



Full wwPDB X-ray Structure Validation Report ⓘ

Jun 11, 2024 – 07:56 PM EDT

PDB ID : 1DGB
Title : HUMAN ERYTHROCYTE CATALASE
Authors : Putnam, C.D.; Arvai, A.S.; Bourne, Y.; Tainer, J.A.
Deposited on : 1999-11-23
Resolution : 2.20 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 : 4.02b-467
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 1.20.1
EDS : 2.36.2
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) : 2.36.2

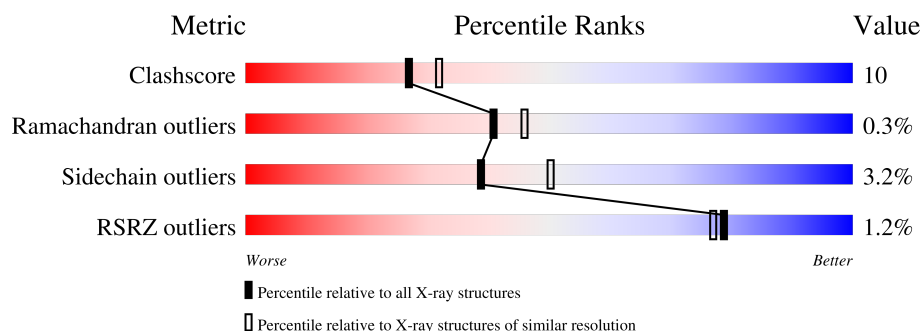
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (2.20-2.20)

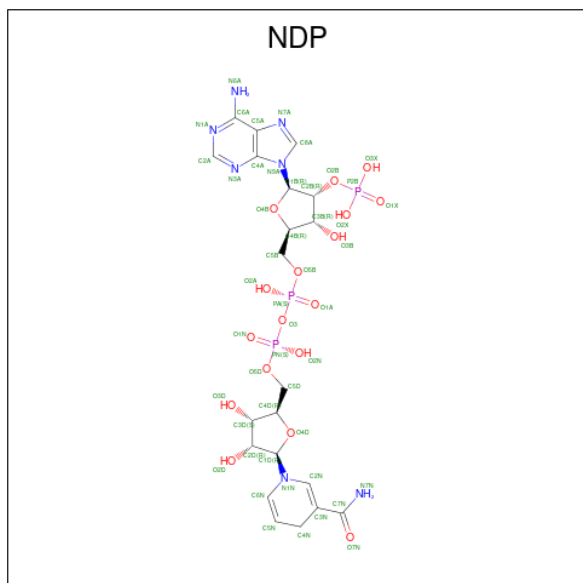
The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. 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	498	<div> <div>%</div> <div> <div></div> <div>83%</div> <div>16%</div> <div>.</div> </div> </div>
1	B	498	<div> <div>%</div> <div> <div></div> <div>77%</div> <div>22%</div> <div>.</div> </div> </div>
1	C	498	<div> <div>2%</div> <div> <div></div> <div>77%</div> <div>21%</div> <div>.</div> </div> </div>
1	D	498	<div> <div>%</div> <div> <div></div> <div>77%</div> <div>21%</div> <div>.</div> </div> </div>

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

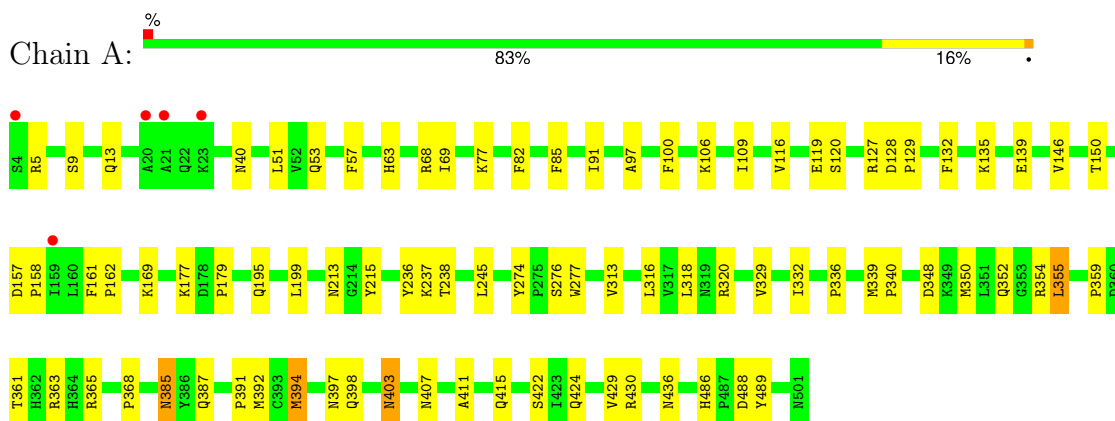
- Molecule 3 is NADPH DIHYDRO-NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (three-letter code: NDP) (formula: $C_{21}H_{30}N_7O_{17}P_3$).



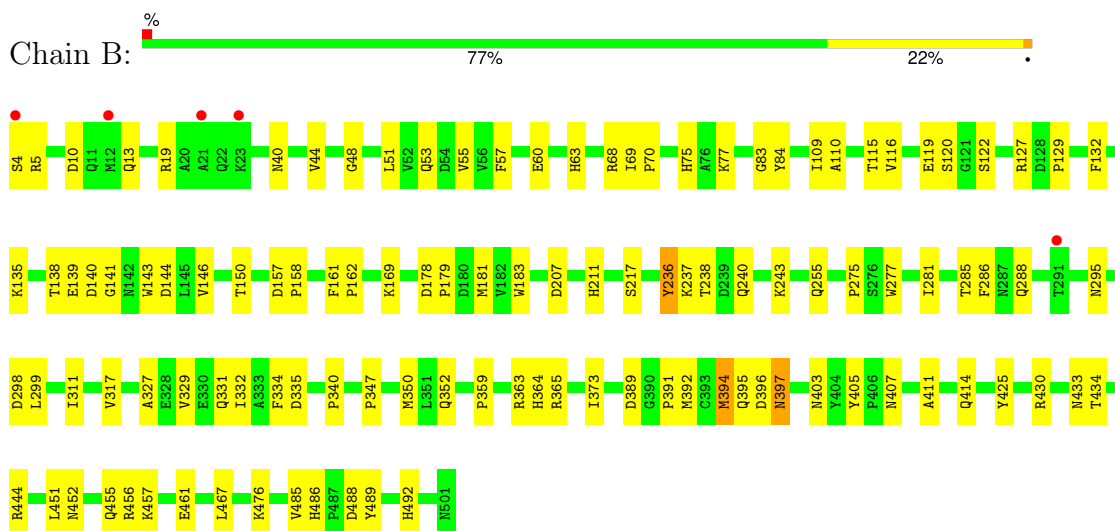
3 Residue-property plots [i](#)

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.

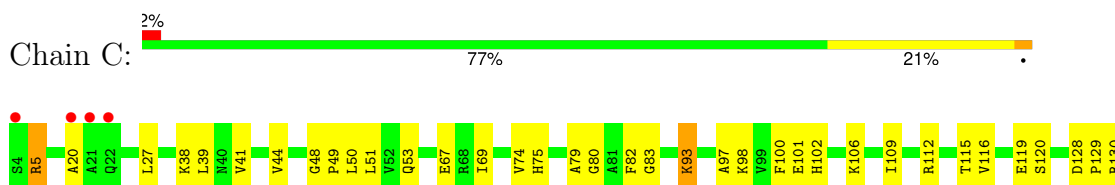
• Molecule 1: CATALASE

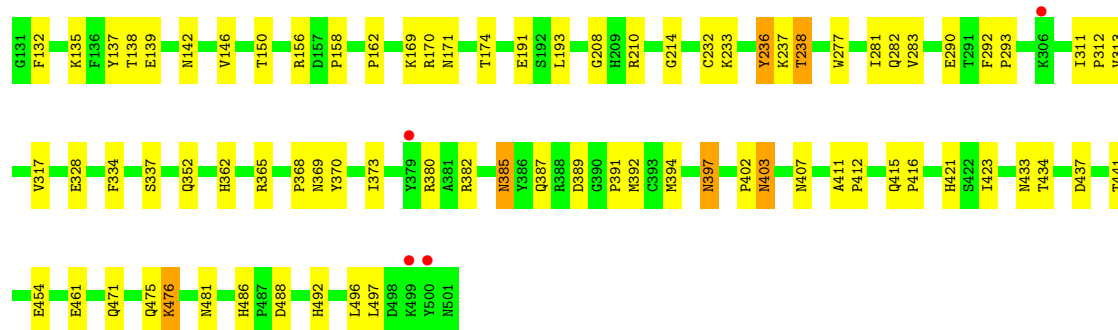


• Molecule 1: CATALASE

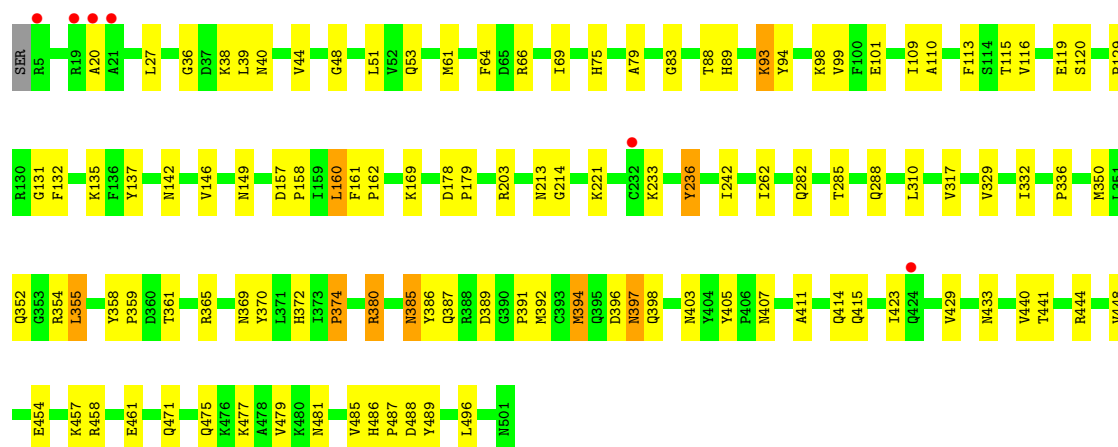
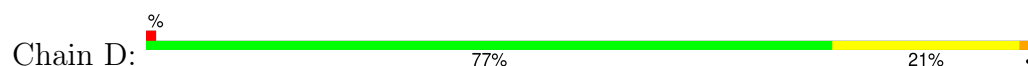


• Molecule 1: CATALASE





● Molecule 1: CATALASE



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	83.50Å 139.93Å 227.89Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.20 19.96 – 2.20	Depositor EDS
% Data completeness (in resolution range)	(Not available) (20.00-2.20) 90.6 (19.96-2.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.11 (at 2.19Å)	Xtriage
Refinement program	X-PLOR 3.851	Depositor
R, R_{free}	0.172 , 0.227 0.169 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	64.4	Xtriage
Anisotropy	0.051	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 55.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.98	EDS
Total number of atoms	17443	wwPDB-VP
Average B, all atoms (Å ²)	63.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.82% 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, NDP

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.38	0/4137	0.62	0/5619
1	B	0.39	0/4137	0.62	0/5619
1	C	0.39	0/4137	0.64	0/5619
1	D	0.40	0/4131	0.63	0/5611
All	All	0.39	0/16542	0.63	0/22468

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	4018	0	3845	81	0
1	B	4018	0	3845	102	0
1	C	4018	0	3845	96	0
1	D	4012	0	3840	104	0
2	A	43	0	30	1	0
2	B	43	0	30	0	0
2	C	43	0	30	0	0
2	D	43	0	30	0	0
3	A	48	0	26	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	C	48	0	26	0	0
4	A	309	0	0	18	0
4	B	263	0	0	10	0
4	C	266	0	0	12	0
4	D	271	0	0	15	0
All	All	17443	0	15547	325	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 10.

