:ARG:NH1	1:B:493:THR:HB	2.22	0.55
1:B:379:ARG:HG2	1:B:379:ARG:HH11	1.72	0.55
1:C:430:THR:HG23	1:C:433:HIS:HB2	1.88	0.55
1:C:406:LYS:HD3	1:C:410:TRP:CE2	2.41	0.55
1:B:431:CYS:CB	1:B:464:MET:HE1	2.36	0.54
1:C:379:ARG:HG2	1:C:379:ARG:HH11	1.72	0.54
1:C:58:ARG:NE	1:C:62:GLU:OE1	2.38	0.54
1:D:406:LYS:HD3	1:D:410:TRP:NE1	2.22	0.54
1:B:429:ILE:HG23	1:B:479:VAL:HG21	1.90	0.54
1:D:254:SER:HA	1:D:280:VAL:HB	1.90	0.54
1:A:119:LYS:HB3	1:A:150:THR:HA	1.90	0.54
1:C:149:ASN:ND2	2:C:601:PLP:H2A1	2.21	0.54
1:D:191:THR:HG21	1:D:203:HIS:HA	1.90	0.54
1:D:510:LEU:HD22	1:D:533:VAL:HG12	1.90	0.54
1:B:281:ASP:OD2	1:B:282:PRO:HD2	2.09	0.53
1:A:430:THR:HG23	1:A:433:HIS:HB2	1.91	0.53
1:C:527:ARG:HG3	1:C:528:GLN:H	1.74	0.52
1:C:430:THR:O	1:C:434:THR:HG23	2.09	0.52
1:C:509:ALA:HB3	1:C:534:VAL:HG13	1.92	0.52
1:D:379:ARG:HG2	1:D:379:ARG:HH11	1.75	0.52
1:C:119:LYS:HB3	1:C:150:THR:HA	1.92	0.52
1:A:458:MET:HE1	1:A:510:LEU:HD21	1.90	0.51
1:A:435:ILE:HG23	1:A:439:ARG:HD2	1.91	0.51
1:B:119:LYS:HB3	1:B:150:THR:HA	1.92	0.51
1:D:404:GLU:N	1:D:404:GLU:OE2	2.42	0.51
1:C:125:ARG:HG3	1:C:227:SER:HB3	1.92	0.51
1:D:115:GLY:N	1:D:120:ASP:OD2	2.43	0.51
1:B:413:ARG:NH1	1:B:493:THR:CB	2.74	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:149:ASN:HD22	2:D:601:PLP:H2A1	1.74	0.50
1:A:149:ASN:HD22	2:A:601:PLP:H2A1	1.75	0.50
3:C:602:HEM:HBB2	3:C:602:HEM:HMB1	1.93	0.50
3:C:602:HEM:HMC1	3:C:602:HEM:HBC2	1.94	0.50
1:C:458:MET:HE1	1:C:533:VAL:HG21	1.93	0.50
1:A:414:VAL:HG23	1:A:494:ASP:O	2.12	0.49
1:D:126:MET:HG3	1:D:227:SER:HB2	1.94	0.49
1:D:303:VAL:HG23	1:D:328:ASP:OD2	2.12	0.49
1:A:58:ARG:NE	1:A:62:GLU:OE1	2.44	0.49
1:D:414:VAL:HG23	1:D:494:ASP:O	2.13	0.49
1:C:510:LEU:HD22	1:C:533:VAL:HG22	1.94	0.49
1:B:126:MET:HG3	1:B:227:SER:HB2	1.95	0.49
1:C:295:GLN:HG3	1:D:478:GLN:OE1	2.13	0.49
1:D:111:PHE:HB2	1:D:377:SER:HB3	1.95	0.48
1:A:379:ARG:HH11	1:A:379:ARG:HG2	1.78	0.48
1:B:149:ASN:HD22	2:B:601:PLP:H2A1	1.77	0.48
1:C:458:MET:HE2	1:C:533:VAL:HG11	1.94	0.48
1:A:406:LYS:HD3	1:A:410:TRP:NE1	2.28	0.48
1:B:414:VAL:HG23	1:B:417:LEU:HD12	1.94	0.48
3:D:602:HEM:HMC1	3:D:602:HEM:HBC2	1.96	0.48
1:A:115:GLY:N	1:A:120:ASP:OD2	2.46	0.47
1:D:58:ARG:NE	1:D:62:GLU:OE1	2.46	0.47
1:D:119:LYS:HB3	1:D:150:THR:HA	1.97	0.47
1:C:115:GLY:N	1:C:120:ASP:OD2	2.47	0.47
1:B:111:PHE:HB2	1:B:377:SER:HB3	1.97	0.47
1:C:149:ASN:HD22	2:C:601:PLP:H2A1	1.80	0.47
1:D:459:VAL:HG21	1:D:479:VAL:CG1	2.45	0.47
1:D:131:GLU:OE2	1:D:161:ARG:NH1	2.48	0.46
1:A:192:PRO:HG2	1:A:195:ALA:HB2	1.97	0.46
1:C:464:MET:HE3	1:C:464:MET:HB3	1.44	0.46
1:A:171:GLU:CD	1:A:192:PRO:HA	2.36	0.46
1:B:398:LYS:NZ	1:C:400:GLU:CD	2.69	0.46
1:C:406:LYS:HD3	1:C:410:TRP:NE1	2.31	0.46
1:A:303:VAL:HG23	1:A:328:ASP:OD2	2.15	0.46
1:D:255:VAL:HG13	1:D:258:GLY:HA2	1.98	0.46
1:A:51:ARG:HB3	3:A:602:HEM:HBA1	1.98	0.45
1:C:126:MET:HG3	1:C:227:SER:HB2	1.98	0.45
1:D:232:HIS:CD2	1:D:260:THR:HA	2.51	0.45
1:C:119:LYS:HD2	1:C:150:THR:OG1	2.16	0.45
1:A:400:GLU:HG2	1:A:400:GLU:H	1.57	0.45
1:C:171:GLU:CD	1:C:192:PRO:HA	2.37	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:255:VAL:HG13	1:C:258:GLY:HA2	1.98	0.45
1:B:430:THR:O	1:B:434:THR:HG23	2.16	0.45
1:A:255:VAL:HG13	1:A:258:GLY:HA2	1.99	0.45
