



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 29, 2025 – 08:35 AM EDT

PDB ID : 3PQ5 / pdb_00003pq5
Title : Structure of I274C variant of E. coli KatE[] - Images 19-24
Authors : Loewen, P.C.; Jha, V.; Louis, S.; Chelikani, P.; Carpena, X.; Fita, I.
Deposited on : 2010-11-25
Resolution : 1.80 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4-5-2 with Phenix2.0rc1
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0rc1
EDS : 3.0
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4 : 9.0.006 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.43.1

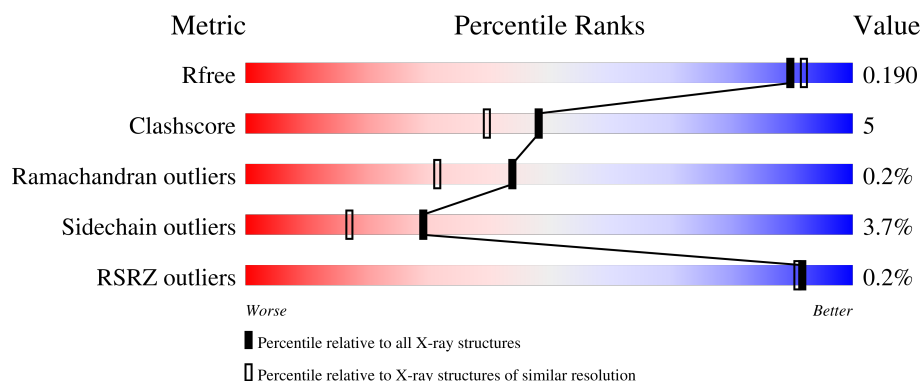
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION





The reported resolution of this entry is 1.80 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}	164625	7108 (1.80-1.80)
Clashscore	180529	8162 (1.80-1.80)
Ramachandran outliers	177936	8077 (1.80-1.80)
Sidechain outliers	177891	8076 (1.80-1.80)
RSRZ outliers	164620	7108 (1.80-1.80)

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	753	
1	B	753	
1	C	753	
1	D	753	

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 26829 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

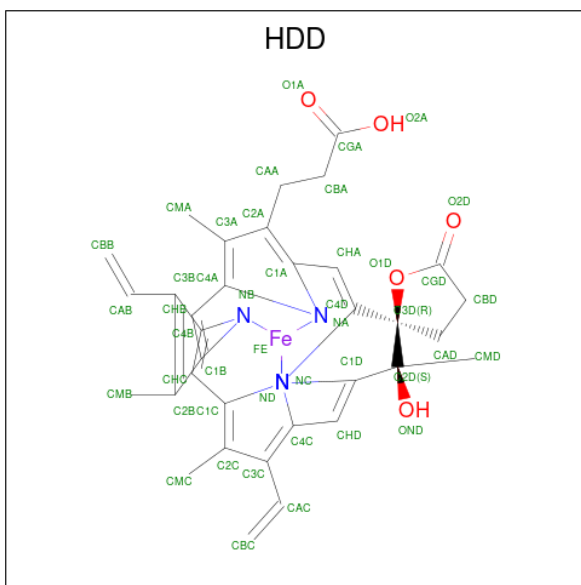
- Molecule 1 is a protein called Catalase HP11.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	726	Total	C	N	O	S	0	5	0
			5755	3652	1009	1083	11			
1	B	726	Total	C	N	O	S	0	5	0
			5757	3654	1009	1083	11			
1	C	726	Total	C	N	O	S	0	2	0
			5747	3649	1007	1080	11			
1	D	726	Total	C	N	O	S	0	9	0
			5771	3662	1013	1085	11			

There are 12 discrepancies between the modelled and reference sequences:

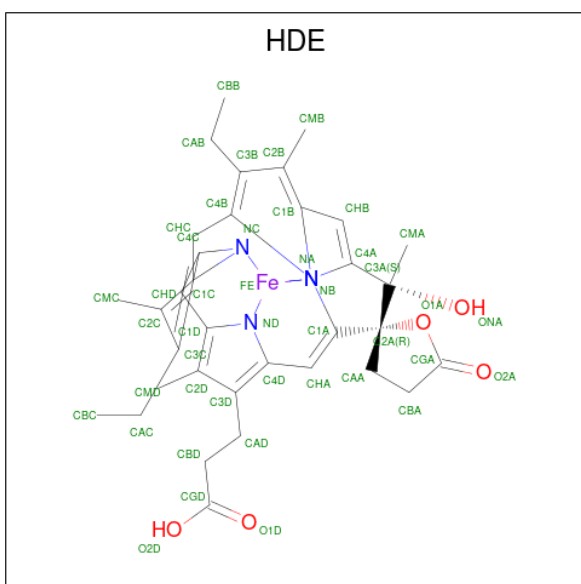
Chain	Residue	Modelled	Actual	Comment	Reference
A	274	CYS	ILE	engineered mutation	UNP P21179
A	438	ALA	CYS	engineered mutation	UNP P21179
A	669	ALA	CYS	engineered mutation	UNP P21179
B	274	CYS	ILE	engineered mutation	UNP P21179
B	438	ALA	CYS	engineered mutation	UNP P21179
B	669	ALA	CYS	engineered mutation	UNP P21179
C	274	CYS	ILE	engineered mutation	UNP P21179
C	438	ALA	CYS	engineered mutation	UNP P21179
C	669	ALA	CYS	engineered mutation	UNP P21179
D	274	CYS	ILE	engineered mutation	UNP P21179
D	438	ALA	CYS	engineered mutation	UNP P21179
D	669	ALA	CYS	engineered mutation	UNP P21179

- Molecule 2 is CIS-HEME D HYDROXYCHLORIN GAMMA-SPIROLACTONE (CCD ID: HDD) (formula: C₃₄H₃₂FeN₄O₅).



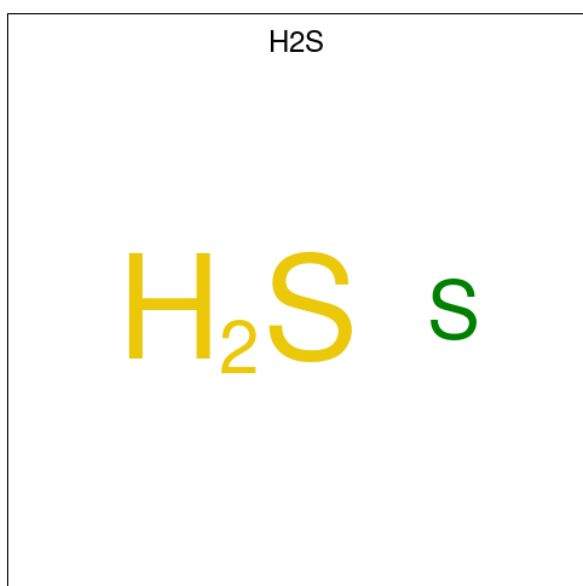
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total 44	C 34	Fe 1	N 4	O 5	0	1
2	B	1	Total 44	C 34	Fe 1	N 4	O 5	0	1
2	C	1	Total 44	C 34	Fe 1	N 4	O 5	0	1
2	D	1	Total 44	C 34	Fe 1	N 4	O 5	0	1

- Molecule 3 is CIS-HEME D HYDROXYCHLORIN GAMMA-SPIROLACTONE 17R, 18S (CCD ID: HDE) (formula: $C_{34}H_{38}FeN_4O_5$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total 44	C 34	Fe 1	N 4	O 5	0	1
3	B	1	Total 44	C 34	Fe 1	N 4	O 5	0	1
3	C	1	Total 44	C 34	Fe 1	N 4	O 5	0	1
3	D	1	Total 44	C 34	Fe 1	N 4	O 5	0	1

- Molecule 4 is HYDROSULFURIC ACID (CCD ID: H2S) (formula: H₂S).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total 1	S 1	0	0
4	B	1	Total 1	S 1	0	0
4	C	1	Total 1	S 1	0	0
4	D	1	Total 1	S 1	0	0

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	893	Total 893	O 893	0	0
5	B	790	Total 790	O 790	0	0

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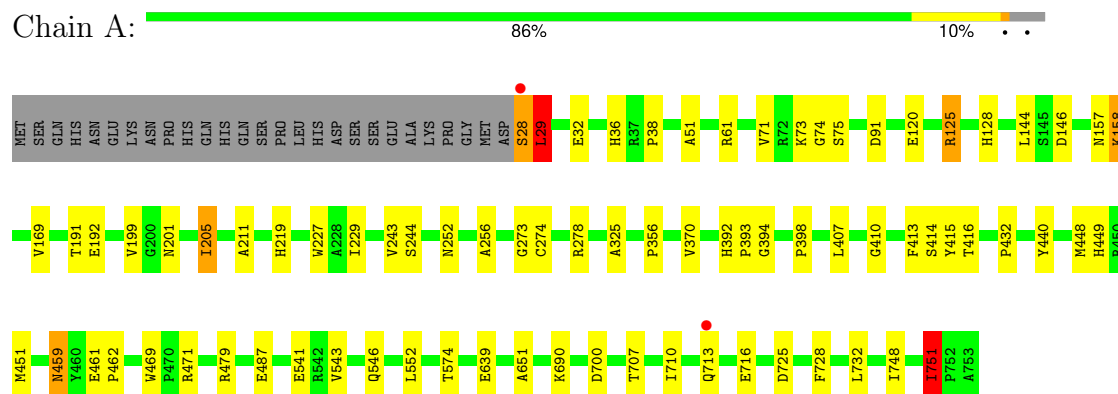
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	C	850	Total 850	O 850	0	0
5	D	910	Total 910	O 910	0	0

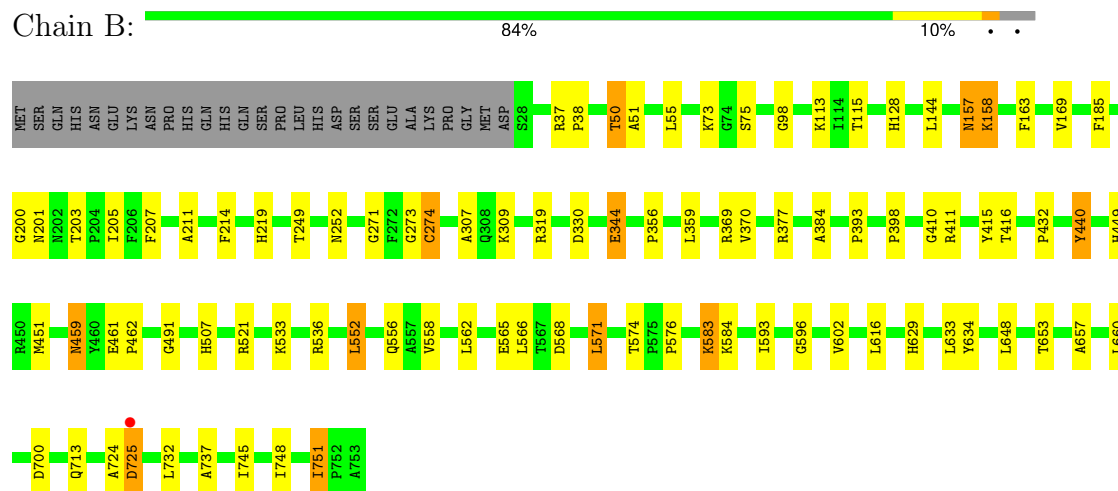
3 Residue-property plots

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

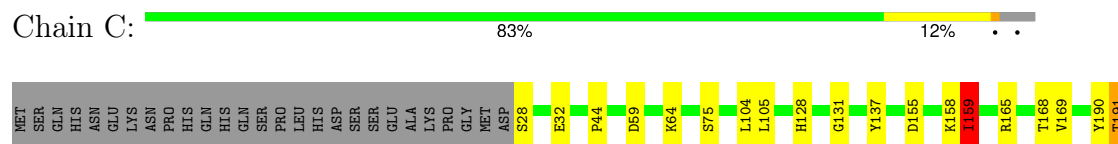
• Molecule 1: Catalase HP11

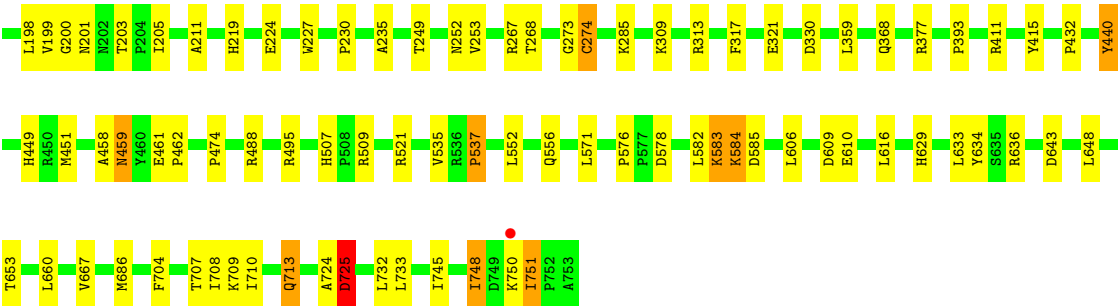


• Molecule 1: Catalase HP11

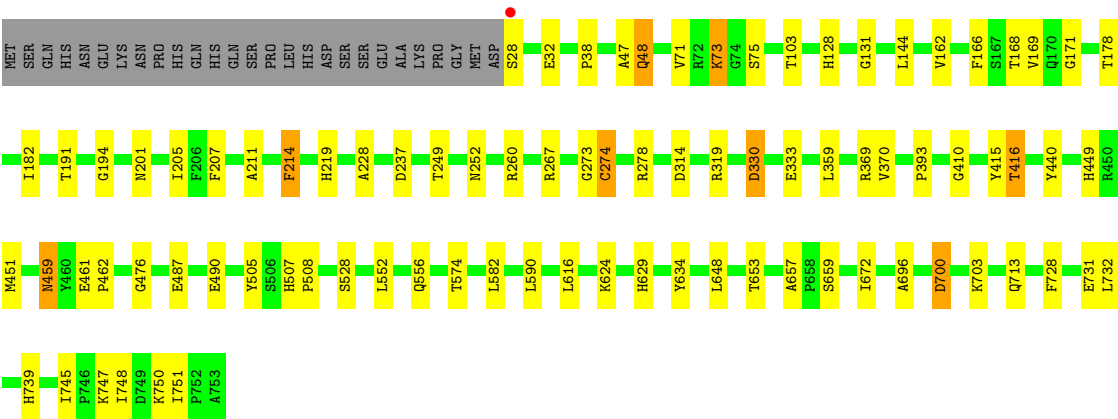
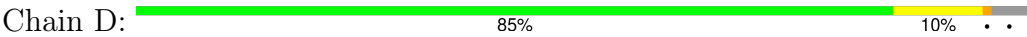


• Molecule 1: Catalase HP11





● Molecule 1: Catalase HPII



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	93.50Å 133.02Å 122.67Å 90.00° 109.40° 90.00°	Depositor
Resolution (Å)	31.96 – 1.80 31.96 – 1.80	Depositor EDS
% Data completeness (in resolution range)	92.7 (31.96-1.80) 93.3 (31.96-1.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.15	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.34 (at 1.79Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.143 , 0.190 0.143 , 0.190	Depositor DCC
R_{free} test set	12197 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	11.5	Xtriage
Anisotropy	0.011	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 42.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.028 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	26829	wwPDB-VP
Average B, all atoms (Å ²)	14.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.64% 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: HDD, H2S, HDE