All (325) 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:138:THR:HG22	1:B:140:ASP:H	1.17	1.05
1:B:452:ASN:H	1:B:455:GLN:HE21	0.99	0.92
1:A:13:GLN:HE21	1:C:471:GLN:HE22	1.12	0.92
1:A:120[B]:SER:O	1:C:120[B]:SER:O	1.89	0.91
1:A:53:GLN:HE21	1:D:352:GLN:HE22	1.19	0.89
1:A:385:ASN:H	1:A:398:GLN:HE22	1.19	0.88
1:A:116:VAL:HG21	1:A:129:PRO:HG2	1.58	0.84
1:B:486:HIS:HD2	1:B:488:ASP:H	1.25	0.82
1:B:13:GLN:HE21	1:D:471:GLN:HE22	1.27	0.81
1:B:452:ASN:H	1:B:455:GLN:NE2	1.78	0.81
1:B:138:THR:HG22	1:B:140:ASP:N	1.95	0.80
1:B:407:ASN:HD21	1:B:411:ALA:HB3	1.48	0.79
1:A:63:HIS:HE1	1:D:369:ASN:HD21	1.31	0.78
1:D:389:ASP:H	1:D:397:ASN:HD21	1.32	0.78
1:B:116:VAL:HG21	1:B:129:PRO:HG2	1.66	0.77
1:B:452:ASN:N	1:B:455:GLN:HE21	1.81	0.74
1:A:13:GLN:NE2	1:C:471:GLN:HE22	1.85	0.73
1:B:63:HIS:HE1	1:C:369:ASN:HD21	1.34	0.73
1:B:53:GLN:HE21	1:C:352:GLN:HE22	1.37	0.72
1:B:120[B]:SER:O	1:D:119:GLU:HB2	1.89	0.72
1:C:385:ASN:HD22	1:C:387:GLN:H	1.36	0.72
1:D:486:HIS:HD2	1:D:488:ASP:H	1.36	0.72
1:D:352:GLN:HA	1:D:355:LEU:HD22	1.72	0.71
1:C:486:HIS:HD2	1:C:488:ASP:H	1.37	0.71
1:A:486:HIS:HD2	1:A:488:ASP:H	1.39	0.70
1:A:13:GLN:HE21	1:C:471:GLN:NE2	1.89	0.70
1:A:486:HIS:CD2	1:A:488:ASP:H	2.09	0.70
1:D:385:ASN:H	1:D:398:GLN:HE22	1.37	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:158:PRO:HG3	1:D:350:MET:HA	1.74	0.69
1:C:475:GLN:HE21	1:C:497:LEU:HD13	1.58	0.68
1:B:158:PRO:HG3	1:B:350:MET:HA	1.75	0.68
1:C:382:ARG:HG3	1:C:382:ARG:HH11	1.58	0.67
1:B:425:TYR:HA	4:B:1356:HOH:O	1.94	0.67
1:D:454:GLU:HB3	1:D:458:ARG:HH21	1.61	0.66
1:D:169:LYS:HB3	4:D:1401:HOH:O	1.93	0.66
1:C:486:HIS:CD2	1:C:488:ASP:H	2.13	0.66
1:B:352:GLN:HE22	1:C:53:GLN:HE21	1.44	0.65
1:B:486:HIS:CD2	1:B:488:ASP:H	2.13	0.65
1:C:385:ASN:ND2	1:C:387:GLN:H	1.95	0.65
1:A:9:SER:HB3	4:A:1307:HOH:O	1.98	0.64
1:B:138:THR:HB	1:B:141:GLY:O	1.98	0.64
1:D:116:VAL:HG21	1:D:129:PRO:HG2	1.79	0.64
1:B:68:ARG:HA	4:B:1292:HOH:O	1.98	0.64
1:D:157:ASP:HB3	1:D:160:LEU:HD12	1.79	0.63
1:D:486:HIS:CD2	1:D:488:ASP:H	2.17	0.63
1:B:407:ASN:ND2	1:B:411:ALA:HB3	2.14	0.63
1:A:407:ASN:HD21	1:A:411:ALA:HB3	1.63	0.62
1:B:63:HIS:HE1	1:C:369:ASN:ND2	1.98	0.62
1:B:63:HIS:HD2	4:B:1237:HOH:O	1.82	0.62
1:B:53:GLN:HE21	1:C:352:GLN:NE2	1.95	0.61
1:A:53:GLN:HE21	1:D:352:GLN:NE2	1.95	0.61
1:D:407:ASN:HD21	1:D:411:ALA:HB3	1.65	0.61
1:B:352:GLN:NE2	1:C:53:GLN:HE21	1.99	0.61
1:A:120[B]:SER:O	1:C:119:GLU:HB2	2.00	0.61
1:B:237:LYS:HE2	4:B:1423:HOH:O	2.00	0.61
1:D:385:ASN:ND2	1:D:387:GLN:H	1.99	0.60
1:B:44:VAL:HG12	1:D:429:VAL:HG22	1.83	0.60
1:D:161:PHE:HB3	1:D:162:PRO:HD3	1.84	0.60
1:C:83:GLY:HA3	1:C:317:VAL:O	2.02	0.59
4:A:1345:HOH:O	1:B:53:GLN:HG3	2.02	0.59
1:B:329:VAL:O	1:B:332:ILE:HG22	2.02	0.59
1:A:361:THR:HG21	2:A:1200:HEM:HBA1	1.83	0.59
1:B:394:MET:HG2	1:C:394:MET:HG3	1.84	0.59
1:C:407:ASN:HD21	1:C:411:ALA:HB3	1.68	0.59
1:C:233:LYS:HB2	1:C:282:GLN:HB2	1.84	0.59
1:A:385:ASN:ND2	1:A:387:GLN:H	1.99	0.58
1:A:352:GLN:O	1:A:355:LEU:HB2	2.03	0.58
1:B:120[B]:SER:O	1:D:119:GLU:CB	2.51	0.58
4:A:1494:HOH:O	1:D:53:GLN:HG3	2.04	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:373:ILE:HD11	1:C:392:MET:HE1	1.84	0.57
1:D:61:MET:HE1	1:D:64:PHE:CD2	2.39	0.57
1:A:486:HIS:HD2	1:A:488:ASP:N	2.00	0.56
1:B:83:GLY:HA3	1:B:317:VAL:O	2.06	0.56
1:B:63:HIS:CE1	1:C:369:ASN:HD21	2.21	0.56
1:A:158:PRO:HG3	1:A:350:MET:HA	1.88	0.56
1:A:237:LYS:HE3	4:A:1533:HOH:O	2.04	0.56
1:D:454:GLU:HB3	1:D:458:ARG:NH2	2.21	0.56
1:A:394:MET:SD	1:D:394:MET:HE2	2.45	0.56
1:D:392:MET:HB3	1:D:394:MET:HE1	1.89	0.55
1:C:106:LYS:HE3	4:C:1485:HOH:O	2.07	0.55
1:D:385:ASN:HD22	1:D:387:GLN:H	1.54	0.55
1:C:137:TYR:HA	1:C:142:ASN:ND2	2.21	0.55
1:C:49:PRO:HB2	1:D:51:LEU:HD12	1.88	0.55
1:B:389:ASP:H	1:B:397:ASN:HD21	1.53	0.55
1:B:19:ARG:HG3	1:B:19:ARG:HH11	1.72	0.55
1:A:392:MET:HE1	1:D:370:TYR:HA	1.89	0.55
1:A:329:VAL:O	1:A:332:ILE:HG22	2.06	0.54
1:A:352:GLN:HE22	1:D:53:GLN:HE21	1.55	0.54
1:D:385:ASN:HD22	1:D:385:ASN:C	2.11	0.54
1:B:116:VAL:CG2	1:B:129:PRO:HG2	2.37	0.54
1:C:75:HIS:HA	1:C:115:THR:O	2.08	0.54
1:C:146:VAL:HG22	1:C:334:PHE:HB3	1.89	0.54
1:B:44:VAL:O	1:B:48:GLY:HA3	2.08	0.54
1:C:139:GLU:HA	1:C:380:ARG:O	2.08	0.54
1:B:451:LEU:HA	1:B:455:GLN:NE2	2.22	0.54
1:A:352:GLN:HA	1:A:355:LEU:HD22	1.90	0.54
1:C:476:LYS:HE3	1:C:476:LYS:HA	1.89	0.54
1:B:161:PHE:HB3	1:B:162:PRO:HD3	1.90	0.53
1:B:13:GLN:NE2	1:D:471:GLN:HE22	2.03	0.53
1:C:128:ASP:O	1:C:130:ARG:NH1	2.41	0.53
1:B:395:GLN:HG3	1:B:396:ASP:H	1.72	0.53
1:C:237:LYS:HE2	4:C:1483:HOH:O	2.07	0.53
1:A:403:ASN:HD21	1:B:181:MET:CE	2.22	0.53
1:D:39:LEU:HB2	4:D:1378:HOH:O	2.09	0.52
1:A:394:MET:HG2	1:D:394:MET:HG2	1.91	0.52
1:B:110:ALA:HB3	1:B:135:LYS:HB3	1.90	0.52
1:B:169:LYS:HB3	4:B:1256:HOH:O	2.08	0.52
1:D:203:ARG:HE	1:D:242:ILE:HG21	1.74	0.52
1:D:444:ARG:HD3	1:D:485:VAL:O	2.10	0.52
1:C:334:PHE:O	1:C:362:HIS:HE1	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:391:PRO:HG3	1:C:69:ILE:HG22	1.92	0.52
1:A:385:ASN:C	1:A:385:ASN:HD22	2.12	0.52
1:D:329:VAL:O	1:D:332:ILE:HG22	2.10	0.52
1:A:486:HIS:CD2	1:A:488:ASP:HB2	2.45	0.52
1:B:486:HIS:HD2	1:B:488:ASP:N	2.00	0.52
1:B:75:HIS:HA	1:B:115:THR:O	2.10	0.51
1:A:63:HIS:HE1	1:D:369:ASN:ND2	2.03	0.51
1:D:415:GLN:HG3	1:D:415:GLN:O	2.10	0.51
1:C:50:LEU:HD12	1:C:51:LEU:H	1.76	0.51
1:D:365:ARG:HD2	4:D:1326:HOH:O	2.10	0.51
1:A:213:ASN:OD1	1:A:238:THR:HG22	2.10	0.51
1:D:83:GLY:HA3	1:D:317:VAL:O	2.10	0.51
1:C:5:ARG:H	1:C:5:ARG:HD2	1.76	0.50
1:A:429:VAL:HG13	1:C:51:LEU:HD22	1.92	0.50
1:C:116:VAL:HG21	1:C:129:PRO:HG2	1.93	0.50
1:B:211:HIS:CG	1:B:243:LYS:HB3	2.47	0.50
1:C:93:LYS:HB2	1:C:93:LYS:NZ	2.26	0.50
1:C:402:PRO:HA	4:C:1362:HOH:O	2.11	0.50
1:D:88:THR:OG1	1:D:89:HIS:HD2	1.95	0.50
1:D:93:LYS:HE3	1:D:94:TYR:CZ	2.46	0.50
1:B:146:VAL:HG22	1:B:334:PHE:HB3	1.94	0.50
1:C:191:GLU:H	1:C:191:GLU:CD	2.15	0.50
1:A:40:ASN:OD1	1:C:433:ASN:HA	2.10	0.50
1:A:82:PHE:HB2	1:A:320:ARG:HB3	1.94	0.50
1:B:40:ASN:ND2	1:D:433:ASN:HA	2.26	0.50
1:B:285:THR:OG1	1:B:288:GLN:HG3	2.11	0.50
1:B:359:PRO:O	1:B:363:ARG:HG3	2.11	0.50
1:A:51:LEU:HD23	1:B:51:LEU:HD13	1.94	0.50
1:D:358:TYR:O	1:D:361:THR:HG22	2.12	0.50
1:D:109:ILE:HA	1:D:135:LYS:O	2.12	0.50
1:B:127:ARG:NH1	4:B:1419:HOH:O	2.44	0.49
1:C:208:GLY:HA3	4:C:1471:HOH:O	2.11	0.49
1:B:444:ARG:HD3	1:B:485:VAL:O	2.11	0.49
1:B:236:TYR:N	1:B:236:TYR:CD2	2.80	0.49
1:D:61:MET:CE	1:D:64:PHE:CD2	2.96	0.49
1:A:63:HIS:HD2	4:D:1397:HOH:O	1.95	0.49
1:A:97:ALA:HB3	1:A:100:PHE:CD2	2.47	0.49
1:B:452:ASN:O	1:B:456:ARG:HG3	2.12	0.49
1:A:391:PRO:HG3	1:D:69:ILE:HG22	1.93	0.49
1:B:217:SER:HB3	1:B:299:LEU:HD11	1.95	0.49
1:B:285:THR:HB	4:B:1445:HOH:O	2.11	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:161:PHE:HB3	1:A:162:PRO:HD3	1.94	0.49
1:B:286:PHE:N	1:B:286:PHE:CD1	2.81	0.48
1:D:214:GLY:HA3	1:D:236:TYR:CE1	2.48	0.48
1:D:352:GLN:O	1:D:355:LEU:HB2	2.13	0.48
1:D:440:VAL:HG23	1:D:441:THR:N	2.28	0.48
1:D:481:ASN:HB2	4:D:1301:HOH:O	2.12	0.48
1:B:138:THR:CG2	1:B:139:GLU:N	2.77	0.48
1:B:77:LYS:HD2	1:B:122:SER:O	2.14	0.48
1:B:286:PHE:N	1:B:286:PHE:HD1	2.11	0.48
1:B:55:VAL:HG11	1:C:337:SER:HB2	1.95	0.48
1:B:144:ASP:HB2	1:B:335:ASP:O	2.13	0.48
1:D:407:ASN:ND2	1:D:411:ALA:HB3	2.28	0.48
1:A:350:MET:O	1:A:354:ARG:HG3	2.14	0.48
1:C:109:ILE:HA	1:C:135:LYS:O	2.13	0.48
