



Full wwPDB X-ray Structure Validation Report

Sep 3, 2014 – 07:50 PM EDT

PDB ID : 4Q1O
Title : Free form of TvNiR, high dose data set
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Deposited on : 2014-04-04
Resolution : 1.75 Å(reported)

This is a full wwPDB validation report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

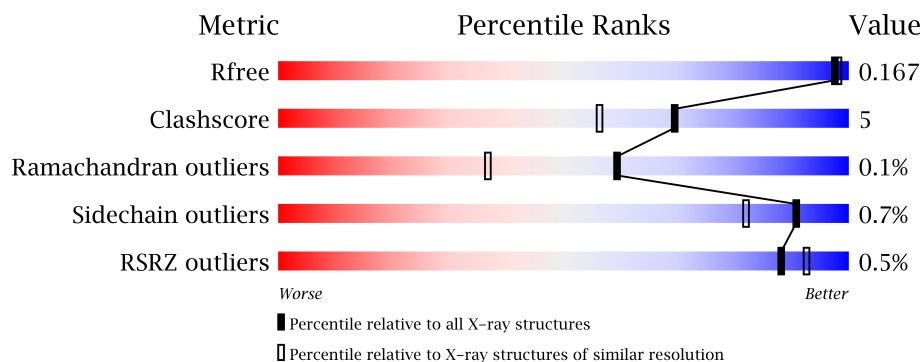
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.16 November 2013
Xtriage (Phenix) : dev-1439
EDS : stable23489
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable23489

1 Overall quality at a glance

The reported resolution of this entry is 1.75 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}	66092	1134 (1.76-1.76)
Clashscore	79885	1304 (1.76-1.76)
Ramachandran outliers	78287	1288 (1.76-1.76)
Sidechain outliers	78261	1288 (1.76-1.76)
RSRZ outliers	66119	1135 (1.76-1.76)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	525	
1	B	525	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
2	HEC	A	605	-	X
2	HEC	B	605	-	X
4	MPD	B	610	-	X
5	GOL	B	611	-	X
6	CIT	B	612	-	X

2 Entry composition i

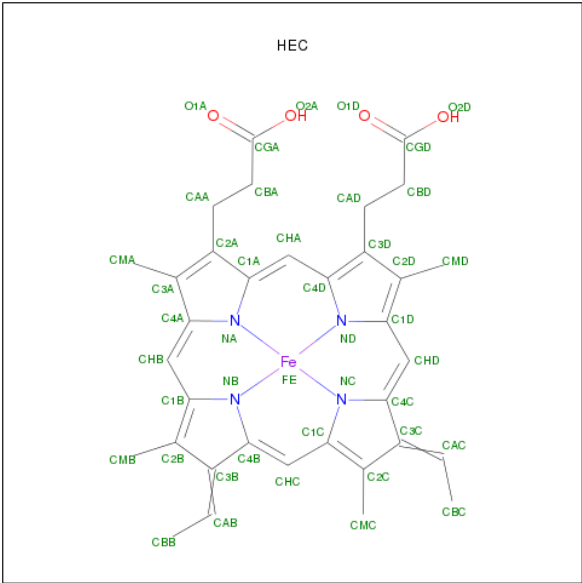
There are 7 unique types of molecules in this entry. The entry contains 10246 atoms, of which 0 are hydrogen and 0 are deuterium.

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 Eight-heme nitrite reductase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	520	Total	C	N	O	S	0	20	0
			4166	2584	759	787	36			
1	B	520	Total	C	N	O	S	0	25	0
			4189	2595	764	794	36			

- Molecule 2 is HEME C (three-letter code: HEC) (formula: $C_{34}H_{34}FeN_4O_4$).



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

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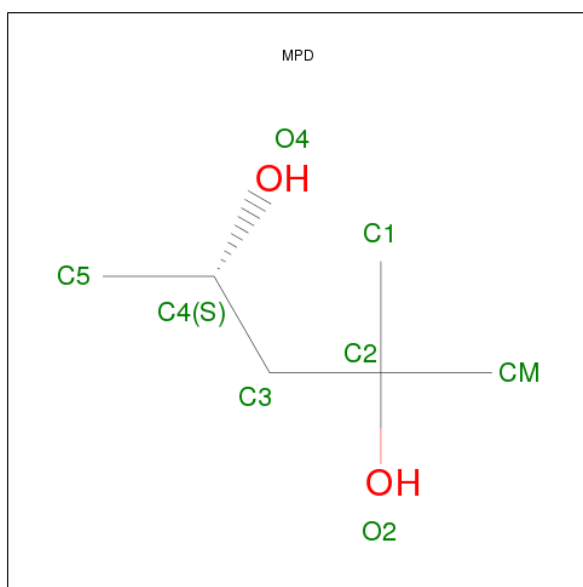
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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total 39	C 32	Fe 1	N 4	O 2	0	0
2	A	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
2	A	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
2	A	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
2	B	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
2	B	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
2	B	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
2	B	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
2	B	1	Total 39	C 32	Fe 1	N 4	O 2	0	0
2	B	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
2	B	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
2	B	1	Total 43	C 34	Fe 1	N 4	O 4	0	0

- Molecule 3 is CALCIUM ION (three-letter code: CA) (formula: Ca).

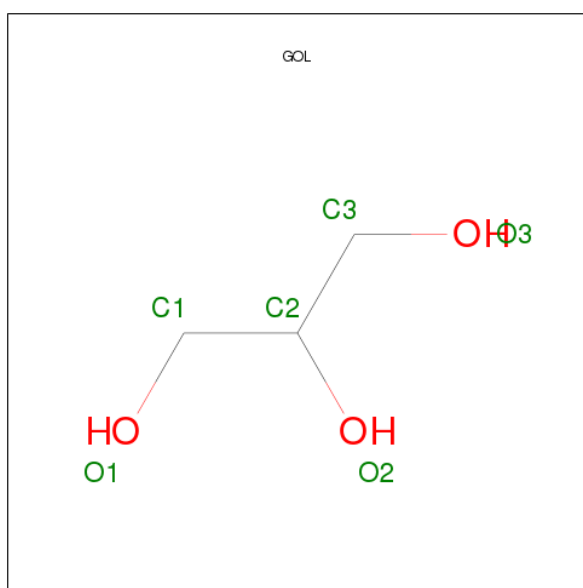
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total	Ca	0	0
			1	1		
3	A	1	Total	Ca	0	0
			1	1		

- Molecule 4 is (4S)-2-METHYL-2,4-PENTANEDIOL (three-letter code: MPD) (formula: C₆H₁₄O₂).



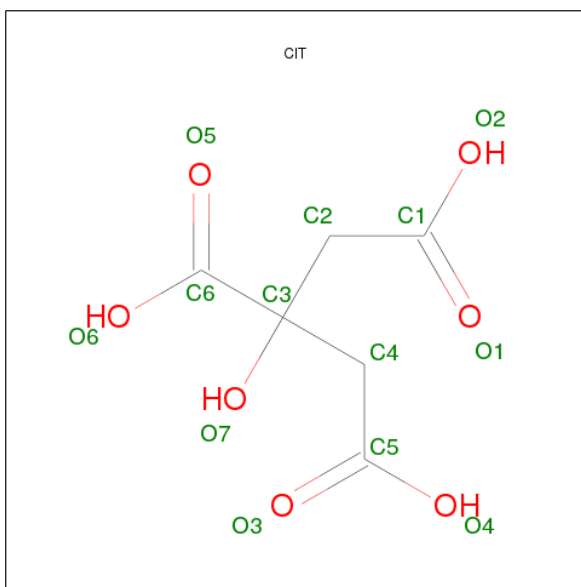
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			8	6	2		
4	B	1	Total	C	O	0	0
			8	6	2		

- Molecule 5 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	B	1	Total	C	O	0	0
			6	3	3		

- Molecule 6 is CITRIC ACID (three-letter code: CIT) (formula: $C_6H_8O_7$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	B	1	Total	C	O	0	0
			13	6	7		

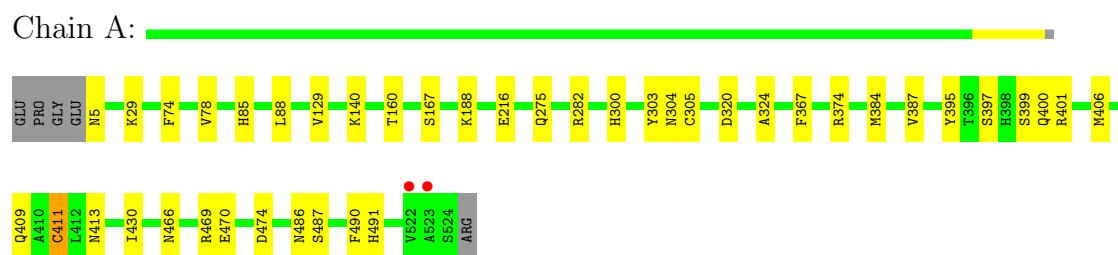
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	577	Total	O	0	0
			577	577		
7	B	597	Total	O	0	0
			597	597		

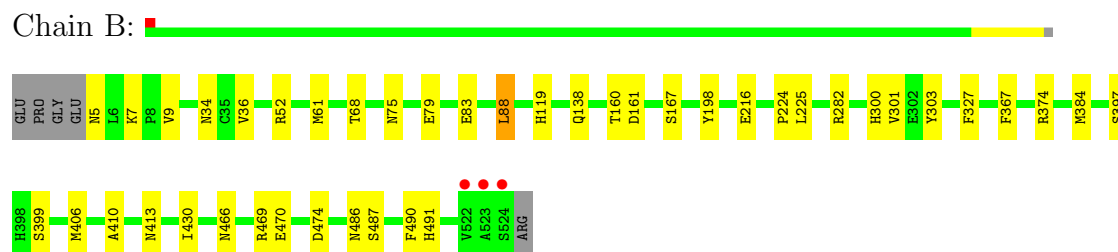
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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: Eight-heme nitrite reductase