1:A:169:MET:O	1:A:190:ARG:HA	2.16	0.45
1:C:169:MET:O	1:C:190:ARG:HA	2.17	0.45
1:A:111:PHE:HB2	1:A:377:SER:HB3	1.99	0.44
1:D:169:MET:HE2	1:D:173:MET:HB2	1.99	0.44
1:D:169:MET:O	1:D:190:ARG:HA	2.16	0.44
1:B:125:ARG:HG3	1:B:227:SER:HB3	1.99	0.44
1:C:426:LEU:O	1:C:429:ILE:HG22	2.18	0.44
1:C:410:TRP:CE2	1:C:497:GLY:HA3	2.52	0.44
1:D:459:VAL:HG21	1:D:479:VAL:HG13	2.00	0.44
1:A:426:LEU:O	1:A:429:ILE:HG22	2.16	0.44
1:D:397:LEU:HD13	1:D:402:LEU:HD12	2.00	0.44
1:B:206:VAL:HG22	1:B:209:ARG:HH21	1.82	0.44
1:B:459:VAL:HG11	1:B:479:VAL:HG13	1.99	0.44
1:B:379:ARG:NH1	1:B:379:ARG:HG2	2.33	0.44
1:B:439:ARG:NH2	1:B:465:LEU:HD21	2.31	0.43
1:B:422:PRO:HD2	1:B:530:VAL:O	2.18	0.43
1:C:191:THR:HG21	1:C:203:HIS:HA	2.00	0.43
1:C:414:VAL:HG12	1:C:494:ASP:O	2.18	0.43
1:C:379:ARG:HG2	1:C:379:ARG:NH1	2.34	0.43
1:A:398:LYS:HB3	1:A:400:GLU:HG2	2.00	0.43
1:C:221:ASP:OD1	1:C:224:ARG:HD3	2.19	0.43
1:D:316:ASP:OD2	1:D:318:THR:OG1	2.27	0.43
1:D:410:TRP:CE2	1:D:497:GLY:HA3	2.54	0.43
1:D:167:ILE:HG13	1:D:181:LEU:HD22	2.01	0.43
1:A:459:VAL:HG21	1:A:479:VAL:HG13	2.00	0.42
1:D:406:LYS:HD3	1:D:410:TRP:CD1	2.54	0.42
1:D:474:GLN:O	1:D:477:ASP:HB2	2.19	0.42
1:A:424:THR:HG22	1:A:447:PRO:HG2	2.01	0.42
1:A:474:GLN:O	1:A:477:ASP:HB2	2.20	0.42
1:D:77:LEU:HA	1:D:78:PRO:HD2	1.89	0.42
1:B:115:GLY:N	1:B:120:ASP:OD2	2.53	0.42
1:B:254:SER:HA	1:B:280:VAL:HB	2.01	0.42
1:C:474:GLN:O	1:C:477:ASP:HB2	2.20	0.42
1:A:125:ARG:HG3	1:A:227:SER:HB3	2.02	0.41
1:C:513:HIS:CG	1:C:514:GLU:N	2.87	0.41
1:A:282:PRO:HD3	1:A:306:ILE:HD12	2.02	0.41
1:C:431:CYS:HB3	1:C:464:MET:CE	2.51	0.41
1:D:379:ARG:HG2	1:D:379:ARG:NH1	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:460:THR:HG22	1:C:463:ASN:H	1.85	0.41
1:D:503:LEU:HD13	1:D:536:ALA:HA	2.01	0.41
1:B:255:VAL:HG13	1:B:258:GLY:HA2	2.01	0.41
1:D:73:SER:HA	1:D:74:PRO:HD2	1.91	0.41
1:B:490:ILE:O	1:B:511:VAL:HA	2.21	0.41
1:B:499:LEU:O	1:B:503:LEU:HG	2.21	0.41
1:C:484:TYR:CD2	1:C:508:PHE:HE2	2.39	0.41
1:B:463:ASN:ND2	1:B:482:VAL:HG22	2.35	0.41
1:D:125:ARG:HG3	1:D:227:SER:HB3	2.03	0.41
1:A:379:ARG:HG2	1:A:379:ARG:NH1	2.35	0.41
1:A:77:LEU:HA	1:A:78:PRO:HD2	1.91	0.41
1:C:431:CYS:HB3	1:C:464:MET:HE2	2.03	0.41
1:A:480:GLY:O	1:A:483:ILE:HG22	2.22	0.40
1:B:527:ARG:HG3	1:B:528:GLN:H	1.86	0.40
1:D:171:GLU:HA	1:D:190:ARG:NH2	2.35	0.40
1:A:144:GLU:HA	1:A:145:PRO:HD2	1.98	0.40
1:A:169:MET:HA	1:A:170:PRO:HD3	1.94	0.40
1:A:400:GLU:O	1:A:404:GLU:HG2	2.22	0.40
1:C:110:GLU:HG2	1:C:118:VAL:HB	2.03	0.40
1:C:144:GLU:HA	1:C:145:PRO:HD2	1.93	0.40
1:C:434:THR:HG21	1:C:479:VAL:HG21	2.03	0.40
1:D:119:LYS:HD2	1:D:150:THR:OG1	2.22	0.40
1:D:241:LEU:HA	1:D:241:LEU:HD23	1.91	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	487/558 (87%)	480 (99%)	7 (1%)	0	100	100
1	B	485/558 (87%)	476 (98%)	9 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	482/558 (86%)	475 (98%)	7 (2%)	0	100	100
1	D	486/558 (87%)	480 (99%)	6 (1%)	0	100	100
All	All	1940/2232 (87%)	1911 (98%)	29 (2%)	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	412/472 (87%)	407 (99%)	5 (1%)	71	86
1	B	413/472 (88%)	410 (99%)	3 (1%)	84	93
1	C	411/472 (87%)	409 (100%)	2 (0%)	88	95
1	D	415/472 (88%)	409 (99%)	6 (1%)	67	84
All	All	1651/1888 (87%)	1635 (99%)	16 (1%)	76	89