1:B:392:MET:HE1	1:C:373:ILE:HD11	1.95	0.47
1:C:238:THR:HA	1:C:277:TRP:CD1	2.48	0.47
1:D:389:ASP:N	1:D:397:ASN:HD21	2.07	0.47
1:C:80:GLY:HA3	4:C:1446:HOH:O	2.13	0.47
1:C:403:ASN:C	1:C:403:ASN:HD22	2.16	0.47
1:D:405:TYR:OH	1:D:414:GLN:HG2	2.15	0.47
1:A:85:PHE:O	1:A:106:LYS:HA	2.14	0.47
1:B:394:MET:CG	1:C:394:MET:HG3	2.45	0.47
1:D:461:GLU:HA	1:D:496:LEU:HD13	1.95	0.47
1:A:415:GLN:O	1:D:36:GLY:HA2	2.14	0.47
1:A:238:THR:HA	1:A:277:TRP:CD1	2.49	0.47
1:A:352:GLN:NE2	1:D:53:GLN:HE21	2.13	0.47
1:D:98:LYS:HD3	4:D:1442:HOH:O	2.14	0.47
1:A:69:ILE:HG22	1:D:391:PRO:HG3	1.96	0.47
1:A:116:VAL:CG2	1:A:129:PRO:HG2	2.38	0.47
1:A:128:ASP:OD2	1:A:129:PRO:HD2	2.15	0.47
1:A:359:PRO:HG2	4:A:1392:HOH:O	2.14	0.47
1:A:40:ASN:CG	1:C:433:ASN:HA	2.35	0.46
1:A:53:GLN:NE2	4:A:1488:HOH:O	2.48	0.46
1:A:385:ASN:HD22	1:A:387:GLN:H	1.63	0.46
1:A:436:ASN:HB2	4:A:1595:HOH:O	2.15	0.46
1:B:178:ASP:HA	1:B:179:PRO:HD2	1.81	0.46
1:C:461:GLU:HA	1:C:496:LEU:HD13	1.95	0.46
1:B:19:ARG:HG3	1:B:19:ARG:NH1	2.30	0.46
1:B:433:ASN:HA	1:D:40:ASN:ND2	2.30	0.46
1:D:359:PRO:HG2	4:D:1308:HOH:O	2.15	0.46
1:C:486:HIS:HD2	1:C:488:ASP:N	2.10	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:444:ARG:O	1:D:448:VAL:HG23	2.15	0.46
1:C:97:ALA:HB3	1:C:100:PHE:CD2	2.51	0.46
1:A:394:MET:HE2	1:D:372:HIS:HB2	1.96	0.46
1:D:233:LYS:HB2	1:D:282:GLN:HB2	1.98	0.46
1:B:119:GLU:HB2	1:D:120[B]:SER:O	2.16	0.45
1:B:392:MET:HE1	1:C:370:TYR:HA	1.97	0.45
1:C:475:GLN:NE2	1:C:497:LEU:HD13	2.30	0.45
1:D:285:THR:OG1	1:D:288:GLN:HG3	2.15	0.45
1:C:232:CYS:HA	1:C:282:GLN:O	2.16	0.45
1:D:352:GLN:HG3	4:D:1448:HOH:O	2.16	0.45
1:D:457:LYS:O	1:D:461:GLU:HG2	2.16	0.45
1:A:215:TYR:HB3	4:A:1389:HOH:O	2.17	0.45
1:C:365:ARG:HD2	4:C:1308:HOH:O	2.17	0.45
1:D:110:ALA:HB3	1:D:135:LYS:HB3	1.99	0.45
1:A:57:PHE:CE1	1:C:158:PRO:HB2	2.51	0.45
1:B:138:THR:HG22	1:B:139:GLU:N	2.32	0.45
1:C:415:GLN:HA	1:C:416:PRO:HD3	1.87	0.45
1:A:339:MET:HA	1:A:340:PRO:HD3	1.73	0.45
1:A:365:ARG:HD2	4:A:1449:HOH:O	2.16	0.45
1:C:210:ARG:HD2	4:C:1365:HOH:O	2.16	0.45
1:A:195:GLN:HA	1:A:195:GLN:OE1	2.17	0.45
1:C:171:ASN:HB3	1:C:174:THR:OG1	2.16	0.45
1:C:193:LEU:HD11	1:C:481:ASN:HB3	1.98	0.45
1:D:98:LYS:O	1:D:101:GLU:HG2	2.16	0.45
1:C:389:ASP:H	1:C:397:ASN:HD21	1.65	0.45
1:A:336:PRO:HD2	4:A:1508:HOH:O	2.16	0.45
1:C:283:VAL:HG23	1:C:311:ILE:HD12	1.98	0.45
1:A:91:ILE:HG21	1:A:313:VAL:HG22	1.99	0.44
1:C:214:GLY:HA3	1:C:236:TYR:CE1	2.52	0.44
1:A:146:VAL:HB	1:A:354:ARG:HH22	1.81	0.44
1:A:368:PRO:HD2	4:A:1431:HOH:O	2.18	0.44
1:A:68:ARG:HA	4:A:1314:HOH:O	2.17	0.44
1:A:429:VAL:HG23	1:B:425:TYR:HD2	1.83	0.44
1:C:44:VAL:HG13	1:C:44:VAL:O	2.18	0.44
1:D:221:LYS:NZ	1:D:423:ILE:HD11	2.33	0.44
1:B:359:PRO:HG2	4:B:1384:HOH:O	2.17	0.44
1:D:79:ALA:HB2	1:D:262:ILE:HG12	2.00	0.44
1:B:44:VAL:O	1:B:44:VAL:HG23	2.18	0.44
1:C:382:ARG:HG3	1:C:382:ARG:NH1	2.29	0.44
1:D:329:VAL:HA	4:D:1418:HOH:O	2.18	0.44
1:D:27:LEU:HD21	1:D:38:LYS:HD3	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:53:GLN:NE2	1:C:352:GLN:HE22	2.11	0.43
1:A:385:ASN:HA	1:D:27:LEU:HD13	2.01	0.43
1:B:143:TRP:HB2	1:B:340:PRO:HD3	2.00	0.43
1:D:149:ASN:HA	1:D:213:ASN:O	2.18	0.43
1:A:179:PRO:HG2	4:A:1560:HOH:O	2.17	0.43
1:C:74:VAL:O	1:C:75:HIS:HB2	2.18	0.43
1:C:411:ALA:HB1	1:C:412:PRO:HD2	2.00	0.43
1:D:75:HIS:CE1	1:D:116:VAL:HG22	2.53	0.43
1:A:157:ASP:HA	1:A:158:PRO:HD3	1.83	0.43
1:B:434:THR:H	1:D:40:ASN:HD21	1.64	0.43
1:D:486:HIS:HD2	1:D:488:ASP:N	2.11	0.43
1:B:476:LYS:HA	1:B:476:LYS:HD3	1.77	0.43
1:C:102:HIS:HB2	4:C:1350:HOH:O	2.18	0.43
1:C:169:LYS:HB3	1:C:170:ARG:H	1.69	0.43
1:C:281:ILE:HG23	1:C:313:VAL:HG21	2.01	0.43
1:C:137:TYR:HA	1:C:142:ASN:HD22	1.83	0.43
1:B:405:TYR:OH	1:B:414:GLN:HG2	2.19	0.43
1:C:27:LEU:HD21	1:C:38:LYS:HD3	2.00	0.43
1:C:403:ASN:C	1:C:403:ASN:ND2	2.72	0.43
1:D:44:VAL:O	1:D:48:GLY:HA3	2.19	0.43
1:B:211:HIS:CB	1:B:243:LYS:HB3	2.49	0.43
1:C:79:ALA:O	1:C:112:ARG:HA	2.19	0.43
1:D:61:MET:CE	1:D:64:PHE:HD2	2.31	0.43
1:D:329:VAL:HG22	4:D:1418:HOH:O	2.18	0.43
1:A:245:LEU:HA	4:A:1482:HOH:O	2.19	0.42
1:B:486:HIS:CD2	1:B:488:ASP:HB3	2.54	0.42
1:D:113:PHE:HA	1:D:131:GLY:O	2.18	0.42
1:A:430:ARG:HB2	4:A:1594:HOH:O	2.18	0.42
1:C:421:HIS:CE1	1:C:423:ILE:HG12	2.54	0.42
1:D:458:ARG:HG2	4:D:1241:HOH:O	2.18	0.42
1:A:109:ILE:HA	1:A:135:LYS:O	2.19	0.42
1:B:327:ALA:HA	1:B:331:GLN:HE21	1.84	0.42
1:D:75:HIS:HA	1:D:115:THR:O	2.19	0.42
1:A:274:TYR:HB3	1:A:318:LEU:O	2.20	0.42
1:A:359:PRO:O	1:A:363:ARG:HG3	2.20	0.42
1:B:352:GLN:HE22	1:C:53:GLN:NE2	2.11	0.42
1:C:39:LEU:HB2	4:C:1354:HOH:O	2.20	0.42
1:D:157:ASP:HA	1:D:158:PRO:HD3	1.91	0.42
1:D:380:ARG:HB3	1:D:380:ARG:HH11	1.84	0.42
1:A:169:LYS:HB3	4:A:1390:HOH:O	2.18	0.42
1:C:98:LYS:O	1:C:101:GLU:HG2	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:57:PHE:CE1	1:D:158:PRO:HB2	2.55	0.42
1:B:157:ASP:HA	1:B:158:PRO:HD3	1.94	0.42
1:B:60:GLU:HB3	4:B:1220:HOH:O	2.19	0.42
1:C:82:PHE:HZ	1:C:328:GLU:HB3	1.84	0.42
1:A:394:MET:CG	1:D:394:MET:HE2	2.50	0.41
1:C:44:VAL:HG21	1:D:44:VAL:HG21	2.00	0.41
1:C:311:ILE:HA	1:C:312:PRO:HD2	1.86	0.41
1:D:146:VAL:HB	1:D:354:ARG:HH22	1.84	0.41
1:D:282:GLN:HG3	1:D:310:LEU:HD23	2.01	0.41
1:D:386:TYR:CE1	1:D:405:TYR:HB2	2.55	0.41
1:B:5:ARG:HD3	1:B:10:ASP:OD1	2.21	0.41
1:B:51:LEU:N	1:B:51:LEU:HD22	2.35	0.41
1:B:457:LYS:HE2	1:B:461:GLU:OE2	2.20	0.41
1:C:292:PHE:HA	1:C:293:PRO:HD3	1.93	0.41
1:D:116:VAL:CG2	1:D:129:PRO:HG2	2.48	0.41
1:D:486:HIS:HA	1:D:487:PRO:HD3	1.90	0.41
1:B:84:TYR:N	1:B:109:ILE:HG12	2.35	0.41
1:C:44:VAL:O	1:C:48:GLY:HA3	2.20	0.41
1:D:336:PRO:HD2	4:D:1309:HOH:O	2.20	0.41
1:D:477:LYS:HA	4:D:1449:HOH:O	2.20	0.41
1:A:119:GLU:HB2	1:C:120[B]:SER:O	2.20	0.41
1:C:53:GLN:NE2	4:C:1521:HOH:O	2.52	0.41
1:C:368:PRO:HB2	1:C:391:PRO:HD2	2.02	0.41
1:A:385:ASN:H	1:A:398:GLN:NE2	2.01	0.41
1:B:69:ILE:HG22	1:C:391:PRO:HG3	2.03	0.41
1:B:183:TRP:CD2	1:B:467:LEU:HD13	2.56	0.41
1:B:240:GLN:OE1	1:B:275:PRO:HA	2.21	0.41
1:D:137:TYR:HA	1:D:142:ASN:OD1	2.21	0.41
1:D:157:ASP:HB3	1:D:160:LEU:CD1	2.48	0.41
1:A:127:ARG:HD2	1:A:199:LEU:O	2.21	0.41
1:C:5:ARG:H	1:C:5:ARG:CD	2.33	0.41
1:D:475:GLN:O	1:D:479:VAL:HG23	2.21	0.41
1:B:70:PRO:HB2	1:B:365:ARG:HB2	2.03	0.41
1:B:207:ASP:HB3	1:B:243:LYS:HG2	2.01	0.41
1:B:281:ILE:HG13	1:B:311:ILE:HB	2.02	0.41
1:B:347:PRO:HG3	4:B:1424:HOH:O	2.20	0.41
1:B:389:ASP:H	1:B:397:ASN:ND2	2.19	0.41
1:D:178:ASP:HA	1:D:179:PRO:HD2	1.89	0.41
1:C:156:ARG:HD2	1:C:434:THR:O	2.21	0.40
1:A:403:ASN:N	1:A:403:ASN:HD22	2.19	0.40
1:B:238:THR:HA	1:B:277:TRP:CD1	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:364:HIS:CD2	1:D:66:ARG:HA	2.56	0.40
1:C:382:ARG:NH1	1:C:382:ARG:CG	2.83	0.40
1:A:348:ASP:HA	4:A:1473:HOH:O	2.21	0.40
1:D:53:GLN:NE2	4:D:1393:HOH:O	2.55	0.40
1:A:276:SER:HA	1:A:316:LEU:O	2.21	0.40
1:C:162:PRO:HD2	4:C:1416:HOH:O	2.22	0.40
1:D:233:LYS:HD2	4:D:1272:HOH:O	2.22	0.40
1:A:422:SER:HA	4:A:1334:HOH:O	2.21	0.40
1:B:295:ASN:HB3	1:B:298:ASP:HB2	2.03	0.40
1:C:233:LYS:HD2	4:C:1432:HOH:O	2.20	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	498/498 (100%)	463 (93%)	35 (7%)	0	100	100
1	B	498/498 (100%)	468 (94%)	30 (6%)	0	100	100
1	C	498/498 (100%)	466 (94%)	30 (6%)	2 (0%)	34	37
1	D	497/498 (100%)	467 (94%)	27 (5%)	3 (1%)	25	26
All	All	1991/1992 (100%)	1864 (94%)	122 (6%)	5 (0%)	41	46