- Molecule 1: Eight-heme nitrite reductase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 3	Depositor
Cell constants a, b, c, α , β , γ	193.97Å 193.97Å 193.97Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	53.86 – 1.75 53.80 – 1.65	Depositor EDS
% Data completeness (in resolution range)	99.2 (53.86-1.75) 94.9 (53.80-1.65)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.12 (at 1.65Å)	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
R, R_{free}	0.155 , 0.166 0.165 , 0.167	Depositor DCC
R_{free} test set	11071 reflections (4.21%)	DCC
Wilson B-factor (Å ²)	18.9	Xtriage
Anisotropy	0.000	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 39.1	EDS
Estimated twinning fraction	0.025 for l,-k,h	Xtriage
L-test for twinning	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 274147 reflections	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	10246	wwPDB-VP
Average B, all atoms (Å ²)	21.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.43% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, MPD, CIT, CA, HEC

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	0.56	0/4383	0.74	3/5945 (0.1%)
1	B	0.60	1/4435 (0.0%)	0.76	2/6012 (0.0%)
All	All	0.58	1/8818 (0.0%)	0.75	5/11957 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	83	GLU	CD-OE1	5.10	1.31	1.25

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	188	LYS	CD-CE-NZ	5.62	124.63	111.70
1	B	282	ARG	NE-CZ-NH1	5.44	123.02	120.30
1	A	282	ARG	NE-CZ-NH2	-5.42	117.59	120.30
1	A	320	ASP	CB-CG-OD1	5.16	122.95	118.30
1	B	161	ASP	CB-CG-OD1	5.07	122.86	118.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4166	0	3866	33	0
1	B	4189	0	3888	39	0
2	A	340	0	236	13	0
2	B	340	0	236	13	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	8	0	14	0	0
4	B	8	0	14	0	0
5	B	6	0	8	1	0
6	B	13	0	5	1	0
7	A	577	0	0	12	0
7	B	597	0	0	13	0
All	All	10246	0	8267	82	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 5.

All (82) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:474[A]:ASP:OD2	7:B:793:HOH:O	1.53	1.27
1:A:399[A]:SER:O	7:A:1252:HOH:O	1.62	1.18
1:A:474[B]:ASP:OD2	7:A:1121:HOH:O	1.60	1.18
1:A:413[B]:ASN:OD1	7:A:1128:HOH:O	1.64	1.14
1:B:138[B]:GLN:OE1	7:B:710:HOH:O	1.73	1.06
1:B:413[B]:ASN:ND2	7:B:1171:HOH:O	1.88	1.03
6:B:612:CIT:O2	7:B:1279:HOH:O	1.76	1.03
1:A:409[B]:GLN:NE2	7:A:1010:HOH:O	1.64	1.02
1:A:470:GLU:OE1	7:A:1061:HOH:O	1.83	0.96
1:B:138[B]:GLN:NE2	7:B:710:HOH:O	2.00	0.94
1:B:138[B]:GLN:CD	7:B:710:HOH:O	2.02	0.92
1:B:399[B]:SER:O	7:B:1278:HOH:O	1.90	0.88
1:B:413[A]:ASN:ND2	7:B:1187:HOH:O	2.05	0.88
1:B:413[B]:ASN:CG	7:B:1171:HOH:O	2.12	0.85
1:A:413[B]:ASN:CG	7:A:1128:HOH:O	2.12	0.83
1:A:401[A]:ARG:NH2	7:A:1201:HOH:O	2.24	0.70
2:A:606:HEC:HBC3	2:A:606:HEC:HMC1	1.74	0.69
2:B:605:HEC:HMC1	2:B:605:HEC:HBC3	1.75	0.67
1:A:140:LYS:HG2	1:A:160[B]:THR:HG23	1.78	0.66
1:B:167:SER:HB2	1:B:216:GLU:HG2	1.79	0.64
2:B:606:HEC:HMC1	2:B:606:HEC:HBC3	1.81	0.62
1:A:367:PHE:CZ	2:A:604:HEC:HMC2	2.36	0.61
1:B:198:TYR:CD2	5:B:611:GOL:H2	2.37	0.60
1:B:384:MET:HB2	1:B:397:SER:O	2.00	0.60

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:9:VAL:HG13	1:B:36[B]:VAL:CG1	2.32	0.60
1:A:384:MET:HB2	1:A:397:SER:O	2.01	0.59
1:A:466:ASN:ND2	1:A:469:ARG:HH11	2.00	0.59
1:A:5:ASN:N	7:A:1259:HOH:O	2.34	0.59
1:A:167:SER:HB2	1:A:216:GLU:HG2	1.85	0.58
1:A:275[B]:GLN:NE2	7:A:1095:HOH:O	2.17	0.57
1:B:367:PHE:CZ	2:B:604:HEC:HMC2	2.39	0.57
1:A:409[A]:GLN:OE1	1:A:413[A]:ASN:ND2	2.36	0.57
1:A:303:TYR:CE2	2:A:601:HEC:HMC2	2.42	0.55
1:A:74:PHE:CZ	1:A:78[A]:VAL:HG11	2.43	0.53
1:B:303:TYR:CE2	2:B:601:HEC:HMC2	2.43	0.53
1:B:68[B]:THR:HG23	7:B:863:HOH:O	2.09	0.53
2:A:607:HEC:HBD1	1:B:68[A]:THR:OG1	2.09	0.53
1:B:410:ALA:O	2:B:605:HEC:HMC3	2.10	0.52
1:B:466:ASN:ND2	1:B:469:ARG:HH11	2.07	0.52
1:B:75:ASN:O	1:B:79[B]:GLU:HG3	2.10	0.52
1:A:486:ASN:HB3	2:A:604:HEC:CAA	2.40	0.51
1:B:486:ASN:HB3	2:B:604:HEC:CAA	2.41	0.51
2:B:606:HEC:HBD2	2:B:606:HEC:HHA	1.93	0.50
2:B:604:HEC:HMC1	2:B:604:HEC:HBC3	1.93	0.50
1:A:430:ILE:HG21	1:A:490:PHE:HA	1.94	0.49
2:A:603:HEC:HMA3	2:A:604:HEC:HBA2	1.96	0.48
1:A:401[A]:ARG:NE	7:A:1201:HOH:O	2.47	0.47
1:A:466:ASN:HD22	1:A:469:ARG:HD2	1.79	0.47
1:B:52:ARG:NE	7:B:1287:HOH:O	2.47	0.47
1:A:85:HIS:HB2	1:A:88[A]:LEU:HD22	1.97	0.47
1:B:430:ILE:HG21	1:B:490:PHE:HA	1.97	0.47
1:A:487:SER:HB3	1:A:491:HIS:CE1	2.51	0.46
1:B:7:LYS:O	1:B:36[B]:VAL:HG11	2.17	0.44
1:B:300:HIS:CE1	2:B:601:HEC:HMD1	2.53	0.44
2:B:603:HEC:HMA3	2:B:604:HEC:HBA2	1.99	0.44
1:B:88[A]:LEU:HD13	7:B:1156:HOH:O	2.17	0.43
1:A:304[B]:ASN:HD22	1:A:324:ALA:HA	1.83	0.43
1:B:466:ASN:HD22	1:B:469:ARG:HD2	1.82	0.43
1:B:5:ASN:HB3	7:B:1073:HOH:O	2.18	0.42
1:B:119:HIS:CD2	2:B:603:HEC:ND	2.88	0.42
1:A:129:VAL:HG11	2:A:601:HEC:HMA1	2.02	0.42
1:B:301:VAL:HG21	1:B:327:PHE:CE2	2.54	0.42
1:A:374:ARG:NE	1:A:374:ARG:HA	2.35	0.42
2:A:608:HEC:HMC1	2:A:608:HEC:HBC3	2.02	0.42
1:B:486:ASN:HB3	2:B:604:HEC:HAA1	2.00	0.41
1:A:300:HIS:CE1	2:A:601:HEC:HMD1	2.55	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:374:ARG:HA	1:B:374:ARG:NE	2.35	0.41
1:A:29:LYS:HD2	2:A:607:HEC:CGA	2.50	0.41
1:A:401[A]:ARG:CZ	7:A:1201:HOH:O	2.64	0.41
2:A:606:HEC:HBD2	2:A:606:HEC:HHA	2.02	0.41
1:A:387[A]:VAL:HG21	1:A:395:TYR:CE1	2.55	0.41
1:A:367:PHE:CE1	2:A:604:HEC:HMC2	2.56	0.41
1:B:224:PRO:O	1:B:225:LEU:C	2.59	0.41
1:B:466:ASN:O	1:B:470:GLU:HG3	2.21	0.41
1:B:34:ASN:OD1	1:B:36[B]:VAL:HG22	2.21	0.41
1:A:401[A]:ARG:NH1	7:A:832:HOH:O	2.54	0.40
1:A:305:CYS:SG	2:A:601:HEC:HMC2	2.60	0.40
1:B:367:PHE:CE1	2:B:604:HEC:HMC2	2.57	0.40
1:B:487:SER:HB3	1:B:491:HIS:CE1	2.56	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	538/525 (102%)	512 (95%)	25 (5%)	1 (0%)	56	34
1	B	543/525 (103%)	520 (96%)	23 (4%)	0	100	100
All	All	1081/1050 (103%)	1032 (96%)	48 (4%)	1 (0%)	59	37

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	411	CYS

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	453/443 (102%)	448 (99%)	5 (1%)	84	70
1	B	460/443 (104%)	454 (99%)	6 (1%)	80	65
All	All	913/886 (103%)	902 (99%)	11 (1%)	91	66

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	400[A]	GLN
1	A	400[B]	GLN
1	A	406[A]	MET
1	A	406[B]	MET
1	A	411	CYS
1	B	61[A]	MET
1	B	61[B]	MET
1	B	88[A]	LEU
1	B	88[B]	LEU
1	B	406[A]	MET
1	B	406[B]	MET