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	1.40	8/5932 (0.1%)	1.16	10/8064 (0.1%)
1	B	1.34	14/5931 (0.2%)	1.15	14/8062 (0.2%)
1	C	1.36	12/5908 (0.2%)	1.15	8/8033 (0.1%)
1	D	1.40	16/5966 (0.3%)	1.14	5/8109 (0.1%)
All	All	1.37	50/23737 (0.2%)	1.15	37/32268 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	C	0	2

All (50) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	200	GLY	N-CA	10.12	1.53	1.44
1	C	474	PRO	CA-C	9.38	1.57	1.51
1	B	384	ALA	N-CA	7.26	1.55	1.46
1	B	200	GLY	N-CA	7.25	1.50	1.44
1	B	558	VAL	CA-CB	6.31	1.62	1.54
1	D	228	ALA	CA-CB	6.25	1.62	1.53
1	C	44	PRO	CA-C	6.21	1.57	1.52
1	A	71	VAL	CA-CB	5.99	1.61	1.54
1	D	194	GLY	N-CA	5.93	1.50	1.45
1	D	657	ALA	CA-CB	5.91	1.60	1.53
1	B	113	LYS	CA-C	5.82	1.60	1.52
1	D	178	THR	CA-CB	5.78	1.60	1.52
1	C	495	ARG	CZ-NH1	5.74	1.40	1.32
1	C	191	THR	CA-CB	5.73	1.62	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	585	ASP	C-O	-5.73	1.18	1.24
1	D	71	VAL	CA-CB	5.72	1.61	1.54
1	D	131	GLY	N-CA	5.70	1.50	1.45
1	D	528	SER	N-CA	5.65	1.53	1.46
1	D	162	VAL	C-O	5.63	1.29	1.23
1	B	98	GLY	N-CA	5.59	1.51	1.45
1	A	256	ALA	CA-CB	5.56	1.62	1.53
1	A	651	ALA	CA-CB	5.56	1.62	1.53
1	D	171	GLY	N-CA	5.55	1.52	1.45
1	B	203	THR	CA-CB	5.54	1.60	1.54
1	A	29	LEU	N-CA	-5.50	1.38	1.46
1	B	185	PHE	CA-C	5.47	1.58	1.53
1	B	50	THR	N-CA	5.44	1.53	1.45
1	B	745	ILE	CA-CB	5.44	1.56	1.54
1	C	203	THR	N-CA	5.41	1.50	1.45
1	D	333	GLU	C-O	5.36	1.30	1.23
1	C	235	ALA	CA-CB	5.33	1.59	1.52
1	B	55	LEU	N-CA	5.28	1.52	1.46
1	A	710	ILE	CA-CB	5.25	1.60	1.54
1	D	103	THR	CA-CB	5.22	1.61	1.53
1	C	131	GLY	C-O	5.21	1.28	1.23
1	B	307	ALA	C-O	-5.19	1.18	1.24
1	A	125	ARG	N-CA	5.16	1.52	1.46
1	B	576	PRO	CA-C	5.15	1.56	1.52
1	D	739	HIS	N-CA	5.15	1.52	1.46
1	D	314	ASP	N-CA	5.14	1.51	1.46
1	B	491	GLY	N-CA	5.13	1.50	1.45
1	A	243	VAL	CA-C	5.12	1.59	1.52
1	C	165	ARG	C-O	5.09	1.30	1.24
1	C	268	THR	CA-CB	5.08	1.60	1.53
1	D	659	SER	N-CA	-5.05	1.39	1.46
1	D	47	ALA	CA-C	5.04	1.59	1.52
1	D	214	PHE	CA-C	5.03	1.58	1.52
1	C	458	ALA	N-CA	5.03	1.52	1.46
1	B	271	GLY	N-CA	5.02	1.50	1.45
1	A	74	GLY	N-CA	5.01	1.50	1.45

All (37) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	536	ARG	CA-C-N	-8.86	110.61	119.56
1	B	536	ARG	C-N-CA	-8.86	110.61	119.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	745	ILE	N-CA-CB	7.41	115.48	110.52
1	C	725	ASP	N-CA-C	6.96	125.64	110.80
1	A	574	THR	CA-C-N	6.75	124.59	119.66
1	A	574	THR	C-N-CA	6.75	124.59	119.66
1	C	159	ILE	CB-CG1-CD1	-6.74	99.64	113.80
1	A	229	ILE	N-CA-C	-6.74	103.67	109.19
1	A	157	ASN	CA-C-N	-6.45	114.19	122.77
1	A	157	ASN	C-N-CA	-6.45	114.19	122.77
1	D	330	ASP	CB-CA-C	-6.09	102.66	111.91
1	A	120	GLU	N-CA-C	6.00	117.82	111.28
1	A	325	ALA	N-CA-C	-5.92	104.91	111.36
1	C	159	ILE	CA-CB-CG2	5.90	120.53	110.50
1	B	574	THR	CA-C-N	-5.88	114.32	120.38
1	B	574	THR	C-N-CA	-5.88	114.32	120.38
1	C	748	ILE	N-CA-C	5.85	116.63	110.72
1	B	163	PHE	N-CA-C	-5.79	98.98	108.76
1	B	356	PRO	N-CA-C	-5.70	108.75	114.68
1	B	648	LEU	CA-C-N	5.54	125.30	119.76
1	B	648	LEU	C-N-CA	5.54	125.30	119.76
1	B	657	ALA	CA-C-N	5.43	125.73	119.92
1	B	657	ALA	C-N-CA	5.43	125.73	119.92
1	C	169	VAL	CB-CA-C	-5.41	106.23	111.05
1	C	745	ILE	O-C-N	5.40	123.88	120.42
1	A	158[A]	LYS	CB-CA-C	5.37	118.88	110.19
1	A	158[B]	LYS	CB-CA-C	5.37	118.88	110.19
1	D	182	ILE	N-CA-C	-5.29	104.23	110.21
1	B	593	ILE	CA-C-N	5.24	126.39	119.84
1	B	593	ILE	C-N-CA	5.24	126.39	119.84
1	D	166	PHE	N-CA-C	-5.17	102.40	110.42
1	A	751	ILE	N-CA-CB	5.13	114.85	110.08
1	B	377	ARG	CA-CB-CG	-5.12	103.86	114.10
1	C	667	VAL	CA-C-N	-5.08	115.49	120.52
1	C	667	VAL	C-N-CA	-5.08	115.49	120.52
1	B	745	ILE	O-C-N	5.06	123.66	120.42
1	D	237	ASP	N-CA-C	5.03	116.45	111.07

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	724	ALA	Peptide
1	C	725	ASP	Peptide

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	5755	0	5582	59	0
1	B	5757	0	5587	58	0
1	C	5747	0	5577	62	1
1	D	5771	0	5598	46	0
2	A	44	0	31	3	0
2	B	44	0	31	10	0
2	C	44	0	31	4	0
2	D	44	0	31	5	0
3	A	44	0	36	11	0
3	B	44	0	36	13	0
3	C	44	0	36	11	0
3	D	44	0	36	8	0
4	A	1	0	0	1	0
4	B	1	0	0	0	0
4	C	1	0	0	1	0
4	D	1	0	0	0	0
5	A	893	0	0	12	2
5	B	790	0	0	10	0
5	C	850	0	0	21	0
5	D	910	0	0	18	2
All	All	26829	0	22612	248	3

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 5.

All (248) 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:D:451:MET:SD	5:D:3617:HOH:O	1.99	1.19
1:A:716:GLU:HG2	5:A:3090:HOH:O	1.43	1.18
3:C:761[B]:HDE:CMC	3:C:761[B]:HDE:HBCB	1.70	1.15
3:B:761[B]:HDE:HMCB	3:B:761[B]:HDE:CBC	1.77	1.14
1:C:578:ASP:HB3	5:C:2919:HOH:O	1.46	1.13
1:A:451:MET:HE2	1:C:451:MET:HE2	1.28	1.11
1:C:267:ARG:HG3	5:C:2916:HOH:O	1.49	1.10