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	396	ASP
1	C	20	ALA
1	D	20	ALA
1	C	441	THR
1	D	374	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	430/429 (100%)	416 (97%)	14 (3%)	38	49
1	B	430/429 (100%)	419 (97%)	11 (3%)	46	58
1	C	430/429 (100%)	413 (96%)	17 (4%)	31	40
1	D	429/429 (100%)	416 (97%)	13 (3%)	41	53
All	All	1719/1716 (100%)	1664 (97%)	55 (3%)	39	50

All (55) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	5	ARG
1	A	77	LYS
1	A	132	PHE
1	A	139	GLU
1	A	150	THR
1	A	177	LYS
1	A	236	TYR
1	A	355	LEU
1	A	385	ASN
1	A	394	MET
1	A	397	ASN
1	A	403	ASN
1	A	424	GLN
1	A	489	TYR
1	B	4	SER
1	B	132	PHE
1	B	150	THR
1	B	236	TYR
1	B	255	GLN
1	B	394	MET
1	B	397	ASN
1	B	403	ASN
1	B	430	ARG
1	B	489	TYR

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Mol	Chain	Res	Type
1	B	492	HIS
1	C	5	ARG
1	C	41	VAL
1	C	67	GLU
1	C	93	LYS
1	C	132	PHE
1	C	138	THR
1	C	150	THR
1	C	236	TYR
1	C	238	THR
1	C	290	GLU
1	C	385	ASN
1	C	397	ASN
1	C	403	ASN
1	C	437	ASP
1	C	454	GLU
1	C	476	LYS
1	C	492	HIS
1	D	93	LYS
1	D	99	VAL
1	D	132	PHE
1	D	160	LEU
1	D	236	TYR
1	D	355	LEU
1	D	374	PRO
1	D	380	ARG
1	D	385	ASN
1	D	394	MET
1	D	397	ASN
1	D	403	ASN
1	D	489	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (59) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	13	GLN
1	A	53	GLN
1	A	63	HIS
1	A	211	HIS
1	A	226	ASN
1	A	338	ASN
1	A	369	ASN

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Mol	Chain	Res	Type
1	A	385	ASN
1	A	395	GLN
1	A	397	ASN
1	A	398	GLN
1	A	403	ASN
1	A	486	HIS
1	B	13	GLN
1	B	40	ASN
1	B	53	GLN
1	B	63	HIS
1	B	211	HIS
1	B	226	ASN
1	B	287	ASN
1	B	338	ASN
1	B	369	ASN
1	B	397	ASN
1	B	403	ASN
1	B	421	HIS
1	B	455	GLN
1	B	475	GLN
1	B	486	HIS
1	B	501	ASN
1	C	40	ASN
1	C	53	GLN
1	C	142	ASN
1	C	226	ASN
1	C	338	ASN
1	C	369	ASN
1	C	385	ASN
1	C	397	ASN
1	C	403	ASN
1	C	415	GLN
1	C	475	GLN
1	C	486	HIS
1	C	501	ASN
1	D	14	HIS
1	D	40	ASN
1	D	53	GLN
1	D	89	HIS
1	D	211	HIS
1	D	255	GLN
1	D	305	HIS

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Mol	Chain	Res	Type
1	D	338	ASN
1	D	369	ASN
1	D	385	ASN
1	D	397	ASN
1	D	398	GLN
1	D	403	ASN
1	D	475	GLN
1	D	486	HIS
1	D	492	HIS
1	D	501	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 monosaccharides in this entry.

5.6 Ligand geometry ⓘ

6 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
3	NDP	C	1301	-	47,52,52	1.30	5 (10%)	61,80,80	1.20	6 (9%)
2	HEM	A	1200	1	42,50,50	1.59	7 (16%)	46,82,82	1.57	11 (23%)
3	NDP	A	1300	-	47,52,52	1.29	5 (10%)	61,80,80	1.32	7 (11%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	HEM	C	1202	1	42,50,50	1.49	7 (16%)	46,82,82	1.45	7 (15%)
2	HEM	D	1203	1	42,50,50	1.47	6 (14%)	46,82,82	1.74	8 (17%)
2	HEM	B	1201	1	42,50,50	1.58	5 (11%)	46,82,82	1.50	10 (21%)

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	NDP	C	1301	-	-	1/30/77/77	0/5/5/5
2	HEM	A	1200	1	-	6/12/54/54	-
3	NDP	A	1300	-	-	1/30/77/77	0/5/5/5
2	HEM	C	1202	1	-	4/12/54/54	-
2	HEM	D	1203	1	-	4/12/54/54	-
2	HEM	B	1201	1	-	4/12/54/54	-