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

Mol	Chain	Res	Type
1	A	138	GLN
1	A	190	GLN
1	A	466	ASN
1	B	466	ASN

5.3.3 RNA ⓘ

There are no RNA chains 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 22 ligands modelled in this entry, 2 are monoatomic - leaving 20 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$
2	HEC	A	601	1,7	50,50,50	2.95	17 (34%)	56,82,82	3.28	26 (46%)
2	HEC	A	602	1	50,50,50	2.75	14 (28%)	56,82,82	3.67	29 (51%)
2	HEC	A	603	1	50,50,50	2.86	18 (36%)	56,82,82	3.90	27 (48%)
2	HEC	A	604	1	50,50,50	2.93	15 (30%)	56,82,82	3.56	24 (42%)
2	HEC	A	605	1	46,46,50	3.87	24 (52%)	49,77,82	4.04	23 (46%)
2	HEC	A	606	1	50,50,50	2.98	14 (28%)	56,82,82	3.40	24 (42%)
2	HEC	A	607	1	50,50,50	2.75	14 (28%)	56,82,82	3.59	27 (48%)
2	HEC	A	608	1	50,50,50	3.27	21 (42%)	56,82,82	3.55	29 (51%)
4	MPD	A	610	-	7,7,7	0.42	0	10,10,10	0.60	0
2	HEC	B	601	1,7	50,50,50	2.95	16 (32%)	56,82,82	3.40	26 (46%)
2	HEC	B	602	1	50,50,50	2.88	14 (28%)	56,82,82	3.67	30 (53%)
2	HEC	B	603	1	50,50,50	2.84	13 (26%)	56,82,82	3.59	27 (48%)
2	HEC	B	604	1	50,50,50	2.88	15 (30%)	56,82,82	3.36	25 (44%)
2	HEC	B	605	1	46,46,50	3.73	23 (50%)	49,77,82	3.91	23 (46%)
2	HEC	B	606	1	50,50,50	2.98	17 (34%)	56,82,82	3.65	28 (50%)
2	HEC	B	607	1	50,50,50	2.76	15 (30%)	56,82,82	3.77	27 (48%)
2	HEC	B	608	1	50,50,50	3.18	19 (38%)	56,82,82	3.91	28 (50%)
4	MPD	B	610	-	7,7,7	0.41	0	10,10,10	0.37	0
5	GOL	B	611	-	5,5,5	0.28	0	5,5,5	0.31	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	CIT	B	612	-	12,12,12	0.91	0	17,17,17	1.48	2 (11%)

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	HEC	A	601	1,7	-	0/10/54/54	0/0/8/8
2	HEC	A	602	1	-	0/10/54/54	0/0/8/8
2	HEC	A	603	1	-	0/10/54/54	0/0/8/8
2	HEC	A	604	1	-	0/10/54/54	0/0/8/8
2	HEC	A	605	1	-	0/5/49/54	0/0/8/8
2	HEC	A	606	1	-	0/10/54/54	0/0/8/8
2	HEC	A	607	1	-	0/10/54/54	0/0/8/8
2	HEC	A	608	1	-	0/10/54/54	0/0/8/8
4	MPD	A	610	-	-	0/5/5/5	0/0/0/0
2	HEC	B	601	1,7	-	0/10/54/54	0/0/8/8
2	HEC	B	602	1	-	0/10/54/54	0/0/8/8
2	HEC	B	603	1	-	0/10/54/54	0/0/8/8
2	HEC	B	604	1	-	0/10/54/54	0/0/8/8
2	HEC	B	605	1	-	0/5/49/54	0/0/8/8
2	HEC	B	606	1	-	0/10/54/54	0/0/8/8
2	HEC	B	607	1	-	0/10/54/54	0/0/8/8
2	HEC	B	608	1	-	0/10/54/54	0/0/8/8
4	MPD	B	610	-	-	0/5/5/5	0/0/0/0
5	GOL	B	611	-	-	0/4/4/4	0/0/0/0
6	CIT	B	612	-	-	0/16/16/16	0/0/0/0

All (269) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	608	HEC	C3C-CAC	12.71	1.51	1.34
2	A	605	HEC	C3D-C4D	12.60	1.50	1.44
2	B	602	HEC	C3C-CAC	12.17	1.51	1.34
2	A	606	HEC	C3C-CAC	12.14	1.51	1.34
2	B	605	HEC	C3C-CAC	12.09	1.51	1.34
2	B	605	HEC	C3D-C4D	12.05	1.50	1.44
2	A	608	HEC	C3B-CAB	11.92	1.50	1.34
2	A	605	HEC	C3C-CAC	11.78	1.50	1.34
2	B	608	HEC	C3C-CAC	11.60	1.50	1.34
2	B	601	HEC	C3B-CAB	11.56	1.50	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	606	HEC	C3C-CAC	11.55	1.50	1.34
2	A	602	HEC	C3C-CAC	11.39	1.50	1.34
2	B	603	HEC	C3C-CAC	11.37	1.50	1.34
2	B	603	HEC	C3B-CAB	11.36	1.50	1.34
2	A	604	HEC	C3B-CAB	11.22	1.49	1.34
2	B	604	HEC	C3B-CAB	11.21	1.49	1.34
2	B	608	HEC	C3B-CAB	11.10	1.49	1.34
2	B	604	HEC	C3C-CAC	11.07	1.49	1.34
2	A	601	HEC	C3B-CAB	10.96	1.49	1.34
2	A	603	HEC	C3C-CAC	10.82	1.49	1.34
2	A	606	HEC	C3B-CAB	10.82	1.49	1.34
2	A	603	HEC	C3B-CAB	10.80	1.49	1.34
2	B	607	HEC	C3C-CAC	10.72	1.49	1.34
2	A	607	HEC	C3C-CAC	10.69	1.49	1.34
2	B	606	HEC	C3B-CAB	10.65	1.49	1.34
2	B	602	HEC	C3B-CAB	10.65	1.49	1.34
2	A	601	HEC	C3C-CAC	10.43	1.48	1.34
2	A	604	HEC	C3C-CAC	10.31	1.48	1.34
2	A	602	HEC	C3B-CAB	10.28	1.48	1.34
2	B	601	HEC	C3C-CAC	10.21	1.48	1.34
2	A	607	HEC	C3B-CAB	10.18	1.48	1.34
2	B	607	HEC	C3B-CAB	10.06	1.48	1.34
2	A	605	HEC	C3B-CAB	9.41	1.47	1.34
2	B	605	HEC	C3B-CAB	9.11	1.46	1.34
2	A	605	HEC	C3B-C2B	6.77	1.47	1.40
2	B	608	HEC	C3C-C2C	6.59	1.47	1.40
2	A	601	HEC	C3C-C2C	6.34	1.47	1.40
2	A	608	HEC	C3C-C2C	5.99	1.46	1.40
2	A	604	HEC	C3B-C2B	5.91	1.46	1.40
2	B	606	HEC	C3B-C2B	5.85	1.46	1.40
2	A	608	HEC	C3B-C2B	5.73	1.46	1.40
2	A	607	HEC	C3B-C2B	5.72	1.46	1.40
2	B	608	HEC	C3B-C2B	5.61	1.46	1.40
2	A	605	HEC	C3C-C2C	5.49	1.46	1.40
2	B	601	HEC	C3B-C2B	5.48	1.46	1.40
2	B	606	HEC	C3C-C2C	5.43	1.46	1.40
2	B	601	HEC	C3C-C2C	5.38	1.46	1.40
2	B	607	HEC	C3B-C2B	5.33	1.46	1.40
2	A	606	HEC	C3B-C2B	5.27	1.46	1.40
2	A	606	HEC	C3C-C2C	5.23	1.46	1.40
2	B	604	HEC	C3C-C2C	5.21	1.46	1.40
2	B	605	HEC	C3C-C2C	5.14	1.46	1.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	605	HEC	C3B-C2B	5.05	1.45	1.40
2	A	604	HEC	C3C-C2C	4.88	1.45	1.40
2	A	602	HEC	C3C-C2C	4.65	1.45	1.40
2	B	602	HEC	C3C-C2C	4.62	1.45	1.40
2	A	605	HEC	C3D-C2D	4.61	1.49	1.41
2	A	605	HEC	FE-NA	4.44	2.11	1.92
2	A	601	HEC	C3B-C2B	4.40	1.45	1.40
2	B	604	HEC	C3B-C2B	4.33	1.45	1.40
2	B	605	HEC	C3D-C2D	4.27	1.49	1.41
2	A	605	HEC	C1D-C2D	4.27	1.50	1.43
2	A	605	HEC	FE-ND	4.22	2.10	1.92
2	B	603	HEC	C3B-C2B	4.19	1.45	1.40
2	A	603	HEC	C3B-C2B	4.17	1.45	1.40
2	B	605	HEC	FE-ND	4.17	2.10	1.92
2	B	603	HEC	C3C-C2C	4.05	1.44	1.40
2	B	605	HEC	C1D-C2D	4.04	1.50	1.43
2	B	605	HEC	FE-NA	3.99	2.09	1.92
2	A	605	HEC	C2A-C3A	3.81	1.49	1.37
2	B	607	HEC	C3C-C2C	3.76	1.44	1.40
2	A	605	HEC	C4D-CHA	3.70	1.50	1.39
2	B	608	HEC	FE-NA	3.65	2.08	1.92
2	B	608	HEC	FE-NC	3.63	2.08	1.92
2	A	601	HEC	C1B-C2B	3.63	1.49	1.43
2	B	602	HEC	C4B-NB	-3.62	1.32	1.36
2	B	608	HEC	C4C-NC	-3.59	1.32	1.36
2	B	603	HEC	C1A-NA	-3.52	1.32	1.36
2	A	608	HEC	FE-NB	3.50	2.07	1.92
2	A	608	HEC	C1A-NA	-3.49	1.32	1.36
2	B	608	HEC	FE-NB	3.48	2.07	1.92
2	B	602	HEC	C3B-C2B	3.47	1.44	1.40
2	B	601	HEC	FE-NB	3.46	2.07	1.92
2	A	605	HEC	FE-NC	3.43	2.07	1.92
2	A	605	HEC	C3C-C4C	3.43	1.50	1.42
2	B	601	HEC	C1B-C2B	3.42	1.49	1.43
2	B	605	HEC	C2A-C3A	3.42	1.47	1.37
2	B	605	HEC	C4D-CHA	3.40	1.49	1.39
2	A	605	HEC	FE-NB	3.40	2.07	1.92
2	B	605	HEC	C3C-C4C	3.39	1.50	1.42
2	A	603	HEC	C1A-NA	-3.38	1.32	1.36
2	A	608	HEC	C1C-C2C	3.38	1.49	1.43
2	A	601	HEC	FE-ND	3.35	2.06	1.92
2	A	604	HEC	FE-NC	3.35	2.06	1.92