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

Mol	Chain	Res	Type
1	A	268	LEU
1	A	338	LEU
1	A	399	GLU
1	A	400	GLU
1	A	405	LYS
1	B	268	LEU
1	B	338	LEU
1	B	399	GLU
1	C	338	LEU
1	C	414	VAL
1	D	268	LEU
1	D	338	LEU
1	D	398	LYS
1	D	400	GLU

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Mol	Chain	Res	Type
1	D	402	LEU
1	D	404	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	66	HIS
1	D	528	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

8 ligands are modelled in this entry.

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	$\# Z > 2$
2	PLP	B	601	1	15,15,16	3.28	7 (46%)	20,22,23	2.19	6 (30%)
3	HEM	D	602	1	27,50,50	2.20	5 (18%)	17,82,82	1.56	2 (11%)
3	HEM	A	602	1	27,50,50	2.19	6 (22%)	17,82,82	1.51	5 (29%)
3	HEM	C	602	1	27,50,50	2.20	6 (22%)	17,82,82	1.23	2 (11%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	PLP	D	601	1	15,15,16	3.26	7 (46%)	20,22,23	2.00	5 (25%)
2	PLP	A	601	1	15,15,16	3.16	7 (46%)	20,22,23	2.03	6 (30%)
3	HEM	B	602	1	27,50,50	2.20	6 (22%)	17,82,82	1.30	3 (17%)
2	PLP	C	601	1	15,15,16	3.24	8 (53%)	20,22,23	2.12	6 (30%)

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
2	PLP	B	601	1	-	0/6/6/8	0/1/1/1
3	HEM	D	602	1	-	0/6/54/54	-
3	HEM	A	602	1	-	0/6/54/54	-
3	HEM	C	602	1	-	0/6/54/54	-
2	PLP	D	601	1	-	0/6/6/8	0/1/1/1
2	PLP	A	601	1	-	0/6/6/8	0/1/1/1
3	HEM	B	602	1	-	1/6/54/54	-
2	PLP	C	601	1	-	0/6/6/8	0/1/1/1

All (52) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	601	PLP	C2A-C2	-7.69	1.37	1.50
2	B	601	PLP	C2A-C2	-7.67	1.37	1.50
2	C	601	PLP	C2A-C2	-7.64	1.37	1.50
2	A	601	PLP	C2A-C2	-7.63	1.37	1.50
2	B	601	PLP	C4A-C4	-7.29	1.36	1.51
2	D	601	PLP	C4A-C4	-7.10	1.36	1.51
2	C	601	PLP	C4A-C4	-7.08	1.36	1.51
2	A	601	PLP	C4A-C4	-6.86	1.37	1.51
3	A	602	HEM	C3C-C2C	-5.33	1.33	1.40
3	B	602	HEM	C3C-C2C	-5.23	1.33	1.40
3	D	602	HEM	C3C-C2C	-5.15	1.33	1.40
3	A	602	HEM	C3B-C2B	-5.12	1.33	1.40
3	D	602	HEM	C3B-C2B	-5.11	1.33	1.40
3	C	602	HEM	C3C-C2C	-5.01	1.33	1.40
3	B	602	HEM	C3D-C2D	5.00	1.52	1.37
3	C	602	HEM	C3D-C2D	4.86	1.52	1.37
3	D	602	HEM	C3D-C2D	4.75	1.51	1.37
3	C	602	HEM	C3B-C2B	-4.73	1.33	1.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	602	HEM	C3D-C2D	4.61	1.51	1.37
3	B	602	HEM	C3B-C2B	-4.57	1.34	1.40
3	D	602	HEM	C3C-CAC	3.78	1.55	1.47
3	C	602	HEM	C3C-CAC	3.62	1.55	1.47
2	D	601	PLP	C3-C2	-3.54	1.37	1.40
3	A	602	HEM	C3C-CAC	3.51	1.55	1.47
3	B	602	HEM	C3B-CAB	3.49	1.55	1.47
3	C	602	HEM	C3B-CAB	3.45	1.55	1.47
3	D	602	HEM	C3B-CAB	3.43	1.54	1.47
3	A	602	HEM	C3B-CAB	3.40	1.54	1.47
3	B	602	HEM	C3C-CAC	3.40	1.54	1.47
2	D	601	PLP	C5A-C5	-3.40	1.41	1.50
2	B	601	PLP	C5A-C5	-3.35	1.41	1.50
2	C	601	PLP	C5A-C5	-3.20	1.42	1.50
2	A	601	PLP	C5A-C5	-3.18	1.42	1.50
2	C	601	PLP	C3-C2	-3.05	1.37	1.40
2	B	601	PLP	C3-C2	-3.04	1.37	1.40
2	A	601	PLP	P-O3P	-2.87	1.43	1.54
2	B	601	PLP	P-O3P	-2.74	1.44	1.54
2	D	601	PLP	P-O3P	-2.74	1.44	1.54
2	C	601	PLP	P-O3P	-2.74	1.44	1.54
2	A	601	PLP	C3-C2	-2.66	1.38	1.40
2	C	601	PLP	P-O2P	-2.64	1.44	1.54
2	B	601	PLP	P-O2P	-2.59	1.44	1.54
2	A	601	PLP	P-O2P	-2.59	1.44	1.54
2	C	601	PLP	C6-N1	2.51	1.39	1.34
2	D	601	PLP	P-O2P	-2.49	1.45	1.54
2	B	601	PLP	C6-N1	2.46	1.39	1.34
3	C	602	HEM	CAA-C2A	2.37	1.55	1.52
3	B	602	HEM	CAA-C2A	2.26	1.55	1.52
3	A	602	HEM	CAA-C2A	2.23	1.55	1.52
2	A	601	PLP	C6-N1	2.20	1.39	1.34
2	D	601	PLP	C6-N1	2.19	1.39	1.34
2	C	601	PLP	P-O1P	-2.04	1.44	1.50

All (35) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	601	PLP	O4P-C5A-C5	5.72	120.24	109.35
2	C	601	PLP	O4P-C5A-C5	5.49	119.80	109.35
2	D	601	PLP	O4P-C5A-C5	4.93	118.75	109.35
2	A	601	PLP	O4P-C5A-C5	4.56	118.04	109.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	601	PLP	O3P-P-O4P	-4.36	95.13	106.73
3	D	602	HEM	CAA-CBA-CGA	-3.71	106.44	112.67
2	B	601	PLP	O3P-P-O4P	-3.70	96.90	106.73
2	C	601	PLP	O3P-P-O4P	-3.70	96.90	106.73
2	D	601	PLP	O3P-P-O4P	-3.66	97.00	106.73
2	D	601	PLP	O4P-P-O1P	-3.39	96.96	106.47
2	A	601	PLP	O4P-P-O1P	-3.23	97.41	106.47
2	C	601	PLP	O4P-P-O1P	-3.14	97.68	106.47
2	B	601	PLP	O4P-P-O1P	-3.05	97.91	106.47
2	C	601	PLP	O3P-P-O2P	2.80	118.35	107.64
2	B	601	PLP	O3P-P-O2P	2.80	118.34	107.64
2	D	601	PLP	O3P-P-O2P	2.69	117.91	107.64
2	A	601	PLP	O3P-P-O2P	2.66	117.79	107.64
3	C	602	HEM	CMC-C2C-C3C	2.60	129.54	124.68
2	B	601	PLP	O2P-P-O4P	-2.58	99.86	106.73
3	A	602	HEM	CAA-CBA-CGA	-2.48	108.51	112.67
3	A	602	HEM	CMA-C3A-C4A	-2.43	124.73	128.46
2	B	601	PLP	C6-C5-C4	-2.43	116.25	118.16
3	B	602	HEM	CMB-C2B-C3B	2.32	129.03	124.68
2	C	601	PLP	C6-C5-C4	-2.31	116.34	118.16
3	A	602	HEM	CMC-C2C-C3C	2.29	128.97	124.68
3	D	602	HEM	C1D-C2D-C3D	-2.29	105.41	107.00
3	A	602	HEM	C1D-C2D-C3D	-2.27	105.42	107.00
3	B	602	HEM	CMA-C3A-C4A	-2.22	125.05	128.46
2	C	601	PLP	O2P-P-O4P	-2.22	100.84	106.73
3	B	602	HEM	CMC-C2C-C3C	2.16	128.72	124.68
2	D	601	PLP	O2P-P-O4P	-2.15	101.00	106.73
3	C	602	HEM	C1D-C2D-C3D	-2.14	105.51	107.00
2	A	601	PLP	O3P-P-O1P	2.10	118.91	110.68
3	A	602	HEM	CAD-CBD-CGD	-2.05	109.23	112.67
2	A	601	PLP	C6-C5-C4	-2.04	116.55	118.16