All (35) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1201	HEM	C3C-C2C	-6.05	1.32	1.40
3	C	1301	NDP	C4N-C3N	-4.79	1.40	1.50
2	D	1203	HEM	C3C-C2C	-4.74	1.34	1.40
3	A	1300	NDP	C4N-C3N	-4.48	1.41	1.50
2	A	1200	HEM	C3C-C2C	-4.39	1.34	1.40
2	C	1202	HEM	C3C-C2C	-4.24	1.34	1.40
2	A	1200	HEM	C1A-CHA	-3.35	1.31	1.41
2	C	1202	HEM	FE-ND	-3.31	1.79	1.98
2	D	1203	HEM	FE-ND	-3.10	1.80	1.98
3	C	1301	NDP	C4N-C5N	-3.05	1.41	1.49
3	A	1300	NDP	C4N-C5N	-3.04	1.41	1.49
2	B	1201	HEM	C4A-CHB	-2.96	1.32	1.41
3	A	1300	NDP	C7N-C3N	2.87	1.54	1.48
2	D	1203	HEM	CHD-C1D	-2.77	1.33	1.40
2	A	1200	HEM	C3D-C2D	-2.77	1.30	1.36
2	B	1201	HEM	FE-NB	-2.74	1.82	1.98
2	D	1203	HEM	CHC-C4B	-2.71	1.33	1.40
3	C	1301	NDP	C7N-C3N	2.69	1.54	1.48
2	A	1200	HEM	CHD-C1D	-2.51	1.33	1.40
3	C	1301	NDP	C6N-C5N	2.40	1.40	1.33
3	A	1300	NDP	O4B-C1B	2.32	1.43	1.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1200	HEM	C4A-CHB	-2.31	1.34	1.41
2	A	1200	HEM	FE-ND	-2.30	1.85	1.98
2	C	1202	HEM	CHC-C4B	-2.27	1.34	1.40
2	C	1202	HEM	CHD-C1D	-2.27	1.34	1.40
2	B	1201	HEM	CHC-C4B	-2.23	1.34	1.40
2	C	1202	HEM	C4A-CHB	-2.22	1.34	1.41
2	D	1203	HEM	C1A-CHA	-2.20	1.34	1.41
3	A	1300	NDP	C6N-C5N	2.20	1.39	1.33
2	B	1201	HEM	C1A-CHA	-2.17	1.35	1.41
2	C	1202	HEM	C4D-ND	-2.16	1.36	1.40
2	C	1202	HEM	C1A-CHA	-2.15	1.35	1.41
2	D	1203	HEM	C2A-C3A	-2.14	1.31	1.37
3	C	1301	NDP	O4B-C1B	2.06	1.43	1.40
2	A	1200	HEM	CHC-C4B	-2.02	1.35	1.40

All (49) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	1203	HEM	C3B-C4B-NB	4.75	112.88	109.47
2	A	1200	HEM	CMA-C3A-C4A	-4.40	122.01	128.46
2	D	1203	HEM	C4A-C3A-C2A	4.37	110.03	107.00
3	A	1300	NDP	N3A-C2A-N1A	-4.20	122.97	128.67
3	C	1301	NDP	N3A-C2A-N1A	-4.09	123.12	128.67
3	A	1300	NDP	C4B-O4B-C1B	-3.82	106.43	109.92
2	D	1203	HEM	CMC-C2C-C3C	3.69	132.05	124.68
2	B	1201	HEM	C3B-C4B-NB	3.43	111.93	109.47
2	C	1202	HEM	CMC-C2C-C3C	3.35	131.37	124.68
2	B	1201	HEM	CMC-C2C-C3C	3.28	131.24	124.68
2	B	1201	HEM	C2B-C1B-NB	3.23	113.55	109.84
3	C	1301	NDP	C4A-C5A-N7A	3.16	112.67	109.34
2	D	1203	HEM	C3D-C4D-ND	3.12	113.59	110.17
2	D	1203	HEM	C3B-C2B-C1B	2.96	108.63	106.41
2	A	1200	HEM	CMA-C3A-C2A	2.87	130.36	124.94
2	C	1202	HEM	CMD-C2D-C1D	-2.80	120.66	125.03
2	C	1202	HEM	C3D-C4D-ND	2.79	113.23	110.17
2	C	1202	HEM	C3B-C4B-NB	2.79	111.47	109.47
2	D	1203	HEM	C4B-C3B-C2B	-2.77	104.73	107.28
2	A	1200	HEM	CMC-C2C-C3C	2.75	130.18	124.68
2	A	1200	HEM	C3D-C4D-ND	2.68	113.11	110.17
2	B	1201	HEM	C3D-C4D-ND	2.63	113.05	110.17
2	A	1200	HEM	CAD-C3D-C4D	2.57	129.18	124.70
3	A	1300	NDP	C5A-C6A-N6A	2.55	124.20	120.31

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1200	HEM	C1D-C2D-C3D	2.52	109.63	106.98
2	B	1201	HEM	C1D-C2D-C3D	2.47	109.57	106.98
2	A	1200	HEM	CHA-C4D-C3D	-2.45	120.71	125.23
3	C	1301	NDP	C6A-C5A-C4A	2.37	122.52	117.90
2	C	1202	HEM	CMA-C3A-C4A	-2.37	124.98	128.46
2	B	1201	HEM	CHA-C4D-C3D	-2.34	120.91	125.23
2	B	1201	HEM	CMA-C3A-C4A	-2.33	125.04	128.46
3	C	1301	NDP	O3X-P2B-O2X	2.32	116.50	107.80
3	A	1300	NDP	C4A-C5A-N7A	2.32	111.79	109.34
2	A	1200	HEM	CBA-CAA-C2A	-2.32	108.64	112.54
2	C	1202	HEM	C3B-C2B-C1B	2.29	108.13	106.41
2	C	1202	HEM	C4D-C3D-C2D	-2.28	103.58	106.89
2	A	1200	HEM	C3B-C4B-NB	2.26	111.09	109.47
2	B	1201	HEM	C3B-C2B-C1B	-2.26	104.71	106.41
2	B	1201	HEM	C1B-NB-C4B	-2.21	102.59	105.21
2	D	1203	HEM	C4D-ND-C1D	-2.21	102.59	105.21
2	A	1200	HEM	C4D-ND-C1D	-2.20	102.60	105.21
3	A	1300	NDP	O3X-P2B-O2X	2.19	116.03	107.80
2	A	1200	HEM	C4D-C3D-C2D	-2.16	103.75	106.89
3	A	1300	NDP	C1B-N9A-C4A	-2.15	122.86	126.64
3	C	1301	NDP	C4B-O4B-C1B	-2.14	107.96	109.92
2	D	1203	HEM	C4D-C3D-C2D	-2.05	103.91	106.89
3	A	1300	NDP	C3N-C2N-N1N	-2.03	120.22	123.20
2	B	1201	HEM	C4D-C3D-C2D	-2.02	103.95	106.89
3	C	1301	NDP	O4B-C1B-N9A	2.02	111.43	108.75

There are no chirality outliers.

All (20) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	1300	NDP	O4D-C1D-N1N-C6N
3	C	1301	NDP	O4D-C1D-N1N-C6N
2	A	1200	HEM	C2B-C3B-CAB-CBB
2	B	1201	HEM	CAD-CBD-CGD-O2D
2	B	1201	HEM	CAD-CBD-CGD-O1D
2	C	1202	HEM	CAD-CBD-CGD-O2D
2	A	1200	HEM	CAD-CBD-CGD-O2D
2	C	1202	HEM	CAD-CBD-CGD-O1D
2	A	1200	HEM	CAD-CBD-CGD-O1D
2	D	1203	HEM	CAD-CBD-CGD-O2D
2	D	1203	HEM	CAD-CBD-CGD-O1D
2	A	1200	HEM	C4B-C3B-CAB-CBB

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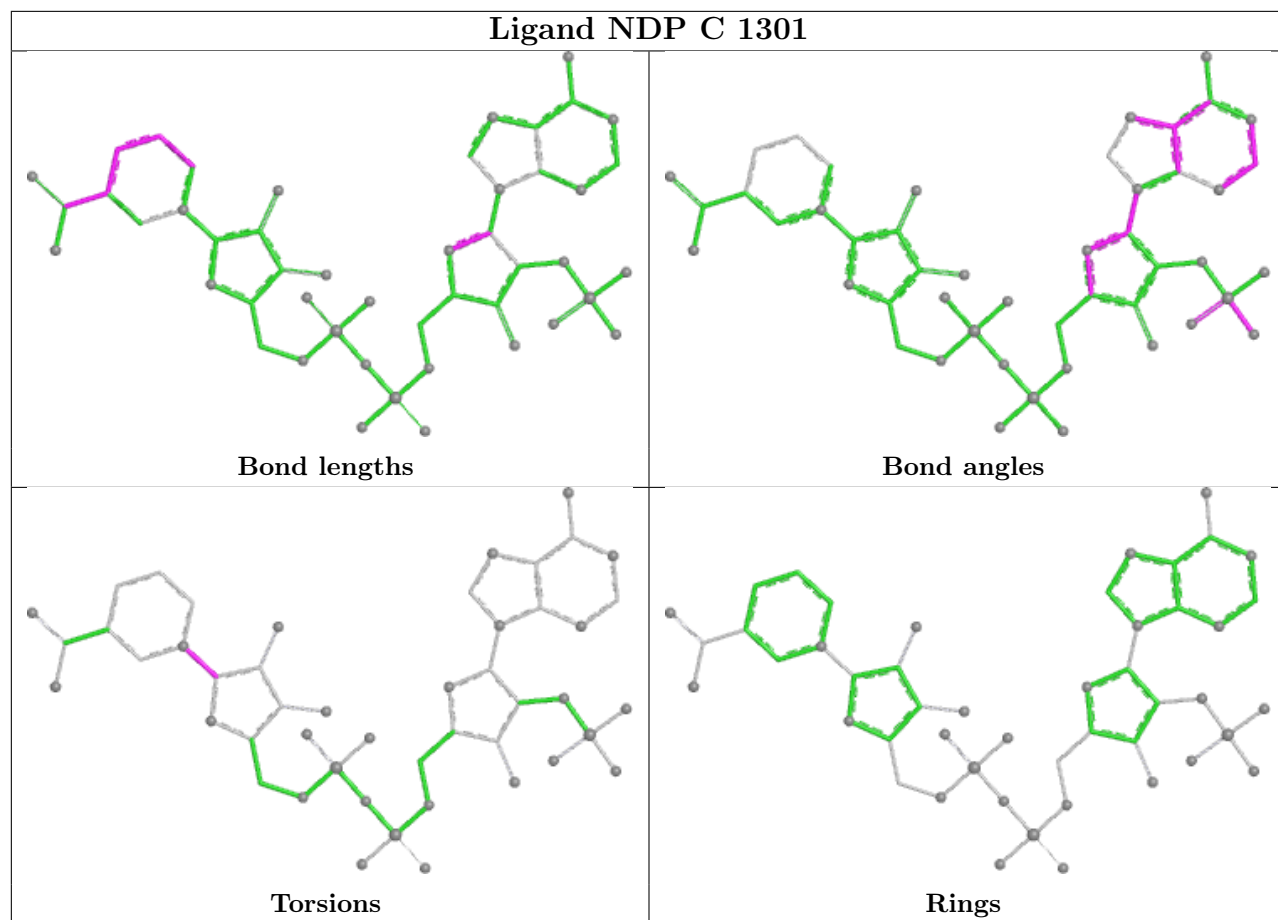
Mol	Chain	Res	Type	Atoms
2	A	1200	HEM	CAA-CBA-CGA-O1A
2	B	1201	HEM	CAA-CBA-CGA-O2A
2	D	1203	HEM	CAA-CBA-CGA-O2A
2	B	1201	HEM	CAA-CBA-CGA-O1A
2	D	1203	HEM	CAA-CBA-CGA-O1A
2	A	1200	HEM	CAA-CBA-CGA-O2A
2	C	1202	HEM	CAA-CBA-CGA-O1A
2	C	1202	HEM	C2B-C3B-CAB-CBB

There are no ring outliers.