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	607	HEC	C3C-C2C	3.33	1.44	1.40
2	A	601	HEC	FE-NB	3.33	2.06	1.92
2	B	605	HEC	FE-NC	3.33	2.06	1.92
2	B	605	HEC	FE-NB	3.31	2.06	1.92
2	B	606	HEC	FE-NB	3.30	2.06	1.92
2	A	608	HEC	FE-NC	3.29	2.06	1.92
2	A	605	HEC	C1D-CHD	3.26	1.48	1.39
2	B	605	HEC	C1D-CHD	3.25	1.48	1.39
2	B	607	HEC	C1A-NA	-3.25	1.32	1.36
2	A	603	HEC	C3C-C2C	3.24	1.44	1.40
2	A	606	HEC	FE-NB	3.24	2.06	1.92
2	A	606	HEC	FE-NC	3.23	2.06	1.92
2	B	608	HEC	C3D-C2D	3.19	1.47	1.37
2	A	604	HEC	FE-ND	3.16	2.06	1.92
2	A	607	HEC	FE-NA	3.13	2.05	1.92
2	B	606	HEC	FE-NC	3.11	2.05	1.92
2	B	601	HEC	FE-NC	3.10	2.05	1.92
2	A	608	HEC	FE-ND	3.09	2.05	1.92
2	A	608	HEC	FE-NA	3.09	2.05	1.92
2	B	602	HEC	C1A-NA	-3.07	1.32	1.36
2	B	605	HEC	C4A-C3A	3.07	1.50	1.42
2	B	604	HEC	C4B-NB	-3.06	1.32	1.36
2	A	603	HEC	C4C-NC	-3.04	1.32	1.36
2	A	601	HEC	C3D-C2D	3.03	1.46	1.37
2	B	604	HEC	FE-ND	3.00	2.05	1.92
2	A	605	HEC	C1A-C2A	2.99	1.50	1.42
2	A	603	HEC	FE-NC	2.98	2.05	1.92
2	B	607	HEC	FE-NC	2.98	2.05	1.92
2	A	601	HEC	FE-NA	2.97	2.05	1.92
2	A	601	HEC	FE-NC	2.93	2.05	1.92
2	A	603	HEC	C3D-C2D	2.90	1.46	1.37
2	B	601	HEC	C1D-C2D	2.90	1.48	1.43
2	A	603	HEC	FE-NA	2.90	2.04	1.92
2	A	607	HEC	C3D-C2D	2.90	1.46	1.37
2	B	602	HEC	FE-NA	2.89	2.04	1.92
2	A	606	HEC	FE-NA	2.89	2.04	1.92
2	B	606	HEC	FE-NA	2.86	2.04	1.92
2	B	605	HEC	C1A-C2A	2.86	1.49	1.42
2	A	602	HEC	FE-ND	2.85	2.04	1.92
2	A	607	HEC	C1C-C2C	2.84	1.48	1.43
2	A	603	HEC	FE-NB	2.83	2.04	1.92
2	A	608	HEC	C3D-C2D	2.83	1.46	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	608	HEC	C4D-C3D	2.82	1.48	1.43
2	A	606	HEC	FE-ND	2.82	2.04	1.92
2	B	604	HEC	C2A-C3A	2.81	1.46	1.37
2	B	608	HEC	FE-ND	2.80	2.04	1.92
2	B	608	HEC	C2A-C3A	2.78	1.45	1.37
2	A	605	HEC	C4A-C3A	2.75	1.49	1.42
2	B	605	HEC	C4B-NB	-2.74	1.33	1.36
2	A	602	HEC	FE-NC	2.74	2.04	1.92
2	B	606	HEC	FE-ND	2.73	2.04	1.92
2	B	606	HEC	C2A-C3A	2.73	1.45	1.37
2	A	604	HEC	C2A-C3A	2.72	1.45	1.37
2	B	606	HEC	C1A-NA	-2.71	1.33	1.36
2	B	608	HEC	C1C-C2C	2.71	1.48	1.43
2	B	604	HEC	FE-NB	2.69	2.04	1.92
2	A	606	HEC	C1C-C2C	2.68	1.48	1.43
2	B	601	HEC	FE-ND	2.68	2.03	1.92
2	A	605	HEC	C1A-CHA	2.68	1.49	1.37
2	A	607	HEC	FE-NC	2.67	2.03	1.92
2	B	607	HEC	FE-NA	2.67	2.03	1.92
2	B	603	HEC	FE-NB	2.65	2.03	1.92
2	A	601	HEC	C1D-C2D	2.65	1.47	1.43
2	B	607	HEC	FE-ND	2.65	2.03	1.92
2	B	608	HEC	C1A-NA	-2.64	1.33	1.36
2	A	604	HEC	C3D-C2D	2.64	1.45	1.37
2	A	606	HEC	C1A-NA	-2.63	1.33	1.36
2	B	603	HEC	FE-NC	2.62	2.03	1.92
2	A	603	HEC	C1C-C2C	2.62	1.47	1.43
2	A	606	HEC	C2A-C3A	2.62	1.45	1.37
2	B	608	HEC	C4A-NA	-2.61	1.33	1.36
2	A	602	HEC	C3D-C2D	2.61	1.45	1.37
2	A	602	HEC	C3B-C2B	2.61	1.43	1.40
2	B	607	HEC	FE-NB	2.61	2.03	1.92
2	B	601	HEC	C3D-C2D	2.60	1.45	1.37
2	B	603	HEC	FE-NA	2.59	2.03	1.92
2	B	605	HEC	CAD-C3D	2.59	1.52	1.40
2	B	601	HEC	FE-NA	2.58	2.03	1.92
2	A	602	HEC	C4B-NB	-2.57	1.33	1.36
2	A	604	HEC	C1D-C2D	2.55	1.47	1.43
2	A	604	HEC	FE-NA	2.55	2.03	1.92
2	A	605	HEC	CAD-C3D	2.55	1.52	1.40
2	B	605	HEC	C1A-CHA	2.54	1.49	1.37
2	B	604	HEC	C1D-C2D	2.54	1.47	1.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	602	HEC	FE-NB	2.52	2.03	1.92
2	A	607	HEC	C2A-C3A	2.52	1.45	1.37
2	A	605	HEC	C1B-CHB	2.52	1.46	1.39
2	A	604	HEC	FE-NB	2.51	2.03	1.92
2	B	601	HEC	C2A-C3A	2.50	1.45	1.37
2	A	607	HEC	FE-ND	2.50	2.03	1.92
2	A	608	HEC	C4D-CHA	2.50	1.46	1.39
2	B	605	HEC	C4C-CHD	2.49	1.48	1.37
2	B	604	HEC	FE-NA	2.48	2.03	1.92
2	B	603	HEC	C4A-NA	-2.47	1.33	1.36
2	B	602	HEC	FE-NB	2.47	2.03	1.92
2	B	608	HEC	C4D-CHA	2.46	1.46	1.39
2	B	605	HEC	C1B-CHB	2.46	1.46	1.39
2	A	603	HEC	C1C-NC	-2.45	1.32	1.36
2	A	604	HEC	C1C-CHC	2.45	1.46	1.39
2	A	603	HEC	FE-ND	2.44	2.02	1.92
2	B	602	HEC	C4A-NA	-2.44	1.33	1.36
2	A	604	HEC	C1D-CHD	2.43	1.46	1.39
2	A	608	HEC	C2A-C3A	2.42	1.44	1.37
2	A	603	HEC	C2A-C3A	2.42	1.44	1.37
2	A	605	HEC	C4C-CHD	2.41	1.48	1.37
2	B	608	HEC	C3C-C4C	2.41	1.48	1.42
2	A	607	HEC	FE-NB	2.41	2.02	1.92
2	A	608	HEC	C3C-C4C	2.41	1.48	1.42
2	A	602	HEC	C2A-C3A	2.40	1.44	1.37
2	B	603	HEC	FE-ND	2.38	2.02	1.92
2	A	601	HEC	C2A-C3A	2.38	1.44	1.37
2	B	601	HEC	C1A-NA	-2.38	1.33	1.36
2	A	608	HEC	C1D-CHD	2.37	1.46	1.39
2	B	603	HEC	C3D-C2D	2.36	1.44	1.37
2	A	602	HEC	C1A-C2A	2.35	1.48	1.42
2	A	603	HEC	C4D-CHA	2.35	1.46	1.39
2	B	607	HEC	C4C-NC	-2.35	1.33	1.36
2	B	602	HEC	FE-ND	2.33	2.02	1.92
2	B	606	HEC	C3B-C4B	2.33	1.48	1.42
2	B	604	HEC	C1B-C2B	2.32	1.47	1.43
2	A	601	HEC	C1B-CHB	2.31	1.46	1.39
2	B	606	HEC	CAD-C3D	-2.31	1.48	1.52
2	B	601	HEC	C1B-CHB	2.29	1.46	1.39
2	B	603	HEC	C1B-C2B	2.28	1.47	1.43
2	A	601	HEC	C1D-CHD	2.28	1.46	1.39
2	A	608	HEC	C1B-CHB	2.28	1.46	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	605	HEC	C1C-CHC	2.28	1.46	1.39
2	A	601	HEC	C3C-C4C	2.28	1.48	1.42
2	A	608	HEC	C3B-C4B	2.27	1.48	1.42
2	B	602	HEC	C3D-C2D	2.27	1.44	1.37
2	A	608	HEC	C1B-C2B	2.26	1.47	1.43
2	A	604	HEC	C4B-NB	-2.25	1.33	1.36
2	A	603	HEC	C3C-C4C	2.25	1.48	1.42
2	B	602	HEC	FE-NC	2.23	2.02	1.92
2	B	602	HEC	O2D-CGD	-2.23	1.22	1.30
2	A	602	HEC	FE-NA	2.23	2.01	1.92
2	B	604	HEC	C4D-ND	-2.22	1.32	1.36
2	B	606	HEC	C3D-C2D	2.22	1.44	1.37
2	B	607	HEC	C2A-C3A	2.21	1.44	1.37
2	B	606	HEC	C4C-NC	-2.21	1.34	1.36
2	A	605	HEC	C4B-NB	-2.20	1.34	1.36
2	A	601	HEC	C1C-CHC	2.19	1.45	1.39
2	A	606	HEC	C3D-C2D	2.19	1.44	1.37
2	A	601	HEC	C4A-NA	-2.18	1.34	1.36
2	A	607	HEC	C1D-CHD	2.17	1.45	1.39
2	B	606	HEC	C1D-CHD	2.17	1.45	1.39
2	B	601	HEC	C4C-NC	-2.17	1.34	1.36
2	A	603	HEC	C4D-C3D	2.16	1.47	1.43
2	A	608	HEC	C1A-C2A	2.16	1.48	1.42
2	B	607	HEC	C4D-CHA	2.16	1.45	1.39
2	B	607	HEC	C3D-C2D	2.15	1.44	1.37
2	B	601	HEC	C1D-CHD	2.15	1.45	1.39
2	B	607	HEC	C1D-CHD	2.15	1.45	1.39
2	A	603	HEC	C1B-CHB	2.14	1.45	1.39
2	B	604	HEC	FE-NC	2.14	2.01	1.92
2	B	604	HEC	C3D-C2D	2.14	1.44	1.37
2	A	605	HEC	C3B-C4B	2.13	1.47	1.42
2	A	604	HEC	C1B-CHB	2.12	1.45	1.39
2	B	606	HEC	C4D-CHA	2.11	1.45	1.39
2	A	605	HEC	C4B-CHC	2.10	1.47	1.37
2	A	608	HEC	C4D-C3D	2.10	1.47	1.43
2	B	607	HEC	C1C-CHC	2.10	1.45	1.39
2	A	602	HEC	C1C-C2C	2.10	1.47	1.43
2	B	608	HEC	C3B-C4B	2.09	1.47	1.42
2	B	602	HEC	C2A-C3A	2.07	1.43	1.37
2	B	606	HEC	C1C-CHC	2.06	1.45	1.39
2	A	608	HEC	CAD-C3D	-2.05	1.48	1.52
2	A	607	HEC	C1B-CHB	2.04	1.45	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	607	HEC	C1D-C2D	2.04	1.47	1.43
2	B	603	HEC	C1B-CHB	2.04	1.45	1.39
2	B	604	HEC	C1B-CHB	2.03	1.45	1.39
2	A	606	HEC	C4D-CHA	2.03	1.45	1.39
2	B	608	HEC	C1B-C2B	2.02	1.47	1.43
2	A	606	HEC	CAA-C2A	-2.02	1.48	1.52
2	A	602	HEC	O2D-CGD	-2.01	1.23	1.30