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:761[B]:HDE:HBCB	3:C:761[B]:HDE:HMC	1.11	1.09
1:B:416:THR:HG21	5:D:2464:HOH:O	1.52	1.08
1:C:451:MET:SD	5:C:3612:HOH:O	2.12	1.06
3:B:761[B]:HDE:HMCB	3:B:761[B]:HDE:HBCA	1.06	1.05
1:B:451:MET:HE2	1:D:451:MET:HE2	1.09	1.05
1:A:416[A]:THR:HG21	5:A:3313:HOH:O	1.54	1.04
3:B:761[B]:HDE:HBCA	3:B:761[B]:HDE:CMC	1.84	1.04
3:B:761[B]:HDE:CBC	3:B:761[B]:HDE:CMC	2.34	1.02
1:A:541:GLU:OE2	5:A:2550:HOH:O	1.79	1.00
3:C:761[B]:HDE:CMC	3:C:761[B]:HDE:CBC	2.42	0.97
1:A:451:MET:SD	5:A:3609:HOH:O	2.25	0.94
1:B:533[A]:LYS:HE2	5:B:3100:HOH:O	1.67	0.94
1:A:28:SER:O	1:A:28:SER:OG	1.78	0.93
1:A:29:LEU:HD22	5:C:2405:HOH:O	1.69	0.92
1:B:451:MET:SD	5:B:3614:HOH:O	2.27	0.91
1:A:201:ASN:CG	2:A:760[A]:HDD:HMB1	1.99	0.88
1:B:201:ASN:CG	2:B:760[A]:HDD:HMB1	1.99	0.87
1:D:201:ASN:CG	2:D:760[A]:HDD:HMB1	1.99	0.86
1:A:751:ILE:HD13	1:A:751:ILE:O	1.78	0.84
1:A:639:GLU:HG3	5:A:2414:HOH:O	1.75	0.84
3:A:761[B]:HDE:CBC	3:A:761[B]:HDE:HMCB	2.07	0.84
3:B:761[B]:HDE:CMC	3:B:761[B]:HDE:HBCB	2.09	0.82
1:C:201:ASN:CG	2:C:760[A]:HDD:HMB1	2.04	0.82
3:D:761[B]:HDE:HMCB	3:D:761[B]:HDE:HBCB	1.61	0.81
1:C:440:TYR:HD1	5:C:3454:HOH:O	1.63	0.79
1:A:29:LEU:HD23	5:C:3144:HOH:O	1.82	0.78
3:C:761[B]:HDE:HBBA	3:C:761[B]:HDE:HMBB	1.67	0.76
3:A:761[B]:HDE:HMB	3:A:761[B]:HDE:HBBB	1.67	0.76
1:D:731:GLU:OE2	5:D:3028:HOH:O	2.03	0.75
3:D:761[B]:HDE:HMB	3:D:761[B]:HDE:HBBB	1.69	0.75
1:B:440:TYR:O	1:D:73[B]:LYS:HE3	1.87	0.74
1:D:748:ILE:O	1:D:751:ILE:HG22	1.86	0.74
3:A:761[B]:HDE:HMB	3:A:761[B]:HDE:CBB	2.16	0.74
3:A:761[B]:HDE:HMCB	3:A:761[B]:HDE:HBCB	1.71	0.73
1:B:451:MET:HE2	1:D:451:MET:CE	2.05	0.73
1:C:28:SER:HA	5:C:2523:HOH:O	1.88	0.72
3:A:761[B]:HDE:HMCB	3:A:761[B]:HDE:HBCA	1.72	0.70
1:B:700:ASP:HB2	5:B:3595:HOH:O	1.91	0.69
1:C:556:GLN:NE2	5:C:2533:HOH:O	2.26	0.68
1:D:672:ILE:HG12	1:D:700:ASP:OD2	1.93	0.68
1:C:725:ASP:O	5:C:2403:HOH:O	2.11	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:440:TYR:O	1:D:73[B]:LYS:CE	2.41	0.68
1:C:629:HIS:HD2	5:C:1129:HOH:O	1.76	0.67
1:B:748:ILE:O	1:B:751:ILE:HG22	1.94	0.67
1:B:330:ASP:OD1	1:B:629:HIS:HE1	1.79	0.66
3:A:761[B]:HDE:HBCB	3:A:761[B]:HDE:CMC	2.26	0.66
1:B:724:ALA:O	1:B:725:ASP:O	2.15	0.65
1:B:201:ASN:CG	2:B:760[A]:HDD:CMB	2.69	0.64
1:B:552:LEU:HD21	1:B:571:LEU:HD12	1.79	0.62
3:C:761[B]:HDE:HMBB	3:C:761[B]:HDE:CBB	2.29	0.62
1:B:73:LYS:HE3	5:D:3517:HOH:O	1.99	0.62
2:B:760[A]:HDD:CMB	2:B:760[A]:HDD:HBB1	2.30	0.62
1:A:416[B]:THR:HG22	5:A:904:HOH:O	2.00	0.61
1:D:629:HIS:HD2	5:D:1554:HOH:O	1.82	0.61
3:B:761[B]:HDE:HMBB	3:B:761[B]:HDE:CBB	2.30	0.61
1:C:708:ILE:HG13	1:C:710:ILE:HG12	1.82	0.61
1:B:37:ARG:HD3	5:B:2886:HOH:O	1.99	0.61
1:C:609:ASP:O	5:C:1764:HOH:O	2.16	0.60
1:C:636:ARG:HD3	5:C:2717:HOH:O	2.00	0.60
1:D:28:SER:HA	5:D:2467:HOH:O	2.00	0.60
1:D:267:ARG:HG3	5:D:1920:HOH:O	2.02	0.60
1:A:201:ASN:CG	2:A:760[A]:HDD:CMB	2.74	0.59
1:B:115:THR:HG21	5:B:3420:HOH:O	2.02	0.59
1:C:274:CYS:CA	4:C:754:H2S:S	2.91	0.59
1:C:368:GLN:NE2	5:C:1787:HOH:O	2.16	0.59
1:A:244:SER:HA	1:A:546[B]:GLN:NE2	2.17	0.59
1:B:73:LYS:CE	5:D:3517:HOH:O	2.51	0.59
1:A:278:ARG:HH12	1:A:487:GLU:CD	2.10	0.59
1:C:634:TYR:O	1:C:653:THR:HA	2.03	0.59
1:C:713:GLN:HB3	5:C:3004:HOH:O	2.03	0.58
1:B:201:ASN:ND2	2:B:760[A]:HDD:CMB	2.67	0.58
1:D:330:ASP:OD1	1:D:629:HIS:HE1	1.88	0.57
2:B:760[A]:HDD:HBC1	2:B:760[A]:HDD:CMC	2.36	0.56
1:C:59:ASP:OD2	5:C:3406:HOH:O	2.18	0.56
3:A:761[B]:HDE:CBC	3:A:761[B]:HDE:CMC	2.75	0.56
1:C:578:ASP:HB2	1:C:582:LEU:O	2.06	0.56
1:C:28:SER:N	5:C:2523:HOH:O	2.39	0.55
1:D:449[A]:HIS:HE1	5:D:1789:HOH:O	1.89	0.55
1:B:629:HIS:HD2	5:B:1055:HOH:O	1.90	0.55
1:D:273:GLY:C	1:D:274:CYS:SG	2.90	0.55
3:D:761[B]:HDE:HMB	3:D:761[B]:HDE:CBB	2.35	0.54
1:D:359:LEU:H	1:D:507:HIS:HD2	1.56	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:761[B]:HDE:HBCB	3:D:761[B]:HDE:CMC	2.34	0.53
1:A:29:LEU:HB2	5:C:2405:HOH:O	2.08	0.53
1:C:28:SER:CA	5:C:2523:HOH:O	2.52	0.53
1:D:556:GLN:NE2	5:D:2773:HOH:O	2.41	0.53
1:A:748:ILE:O	1:A:751:ILE:HD12	2.09	0.53
1:A:690:LYS:HG3	1:A:751:ILE:HD11	1.91	0.52
1:B:449[B]:HIS:HE1	5:D:1789:HOH:O	1.92	0.52
1:B:411:ARG:HG2	3:B:761[B]:HDE:C3B	2.39	0.52
1:C:359:LEU:H	1:C:507:HIS:HD2	1.58	0.52
1:B:521:ARG:HG3	5:B:3553:HOH:O	2.10	0.52
1:A:201:ASN:ND2	2:A:760[A]:HDD:CMB	2.73	0.52
1:C:610:GLU:HG2	5:C:3224:HOH:O	2.09	0.52
1:C:201:ASN:CG	2:C:760[A]:HDD:CMB	2.80	0.52
1:C:583:LYS:HG2	5:C:2919:HOH:O	2.10	0.52
1:B:73:LYS:CD	5:D:3517:HOH:O	2.58	0.52
1:B:157:ASN:C	1:B:157:ASN:HD22	2.19	0.51
1:B:583:LYS:O	1:B:584:LYS:HB3	2.11	0.51
1:A:459:ASN:ND2	1:B:219:HIS:HB3	2.26	0.51
1:B:201:ASN:ND2	2:B:760[A]:HDD:HMB3	2.26	0.51
1:A:392:HIS:CD2	1:A:394:GLY:H	2.29	0.51
3:B:761[B]:HDE:HMBB	3:B:761[B]:HDE:HBBA	1.91	0.51
1:C:137:TYR:HB2	1:C:159:ILE:CD1	2.41	0.51
1:B:144:LEU:HD11	1:B:370:VAL:HG13	1.93	0.50
1:A:219:HIS:HB3	1:B:459:ASN:ND2	2.26	0.50
3:D:761[B]:HDE:CBB	3:D:761[B]:HDE:CMB	2.88	0.50
1:A:36:HIS:HE1	5:A:1872:HOH:O	1.95	0.50
1:C:330:ASP:OD1	1:C:629:HIS:HE1	1.94	0.50
1:A:61:ARG:HD2	5:A:3208:HOH:O	2.10	0.50
1:A:125:ARG:HG2	3:A:761[B]:HDE:HBA	1.94	0.50
1:C:459:ASN:ND2	1:D:219:HIS:HB3	2.27	0.50
3:C:761[B]:HDE:CBB	3:C:761[B]:HDE:CMB	2.89	0.50
1:A:700:ASP:HB2	5:A:3594:HOH:O	2.11	0.49
1:B:359:LEU:H	1:B:507:HIS:HD2	1.60	0.49
1:D:201:ASN:CG	2:D:760[A]:HDD:CMB	2.79	0.49
1:A:725:ASP:H	1:A:728:PHE:HB3	1.78	0.49
1:B:369:ARG:HG2	5:B:1639:HOH:O	2.12	0.48
1:A:469:TRP:CE3	1:A:471:ARG:HG3	2.48	0.48
1:A:543:VAL:HA	1:A:546[B]:GLN:HE21	1.78	0.48
5:A:1788:HOH:O	1:C:449[A]:HIS:HE1	1.96	0.48
1:B:732:LEU:C	1:B:732:LEU:HD13	2.39	0.48
1:C:273:GLY:C	1:C:274:CYS:SG	2.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:201:ASN:ND2	2:D:760[A]:HDD:CMB	2.76	0.48
1:B:273:GLY:C	1:B:274:CYS:SG	2.97	0.48
1:D:416[B]:THR:HG22	5:D:1415:HOH:O	2.14	0.48
1:D:207:PHE:O	1:D:249:THR:HA	2.13	0.48
1:D:214:PHE:CD1	2:D:760[A]:HDD:HAC	2.49	0.47
1:A:144:LEU:HD11	1:A:370:VAL:HG13	1.97	0.47
1:C:211:ALA:CB	3:C:761[B]:HDE:HBB	2.44	0.47
1:C:610:GLU:OE1	1:C:643:ASP:HA	2.15	0.47
2:B:760[A]:HDD:CMB	2:B:760[A]:HDD:CBB	2.93	0.47
1:A:199:VAL:HG12	3:A:761[B]:HDE:HHDA	1.97	0.47
1:B:552:LEU:HD22	1:B:556:GLN:HG3	1.97	0.47
3:B:761[B]:HDE:HMBB	3:B:761[B]:HDE:HBBB	1.96	0.47
1:A:274:CYS:CA	4:A:754:H2S:S	3.03	0.47
1:B:596:GLY:HA3	1:B:737:ALA:O	2.15	0.47
1:B:634:TYR:O	1:B:653:THR:HA	2.14	0.47
1:C:219:HIS:HB3	1:D:459:ASN:ND2	2.30	0.46
1:C:748:ILE:O	1:C:751:ILE:HG22	2.15	0.46
1:D:672:ILE:CG1	1:D:700:ASP:OD2	2.61	0.46
5:B:3557:HOH:O	1:C:686:MET:HE1	2.14	0.46
1:D:128:HIS:CE1	1:D:169:VAL:HG22	2.50	0.46
1:B:38:PRO:HG2	1:B:51:ALA:HB2	1.98	0.46
1:B:207:PHE:O	1:B:249:THR:HA	2.15	0.46
1:B:440:TYR:O	1:D:73[B]:LYS:HE2	2.12	0.46
3:B:761[B]:HDE:CBB	3:B:761[B]:HDE:CMB	2.94	0.46
1:D:211:ALA:CB	1:D:410:GLY:HA3	2.46	0.46
2:B:760[A]:HDD:HMD2	2:B:760[A]:HDD:HAD2	1.72	0.46
3:D:761[B]:HDE:HAAA	3:D:761[B]:HDE:HMAB	1.59	0.46
1:A:751:ILE:HD13	1:A:751:ILE:C	2.38	0.46
1:D:476:GLY:HA3	5:D:1112:HOH:O	2.14	0.46
1:C:583:LYS:O	1:C:584:LYS:HB3	2.15	0.45
3:D:761[B]:HDE:HBBB	3:D:761[B]:HDE:CMB	2.44	0.45
1:C:440:TYR:CD1	5:C:3454:HOH:O	2.51	0.45
1:C:440:TYR:C	1:C:440:TYR:CD2	2.94	0.45
3:C:761[B]:HDE:CMC	3:C:761[B]:HDE:HBCA	2.42	0.45
1:B:128:HIS:CE1	1:B:169:VAL:HG22	2.52	0.45
1:D:703:LYS:NZ	5:D:2744:HOH:O	2.30	0.45
1:A:273:GLY:C	1:A:274:CYS:SG	3.00	0.45
1:B:319:ARG:HD3	1:C:227:TRP:O	2.16	0.45
1:C:359:LEU:H	1:C:507:HIS:CD2	2.36	0.45
1:C:461:GLU:HA	1:C:462:PRO:C	2.41	0.44
1:B:309:LYS:HD2	1:B:660:LEU:HD11	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:411:ARG:HG2	3:C:761[B]:HDE:C3B	2.46	0.44
1:B:583:LYS:NZ	1:B:583:LYS:H	2.15	0.44
1:A:211:ALA:CB	1:A:410:GLY:HA3	2.48	0.44
1:C:201:ASN:OD1	2:C:760[A]:HDD:HMB1	2.17	0.44
1:B:115:THR:CG2	5:B:3420:HOH:O	2.62	0.43
1:B:393:PRO:HD2	1:B:415:TYR:CG	2.53	0.43
3:D:761[B]:HDE:HMCB	3:D:761[B]:HDE:CBC	2.40	0.43
1:A:393:PRO:HD2	1:A:415:TYR:CG	2.53	0.43
1:D:359:LEU:H	1:D:507:HIS:CD2	2.33	0.43
1:C:393:PRO:HD2	1:C:415:TYR:CG	2.52	0.43
3:C:761[B]:HDE:HMAB	3:C:761[B]:HDE:HAAA	1.69	0.43
1:D:48:GLN:HE21	1:D:48:GLN:HB3	1.63	0.43
1:A:36:HIS:CD2	1:A:36:HIS:H	2.37	0.43
1:D:369:ARG:CG	5:D:3574:HOH:O	2.67	0.43
1:A:146:ASP:HB2	5:A:2592:HOH:O	2.19	0.43
1:D:144:LEU:HD11	1:D:370:VAL:HG13	2.00	0.43
1:C:704:PHE:O	1:C:707:THR:HG22	2.18	0.43
1:A:192:GLU:OE1	1:A:479:ARG:NH2	2.52	0.42
5:A:1016:HOH:O	1:C:104:LEU:HB3	2.19	0.42
1:D:38:PRO:HA	1:D:48:GLN:HE21	1.84	0.42
1:D:128:HIS:HA	1:D:168:THR:O	2.18	0.42
1:A:205:ILE:HD13	1:A:205:ILE:H	1.84	0.42
1:C:309:LYS:HD2	1:C:660:LEU:HD11	2.01	0.42
1:D:214:PHE:CD1	2:D:760[A]:HDD:CAC	3.02	0.42
1:A:219:HIS:HB3	1:B:459:ASN:CG	2.45	0.42
1:A:414:SER:OG	3:A:761[B]:HDE:HBB	2.19	0.42
1:A:461:GLU:HA	1:A:462:PRO:C	2.44	0.42
1:C:509:ARG:HD2	1:C:576:PRO:HD2	2.02	0.42
1:D:260:ARG:HD3	1:D:590:LEU:HD21	2.02	0.42
1:B:211:ALA:CB	1:B:410:GLY:HA3	2.49	0.42
1:A:227:TRP:O	1:D:319:ARG:HD3	2.19	0.42
3:A:761[B]:HDE:HMB	3:A:761[B]:HDE:HBBA	1.97	0.42
1:C:128:HIS:HA	1:C:168:THR:O	2.19	0.42
1:A:244:SER:HA	1:A:546[B]:GLN:CD	2.44	0.42
1:B:73:LYS:HD2	5:D:3517:HOH:O	2.17	0.42
1:B:602:VAL:HG22	1:B:629:HIS:HB2	2.02	0.42
3:B:761[B]:HDE:HBBB	3:B:761[B]:HDE:CMB	2.50	0.42
1:A:356:PRO:HG3	1:A:407:LEU:HB2	2.02	0.42
1:B:214:PHE:CD2	2:B:760[A]:HDD:CMC	3.03	0.42
1:C:201:ASN:ND2	2:C:760[A]:HDD:CMB	2.83	0.41
1:C:155:ASP:HB3	1:C:158:LYS:HB2	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:201:ASN:OD1	2:B:760[A]:HDD:HMB1	2.17	0.41
1:C:535:VAL:O	1:C:537:PRO:HD3	2.21	0.41
1:D:278:ARG:HH12	1:D:487:GLU:CD	2.29	0.41
1:A:128:HIS:CE1	1:A:169:VAL:HG22	2.55	0.41
1:C:224:GLU:HB3	5:D:3120:HOH:O	2.21	0.41
1:A:91:ASP:OD1	1:C:461:GLU:OE1	2.38	0.41
1:D:696:ALA:HB1	1:D:728:PHE:CZ	2.56	0.41
1:C:313:ARG:HG3	1:C:660:LEU:HD12	2.03	0.41
1:C:317:PHE:O	1:C:321:GLU:HB2	2.20	0.41
1:A:38:PRO:HG2	1:A:51:ALA:HB2	2.02	0.41
1:A:413:PHE:HB2	1:C:105:LEU:HD11	2.03	0.41
1:A:459:ASN:HD22	1:A:459:ASN:C	2.28	0.41
1:B:50:THR:HG21	1:C:227:TRP:CZ3	2.56	0.41
1:B:461:GLU:HA	1:B:462:PRO:C	2.46	0.41
1:D:393:PRO:HD2	1:D:415:TYR:CG	2.55	0.41
1:A:461:GLU:HB2	1:A:462:PRO:HA	2.04	0.41
1:B:157:ASN:HD22	1:B:158:LYS:N	2.19	0.41
3:B:761[B]:HDE:HBCB	3:B:761[B]:HDE:HMCA	1.97	0.41
1:D:505:TYR:C	1:D:508:PRO:HD2	2.46	0.41
1:A:73:LYS:HE3	1:C:440:TYR:O	2.21	0.40
1:C:64:LYS:HE2	1:C:190:TYR:CE1	2.55	0.40
1:D:461:GLU:HA	1:D:462:PRO:C	2.46	0.40
1:D:634:TYR:O	1:D:653:THR:HA	2.20	0.40
1:C:199:VAL:HG12	3:C:761[B]:HDE:HHDA	2.03	0.40
1:A:448:MET:HG3	1:A:449[B]:HIS:CD2	2.57	0.40
1:B:157:ASN:C	1:B:157:ASN:ND2	2.79	0.40
1:B:359:LEU:H	1:B:507:HIS:CD2	2.37	0.40
1:B:344:GLU:CD	1:B:344:GLU:H	2.30	0.40
3:B:761[B]:HDE:HMAB	3:B:761[B]:HDE:HAAA	1.66	0.40
1:C:249:THR:O	1:C:253:VAL:HG23	2.21	0.40

All (3) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:584:LYS:NZ	5:A:1624:HOH:O[1_554]	2.13	0.07
5:A:3241:HOH:O	5:D:2457:HOH:O[2_646]	2.14	0.06
5:D:2178:HOH:O	5:D:2976:HOH:O[1_655]	2.18	0.02

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	729/753 (97%)	707 (97%)	21 (3%)	1 (0%)	48	34
1	B	729/753 (97%)	705 (97%)	22 (3%)	2 (0%)	37	25
1	C	726/753 (96%)	702 (97%)	22 (3%)	2 (0%)	37	25
1	D	733/753 (97%)	713 (97%)	19 (3%)	1 (0%)	48	34
All	All	2917/3012 (97%)	2827 (97%)	84 (3%)	6 (0%)	44	31

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	725	ASP
1	A	75	SER
1	C	75	SER
1	B	75	SER
1	D	75	SER
1	C	725	ASP

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	614/634 (97%)	599 (98%)	15 (2%)	44	32
1	B	614/634 (97%)	593 (97%)	21 (3%)	32	20
1	C	611/634 (96%)	580 (95%)	31 (5%)	20	9
1	D	618/634 (98%)	594 (96%)	24 (4%)	27	15

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
All	All	2457/2536 (97%)	2366 (96%)	91 (4%)	29	17

All (91) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	28	SER
1	A	29	LEU
1	A	32	GLU
1	A	191	THR
1	A	205	ILE
1	A	252	ASN
1	A	398	PRO
1	A	432	PRO
1	A	440	TYR
1	A	459	ASN
1	A	552	LEU
1	A	707	THR
1	A	713	GLN
1	A	732	LEU
1	A	751	ILE
1	B	157	ASN
1	B	158	LYS
1	B	205	ILE
1	B	252	ASN
1	B	274	CYS
1	B	344	GLU
1	B	398	PRO
1	B	432	PRO
1	B	440	TYR
1	B	459	ASN
1	B	552	LEU
1	B	562	LEU
1	B	565	GLU
1	B	566	LEU
1	B	568	ASP
1	B	571	LEU
1	B	583	LYS
1	B	616	LEU
1	B	633	LEU
1	B	713	GLN
1	B	751	ILE
1	C	32	GLU