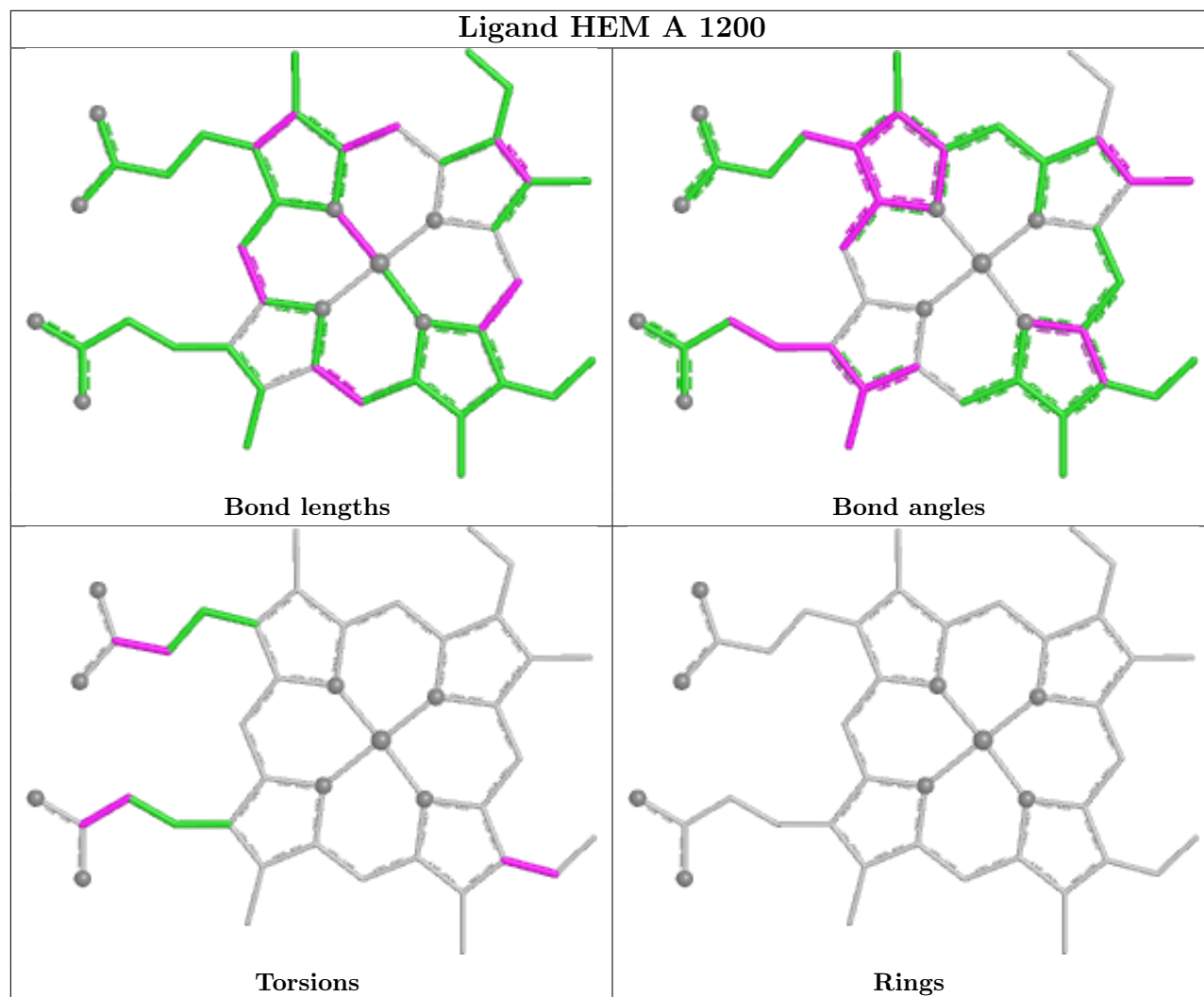
1 monomer is involved in 1 short contact:

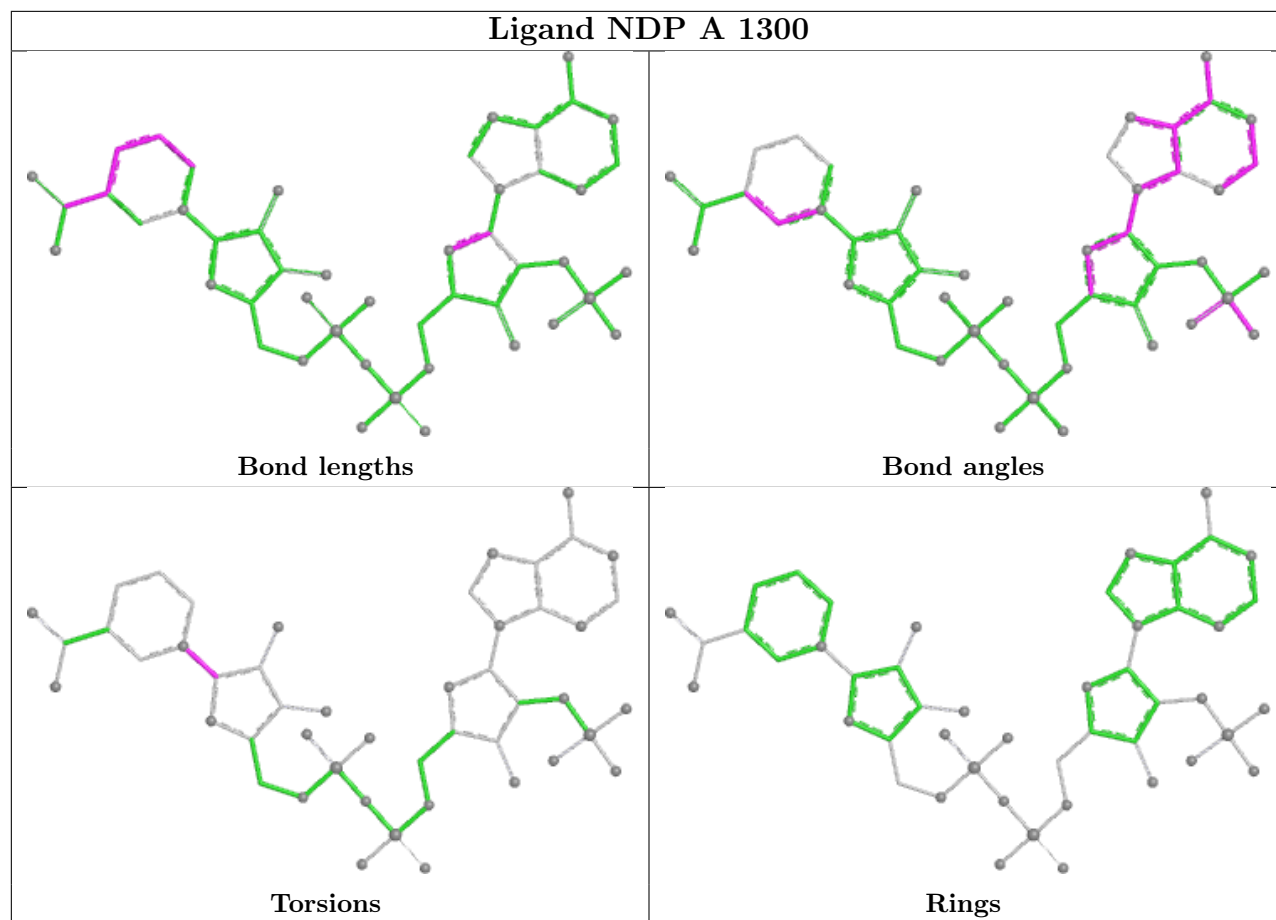
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1200	HEM	1	0

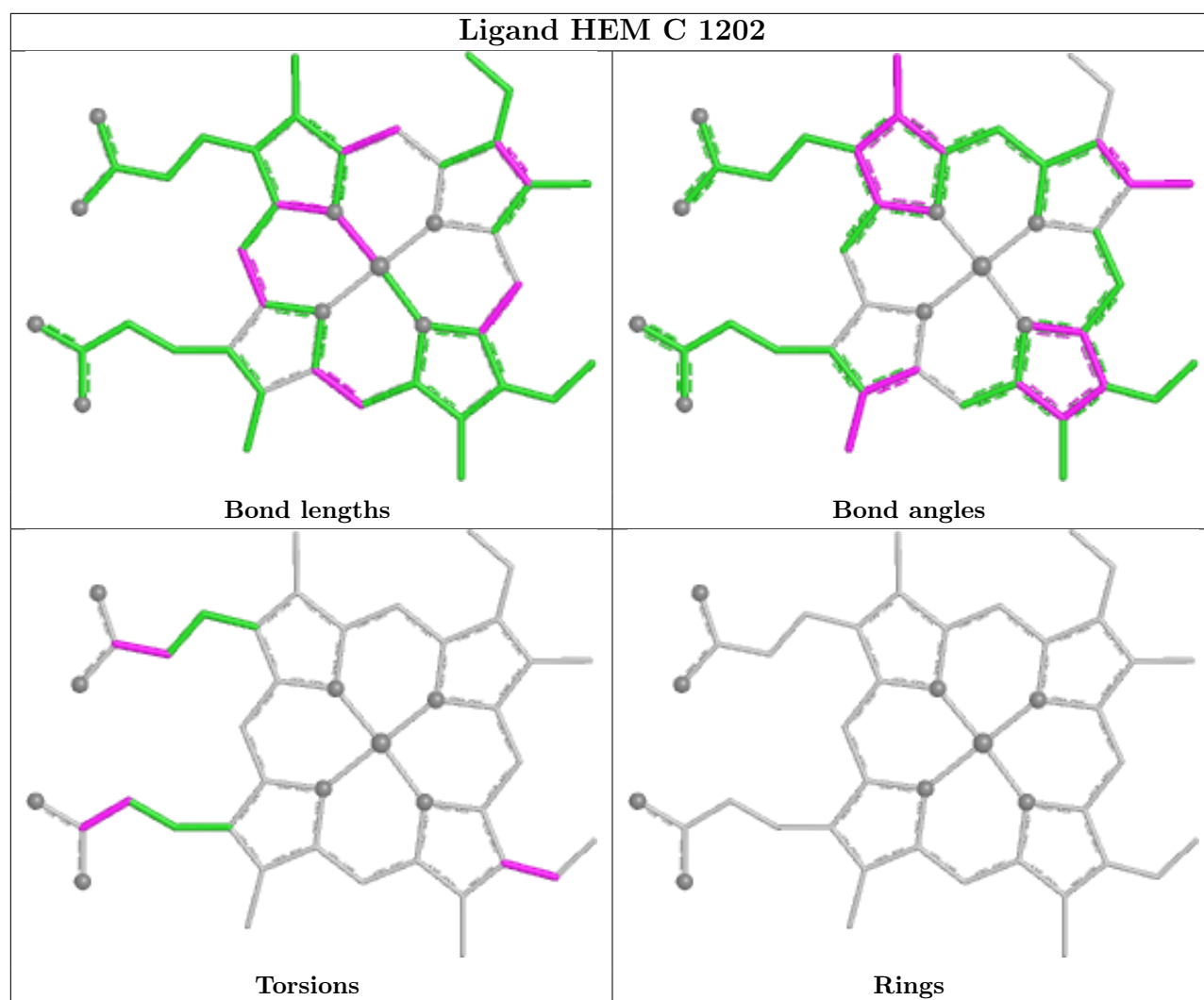
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.