All (425) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	605	HEC	C2C-C1C-NC	13.49	118.51	109.50
2	B	605	HEC	C2C-C1C-NC	12.61	117.92	109.50
2	B	608	HEC	C2B-C1B-NB	11.38	117.10	109.50
2	B	606	HEC	C2C-C1C-NC	11.25	117.02	109.50
2	A	604	HEC	C2C-C1C-NC	11.06	116.89	109.50
2	B	607	HEC	C2B-C1B-NB	10.93	116.80	109.50
2	A	603	HEC	C2D-C1D-ND	10.82	116.73	109.50
2	A	608	HEC	C2B-C1B-NB	10.76	116.69	109.50
2	A	607	HEC	C2C-C1C-NC	10.69	116.64	109.50
2	A	603	HEC	C2B-C1B-NB	10.62	116.59	109.50
2	B	607	HEC	C2C-C1C-NC	10.61	116.59	109.50
2	A	602	HEC	C2B-C1B-NB	10.57	116.56	109.50
2	B	603	HEC	C2D-C1D-ND	10.45	116.48	109.50
2	B	604	HEC	C2C-C1C-NC	10.43	116.46	109.50
2	B	602	HEC	C2C-C1C-NC	10.31	116.38	109.50
2	B	608	HEC	C2D-C1D-ND	10.25	116.35	109.50
2	A	602	HEC	C2C-C1C-NC	9.75	116.01	109.50
2	B	606	HEC	C2B-C1B-NB	9.56	115.89	109.50
2	B	608	HEC	C2C-C1C-NC	9.45	115.81	109.50
2	B	604	HEC	CBB-CAB-C3B	-9.35	106.93	127.36
2	A	606	HEC	C2C-C1C-NC	9.34	115.73	109.50
2	B	601	HEC	C2B-C1B-NB	9.30	115.71	109.50
2	B	603	HEC	C2B-C1B-NB	9.26	115.69	109.50
2	A	608	HEC	C2C-C1C-NC	9.25	115.68	109.50
2	B	602	HEC	C2B-C1B-NB	9.21	115.65	109.50
2	A	607	HEC	C2B-C1B-NB	9.09	115.57	109.50
2	B	601	HEC	C2C-C1C-NC	8.96	115.48	109.50
2	B	607	HEC	C2D-C1D-ND	8.90	115.44	109.50
2	A	602	HEC	CBB-CAB-C3B	-8.87	107.97	127.36
2	A	601	HEC	C2C-C1C-NC	8.84	115.40	109.50
2	A	604	HEC	CBB-CAB-C3B	-8.83	108.06	127.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	603	HEC	C2C-C1C-NC	8.80	115.38	109.50
2	A	605	HEC	CMC-C2C-C3C	8.76	134.40	126.22
2	A	601	HEC	C2B-C1B-NB	8.74	115.33	109.50
2	B	606	HEC	C2D-C1D-ND	8.65	115.28	109.50
2	A	606	HEC	C2D-C1D-ND	8.63	115.26	109.50
2	B	605	HEC	C2B-C1B-NB	8.58	115.23	109.50
2	A	605	HEC	CMB-C2B-C3B	8.56	134.21	126.22
2	A	601	HEC	C2D-C1D-ND	8.51	115.19	109.50
2	B	602	HEC	CBB-CAB-C3B	-8.48	108.83	127.36
2	B	601	HEC	CBB-CAB-C3B	-8.43	108.92	127.36
2	A	607	HEC	CBB-CAB-C3B	-8.37	109.07	127.36
2	A	608	HEC	C2D-C1D-ND	8.35	115.07	109.50
2	B	605	HEC	CMB-C2B-C3B	8.11	133.79	126.22
2	B	603	HEC	CBB-CAB-C3B	-8.10	109.65	127.36
2	A	603	HEC	CBB-CAB-C3B	-8.09	109.67	127.36
2	A	605	HEC	C2B-C1B-NB	7.98	114.83	109.50
2	B	606	HEC	CMC-C2C-C3C	7.91	133.60	126.22
2	A	607	HEC	C2D-C1D-ND	7.86	114.75	109.50
2	A	606	HEC	C2B-C1B-NB	7.77	114.69	109.50
2	B	607	HEC	CBB-CAB-C3B	-7.71	110.50	127.36
2	A	602	HEC	C2D-C1D-ND	7.58	114.56	109.50
2	B	602	HEC	C2D-C1D-ND	7.58	114.56	109.50
2	A	601	HEC	C1D-C2D-C3D	-7.53	101.76	107.00
2	B	601	HEC	C2D-C1D-ND	7.48	114.49	109.50
2	A	608	HEC	CBB-CAB-C3B	-7.41	111.16	127.36
2	B	605	HEC	CBB-CAB-C3B	-7.39	111.21	127.36
2	A	604	HEC	CBA-CAA-C2A	-7.30	100.47	112.63
2	B	603	HEC	CBC-CAC-C3C	-7.26	111.49	127.36
2	A	603	HEC	C1D-C2D-C3D	-7.25	101.95	107.00
2	A	604	HEC	C2B-C1B-NB	7.17	114.29	109.50
2	B	608	HEC	C1D-C2D-C3D	-7.05	102.09	107.00
2	B	608	HEC	CBB-CAB-C3B	-7.03	112.00	127.36
2	A	606	HEC	CMC-C2C-C3C	7.01	132.76	126.22
2	A	605	HEC	C3C-C2C-C1C	-6.93	99.81	107.11
2	A	603	HEC	CMC-C2C-C3C	6.91	132.67	126.22
2	A	601	HEC	CBB-CAB-C3B	-6.89	112.31	127.36
2	B	604	HEC	CBA-CAA-C2A	-6.75	101.39	112.63
2	B	607	HEC	C1D-C2D-C3D	-6.73	102.32	107.00
2	A	606	HEC	CBC-CAC-C3C	-6.71	112.70	127.36
2	A	602	HEC	C1D-C2D-C3D	-6.70	102.33	107.00
2	B	601	HEC	CMB-C2B-C3B	6.68	132.46	126.22
2	A	605	HEC	C2D-C1D-ND	6.66	113.95	109.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	602	HEC	CMC-C2C-C3C	6.65	132.43	126.22
2	A	606	HEC	CBB-CAB-C3B	-6.64	112.86	127.36
2	B	605	HEC	C2D-C1D-ND	6.62	113.92	109.50
2	B	608	HEC	CMC-C2C-C3C	6.57	132.35	126.22
2	A	603	HEC	CBC-CAC-C3C	-6.48	113.19	127.36
2	B	608	HEC	CBA-CAA-C2A	-6.48	101.85	112.63
2	B	608	HEC	C3C-C2C-C1C	-6.47	100.30	107.11
2	B	606	HEC	C3C-C2C-C1C	-6.44	100.33	107.11
2	B	601	HEC	C1D-C2D-C3D	-6.43	102.52	107.00
2	A	608	HEC	C1D-C2D-C3D	-6.40	102.54	107.00
2	A	602	HEC	C3B-C2B-C1B	-6.40	100.37	107.11
2	B	603	HEC	C1D-C2D-C3D	-6.39	102.55	107.00
2	B	605	HEC	CBA-CAA-C2A	-6.37	102.03	112.63
2	A	608	HEC	CMC-C2C-C3C	6.29	132.09	126.22
2	B	606	HEC	CBC-CAC-C3C	-6.24	113.73	127.36
2	B	602	HEC	C1D-C2D-C3D	-6.22	102.67	107.00
2	A	602	HEC	CMC-C2C-C3C	6.20	132.01	126.22
2	B	606	HEC	CBB-CAB-C3B	-6.20	113.80	127.36
2	B	604	HEC	C2B-C1B-NB	6.18	113.62	109.50
2	A	604	HEC	CBD-CAD-C3D	-6.14	102.41	112.63
2	A	607	HEC	C1D-C2D-C3D	-6.13	102.73	107.00
2	B	605	HEC	CMC-C2C-C3C	6.11	131.92	126.22
2	B	608	HEC	CBD-CAD-C3D	-6.06	102.53	112.63
2	A	607	HEC	CMC-C2C-C3C	6.06	131.87	126.22
2	B	603	HEC	C2C-C1C-NC	5.92	113.45	109.50
2	A	606	HEC	C1D-C2D-C3D	-5.89	102.90	107.00
2	A	605	HEC	CBB-CAB-C3B	-5.87	114.53	127.36
2	B	605	HEC	C3C-C2C-C1C	-5.82	100.98	107.11
2	B	605	HEC	C3B-C2B-C1B	-5.81	100.99	107.11
2	A	603	HEC	CBA-CAA-C2A	-5.78	103.01	112.63
2	B	602	HEC	C3B-C2B-C1B	-5.75	101.06	107.11
2	A	607	HEC	CBA-CAA-C2A	-5.73	103.09	112.63
2	A	604	HEC	C3C-C2C-C1C	-5.73	101.08	107.11
2	B	607	HEC	C3C-C2C-C1C	-5.71	101.10	107.11
2	B	607	HEC	C3B-C2B-C1B	-5.71	101.10	107.11
2	B	604	HEC	CBC-CAC-C3C	-5.69	114.93	127.36
2	A	602	HEC	CMB-C2B-C3B	5.60	131.45	126.22
2	B	608	HEC	C3B-C2B-C1B	-5.60	101.22	107.11
2	B	601	HEC	C3B-C2B-C1B	-5.59	101.22	107.11
2	B	604	HEC	CBD-CAD-C3D	-5.58	103.34	112.63
2	A	605	HEC	CBA-CAA-C2A	-5.57	103.35	112.63
2	B	602	HEC	CMB-C2B-C3B	5.56	131.41	126.22