There are no chirality outliers.

All (1) torsion outliers are listed below:

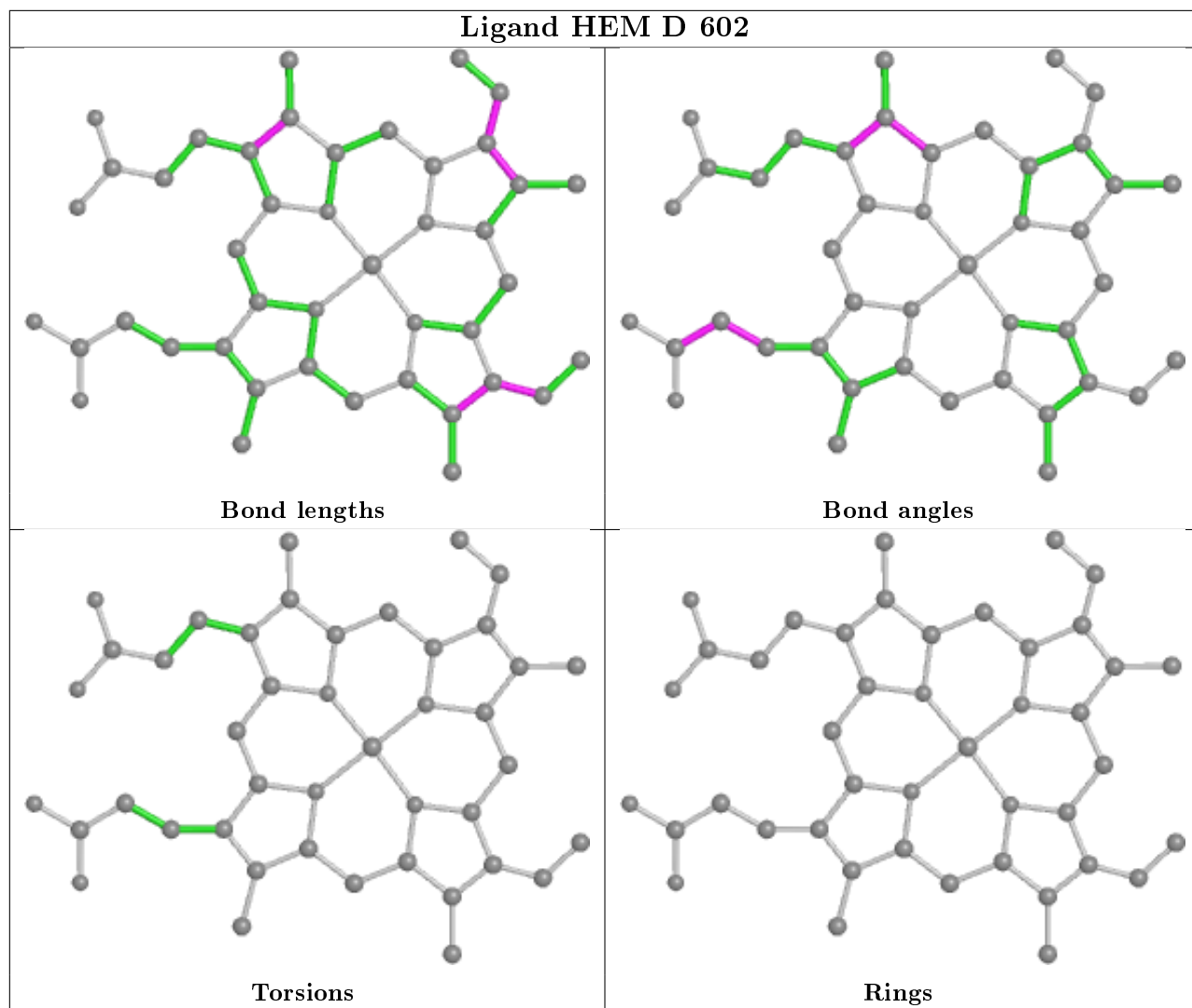
Mol	Chain	Res	Type	Atoms
3	B	602	HEM	C1A-C2A-CAA-CBA