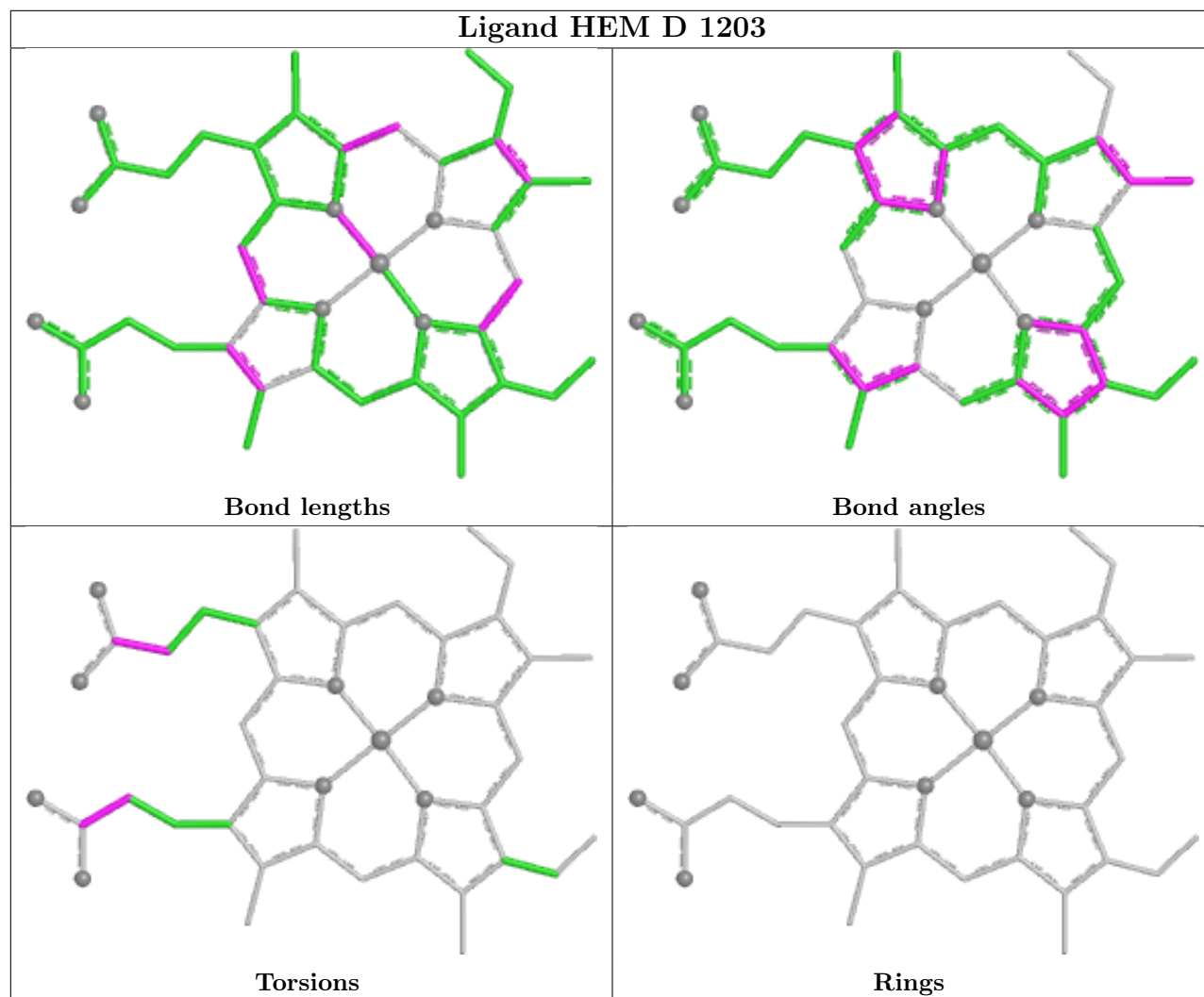
Ligand HEM A 1200

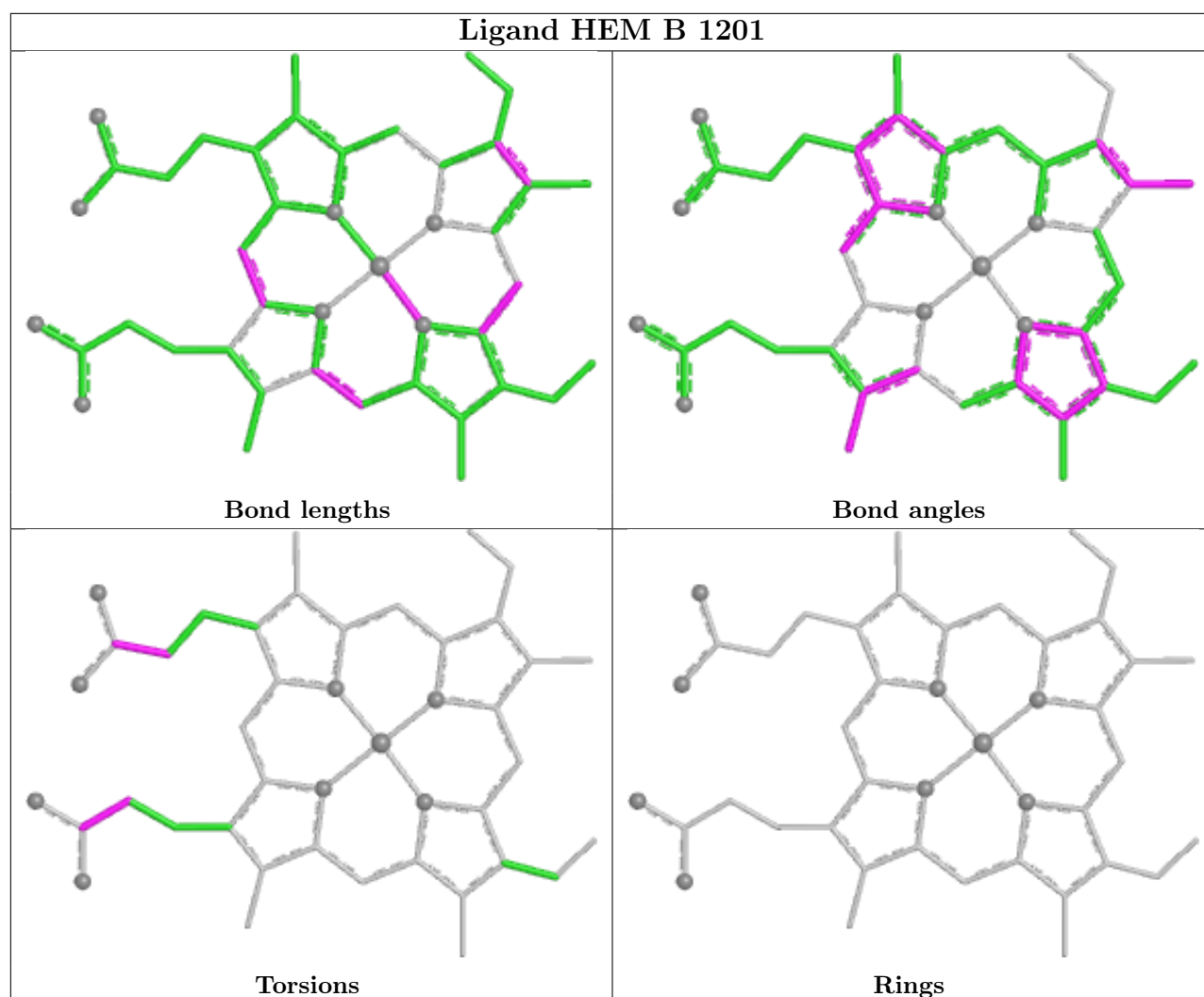






Ligand HEM D 1203





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	498/498 (100%)	-0.33	5 (1%) 82 81	55, 62, 71, 83	0
1	B	498/498 (100%)	-0.34	5 (1%) 82 81	55, 62, 72, 82	0
1	C	498/498 (100%)	-0.35	8 (1%) 72 70	54, 62, 74, 86	0
1	D	497/498 (99%)	-0.31	6 (1%) 79 77	54, 61, 73, 85	0
All	All	1991/1992 (99%)	-0.33	24 (1%) 79 77	54, 62, 73, 86	0

All (24) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	4	SER	5.9
1	B	4	SER	5.7
1	A	4	SER	5.2
1	D	21	ALA	5.2
1	A	21	ALA	4.6
1	C	21	ALA	4.5
1	B	21	ALA	4.5
1	D	20	ALA	4.2
1	C	22	GLN	3.2
1	D	424	GLN	3.1
1	C	500	TYR	2.7
1	C	20	ALA	2.5
1	C	499	LYS	2.4
1	A	23	LYS	2.3
1	D	5	ARG	2.3
1	B	12	MET	2.3
1	A	20	ALA	2.2
1	B	291	THR	2.2
1	D	19	ARG	2.1
1	A	159	ILE	2.1
1	B	23	LYS	2.0

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Mol	Chain	Res	Type	RSRZ
1	C	379	TYR	2.0
1	D	232	CYS	2.0
1	C	306	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 monosaccharides in this entry.

6.4 Ligands [i](#)

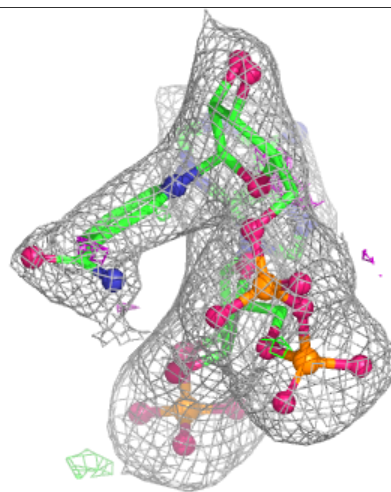
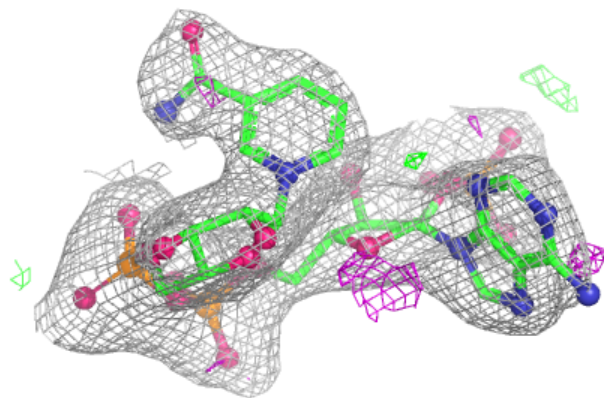
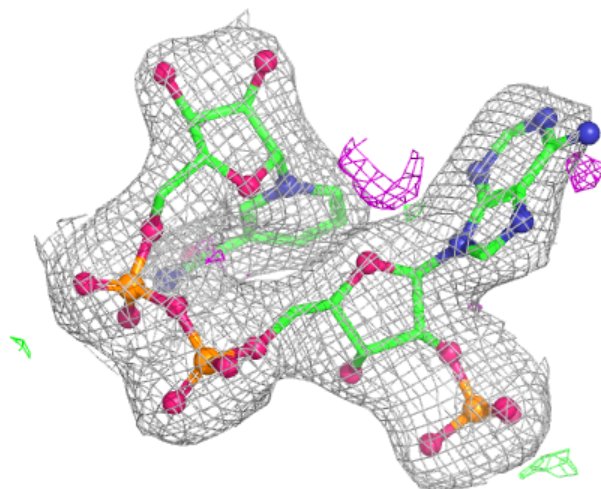
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	NDP	C	1301	48/48	0.95	0.11	73,79,83,83	0
3	NDP	A	1300	48/48	0.96	0.09	67,71,74,74	0
2	HEM	C	1202	43/43	0.97	0.10	58,60,61,61	0
2	HEM	D	1203	43/43	0.97	0.12	54,56,56,57	0
2	HEM	A	1200	43/43	0.98	0.09	56,57,58,58	0
2	HEM	B	1201	43/43	0.98	0.09	56,57,58,59	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.