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Mol	Chain	Res	Type
1	C	159	ILE
1	C	191	THR
1	C	198	LEU
1	C	205	ILE
1	C	230	PRO
1	C	252	ASN
1	C	274	CYS
1	C	285	LYS
1	C	377	ARG
1	C	432	PRO
1	C	440	TYR
1	C	459	ASN
1	C	488	ARG
1	C	521	ARG
1	C	537	PRO
1	C	552	LEU
1	C	571	LEU
1	C	583	LYS
1	C	584	LYS
1	C	606	LEU
1	C	616	LEU
1	C	633	LEU
1	C	648	LEU
1	C	709	LYS
1	C	713	GLN
1	C	725	ASP
1	C	732	LEU
1	C	733	LEU
1	C	750	LYS
1	C	751	ILE
1	D	32	GLU
1	D	48	GLN
1	D	73[A]	LYS
1	D	73[B]	LYS
1	D	191	THR
1	D	205	ILE
1	D	252	ASN
1	D	274	CYS
1	D	416[A]	THR
1	D	416[B]	THR
1	D	440	TYR
1	D	459	ASN

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Mol	Chain	Res	Type
1	D	490	GLU
1	D	552	LEU
1	D	574	THR
1	D	582	LEU
1	D	616	LEU
1	D	624	LYS
1	D	648	LEU
1	D	700	ASP
1	D	713	GLN
1	D	732	LEU
1	D	747	LYS
1	D	750	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (30) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	36	HIS
1	A	77	ASN
1	A	139	GLN
1	A	246	GLN
1	A	252	ASN
1	A	459	ASN
1	A	515	GLN
1	B	157	ASN
1	B	252	ASN
1	B	459	ASN
1	B	507	HIS
1	B	629	HIS
1	C	84	GLN
1	C	246	GLN
1	C	252	ASN
1	C	459	ASN
1	C	486	GLN
1	C	507	HIS
1	C	546	GLN
1	C	556	GLN
1	C	629	HIS
1	C	671	ASN
1	C	682	ASN
1	D	48	GLN
1	D	252	ASN
1	D	459	ASN

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Mol	Chain	Res	Type
1	D	507	HIS
1	D	556	GLN
1	D	629	HIS
1	D	671	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 12 ligands modelled in this entry, 4 are modelled with single atom - leaving 8 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	HDE	C	761[B]	1,5	44,52,52	2.24	13 (29%)	42,89,89	3.39	17 (40%)
2	HDD	A	760[A]	1,5	41,52,52	2.47	12 (29%)	34,89,89	2.24	11 (32%)
3	HDE	A	761[B]	1,5	44,52,52	2.52	14 (31%)	42,89,89	3.01	15 (35%)
2	HDD	B	760[A]	1,5	41,52,52	2.08	15 (36%)	34,89,89	2.51	11 (32%)
3	HDE	D	761[B]	1,5	44,52,52	2.46	13 (29%)	42,89,89	3.37	21 (50%)
2	HDD	D	760[A]	1,5	41,52,52	2.40	15 (36%)	34,89,89	2.25	13 (38%)
3	HDE	B	761[B]	1,5	44,52,52	2.51	13 (29%)	42,89,89	3.46	17 (40%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	HDD	C	760[A]	1,5	41,52,52	2.15	12 (29%)	34,89,89	2.39	12 (35%)

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	HDE	C	761[B]	1,5	-	6/9/89/89	0/1/9/9
2	HDD	A	760[A]	1,5	-	2/5/89/89	0/1/9/9
3	HDE	A	761[B]	1,5	-	6/9/89/89	0/1/9/9
2	HDD	B	760[A]	1,5	-	2/5/89/89	0/1/9/9
3	HDE	D	761[B]	1,5	-	6/9/89/89	0/1/9/9
2	HDD	D	760[A]	1,5	-	2/5/89/89	0/1/9/9
3	HDE	B	761[B]	1,5	-	6/9/89/89	0/1/9/9
2	HDD	C	760[A]	1,5	-	2/5/89/89	0/1/9/9

All (107) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	760[A]	HDD	FE-ND	8.29	2.26	1.95
3	B	761[B]	HDE	CHC-C4B	-7.82	1.43	1.51
2	C	760[A]	HDD	FE-ND	7.36	2.23	1.95
3	D	761[B]	HDE	CHC-C4B	-6.83	1.44	1.51
3	A	761[B]	HDE	CHC-C1C	-6.28	1.44	1.51
2	A	760[A]	HDD	O1D-C3D	-6.18	1.36	1.46
2	A	760[A]	HDD	FE-ND	6.17	2.18	1.95
3	D	761[B]	HDE	CHD-C1D	-6.13	1.44	1.51
3	B	761[B]	HDE	O1A-CGA	6.07	1.45	1.35
3	C	761[B]	HDE	CHC-C4B	-6.06	1.44	1.51
3	A	761[B]	HDE	O1A-CGA	6.03	1.45	1.35
2	A	760[A]	HDD	C3B-C2B	-5.93	1.32	1.40
3	A	761[B]	HDE	CHC-C4B	-5.81	1.45	1.51
2	D	760[A]	HDD	C3B-C2B	-5.43	1.33	1.40
2	A	760[A]	HDD	C3B-C4B	5.38	1.49	1.41
3	C	761[B]	HDE	O1A-CGA	5.15	1.43	1.35
3	B	761[B]	HDE	CHD-C4C	-5.05	1.46	1.51
3	C	761[B]	HDE	CHD-C1D	-4.90	1.46	1.51
3	D	761[B]	HDE	O1A-CGA	4.88	1.43	1.35
3	C	761[B]	HDE	CHD-C4C	-4.86	1.46	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	761[B]	HDE	CHD-C1D	-4.85	1.46	1.51
3	B	761[B]	HDE	CHD-C1D	-4.84	1.46	1.51
3	D	761[B]	HDE	CHD-C4C	-4.83	1.46	1.51
2	B	760[A]	HDD	C3C-C2C	-4.79	1.33	1.40
2	C	760[A]	HDD	C3B-C2B	-4.55	1.34	1.40
2	D	760[A]	HDD	O1D-C3D	-4.48	1.39	1.46
3	B	761[B]	HDE	CHC-C1C	-4.40	1.46	1.51
3	D	761[B]	HDE	CHC-C1C	-4.34	1.46	1.51
3	A	761[B]	HDE	C4C-C3C	4.32	1.48	1.38
2	B	760[A]	HDD	C3B-C4B	4.20	1.47	1.41
3	A	761[B]	HDE	C1A-NA	4.14	1.44	1.37
2	A	760[A]	HDD	C3C-C2C	-4.12	1.34	1.40
3	D	761[B]	HDE	C3B-C2B	4.10	1.49	1.37
3	B	761[B]	HDE	C4C-C3C	4.07	1.47	1.38
2	B	760[A]	HDD	C3B-C2B	-3.99	1.35	1.40
3	D	761[B]	HDE	C1A-NA	3.92	1.44	1.37
3	C	761[B]	HDE	C3B-C2B	3.92	1.49	1.37
2	D	760[A]	HDD	CHD-C1D	3.87	1.42	1.35
3	D	761[B]	HDE	C4A-NA	3.80	1.44	1.37
2	B	760[A]	HDD	FE-ND	3.79	2.10	1.95
3	B	761[B]	HDE	C1A-NA	3.78	1.44	1.37
2	C	760[A]	HDD	C3B-C4B	3.78	1.46	1.41
3	A	761[B]	HDE	C3C-C2C	3.77	1.48	1.37
3	D	761[B]	HDE	C4C-C3C	3.76	1.47	1.38
2	C	760[A]	HDD	C3C-C2C	-3.76	1.35	1.40
3	B	761[B]	HDE	C3B-C2B	3.70	1.48	1.37
3	A	761[B]	HDE	C4A-NA	3.65	1.43	1.37
3	B	761[B]	HDE	C3C-C2C	3.64	1.48	1.37
3	C	761[B]	HDE	C4C-C3C	3.57	1.46	1.38
2	B	760[A]	HDD	CMD-C2D	3.57	1.58	1.53
3	A	761[B]	HDE	C3B-C2B	3.56	1.48	1.37
3	C	761[B]	HDE	C3D-C2D	3.49	1.48	1.37
3	D	761[B]	HDE	C3C-C2C	3.43	1.47	1.37
3	C	761[B]	HDE	CHC-C1C	-3.42	1.47	1.51
2	B	760[A]	HDD	O1D-C3D	-3.40	1.41	1.46
3	A	761[B]	HDE	CHD-C4C	-3.31	1.47	1.51
3	A	761[B]	HDE	C3D-C2D	3.30	1.47	1.37
3	A	761[B]	HDE	C1B-CHB	3.23	1.50	1.41
2	A	760[A]	HDD	C3B-CAB	3.21	1.54	1.47
2	B	760[A]	HDD	CHD-C1D	3.12	1.41	1.35
2	D	760[A]	HDD	C3B-C4B	3.12	1.46	1.41
3	C	761[B]	HDE	C1A-NA	3.08	1.42	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	760[A]	HDD	CHD-C1D	3.07	1.41	1.35
2	C	760[A]	HDD	O1D-C3D	-3.06	1.41	1.46
2	A	760[A]	HDD	CHD-C1D	3.02	1.41	1.35
2	D	760[A]	HDD	C3B-CAB	2.99	1.54	1.47
3	A	761[B]	HDE	C1B-NB	2.97	1.42	1.36
2	C	760[A]	HDD	C3B-CAB	2.91	1.54	1.47
2	A	760[A]	HDD	CMC-C2C	2.91	1.57	1.51
2	B	760[A]	HDD	C3B-CAB	2.91	1.54	1.47
2	D	760[A]	HDD	CMD-C2D	2.91	1.57	1.53
2	C	760[A]	HDD	CHA-C4D	2.89	1.40	1.35
3	D	761[B]	HDE	C4D-CHA	2.87	1.49	1.41
2	B	760[A]	HDD	C4D-ND	2.76	1.42	1.37
3	C	761[B]	HDE	C3C-C2C	2.72	1.45	1.37
3	D	761[B]	HDE	C1B-NB	2.72	1.41	1.36
3	D	761[B]	HDE	C3D-C2D	2.67	1.45	1.37
3	C	761[B]	HDE	C4A-NA	2.65	1.42	1.37
3	B	761[B]	HDE	C4A-NA	2.63	1.42	1.37
2	D	760[A]	HDD	C3C-C2C	-2.59	1.36	1.40
2	B	760[A]	HDD	CMA-C3A	2.56	1.56	1.51
3	B	761[B]	HDE	C3D-C2D	2.54	1.45	1.37
2	C	760[A]	HDD	C1A-NA	2.54	1.41	1.36
3	B	761[B]	HDE	C4D-CHA	2.52	1.48	1.41
2	D	760[A]	HDD	CHA-C4D	2.49	1.40	1.35
3	A	761[B]	HDE	C4D-CHA	2.49	1.47	1.41
2	D	760[A]	HDD	CMC-C2C	2.44	1.56	1.51
2	B	760[A]	HDD	C1A-NA	2.38	1.41	1.36
2	D	760[A]	HDD	C4C-NC	2.35	1.41	1.36
3	B	761[B]	HDE	C1B-NB	2.34	1.41	1.36
3	C	761[B]	HDE	C1B-NB	2.32	1.41	1.36
2	A	760[A]	HDD	O2D-CGD	2.32	1.29	1.22
2	A	760[A]	HDD	CMA-C3A	2.30	1.56	1.51
2	D	760[A]	HDD	C4D-ND	2.30	1.41	1.37
2	A	760[A]	HDD	C4A-NA	2.27	1.41	1.36
2	C	760[A]	HDD	CMC-C2C	2.26	1.56	1.51
2	D	760[A]	HDD	OND-C2D	2.25	1.47	1.42
2	C	760[A]	HDD	C4D-ND	2.22	1.41	1.37
2	D	760[A]	HDD	O1D-CGD	-2.22	1.32	1.35
2	D	760[A]	HDD	C1A-NA	2.15	1.40	1.36
2	C	760[A]	HDD	CMD-C2D	2.14	1.56	1.53
2	B	760[A]	HDD	C2A-C3A	-2.12	1.31	1.37
2	B	760[A]	HDD	CHA-C4D	2.10	1.39	1.35
3	C	761[B]	HDE	C1B-CHB	2.08	1.46	1.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	760[A]	HDD	C1A-NA	2.06	1.40	1.36
2	B	760[A]	HDD	C1D-ND	2.03	1.41	1.37
2	B	760[A]	HDD	OND-C2D	2.03	1.46	1.42

All (117) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	761[B]	HDE	C2D-C1D-ND	11.12	117.64	109.44
3	B	761[B]	HDE	C2D-C1D-ND	10.32	117.05	109.44
3	A	761[B]	HDE	C2D-C1D-ND	10.25	117.00	109.44
3	D	761[B]	HDE	C2D-C1D-ND	10.18	116.94	109.44
3	B	761[B]	HDE	C2C-C1C-NC	9.88	116.72	109.44
3	D	761[B]	HDE	C2C-C1C-NC	9.42	116.38	109.44
3	A	761[B]	HDE	C2C-C1C-NC	8.86	115.97	109.44
3	B	761[B]	HDE	C3B-C4B-NB	8.83	115.66	109.51
2	B	760[A]	HDD	O1D-CGD-O2D	8.76	128.19	120.81
3	C	761[B]	HDE	C2C-C1C-NC	8.52	115.72	109.44
3	C	761[B]	HDE	C3B-C4B-NB	8.36	115.34	109.51
3	D	761[B]	HDE	C3B-C4B-NB	8.14	115.18	109.51
2	C	760[A]	HDD	O1D-CGD-O2D	8.00	127.55	120.81
2	A	760[A]	HDD	O1D-CGD-CBD	-7.68	103.16	110.17
3	A	761[B]	HDE	C3B-C4B-NB	6.83	114.27	109.51
2	D	760[A]	HDD	O1D-CGD-CBD	-6.43	104.31	110.17
3	C	761[B]	HDE	CBC-CAC-C3C	-6.30	97.21	112.32
2	B	760[A]	HDD	O1D-CGD-CBD	-5.59	105.07	110.17
3	B	761[B]	HDE	CBC-CAC-C3C	-5.56	98.99	112.32
3	D	761[B]	HDE	C1B-CHB-C4A	-4.99	120.52	130.04
3	B	761[B]	HDE	C1B-C2B-C3B	-4.91	103.58	107.00
2	C	760[A]	HDD	O1D-CGD-CBD	-4.62	105.95	110.17
3	C	761[B]	HDE	C1B-CHB-C4A	-4.57	121.32	130.04
2	A	760[A]	HDD	C3D-O1D-CGD	4.55	115.38	111.14
3	A	761[B]	HDE	CBA-CAA-C2A	4.47	110.36	103.98
3	B	761[B]	HDE	CBA-CAA-C2A	4.40	110.26	103.98
3	D	761[B]	HDE	C3A-C4A-CHB	-4.32	117.55	124.27
3	B	761[B]	HDE	C4C-CHD-C1D	4.23	123.98	113.19
3	D	761[B]	HDE	CAD-CBD-CGD	-4.12	102.73	113.83
3	A	761[B]	HDE	CAD-CBD-CGD	-4.06	102.89	113.83
3	B	761[B]	HDE	O1A-CGA-O2A	4.04	124.22	120.81
2	D	760[A]	HDD	O1D-CGD-O2D	4.00	124.18	120.81
3	D	761[B]	HDE	C1B-C2B-C3B	-3.99	104.22	107.00
3	D	761[B]	HDE	C4C-CHD-C1D	3.95	123.27	113.19
3	A	761[B]	HDE	C1B-CHB-C4A	-3.89	122.61	130.04