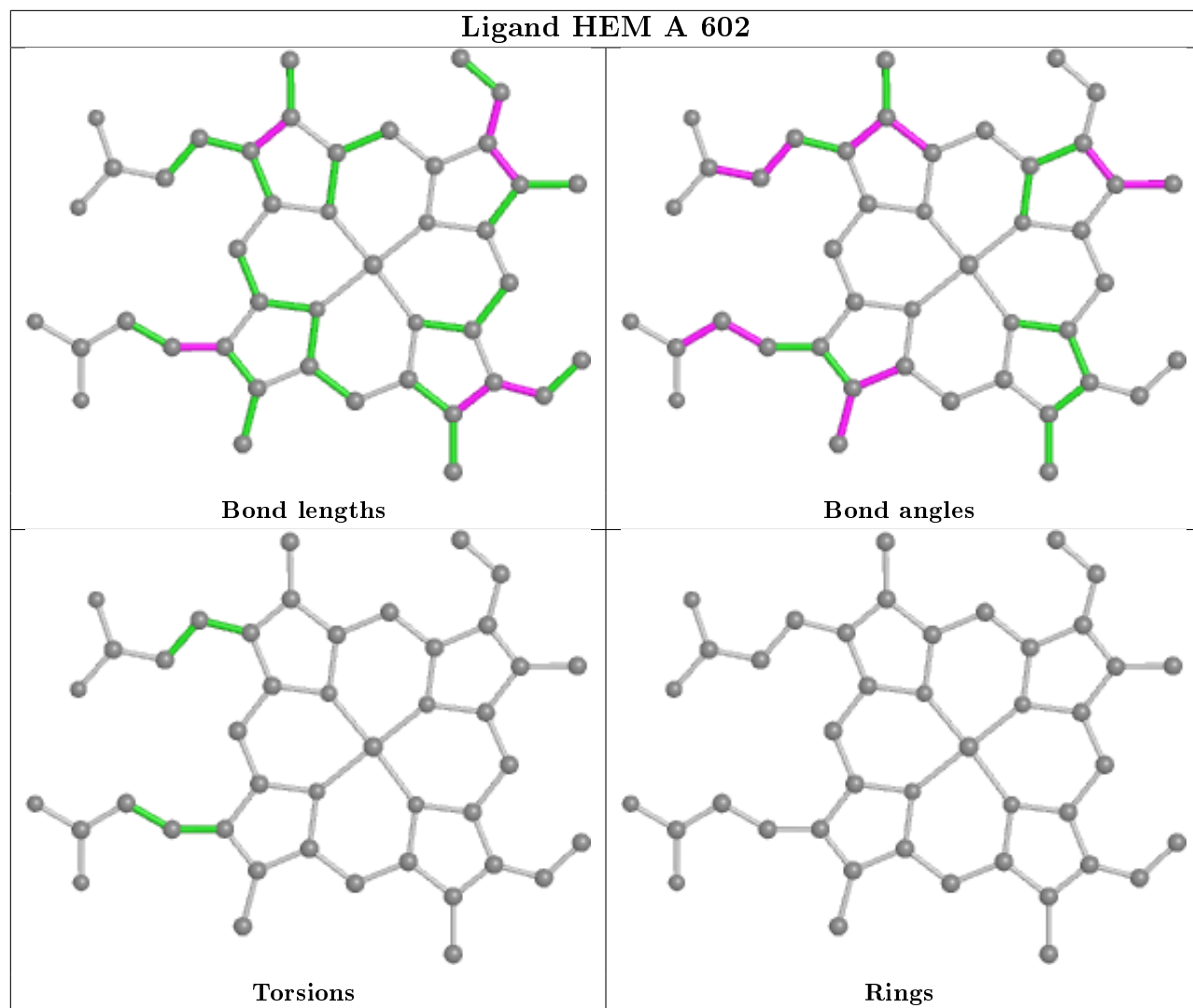
There are no ring outliers.

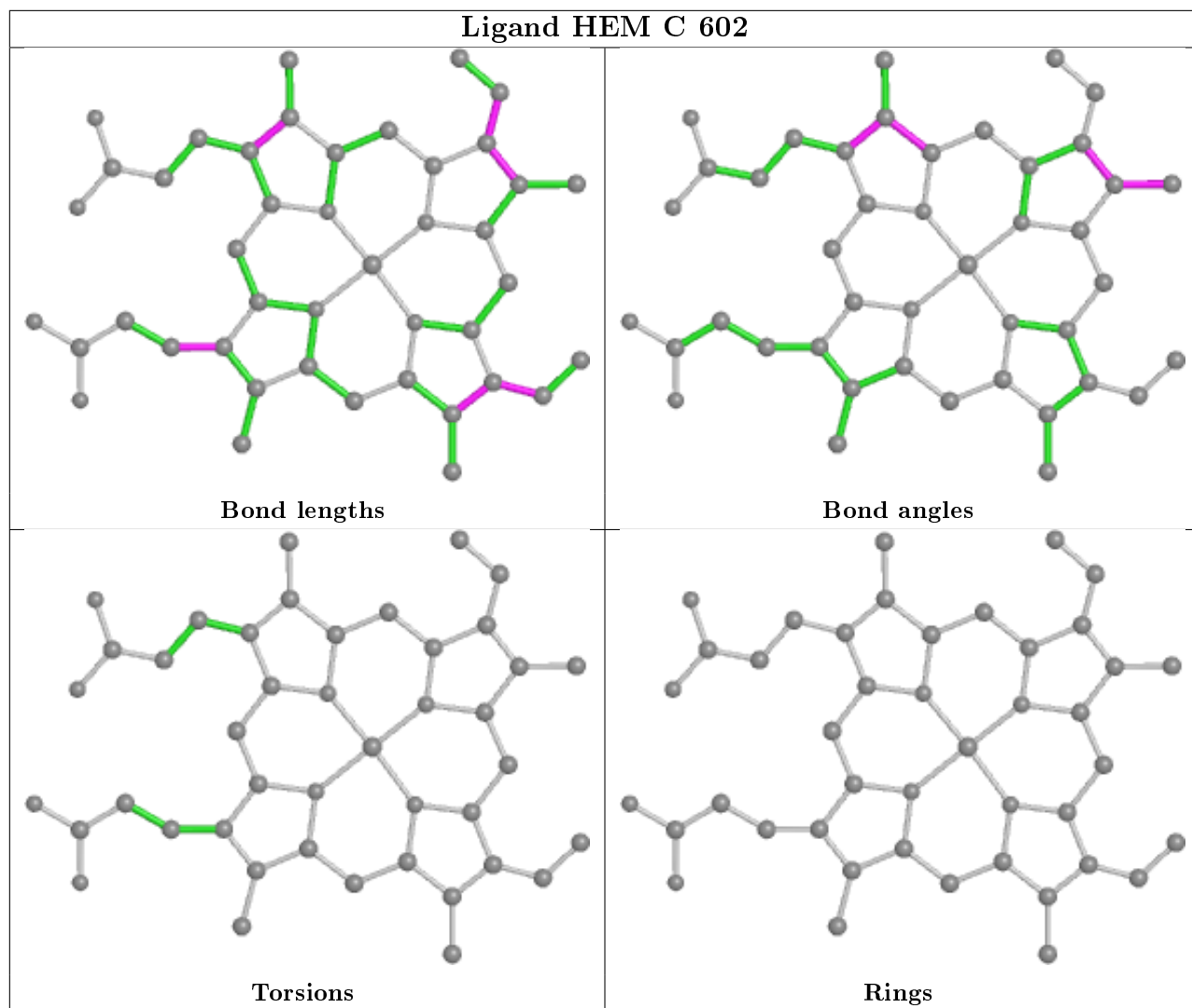
8 monomers are involved in 15 short contacts:

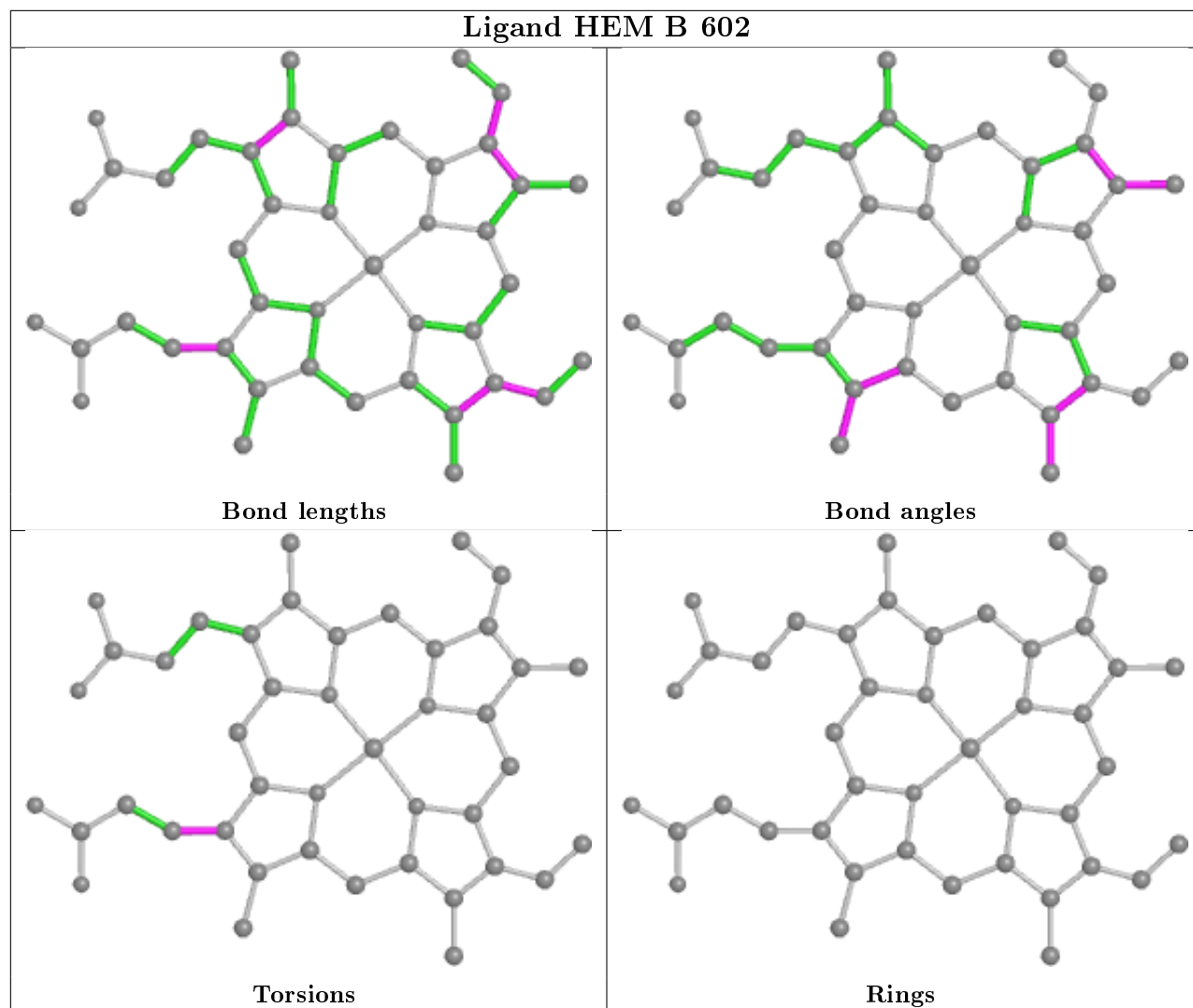
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	601	PLP	2	0
3	D	602	HEM	2	0
3	A	602	HEM	2	0
3	C	602	HEM	2	0
2	D	601	PLP	2	0
2	A	601	PLP	2	0
3	B	602	HEM	1	0
2	C	601	PLP	2	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.









5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

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	493/558 (88%)	0.49	30 (6%) 21 16	58, 82, 128, 160	0
1	B	494/558 (88%)	0.55	48 (9%) 7 5	60, 85, 130, 158	0
1	C	491/558 (87%)	0.55	44 (8%) 9 6	58, 83, 127, 162	0
1	D	493/558 (88%)	0.56	38 (7%) 13 10	55, 80, 127, 159	0
All	All	1971/2232 (88%)	0.54	160 (8%) 12 8	55, 83, 128, 162	0

All (160) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	400	GLU	6.9
1	C	400	GLU	6.7
1	A	71	ALA	6.1
1	C	402	LEU	5.9
1	B	550	GLN	5.6
1	A	398	LYS	5.6
1	D	399	GLU	5.4
1	D	398	LYS	5.3
1	D	528	GLN	5.1
1	A	42	LEU	5.0
1	C	58	ARG	4.9
1	C	398	LYS	4.8
1	B	490	ILE	4.8
1	B	397	LEU	4.7
1	A	69	ALA	4.6
1	C	406	LYS	4.6
1	A	440	GLU	4.5
1	D	406	LYS	4.5
1	B	58	ARG	4.5
1	C	298	GLN	4.5
1	B	398	LYS	4.4

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Mol	Chain	Res	Type	RSRZ
1	A	70	PRO	4.3
1	D	402	LEU	4.3
1	D	479	VAL	4.3
1	C	545	ALA	4.3
1	D	71	ALA	4.2
1	A	401	ASP	4.1
1	C	397	LEU	4.1
1	B	548	ARG	4.1
1	A	399	GLU	4.0
1	D	443	PHE	4.0
1	B	549	ASP	4.0
1	B	547	GLU	3.9
1	C	59	PRO	3.8
1	A	406	LYS	3.7
1	A	403	THR	3.7
1	D	69	ALA	3.6
1	B	413	ARG	3.6
1	B	411	HIS	3.6
1	D	400	GLU	3.5
1	C	295	GLN	3.5
1	C	439	ARG	3.5
1	D	545	ALA	3.5
1	D	298	GLN	3.5
1	D	297	GLU	3.4
1	D	389	ARG	3.4
1	D	405	LYS	3.3
1	A	400	GLU	3.3
1	C	399	GLU	3.2
1	B	464	MET	3.2
1	B	367	GLY	3.2
1	C	53	THR	3.1
1	B	42	LEU	3.1
1	A	392	LEU	3.1
1	C	389	ARG	3.1
1	B	441	LYS	3.1
1	B	417	LEU	3.1
1	C	329	GLU	3.1
1	A	72	LYS	3.0
1	A	66	HIS	3.0
1	A	132	ARG	3.0
1	A	548	ARG	3.0
1	C	61	SER	3.0