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	604	HEC	C2D-C1D-ND	5.54	113.20	109.50
2	B	603	HEC	CMC-C2C-C3C	5.53	131.38	126.22
2	A	606	HEC	C3C-C2C-C1C	-5.52	101.30	107.11
2	B	603	HEC	CBA-CAA-C2A	-5.51	103.46	112.63
2	B	607	HEC	CBA-CAA-C2A	-5.50	103.47	112.63
2	A	608	HEC	C3C-C2C-C1C	-5.49	101.33	107.11
2	A	608	HEC	CMB-C2B-C3B	5.43	131.29	126.22
2	A	603	HEC	CMB-C2B-C3B	5.43	131.28	126.22
2	A	605	HEC	C3A-C4A-NA	5.42	116.89	109.32
2	B	602	HEC	C3A-C4A-NA	5.40	116.85	109.32
2	A	604	HEC	CBC-CAC-C3C	-5.38	115.61	127.36
2	A	605	HEC	C3B-C2B-C1B	-5.37	101.45	107.11
2	A	604	HEC	C3A-C4A-NA	5.37	116.81	109.32
2	A	607	HEC	C3C-C2C-C1C	-5.34	101.49	107.11
2	A	603	HEC	CBD-CAD-C3D	-5.27	103.86	112.63
2	B	607	HEC	CMB-C2B-C3B	5.27	131.13	126.22
2	A	608	HEC	C3B-C2B-C1B	-5.26	101.57	107.11
2	A	602	HEC	C3C-C2C-C1C	-5.20	101.64	107.11
2	B	604	HEC	C3C-C2C-C1C	-5.16	101.67	107.11
2	A	601	HEC	C3B-C2B-C1B	-5.16	101.67	107.11
2	B	608	HEC	CBC-CAC-C3C	-5.16	116.08	127.36
2	B	607	HEC	CMC-C2C-C3C	5.14	131.01	126.22
2	B	601	HEC	C3C-C2C-C1C	-5.12	101.71	107.11
2	A	603	HEC	C3C-C2C-C1C	-5.11	101.73	107.11
2	B	602	HEC	C3C-C2C-C1C	-5.05	101.79	107.11
2	A	602	HEC	C3A-C4A-NA	5.05	116.36	109.32
2	A	608	HEC	CBC-CAC-C3C	-5.04	116.34	127.36
2	B	605	HEC	C3A-C4A-NA	5.02	116.32	109.32
2	B	603	HEC	CMB-C2B-C3B	5.01	130.90	126.22
2	B	603	HEC	CBD-CAD-C3D	-5.00	104.30	112.63
2	B	603	HEC	C4D-ND-C1D	-4.98	102.33	107.12
2	B	606	HEC	C1D-C2D-C3D	-4.96	103.55	107.00
2	B	607	HEC	CBC-CAC-C3C	-4.89	116.67	127.36
2	B	608	HEC	C1A-C2A-C3A	-4.89	102.76	106.70
2	A	604	HEC	C3B-C2B-C1B	-4.87	101.98	107.11
2	A	605	HEC	C4A-C3A-C2A	-4.87	101.29	106.69
2	A	607	HEC	C3B-C2B-C1B	-4.85	102.00	107.11
2	A	604	HEC	C1D-C2D-C3D	-4.82	103.64	107.00
2	A	606	HEC	CMB-C2B-C3B	4.79	130.69	126.22
2	A	603	HEC	C3B-C2B-C1B	-4.75	102.11	107.11
2	A	602	HEC	C1A-C2A-C3A	-4.74	102.88	106.70
2	B	604	HEC	CMB-C2B-C3B	4.74	130.65	126.22

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	601	HEC	C1A-C2A-C3A	-4.72	102.90	106.70
2	A	604	HEC	CMB-C2B-C3B	4.69	130.60	126.22
2	B	606	HEC	C3B-C2B-C1B	-4.69	102.17	107.11
2	B	602	HEC	CBC-CAC-C3C	-4.69	117.11	127.36
2	A	601	HEC	C3C-C2C-C1C	-4.69	102.17	107.11
2	A	605	HEC	C2C-C1C-CHC	-4.66	117.17	126.00
2	A	604	HEC	CMC-C2C-C3C	4.60	130.52	126.22
2	B	608	HEC	CMB-C2B-C3B	4.60	130.52	126.22
2	B	604	HEC	C3A-C4A-NA	4.60	115.74	109.32
2	A	601	HEC	CMB-C2B-C3B	4.56	130.47	126.22
2	B	607	HEC	C3A-C4A-NA	4.51	115.61	109.32
2	A	601	HEC	C1A-C2A-C3A	-4.50	103.08	106.70
2	A	607	HEC	CBC-CAC-C3C	-4.47	117.58	127.36
2	A	603	HEC	C4D-ND-C1D	-4.47	102.81	107.12
2	A	606	HEC	C3B-C2B-C1B	-4.46	102.41	107.11
2	B	604	HEC	C2D-C1D-ND	4.46	112.48	109.50
2	A	604	HEC	C4A-C3A-C2A	-4.45	101.75	106.69
2	B	605	HEC	C2C-C1C-CHC	-4.43	117.59	126.00
2	A	603	HEC	C4A-C3A-C2A	-4.42	101.79	106.69
2	A	607	HEC	C3D-C4D-ND	4.41	115.87	109.73
2	B	602	HEC	C4A-C3A-C2A	-4.41	101.80	106.69
2	B	602	HEC	C1A-C2A-C3A	-4.38	103.17	106.70
2	B	604	HEC	C1D-C2D-C3D	-4.37	103.96	107.00
2	B	604	HEC	C3B-C2B-C1B	-4.35	102.53	107.11
2	A	601	HEC	CBC-CAC-C3C	-4.35	117.86	127.36
2	B	606	HEC	CMB-C2B-C3B	4.34	130.27	126.22
2	B	607	HEC	C4D-ND-C1D	-4.34	102.94	107.12
2	B	605	HEC	C1A-C2A-C3A	-4.33	103.21	106.70
2	A	606	HEC	CBA-CAA-C2A	-4.32	105.44	112.63
2	B	605	HEC	C4A-C3A-C2A	-4.29	101.93	106.69
2	B	607	HEC	C3D-C4D-ND	4.29	115.69	109.73
2	B	603	HEC	C3D-C4D-ND	4.26	115.65	109.73
6	B	612	CIT	O6-C6-C3	4.24	119.06	112.89
2	B	602	HEC	C2A-C1A-NA	4.21	115.59	109.73
2	A	607	HEC	C3A-C4A-NA	4.20	115.18	109.32
2	A	602	HEC	CBC-CAC-C3C	-4.15	118.29	127.36
2	B	603	HEC	C3C-C2C-C1C	-4.14	102.75	107.11
2	B	606	HEC	C4D-ND-C1D	-4.13	103.14	107.12
2	A	607	HEC	C4A-C3A-C2A	-4.07	102.18	106.69
2	B	606	HEC	C4A-C3A-C2A	-4.06	102.19	106.69
2	A	604	HEC	C1A-C2A-C3A	-4.05	103.44	106.70
2	B	605	HEC	C2A-C1A-NA	3.99	115.28	109.73