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	761[B]	HDE	C4D-CHA-C1A	-3.84	122.72	130.04
2	B	760[A]	HDD	CMC-C2C-C1C	-3.83	122.84	128.46
3	C	761[B]	HDE	CAD-CBD-CGD	-3.83	103.52	113.83
2	D	760[A]	HDD	CBD-CAD-C3D	-3.75	98.64	103.98
2	B	760[A]	HDD	C1A-CHA-C4D	-3.72	122.94	130.04
3	B	761[B]	HDE	C1B-CHB-C4A	-3.72	122.95	130.04
3	D	761[B]	HDE	C4D-CHA-C1A	-3.65	123.08	130.04
3	D	761[B]	HDE	CMA-C3A-C4A	-3.63	106.53	112.68
3	B	761[B]	HDE	CAD-CBD-CGD	-3.62	104.09	113.83
3	A	761[B]	HDE	O1A-CGA-O2A	3.59	123.83	120.81
3	C	761[B]	HDE	CMA-C3A-C4A	-3.58	106.62	112.68
2	C	760[A]	HDD	OND-C2D-CMD	-3.54	102.61	109.45
3	C	761[B]	HDE	C4C-CHD-C1D	3.51	122.16	113.19
3	C	761[B]	HDE	C3A-C4A-CHB	-3.41	118.96	124.27
2	D	760[A]	HDD	C2B-C3B-C4B	3.37	109.25	106.90
2	D	760[A]	HDD	C3D-O1D-CGD	3.36	114.28	111.14
2	B	760[A]	HDD	CAA-CBA-CGA	-3.35	104.80	113.83
3	D	761[B]	HDE	CMC-C2C-C3C	3.27	131.11	124.94
2	A	760[A]	HDD	C2B-C3B-C4B	3.24	109.16	106.90
3	B	761[B]	HDE	CMC-C2C-C1C	3.22	130.84	127.28
3	D	761[B]	HDE	CAC-C3C-C4C	-3.21	123.33	127.19
3	C	761[B]	HDE	CMC-C2C-C1C	3.20	130.82	127.28
3	B	761[B]	HDE	C4D-CHA-C1A	-3.19	123.95	130.04
3	A	761[B]	HDE	CMD-C2D-C3D	3.18	130.94	124.94
2	A	760[A]	HDD	CAD-CBD-CGD	-3.17	99.78	104.48
2	C	760[A]	HDD	C2B-C3B-C4B	3.16	109.11	106.90
2	C	760[A]	HDD	CMC-C2C-C1C	-3.07	123.96	128.46
3	D	761[B]	HDE	CHB-C4A-NA	3.03	128.46	124.28
3	B	761[B]	HDE	CMB-C2B-C3B	2.99	130.58	124.94
3	A	761[B]	HDE	C4B-CHC-C1C	2.96	120.75	113.19
3	D	761[B]	HDE	CMB-C2B-C3B	2.93	130.47	124.94
3	D	761[B]	HDE	O1A-CGA-O2A	2.92	123.27	120.81
3	D	761[B]	HDE	CBA-CAA-C2A	2.89	108.11	103.98
3	C	761[B]	HDE	CMD-C2D-C3D	2.89	130.39	124.94
2	D	760[A]	HDD	CAA-CBA-CGA	-2.88	106.08	113.83
2	D	760[A]	HDD	CMC-C2C-C1C	-2.87	124.25	128.46
2	A	760[A]	HDD	OND-C2D-CMD	-2.86	103.93	109.45
2	A	760[A]	HDD	C3B-C4B-NB	-2.85	105.56	110.94
3	B	761[B]	HDE	C3A-C4A-CHB	-2.85	119.84	124.27
3	D	761[B]	HDE	CBC-CAC-C3C	-2.82	105.55	112.32
2	A	760[A]	HDD	CBD-CAD-C3D	-2.82	99.96	103.98
2	C	760[A]	HDD	CHA-C4D-ND	-2.80	120.42	124.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	760[A]	HDD	CAA-CBA-CGA	-2.78	106.35	113.83
3	A	761[B]	HDE	C4C-CHD-C1D	2.77	120.26	113.19
2	D	760[A]	HDD	C4A-C3A-C2A	2.77	108.92	107.00
3	C	761[B]	HDE	C4B-CHC-C1C	2.76	120.25	113.19
3	A	761[B]	HDE	CBC-CAC-C3C	-2.70	105.85	112.32
2	D	760[A]	HDD	CMA-C3A-C4A	-2.69	124.51	128.46
3	C	761[B]	HDE	CBA-CAA-C2A	2.66	107.77	103.98
3	D	761[B]	HDE	C4B-CHC-C1C	2.66	119.97	113.19
3	B	761[B]	HDE	C4B-CHC-C1C	2.65	119.97	113.19
2	C	760[A]	HDD	C3C-C4C-NC	-2.63	105.81	109.21
2	C	760[A]	HDD	C3D-O1D-CGD	2.61	113.57	111.14
3	A	761[B]	HDE	C4D-CHA-C1A	-2.60	125.09	130.04
2	D	760[A]	HDD	C2D-C1D-CHD	2.54	128.22	124.27
2	B	760[A]	HDD	CBD-CAD-C3D	-2.53	100.38	103.98
3	C	761[B]	HDE	O1A-C2A-CAA	2.50	107.68	103.06
2	B	760[A]	HDD	C3D-O1D-CGD	2.48	113.45	111.14
2	C	760[A]	HDD	CBD-CAD-C3D	-2.47	100.46	103.98
2	B	760[A]	HDD	CMC-C2C-C3C	2.45	129.59	124.68
3	B	761[B]	HDE	C1C-C2C-C3C	-2.40	100.81	106.20
2	C	760[A]	HDD	CAA-CBA-CGA	-2.37	107.45	113.83
2	D	760[A]	HDD	O2A-CGA-CBA	2.36	121.45	114.00
2	A	760[A]	HDD	C3C-C4C-NC	-2.27	106.27	109.21
3	A	761[B]	HDE	CAB-C3B-C4B	-2.26	124.47	127.19
2	B	760[A]	HDD	C4A-C3A-C2A	2.20	108.53	107.00
3	B	761[B]	HDE	CMA-C3A-C4A	-2.18	108.99	112.68
3	D	761[B]	HDE	CMB-C2B-C1B	-2.16	125.30	128.46
3	A	761[B]	HDE	C2A-O1A-CGA	2.15	113.15	111.14
2	C	760[A]	HDD	CMA-C3A-C4A	-2.14	125.32	128.46
2	A	760[A]	HDD	CMA-C3A-C4A	-2.14	125.33	128.46
2	B	760[A]	HDD	CMA-C3A-C4A	-2.11	125.37	128.46
3	D	761[B]	HDE	CBB-CAB-C3B	-2.11	107.27	112.32
3	C	761[B]	HDE	O1A-CGA-O2A	2.10	122.58	120.81
2	A	760[A]	HDD	C4A-C3A-C2A	2.08	108.44	107.00
2	D	760[A]	HDD	C3B-C4B-NB	-2.08	107.02	110.94
3	D	761[B]	HDE	O1A-C2A-CAA	2.06	106.87	103.06
3	C	761[B]	HDE	C1C-C2C-C3C	-2.06	101.58	106.20
2	B	760[A]	HDD	OND-C2D-CMD	-2.04	105.50	109.45
2	C	760[A]	HDD	CMC-C2C-C3C	2.03	128.75	124.68
3	A	761[B]	HDE	CMC-C2C-C3C	2.01	128.73	124.94
2	D	760[A]	HDD	OND-C2D-CMD	-2.01	105.57	109.45

There are no chirality outliers.

All (32) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	761[B]	HDE	C2B-C3B-CAB-CBB
3	A	761[B]	HDE	C4B-C3B-CAB-CBB
3	A	761[B]	HDE	C2C-C3C-CAC-CBC
3	A	761[B]	HDE	C4C-C3C-CAC-CBC
3	B	761[B]	HDE	C2B-C3B-CAB-CBB
3	B	761[B]	HDE	C4B-C3B-CAB-CBB
3	B	761[B]	HDE	C2C-C3C-CAC-CBC
3	B	761[B]	HDE	C4C-C3C-CAC-CBC
3	C	761[B]	HDE	C2B-C3B-CAB-CBB
3	C	761[B]	HDE	C4B-C3B-CAB-CBB
3	C	761[B]	HDE	C2C-C3C-CAC-CBC
3	C	761[B]	HDE	C4C-C3C-CAC-CBC
3	D	761[B]	HDE	C2B-C3B-CAB-CBB
3	D	761[B]	HDE	C4B-C3B-CAB-CBB
3	D	761[B]	HDE	C2C-C3C-CAC-CBC
3	D	761[B]	HDE	C4C-C3C-CAC-CBC
2	D	760[A]	HDD	CAA-CBA-CGA-O2A
2	A	760[A]	HDD	CAA-CBA-CGA-O1A
3	A	761[B]	HDE	CAD-CBD-CGD-O2D
2	C	760[A]	HDD	CAA-CBA-CGA-O1A
2	D	760[A]	HDD	CAA-CBA-CGA-O1A
3	C	761[B]	HDE	CAD-CBD-CGD-O2D
3	D	761[B]	HDE	CAD-CBD-CGD-O2D
2	A	760[A]	HDD	CAA-CBA-CGA-O2A
3	D	761[B]	HDE	CAD-CBD-CGD-O1D
2	B	760[A]	HDD	CAA-CBA-CGA-O1A
3	A	761[B]	HDE	CAD-CBD-CGD-O1D
2	C	760[A]	HDD	CAA-CBA-CGA-O2A
3	C	761[B]	HDE	CAD-CBD-CGD-O1D
3	B	761[B]	HDE	CAD-CBD-CGD-O2D
2	B	760[A]	HDD	CAA-CBA-CGA-O2A
3	B	761[B]	HDE	CAD-CBD-CGD-O1D

There are no ring outliers.

8 monomers are involved in 65 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	761[B]	HDE	11	0
2	A	760[A]	HDD	3	0
3	A	761[B]	HDE	11	0
2	B	760[A]	HDD	10	0

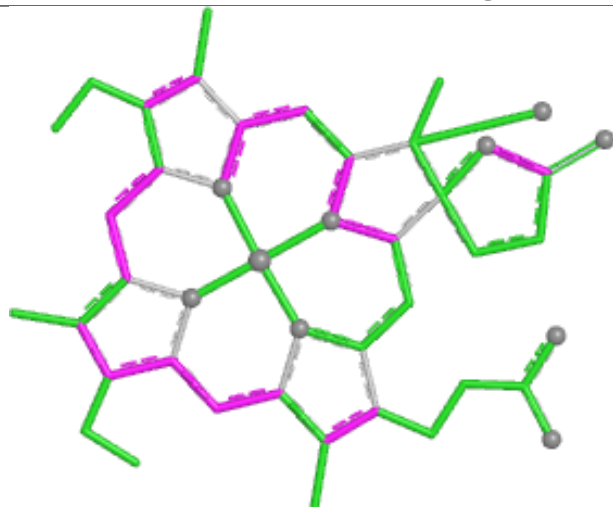
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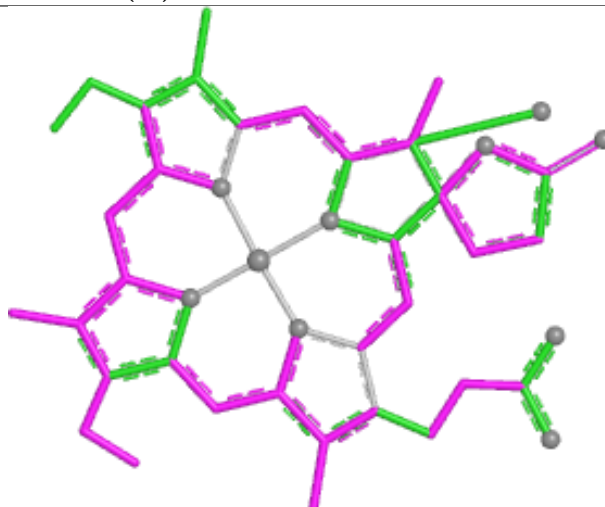
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	D	761[B]	HDE	8	0
2	D	760[A]	HDD	5	0
3	B	761[B]	HDE	13	0
2	C	760[A]	HDD	4	0

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.

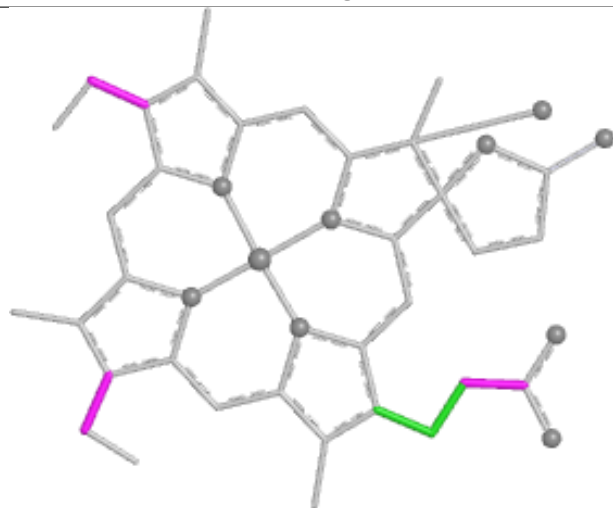
Ligand HDE C 761 (B)



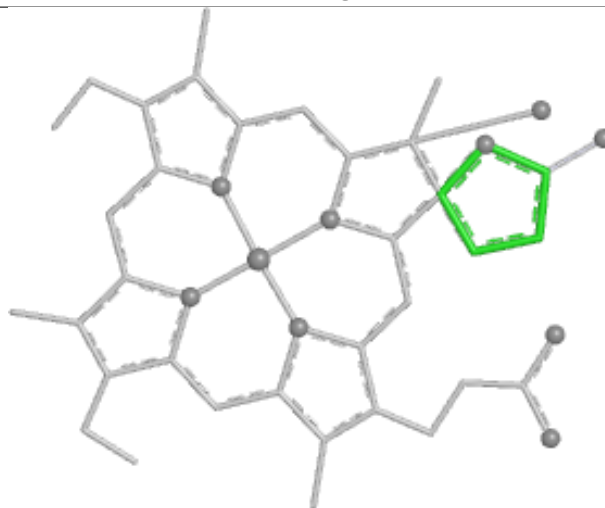
Bond lengths



Bond angles

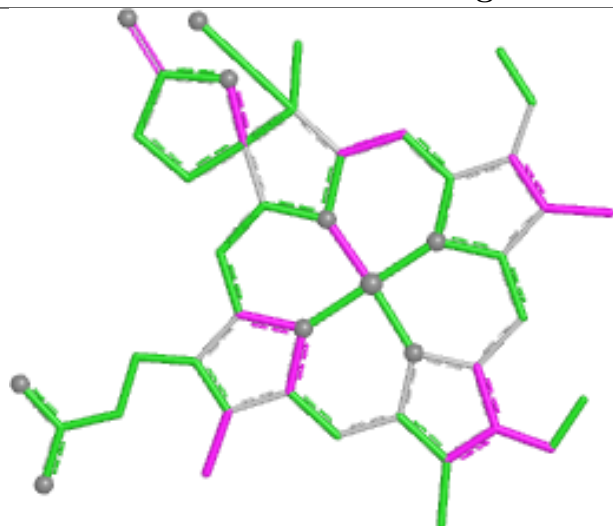


Torsions

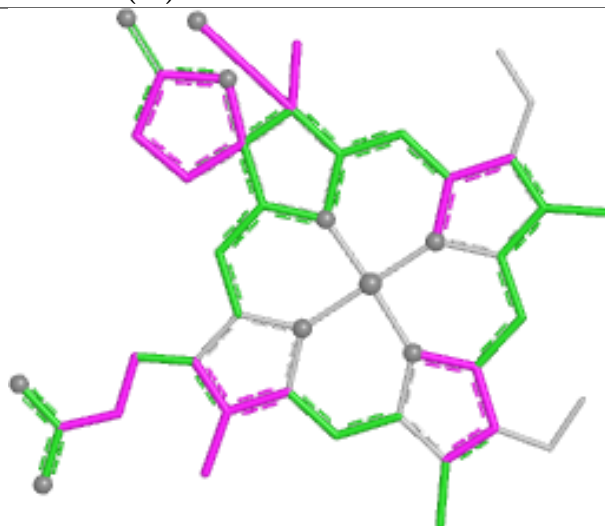


Rings

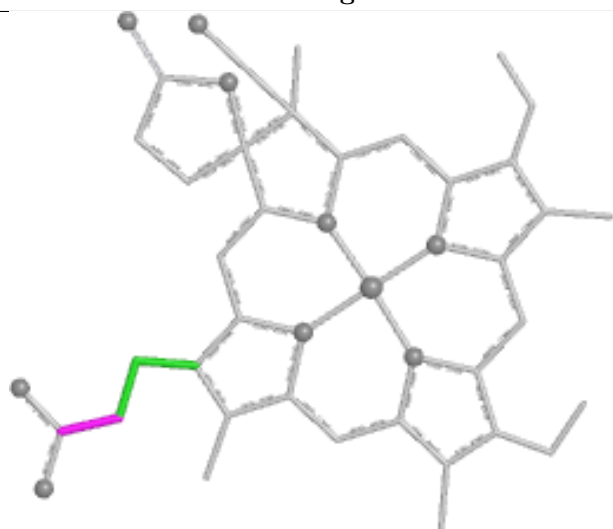
Ligand HDD A 760 (A)