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Mol	Chain	Res	Type	RSRZ
1	B	61	SER	2.9
1	C	417	LEU	2.9
1	B	399	GLU	2.9
1	A	68	THR	2.9
1	D	473	VAL	2.9
1	D	440	GLU	2.8
1	C	361	ALA	2.8
1	D	417	LEU	2.8
1	C	247	LYS	2.8
1	B	366	GLU	2.7
1	D	111	PHE	2.7
1	C	366	GLU	2.7
1	D	132	ARG	2.7
1	C	60	ALA	2.7
1	C	224	ARG	2.7
1	A	298	GLN	2.7
1	C	364	LEU	2.7
1	B	363	GLU	2.7
1	A	448	VAL	2.7
1	D	434	THR	2.7
1	C	411	HIS	2.6
1	A	529	MET	2.6
1	B	120	ASP	2.6
1	C	57	GLY	2.6
1	A	397	LEU	2.6
1	D	72	LYS	2.6
1	B	278	ILE	2.6
1	B	51	ARG	2.6
1	C	409	TRP	2.6
1	A	73	SER	2.6
1	D	542	PHE	2.6
1	C	441	LYS	2.5
1	A	489	GLN	2.5
1	B	546	GLN	2.5
1	B	545	ALA	2.5
1	A	410	TRP	2.5
1	B	392	LEU	2.5
1	B	499	LEU	2.5
1	C	496	LEU	2.5
1	D	155	ALA	2.5
1	B	298	GLN	2.4
1	D	151	GLY	2.4

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Mol	Chain	Res	Type	RSRZ
1	C	453	GLY	2.4
1	C	392	LEU	2.4
1	B	415	GLN	2.4
1	B	132	ARG	2.4
1	C	440	GLU	2.4
1	D	437	ILE	2.4
1	D	413	ARG	2.4
1	B	63	SER	2.4
1	C	296	THR	2.4
1	A	61	SER	2.4
1	C	443	PHE	2.4
1	C	437	ILE	2.4
1	C	410	TRP	2.4
1	D	548	ARG	2.4
1	A	411	HIS	2.3
1	D	165	CYS	2.3
1	B	59	PRO	2.3
1	B	542	PHE	2.3
1	D	169	MET	2.3
1	D	419	LEU	2.3
1	C	542	PHE	2.3
1	D	148	GLY	2.3
1	B	224	ARG	2.3
1	D	213	GLU	2.3
1	B	395	GLY	2.2
1	B	440	GLU	2.2
1	C	72	LYS	2.2
1	A	404	GLU	2.2
1	C	245	ASP	2.2
1	D	241	LEU	2.2
1	B	116	GLY	2.2
1	B	53	THR	2.2
1	B	329	GLU	2.1
1	C	109	CYS	2.1
1	C	55	GLN	2.1
1	D	70	PRO	2.1
1	B	389	ARG	2.1
1	B	493	THR	2.1
1	D	68	THR	2.1
1	A	474	GLN	2.1
1	A	329	GLU	2.1
1	B	62	GLU	2.1

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Mol	Chain	Res	Type	RSRZ
1	C	490	ILE	2.1
1	D	168	VAL	2.1
1	B	60	ALA	2.1
1	A	508	PHE	2.1
1	B	247	LYS	2.0
1	B	343	GLY	2.0
1	B	291	GLU	2.0
1	D	530	VAL	2.0
1	C	116	GLY	2.0
1	B	423	LEU	2.0
1	C	499	LEU	2.0
1	C	548	ARG	2.0
1	B	72	LYS	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 carbohydrates in this entry.

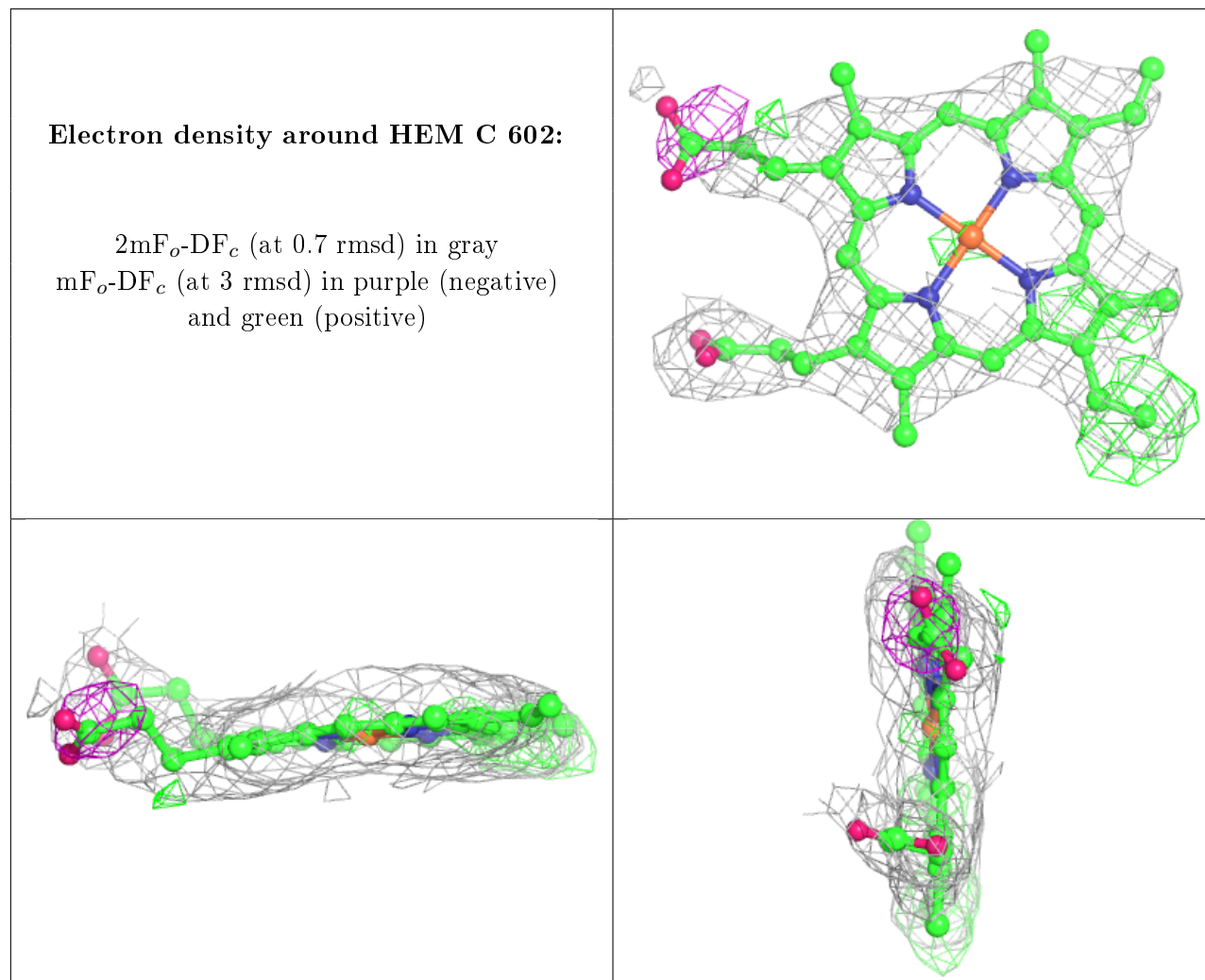
6.4 Ligands [i](#)