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	605	HEC	C4D-C3D-C2D	-3.99	102.94	107.04
2	A	602	HEC	C2A-C1A-NA	3.97	115.25	109.73
2	A	604	HEC	C2A-C1A-NA	3.96	115.23	109.73
2	A	604	HEC	C4D-C3D-C2D	-3.96	102.82	106.92
2	B	603	HEC	C3B-C2B-C1B	-3.95	102.94	107.11
2	A	605	HEC	C2B-C1B-CHB	-3.94	118.53	126.00
2	B	604	HEC	C4A-C3A-C2A	-3.93	102.33	106.69
2	B	604	HEC	C4D-C3D-C2D	-3.90	102.89	106.92
2	A	604	HEC	C3D-C4D-ND	3.88	115.13	109.73
2	B	601	HEC	C3D-C4D-ND	3.88	115.12	109.73
2	A	603	HEC	C3D-C4D-ND	3.88	115.12	109.73
2	B	607	HEC	C4A-C3A-C2A	-3.83	102.44	106.69
2	B	603	HEC	C4D-C3D-C2D	-3.82	102.96	106.92
2	A	608	HEC	CBD-CAD-C3D	-3.80	106.30	112.63
2	A	606	HEC	CAA-CBA-CGA	-3.79	101.33	113.66
2	B	605	HEC	CBC-CAC-C3C	-3.79	119.08	127.36
2	A	605	HEC	C4D-C3D-C2D	-3.78	103.16	107.04
2	A	605	HEC	CBC-CAC-C3C	-3.76	119.14	127.36
2	B	604	HEC	C3D-C4D-ND	3.75	114.95	109.73
2	A	606	HEC	C3A-C4A-NA	3.75	114.54	109.32
2	B	601	HEC	C3A-C4A-NA	3.73	114.52	109.32
2	B	606	HEC	CBA-CAA-C2A	-3.72	106.44	112.63
2	B	606	HEC	C4D-C3D-C2D	-3.70	103.09	106.92
2	A	607	HEC	C4D-C3D-C2D	-3.70	103.09	106.92
2	A	607	HEC	C4D-ND-C1D	-3.70	103.56	107.12
2	A	601	HEC	C3A-C4A-NA	3.69	114.47	109.32
2	B	606	HEC	C3D-C4D-ND	3.69	114.86	109.73
2	A	605	HEC	C1A-C2A-C3A	-3.67	103.74	106.70
2	A	606	HEC	C4A-C3A-C2A	-3.66	102.63	106.69
2	A	605	HEC	C2A-C1A-NA	3.66	114.81	109.73
2	B	606	HEC	C2C-C1C-CHC	-3.65	119.09	126.00
2	A	603	HEC	C2C-C1C-CHC	-3.64	119.09	126.00
2	A	603	HEC	C3A-C4A-NA	3.63	114.39	109.32
2	B	601	HEC	C2A-C1A-NA	3.63	114.77	109.73
2	B	608	HEC	C3A-C4A-NA	3.61	114.36	109.32
2	B	608	HEC	C4D-ND-C1D	-3.61	103.64	107.12
2	B	601	HEC	CBC-CAC-C3C	-3.60	119.48	127.36
2	B	604	HEC	C4C-NC-C1C	-3.59	101.62	106.77
2	B	602	HEC	C3D-C4D-ND	3.58	114.70	109.73
2	A	607	HEC	C2A-C1A-NA	3.58	114.70	109.73
2	A	603	HEC	CMD-C2D-C3D	3.58	131.68	124.94
2	B	607	HEC	C1A-C2A-C3A	-3.57	103.82	106.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	601	HEC	C3D-C4D-ND	3.57	114.69	109.73
2	B	608	HEC	C2A-C1A-NA	3.57	114.69	109.73
2	B	606	HEC	C3A-C4A-NA	3.57	114.29	109.32
2	A	602	HEC	C3D-C4D-ND	3.56	114.69	109.73
2	B	606	HEC	CAA-CBA-CGA	-3.54	102.14	113.66
2	A	603	HEC	C4D-C3D-C2D	-3.52	103.28	106.92
2	A	601	HEC	CMC-C2C-C3C	3.51	129.50	126.22
2	B	605	HEC	C2B-C1B-CHB	-3.48	119.39	126.00
2	A	602	HEC	C4A-C3A-C2A	-3.47	102.84	106.69
2	A	608	HEC	C4A-C3A-C2A	-3.47	102.84	106.69
2	A	606	HEC	C4D-ND-C1D	-3.47	103.78	107.12
2	B	608	HEC	C3D-C4D-ND	3.46	114.54	109.73
2	B	608	HEC	C4D-C3D-C2D	-3.45	103.35	106.92
2	A	606	HEC	C3D-C4D-ND	3.41	114.47	109.73
2	B	607	HEC	CBD-CAD-C3D	-3.38	107.01	112.63
2	B	608	HEC	C2C-C1C-CHC	-3.37	119.61	126.00
2	A	608	HEC	C3D-C4D-ND	3.36	114.40	109.73
2	B	601	HEC	C4D-ND-C1D	-3.36	103.89	107.12
2	B	602	HEC	C4C-NC-C1C	-3.31	102.04	106.77
2	A	608	HEC	CBA-CAA-C2A	-3.30	107.13	112.63
2	A	601	HEC	CAA-C2A-C1A	3.30	130.62	124.67
2	A	608	HEC	CAD-CBD-CGD	-3.28	103.00	113.66
2	B	604	HEC	C2A-C1A-NA	3.28	114.29	109.73
2	A	606	HEC	C4D-C3D-C2D	-3.27	103.53	106.92
2	A	608	HEC	C2C-C1C-CHC	-3.26	119.81	126.00
2	A	601	HEC	C2A-C1A-NA	3.23	114.22	109.73
2	B	608	HEC	C4A-C3A-C2A	-3.23	103.11	106.69
2	B	607	HEC	C4D-C3D-C2D	-3.22	103.58	106.92
2	B	602	HEC	C4D-ND-C1D	-3.21	104.03	107.12
2	A	607	HEC	CMB-C2B-C3B	3.20	129.21	126.22
2	A	607	HEC	C2B-C1B-CHB	-3.19	119.95	126.00
2	B	603	HEC	C4A-C3A-C2A	-3.19	103.16	106.69
2	A	608	HEC	C4D-ND-C1D	-3.19	104.05	107.12
2	A	605	HEC	C3D-C2D-C1D	-3.17	103.18	106.69
2	A	608	HEC	C3A-C4A-NA	3.16	113.73	109.32
2	B	604	HEC	C1A-C2A-C3A	-3.16	104.16	106.70
2	B	607	HEC	C2A-C1A-NA	3.16	114.12	109.73
2	B	604	HEC	CMC-C2C-C3C	3.15	129.16	126.22
2	B	601	HEC	C4D-C3D-C2D	-3.15	103.66	106.92
2	A	607	HEC	C4C-NC-C1C	-3.14	102.28	106.77
2	B	603	HEC	C1A-C2A-C3A	-3.13	104.18	106.70
2	B	608	HEC	C2B-C1B-CHB	-3.12	120.08	126.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	607	HEC	C1A-C2A-C3A	-3.11	104.19	106.70
2	A	601	HEC	C2C-C1C-CHC	-3.09	120.15	126.00
2	A	602	HEC	C4D-C3D-C2D	-3.07	103.74	106.92
2	A	607	HEC	C3D-C4D-CHA	-3.07	120.17	126.00
2	A	602	HEC	C4C-NC-C1C	-3.06	102.39	106.77
2	B	603	HEC	C3A-C4A-NA	3.06	113.59	109.32
2	B	603	HEC	C2D-C1D-CHD	-3.06	120.20	126.00
2	A	601	HEC	C4D-ND-C1D	-3.05	104.19	107.12
2	A	603	HEC	C2B-C1B-CHB	-3.04	120.24	126.00
2	B	603	HEC	C4B-NB-C1B	-3.03	102.44	106.77
2	B	605	HEC	C3D-C2D-C1D	-3.01	103.35	106.69
2	B	602	HEC	CMA-C3A-C2A	3.00	130.61	124.94
2	B	607	HEC	C2B-C1B-CHB	-3.00	120.31	126.00
2	B	603	HEC	C2C-C1C-CHC	-2.99	120.32	126.00
2	A	608	HEC	C1A-C2A-C3A	-2.98	104.30	106.70
2	A	602	HEC	CAD-CBD-CGD	-2.96	104.03	113.66
2	B	601	HEC	C2C-C1C-CHC	-2.94	120.43	126.00
2	A	606	HEC	C1A-C2A-C3A	-2.94	104.33	106.70
2	A	608	HEC	C4D-C3D-C2D	-2.92	103.89	106.92
2	A	601	HEC	CBA-CAA-C2A	-2.92	107.76	112.63
2	B	605	HEC	C3D-C4D-ND	2.92	113.80	109.73
2	A	606	HEC	C2C-C1C-CHC	-2.91	120.49	126.00
2	A	608	HEC	C2B-C1B-CHB	-2.90	120.50	126.00
2	A	607	HEC	CBD-CAD-C3D	-2.89	107.82	112.63
2	B	601	HEC	C4A-C3A-C2A	-2.88	103.49	106.69
2	A	603	HEC	C2D-C1D-CHD	-2.88	120.53	126.00
2	B	608	HEC	C4B-NB-C1B	-2.88	102.64	106.77
2	A	606	HEC	C2D-C1D-CHD	-2.88	120.55	126.00
2	B	602	HEC	CAA-CBA-CGA	-2.86	104.35	113.66
2	B	606	HEC	C2B-C1B-CHB	-2.85	120.59	126.00
2	A	605	HEC	C3D-C4D-ND	2.85	113.69	109.73
2	B	606	HEC	C2A-C1A-NA	2.83	113.66	109.73
2	B	601	HEC	C3D-C4D-CHA	-2.81	120.68	126.00
2	B	602	HEC	C4D-C3D-C2D	-2.80	104.02	106.92
2	B	601	HEC	CAA-C2A-C1A	2.80	129.72	124.67
2	A	601	HEC	C4D-C3D-C2D	-2.80	104.02	106.92
2	B	604	HEC	C3D-C4D-CHA	-2.80	120.69	126.00
2	A	604	HEC	C4C-NC-C1C	-2.78	102.79	106.77
2	B	603	HEC	C4B-C3B-C2B	-2.77	103.36	106.35
2	A	604	HEC	C3D-C4D-CHA	-2.76	120.76	126.00
2	B	608	HEC	CMA-C3A-C2A	2.76	130.15	124.94
2	B	604	HEC	C3C-C4C-NC	2.76	116.15	110.94