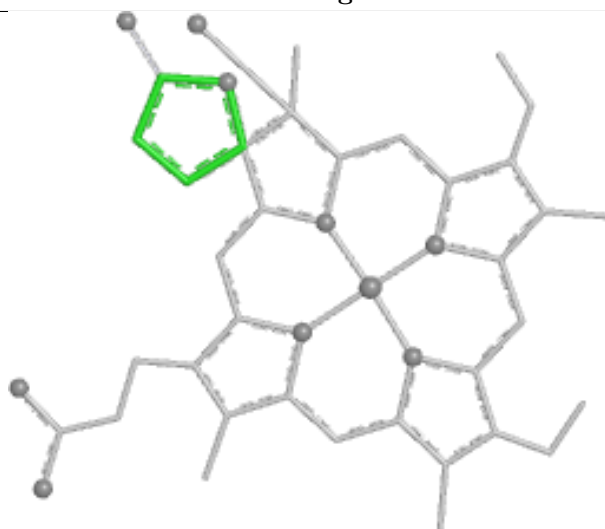
Bond lengths



Bond angles

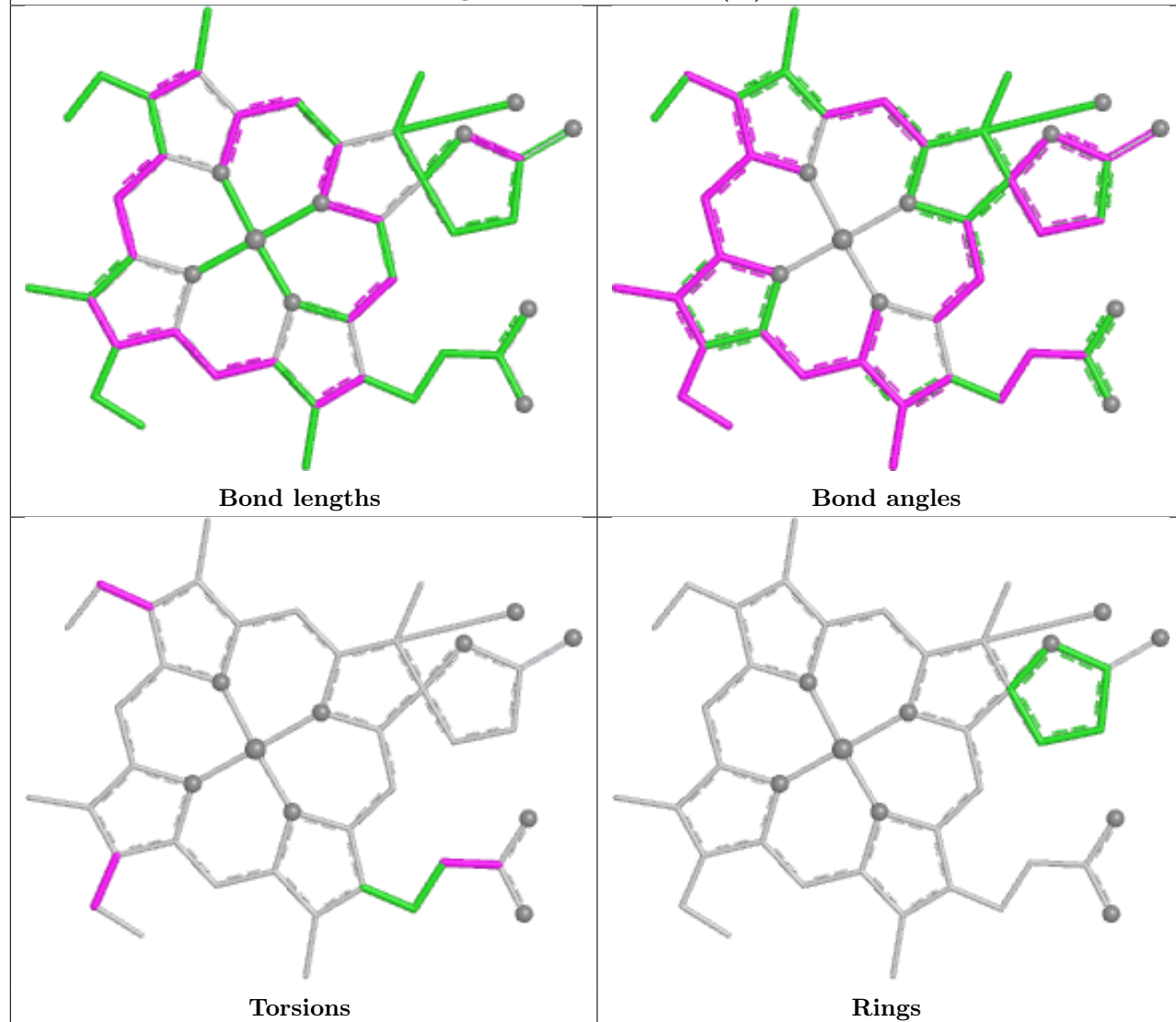


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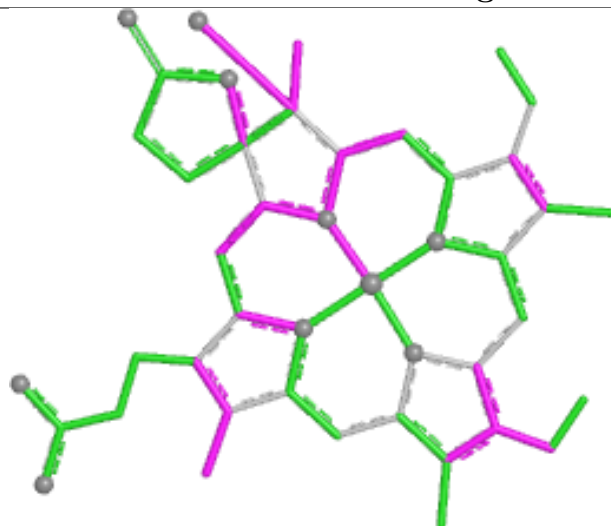


Rings

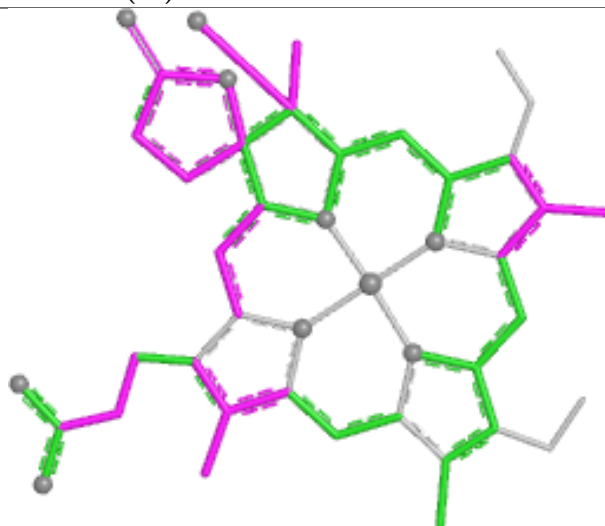
Ligand HDE A 761 (B)



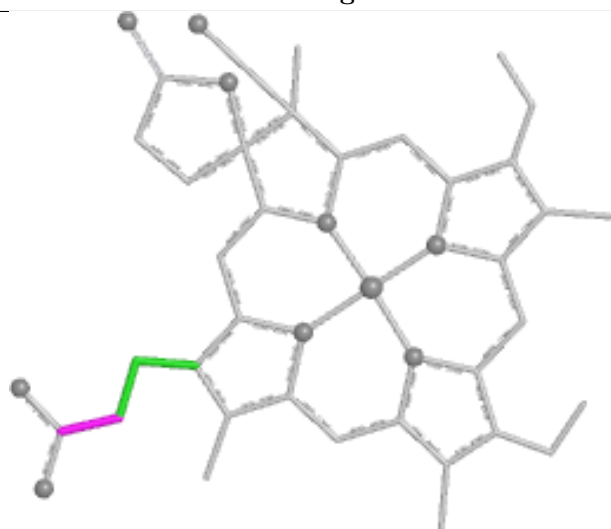
Ligand HDD B 760 (A)



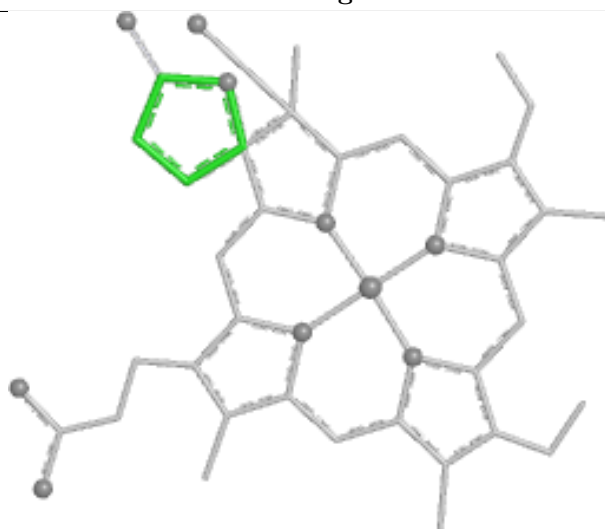
Bond lengths



Bond angles

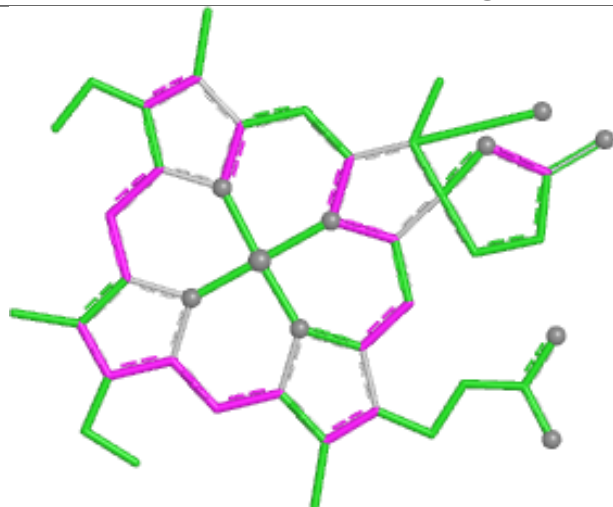


Torsions

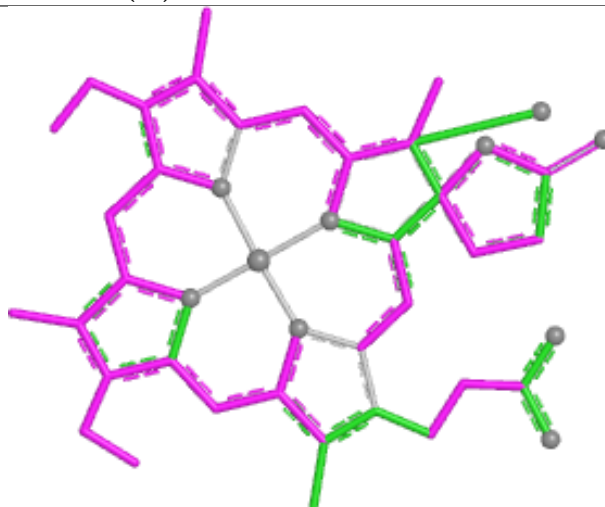


Rings

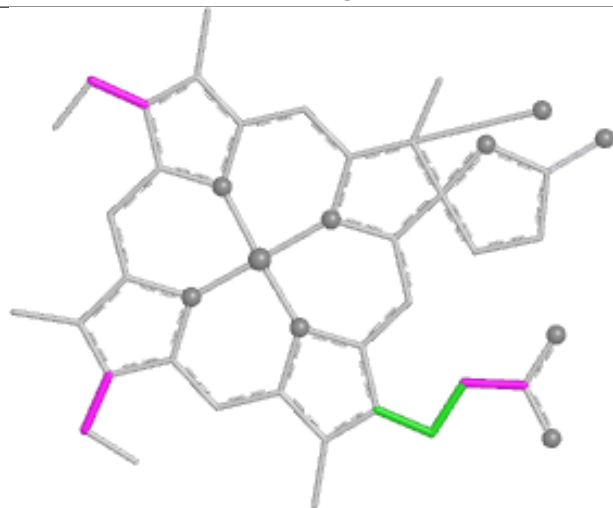
Ligand HDE D 761 (B)