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(\AA^2)	Q<0.9
3	HEM	C	602	43/43	0.89	0.25	90,91,91,92	0
3	HEM	B	602	43/43	0.92	0.23	102,102,103,103	0
2	PLP	C	601	15/16	0.93	0.20	60,72,75,78	0
2	PLP	B	601	15/16	0.94	0.23	61,74,84,85	0
2	PLP	A	601	15/16	0.95	0.23	53,69,79,80	0
3	HEM	A	602	43/43	0.95	0.21	71,72,72,72	0
3	HEM	D	602	43/43	0.95	0.18	74,74,75,75	0
2	PLP	D	601	15/16	0.96	0.20	63,69,78,79	0

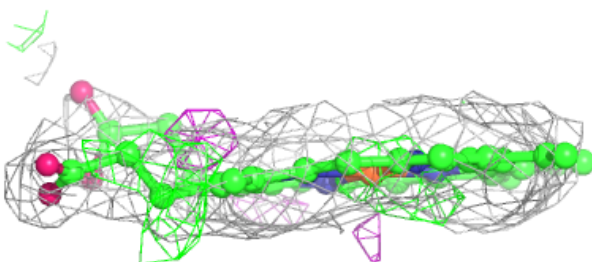
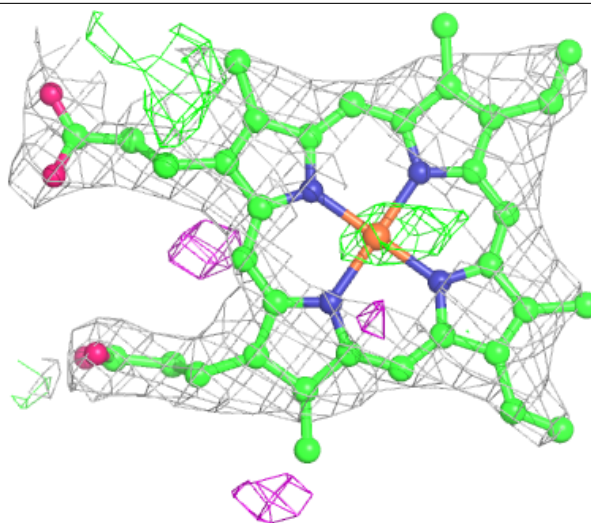
The following is a graphical depiction of the model fit to experimental electron density of all

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.



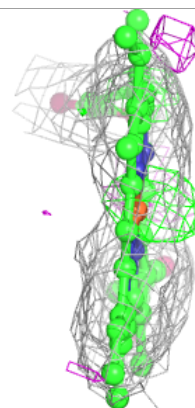
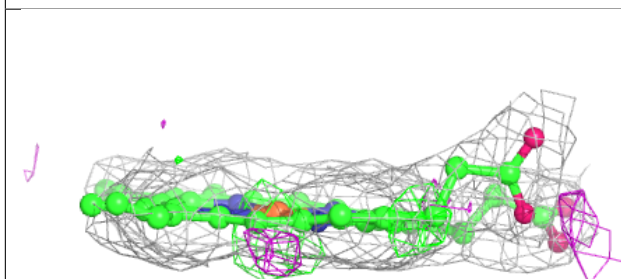
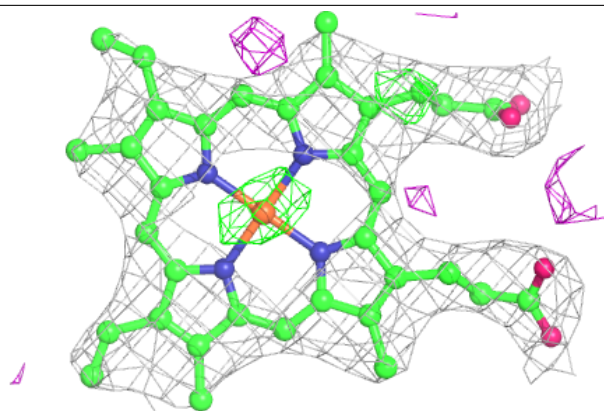
Electron density around HEM B 602:

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

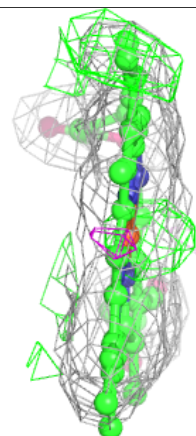
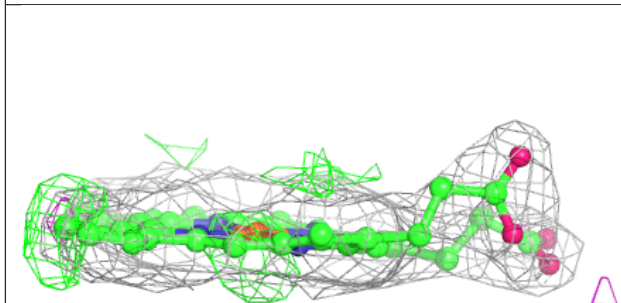
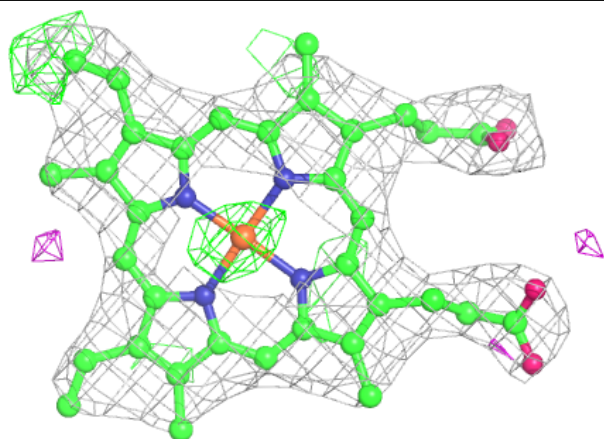


Electron density around HEM A 602:

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

**Electron density around HEM D 602:**

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



6.5 Other polymers

There are no such residues in this entry.