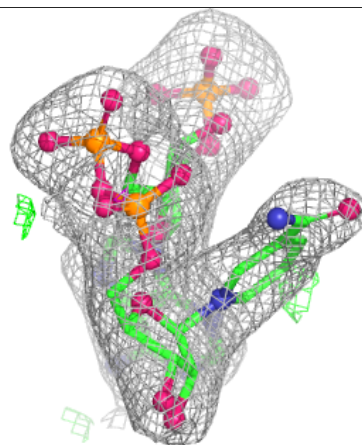
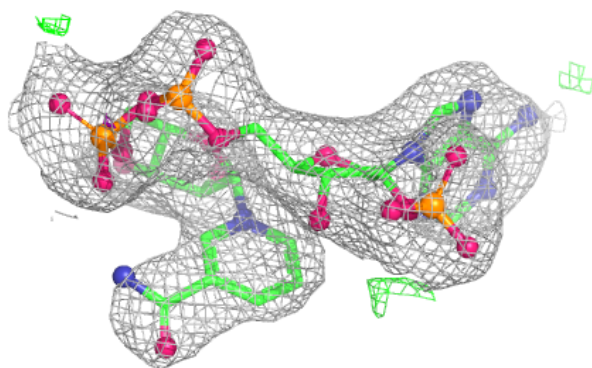
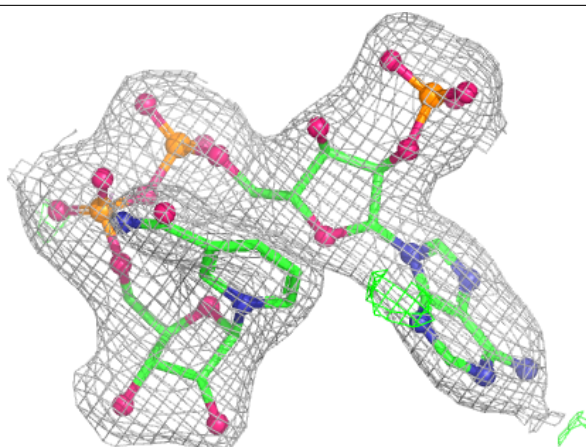
Electron density around NDP C 1301:

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



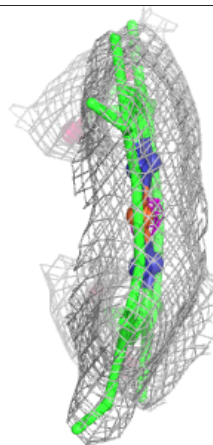
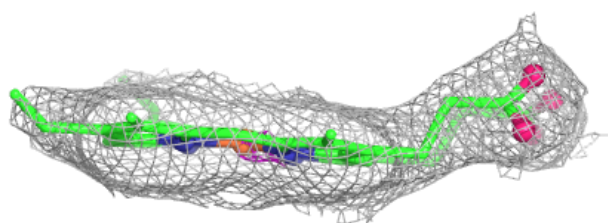
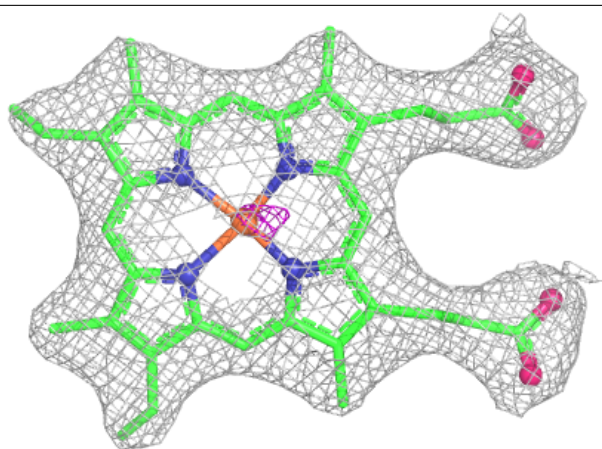
Electron density around NDP A 1300:

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



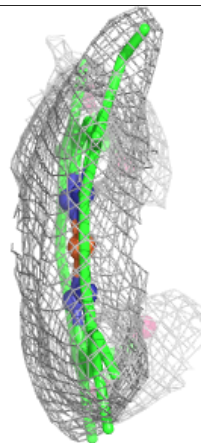
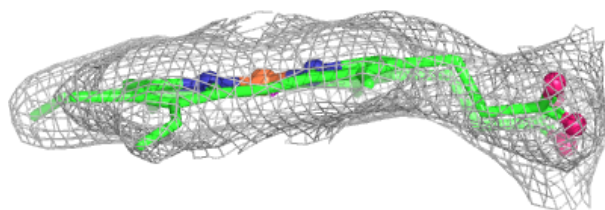
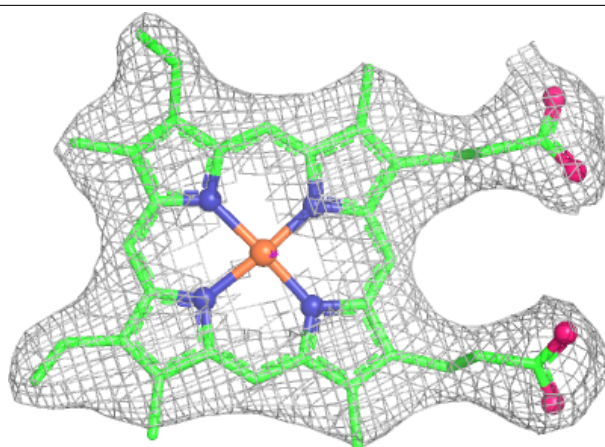
Electron density around HEM C 1202:

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



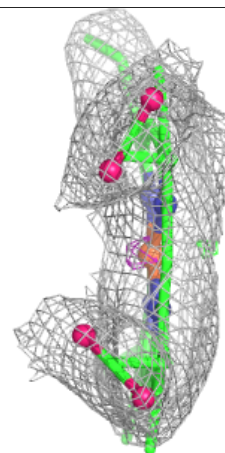
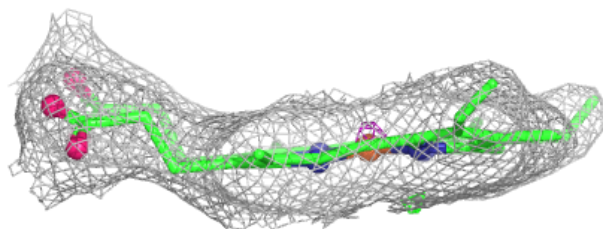
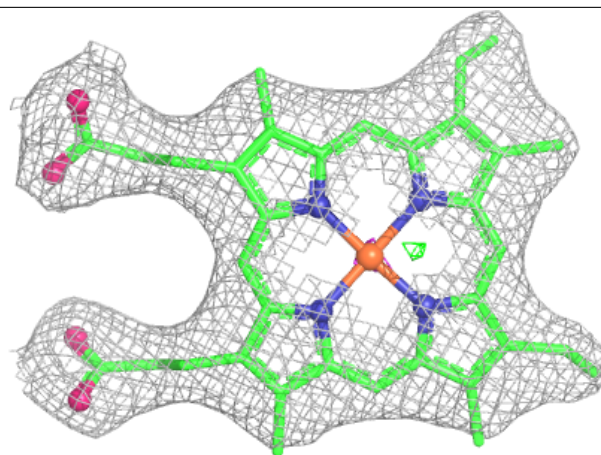
Electron density around HEM D 1203:

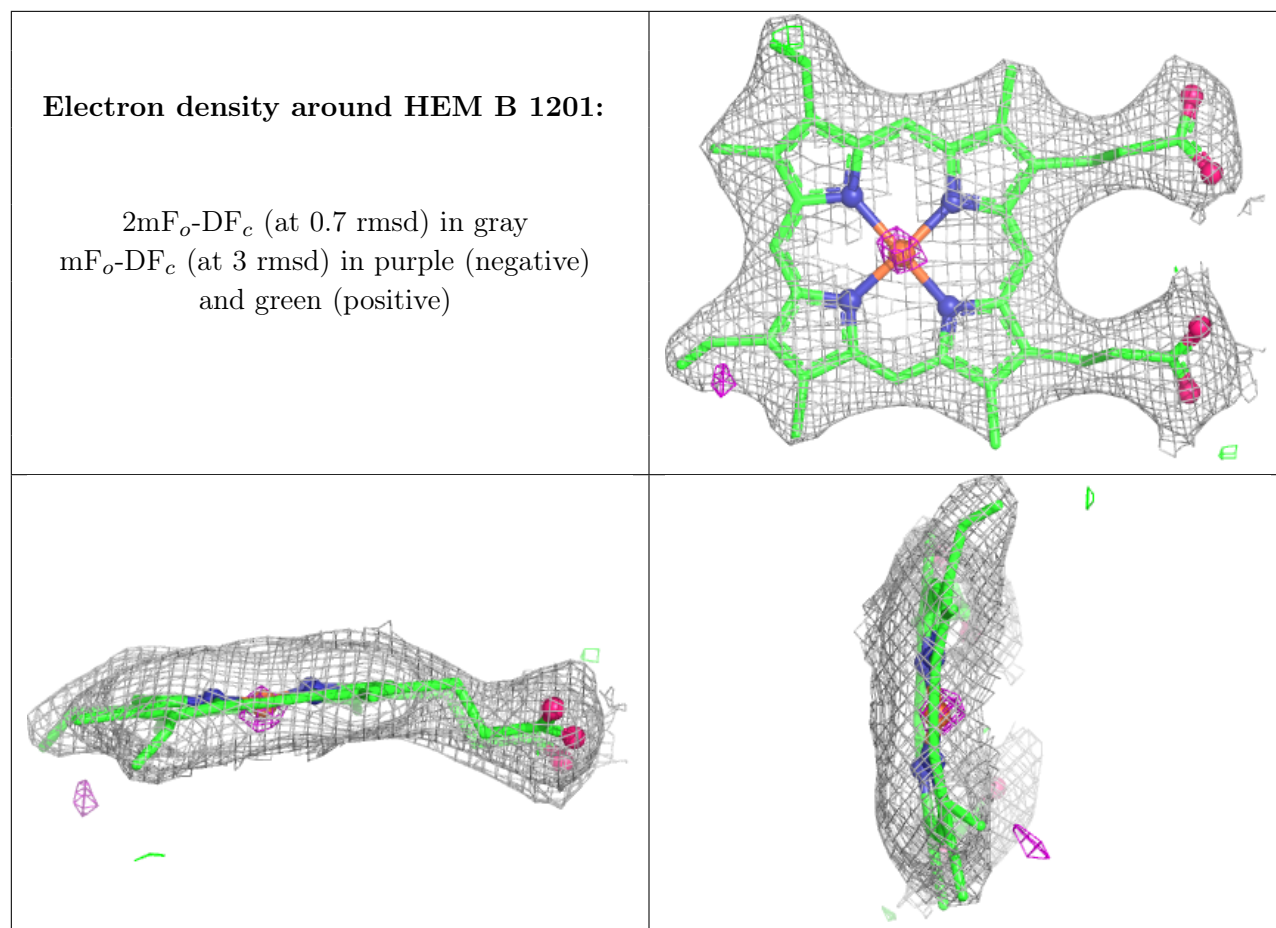
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around HEM A 1200:

$2mF_o-DF_c$ (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.