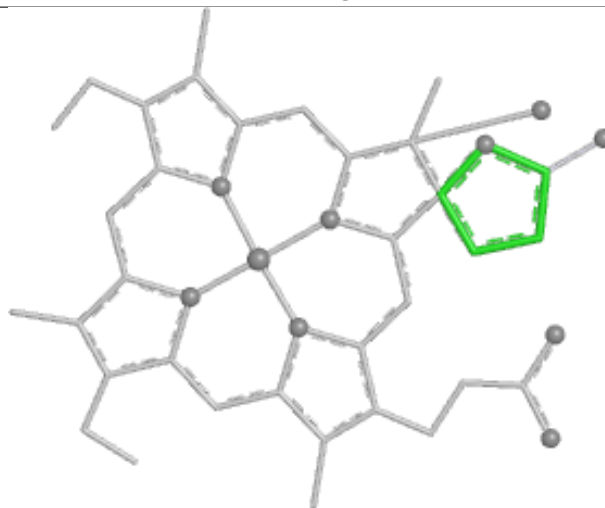
Bond lengths



Bond angles

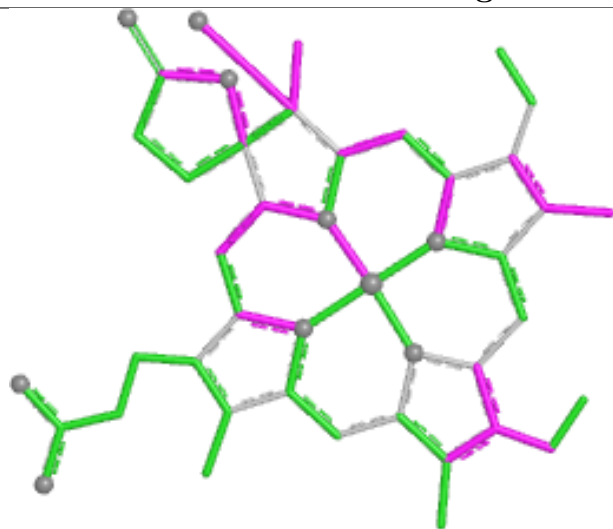


Torsions

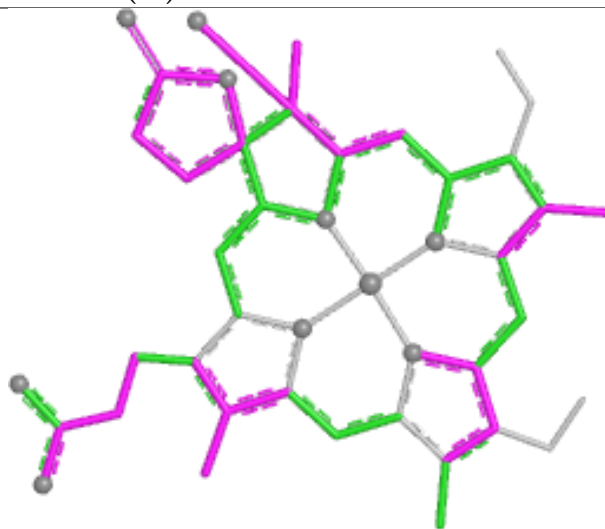


Rings

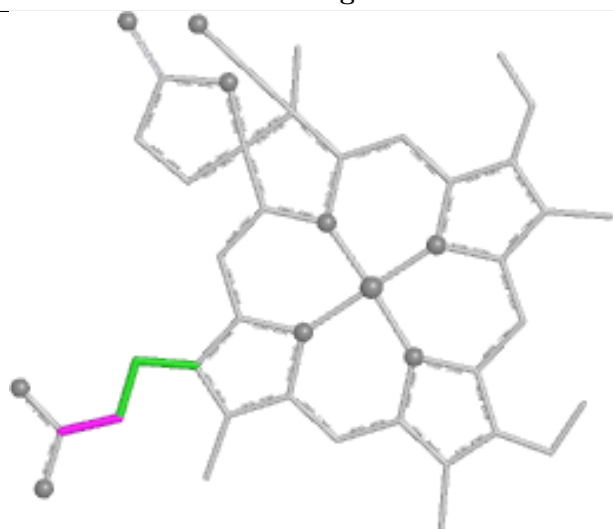
Ligand HDD D 760 (A)



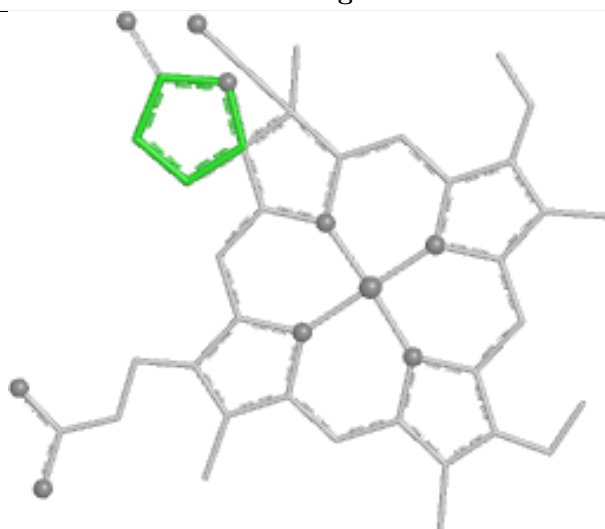
Bond lengths



Bond angles

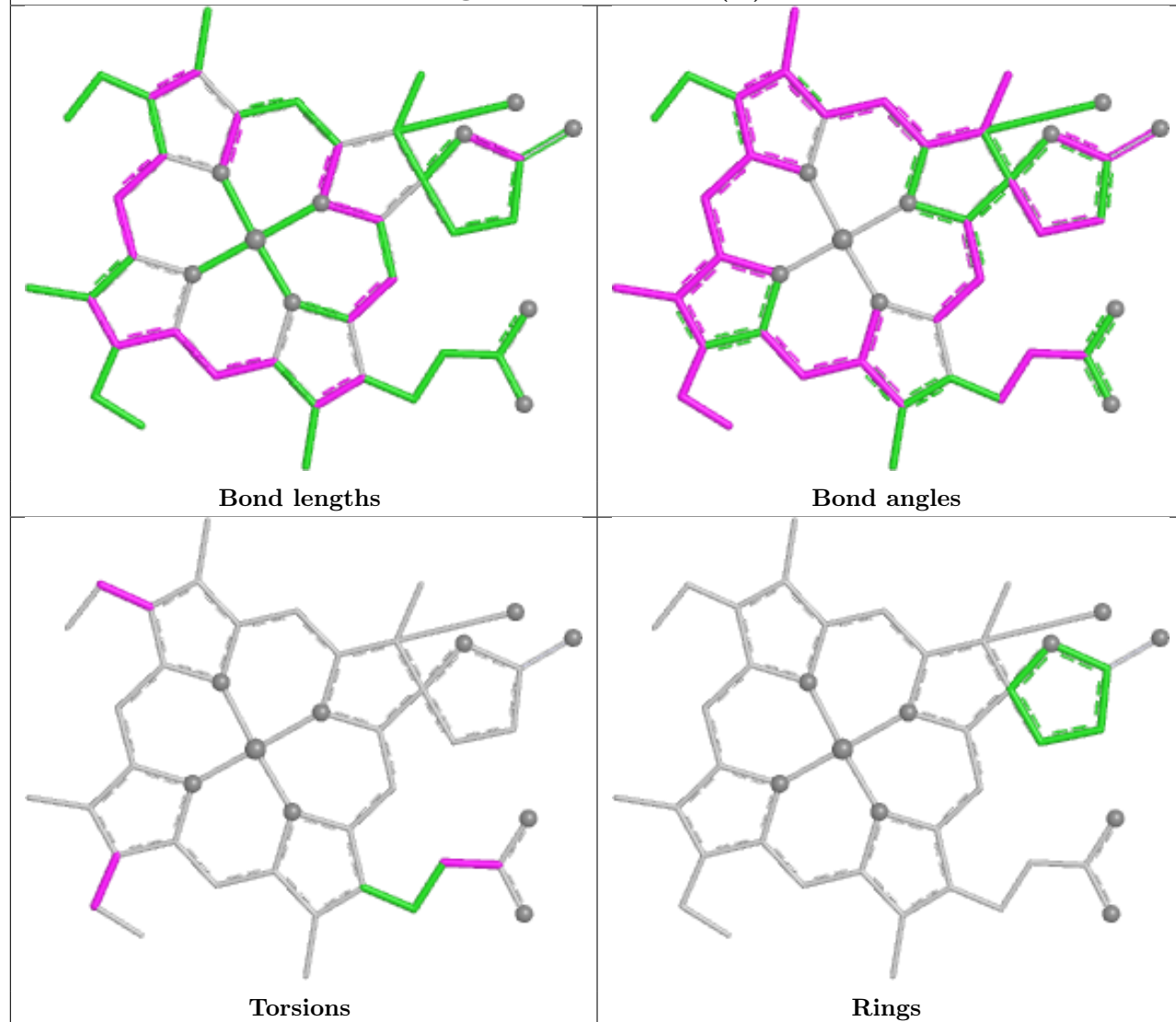


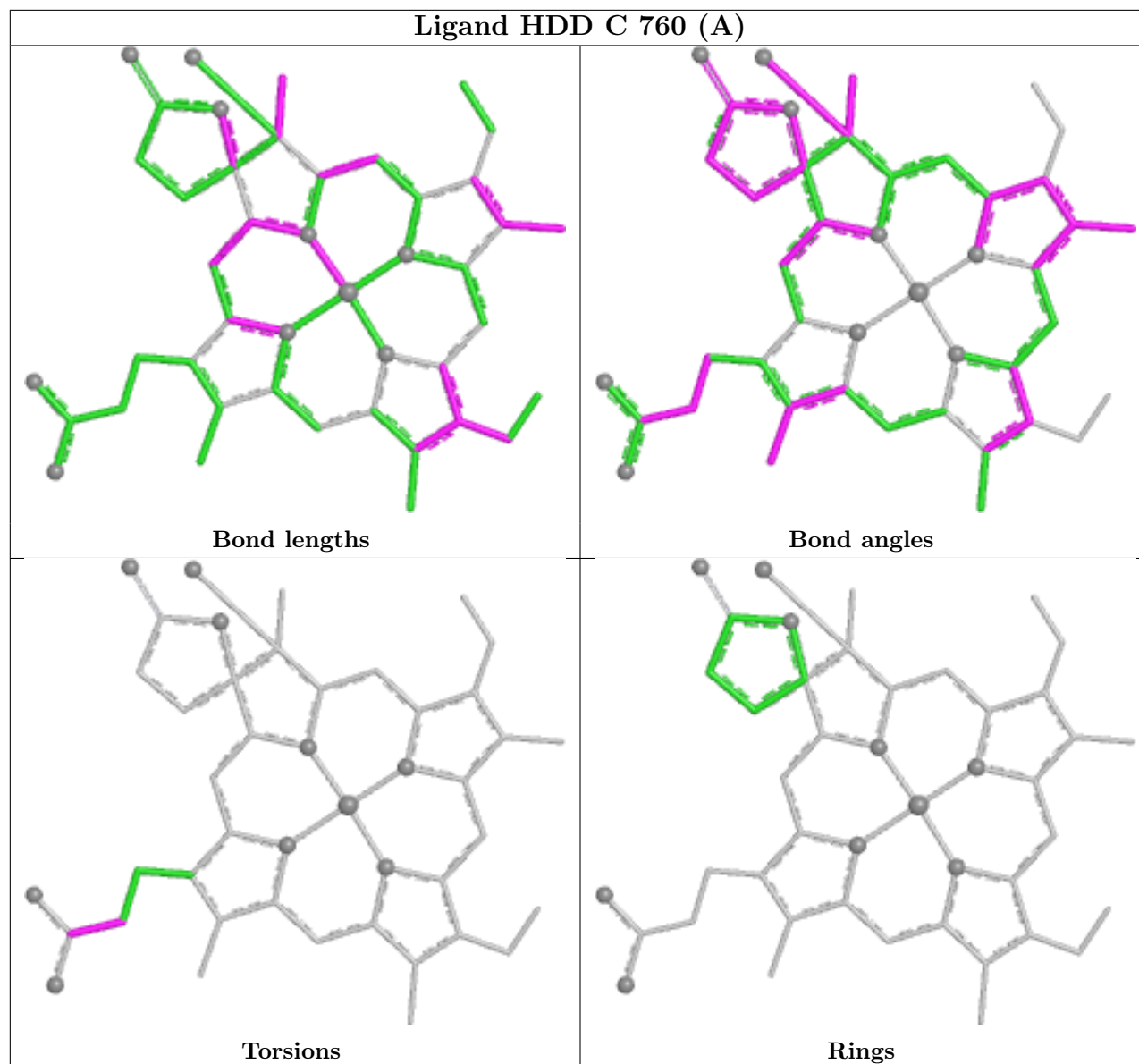
Torsions



Rings

Ligand HDE B 761 (B)





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	726/753 (96%)	-0.92	2 (0%) 90 90	3, 10, 27, 44	7 (0%)
1	B	726/753 (96%)	-0.76	1 (0%) 92 91	2, 12, 32, 45	7 (0%)
1	C	726/753 (96%)	-0.79	1 (0%) 92 91	2, 12, 31, 45	4 (0%)
1	D	726/753 (96%)	-0.90	1 (0%) 92 91	3, 10, 28, 45	10 (1%)
All	All	2904/3012 (96%)	-0.84	5 (0%) 92 91	2, 11, 30, 45	28 (0%)

All (5) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	28	SER	2.9
1	D	28	SER	2.9
1	C	750	LYS	2.2
1	B	725	ASP	2.1
1	A	713	GLN	2.1

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,

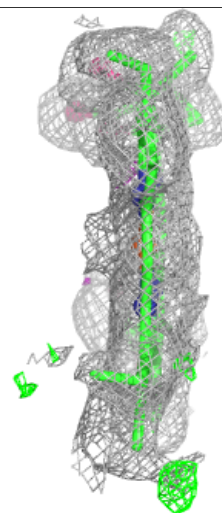
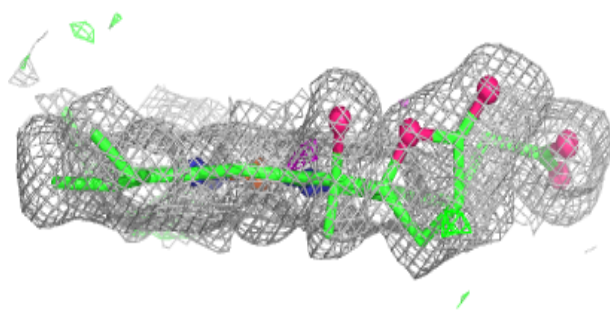
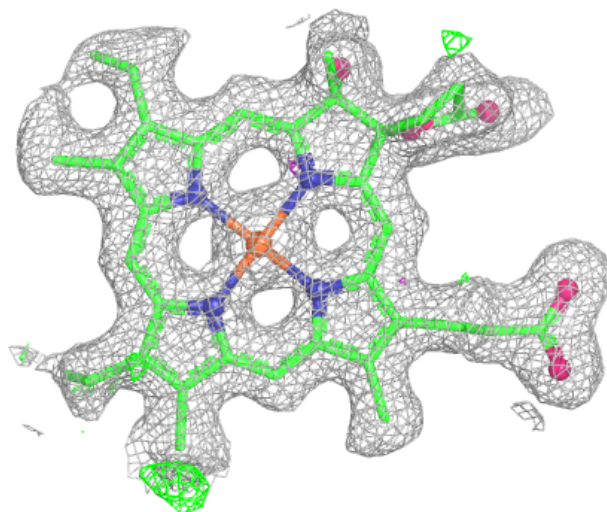
median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	H2S	D	754	1/1	0.94	0.15	25,25,25,25	1
4	H2S	C	754	1/1	0.95	0.10	19,19,19,19	1
4	H2S	A	754	1/1	0.95	0.12	29,29,29,29	1
4	H2S	B	754	1/1	0.96	0.07	20,20,20,20	1
2	HDD	A	760[A]	44/44	0.98	0.05	2,3,8,10	44
3	HDE	B	761[B]	44/44	0.98	0.06	3,9,13,15	44
3	HDE	C	761[B]	44/44	0.98	0.05	3,11,13,13	44
3	HDE	D	761[B]	44/44	0.98	0.05	2,8,13,17	44
3	HDE	A	761[B]	44/44	0.99	0.05	2,7,11,15	44
2	HDD	B	760[A]	44/44	0.99	0.05	3,4,8,8	44
2	HDD	C	760[A]	44/44	0.99	0.04	3,4,9,15	44
2	HDD	D	760[A]	44/44	0.99	0.04	2,3,7,14	44

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.