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	606	HEC	CMA-C3A-C4A	2.75	131.59	126.16
2	B	604	HEC	CHC-C1C-NC	-2.74	120.06	124.70
2	B	602	HEC	C3C-C4C-NC	2.72	116.09	110.94
2	A	602	HEC	C4B-NB-C1B	-2.71	102.88	106.77
2	B	602	HEC	C4C-C3C-C2C	-2.71	103.42	106.35
2	B	607	HEC	C4B-NB-C1B	-2.71	102.89	106.77
2	B	608	HEC	C2D-C1D-CHD	-2.70	120.88	126.00
2	A	606	HEC	C2A-C1A-NA	2.70	113.48	109.73
2	A	605	HEC	CMB-C2B-C1B	-2.69	124.33	128.46
2	B	608	HEC	CMD-C2D-C3D	2.68	129.99	124.94
2	B	606	HEC	C1A-CHA-C4D	-2.67	121.40	126.92
2	B	601	HEC	CMC-C2C-C3C	2.65	128.70	126.22
2	A	608	HEC	C4B-NB-C1B	-2.65	102.98	106.77
2	A	608	HEC	CAA-CBA-CGA	-2.64	105.06	113.66
2	A	601	HEC	C4A-C3A-C2A	-2.62	103.78	106.69
2	B	602	HEC	CAD-CBD-CGD	-2.62	105.14	113.66
2	B	607	HEC	C3D-C4D-CHA	-2.59	121.08	126.00
2	B	602	HEC	C2C-C1C-CHC	-2.57	121.13	126.00
2	B	607	HEC	C4C-NC-C1C	-2.57	103.10	106.77
2	A	602	HEC	C4D-ND-C1D	-2.55	104.66	107.12
2	B	606	HEC	C2D-C1D-CHD	-2.55	121.17	126.00
2	A	603	HEC	C4B-NB-C1B	-2.55	103.12	106.77
6	B	612	CIT	O5-C6-C3	-2.54	118.69	122.20
2	B	606	HEC	C1A-C2A-C3A	-2.54	104.65	106.70
2	A	602	HEC	CBD-CAD-C3D	-2.54	108.40	112.63
2	A	608	HEC	C2A-C1A-NA	2.53	113.25	109.73
2	A	608	HEC	C2D-C1D-CHD	-2.53	121.21	126.00
2	B	606	HEC	C3D-C4D-CHA	-2.53	121.21	126.00
2	A	605	HEC	CMA-C3A-C2A	2.52	129.69	124.94
2	A	608	HEC	CMA-C3A-C2A	2.50	129.65	124.94
2	B	602	HEC	C4B-NB-C1B	-2.49	103.21	106.77
2	A	602	HEC	C3C-C4C-NC	2.48	115.62	110.94
2	A	607	HEC	CAD-CBD-CGD	-2.48	105.61	113.66
2	B	601	HEC	C4B-NB-C1B	-2.46	103.24	106.77
2	B	603	HEC	C3B-C4B-NB	2.44	115.56	110.94
2	A	601	HEC	C3D-C4D-CHA	-2.43	121.39	126.00
2	B	606	HEC	C4B-C3B-C2B	-2.42	103.73	106.35
2	B	603	HEC	CMD-C2D-C3D	2.42	129.50	124.94
2	B	601	HEC	CBA-CAA-C2A	-2.40	108.63	112.63
2	A	602	HEC	C2B-C1B-CHB	-2.40	121.46	126.00
2	B	601	HEC	CMD-C2D-C3D	2.39	129.45	124.94
2	A	607	HEC	C2C-C1C-CHC	-2.39	121.47	126.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	602	HEC	CMA-C3A-C2A	2.39	129.45	124.94
2	A	607	HEC	C3C-C4C-NC	2.38	115.43	110.94
2	B	603	HEC	CMA-C3A-C2A	2.37	129.42	124.94
2	B	608	HEC	C3D-C4D-CHA	-2.37	121.51	126.00
2	B	601	HEC	C2D-C1D-CHD	-2.36	121.52	126.00
2	A	602	HEC	CAA-CBA-CGA	-2.34	106.04	113.66
2	A	608	HEC	C4B-C3B-C2B	-2.34	103.83	106.35
2	B	602	HEC	CBD-CAD-C3D	-2.34	108.74	112.63
2	A	603	HEC	CMA-C3A-C2A	2.32	129.32	124.94
2	A	602	HEC	CAA-C2A-C1A	2.32	128.86	124.67
2	B	603	HEC	C2B-C1B-CHB	-2.32	121.61	126.00
2	B	604	HEC	C4C-C3C-C2C	-2.32	103.85	106.35
2	A	603	HEC	C2A-C1A-NA	2.30	112.93	109.73
2	A	601	HEC	CMD-C2D-C3D	2.29	129.25	124.94
2	A	606	HEC	C2B-C1B-CHB	-2.27	121.69	126.00
2	B	602	HEC	O1A-CGA-CBA	-2.27	115.38	123.06
2	B	607	HEC	CAD-CBD-CGD	-2.26	106.31	113.66
2	B	601	HEC	C3B-C4B-NB	2.26	115.21	110.94
2	B	607	HEC	C2C-C1C-CHC	-2.26	121.72	126.00
2	B	605	HEC	C4C-NC-C1C	-2.25	103.54	106.77
2	B	603	HEC	C2A-C1A-NA	2.24	112.85	109.73
2	A	601	HEC	C2B-C1B-CHB	-2.20	121.84	126.00
2	B	602	HEC	C3D-C4D-CHA	-2.17	121.88	126.00
2	A	604	HEC	C2C-C1C-CHC	-2.17	121.89	126.00
2	B	605	HEC	CMD-C2D-C3D	2.17	129.03	124.94
2	B	607	HEC	C2D-C1D-CHD	-2.17	121.89	126.00
2	A	605	HEC	C4C-NC-C1C	-2.17	103.67	106.77
2	A	602	HEC	C4C-C3C-C2C	-2.16	104.02	106.35
2	B	601	HEC	CMA-C3A-C2A	2.16	129.01	124.94
2	A	605	HEC	O1A-CGA-CBA	-2.16	115.77	123.06
2	A	601	HEC	C4B-NB-C1B	-2.15	103.69	106.77
2	A	604	HEC	CHC-C1C-NC	-2.15	121.06	124.70
2	A	603	HEC	C4B-C3B-C2B	-2.15	104.04	106.35
2	B	608	HEC	C4B-C3B-C2B	-2.14	104.04	106.35
2	A	601	HEC	C2D-C1D-CHD	-2.14	121.94	126.00
2	B	605	HEC	CMB-C2B-C1B	-2.13	125.20	128.46
2	A	601	HEC	C4C-C3C-C2C	-2.12	104.06	106.35
2	B	608	HEC	C3B-C4B-NB	2.12	114.94	110.94
2	A	608	HEC	C3B-C4B-NB	2.11	114.93	110.94
2	A	607	HEC	C4C-C3C-C2C	-2.10	104.08	106.35
2	B	606	HEC	C4C-NC-C1C	-2.08	103.79	106.77
2	A	602	HEC	C2C-C1C-CHC	-2.08	122.06	126.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	607	HEC	CMA-C3A-C2A	2.08	128.86	124.94
2	B	604	HEC	CMA-C3A-C2A	2.06	128.83	124.94
2	A	603	HEC	C3D-C4D-CHA	-2.06	122.10	126.00
2	A	606	HEC	CMA-C3A-C4A	2.06	130.23	126.16
2	A	602	HEC	C3D-C4D-CHA	-2.06	122.10	126.00
2	B	602	HEC	CAA-C2A-C1A	2.06	128.38	124.67
2	B	606	HEC	C4B-CHC-C1C	-2.05	122.69	126.92
2	B	604	HEC	C4B-C3B-C2B	-2.04	104.15	106.35
2	A	604	HEC	C4D-ND-C1D	-2.03	105.17	107.12
2	B	605	HEC	O1A-CGA-CBA	-2.03	116.19	123.06
2	A	608	HEC	C3D-C4D-CHA	-2.02	122.17	126.00
2	B	607	HEC	C3B-C4B-NB	2.01	114.74	110.94
2	B	602	HEC	C3B-C4B-NB	2.01	114.74	110.94
2	A	606	HEC	C3D-C4D-CHA	-2.01	122.19	126.00
2	A	603	HEC	C4C-C3C-C2C	-2.01	104.19	106.35
2	A	604	HEC	C2B-C1B-CHB	-2.01	122.19	126.00

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

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	520/525 (99%)	-0.61	2 (0%) 90 94	13, 20, 32, 57	1 (0%)
1	B	520/525 (99%)	-0.58	3 (0%) 86 92	11, 18, 32, 53	0
All	All	1040/1050 (99%)	-0.60	5 (0%) 88 92	11, 19, 32, 57	1 (0%)

All (5) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	523	ALA	3.7
1	B	522	VAL	3.1
1	A	523	ALA	2.5
1	B	524	SER	2.3
1	A	522	VAL	2.0

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	RSR	LLDF	B-factors(\AA^2)	Q<0.9
5	GOL	B	611	6/6	0.16	15.65	50,53,60,62	0
6	CIT	B	612	13/13	0.21	4.35	25,28,30,30	13
2	HEC	B	605	39/43	0.14	3.22	21,30,44,45	0
2	HEC	A	605	39/43	0.14	3.18	22,31,45,45	0
4	MPD	B	610	8/8	0.09	2.66	22,26,29,29	0
4	MPD	A	610	8/8	0.08	1.71	23,26,29,30	0
2	HEC	B	602	43/43	0.07	0.99	11,12,19,26	0
2	HEC	B	607	43/43	0.07	0.87	12,14,26,36	0
2	HEC	A	601	43/43	0.06	0.84	13,15,17,18	0
2	HEC	B	601	43/43	0.07	0.76	11,13,15,16	0
2	HEC	A	607	43/43	0.07	0.66	13,14,27,39	0
2	HEC	B	604	43/43	0.06	0.59	10,11,15,18	0
2	HEC	A	602	43/43	0.06	0.49	12,13,20,30	0
2	HEC	B	603	43/43	0.06	0.30	9,11,12,15	0
2	HEC	B	606	43/43	0.06	0.30	12,15,18,20	0
2	HEC	A	604	43/43	0.06	0.23	12,13,17,20	0
2	HEC	A	606	43/43	0.06	-0.12	14,15,18,19	0
2	HEC	A	603	43/43	0.06	-0.16	11,12,14,16	0
2	HEC	B	608	43/43	0.06	-0.41	15,19,23,29	0
2	HEC	A	608	43/43	0.06	-0.50	15,17,26,35	0
3	CA	A	609	1/1	0.03	-2.31	21,21,21,21	0
3	CA	B	609	1/1	0.03	-4.42	19,19,19,19	0

6.5 Other polymers ⓘ

There are no such residues in this entry.