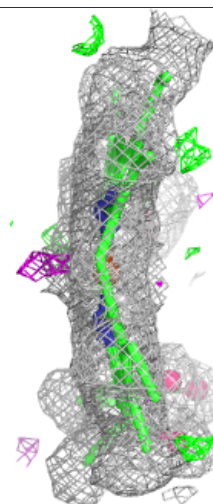
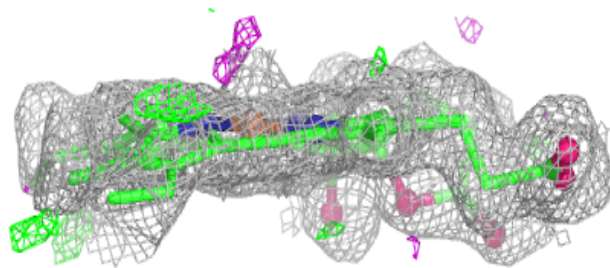
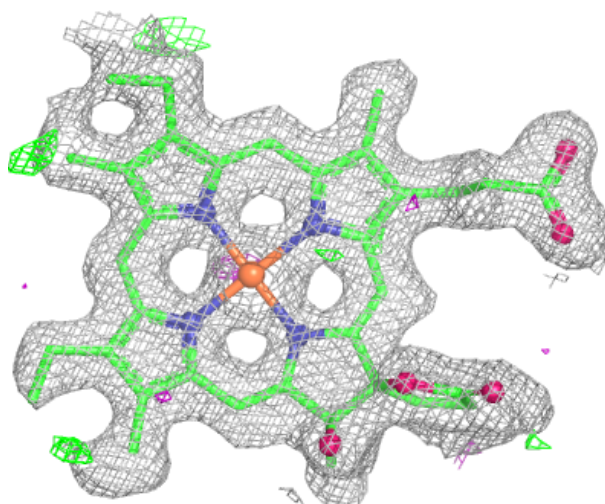
Electron density around HDD A 760 (A):

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



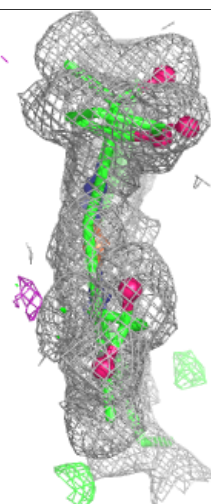
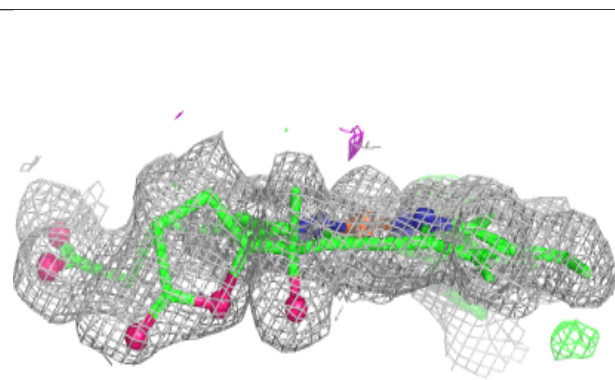
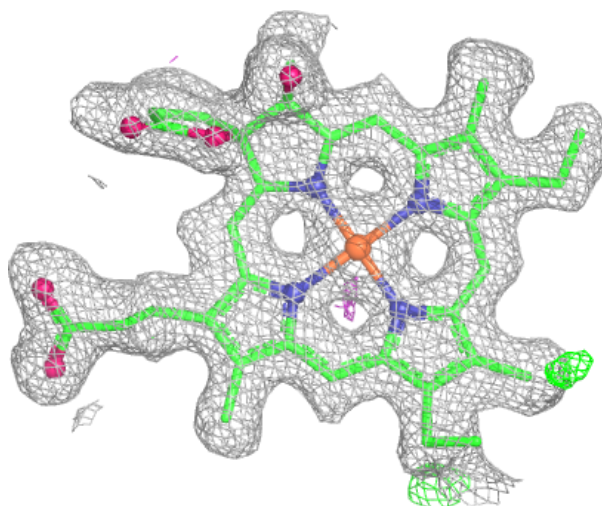
Electron density around HDE B 761 (B):

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



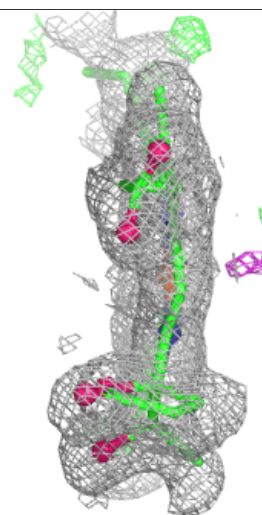
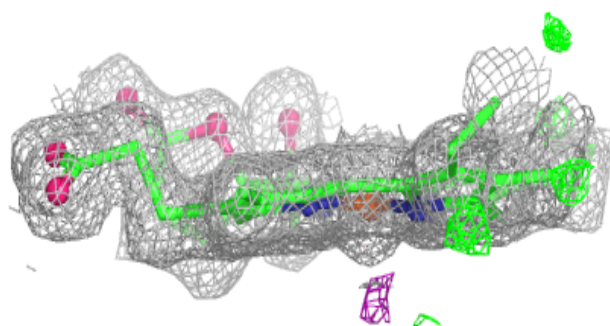
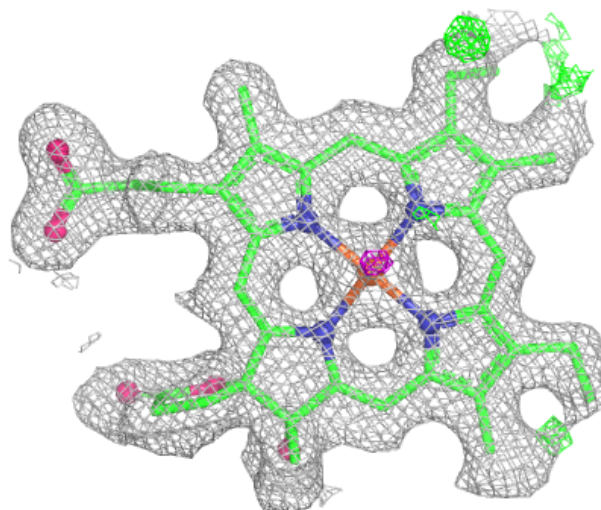
Electron density around HDE C 761 (B):

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



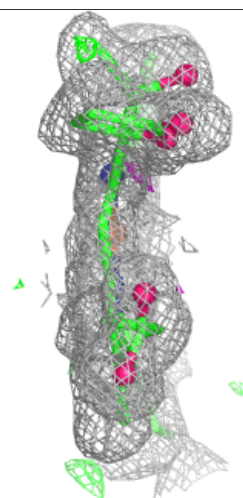
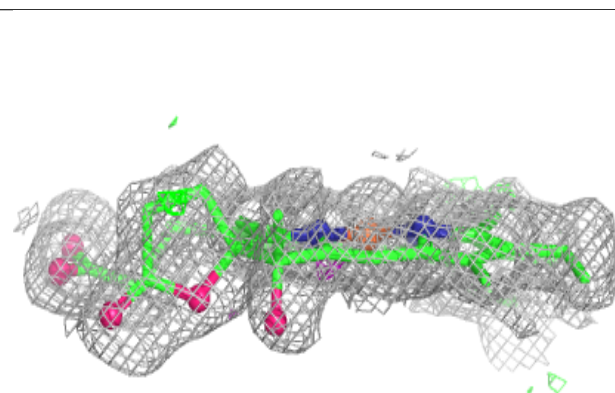
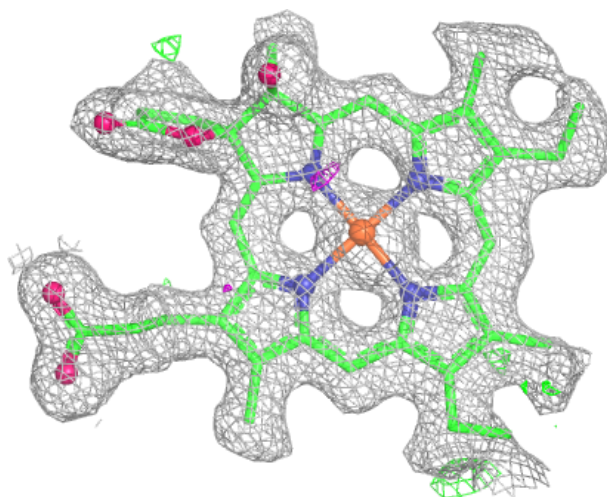
Electron density around HDE D 761 (B):

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



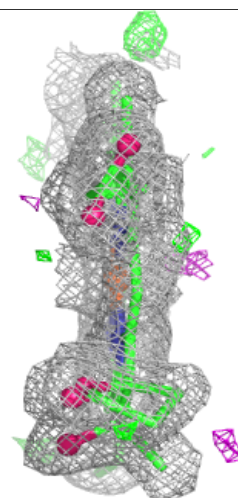
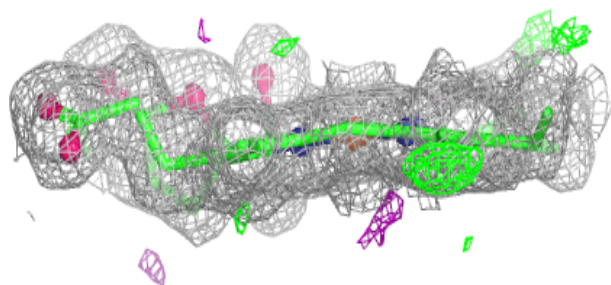
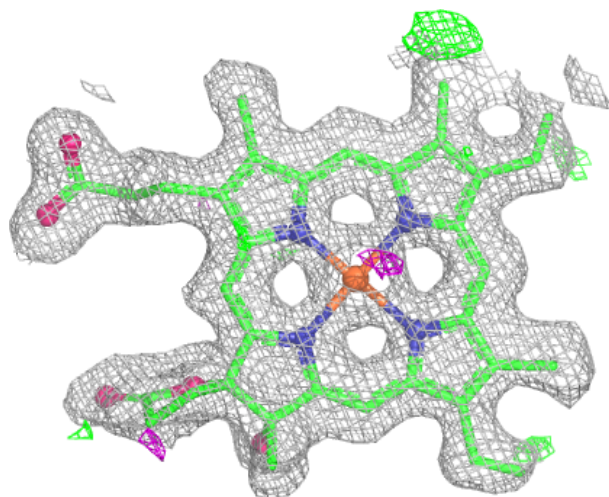
Electron density around HDE A 761 (B):

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



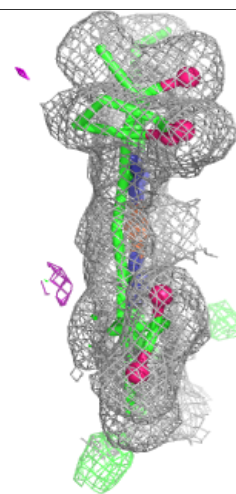
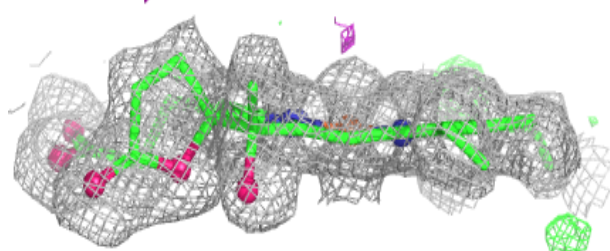
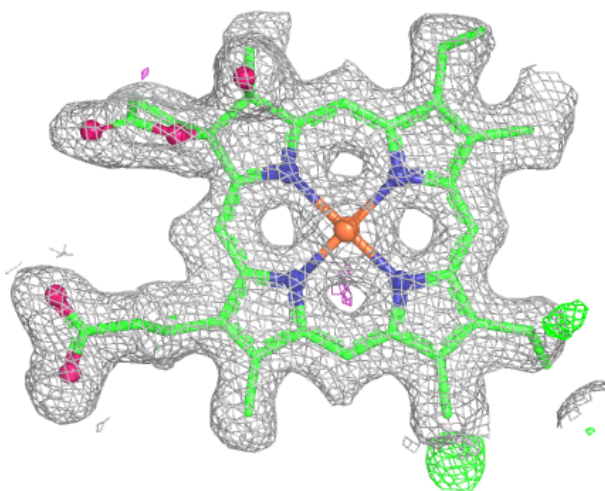
Electron density around HDD B 760 (A):

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



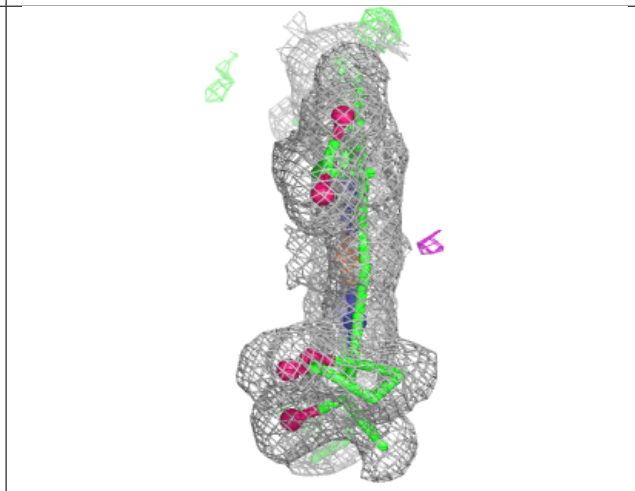
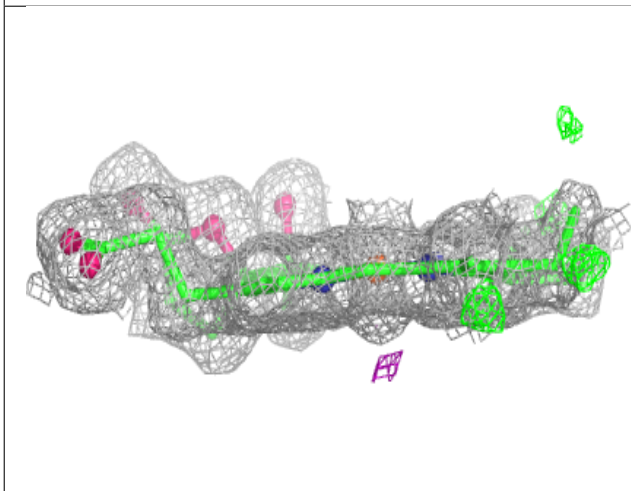
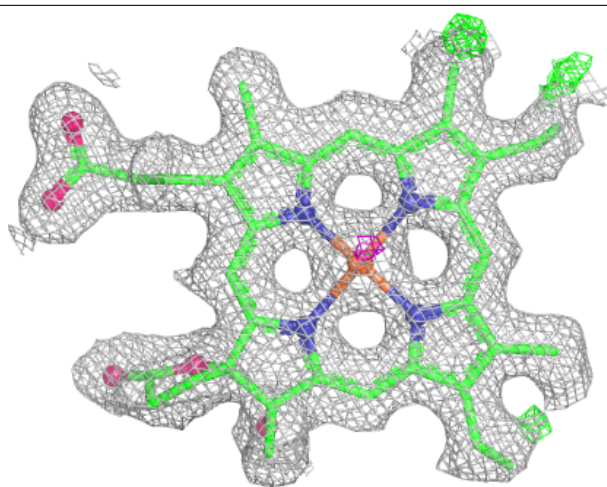
Electron density around HDD C 760 (A):

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



Electron density around HDD D 760 (A):

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



6.5 Other polymers [i](#)

There are no such residues in this entry.