



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 12:22 AM UTC

PDB ID : 1EZV / pdb_00001ezv
Title : STRUCTURE OF THE YEAST CYTOCHROME BC1 COMPLEX CO-CRYSTALLIZED WITH AN ANTIBODY FV-FRAGMENT
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Deposited on : 2000-05-12
Resolution : 2.30 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 Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

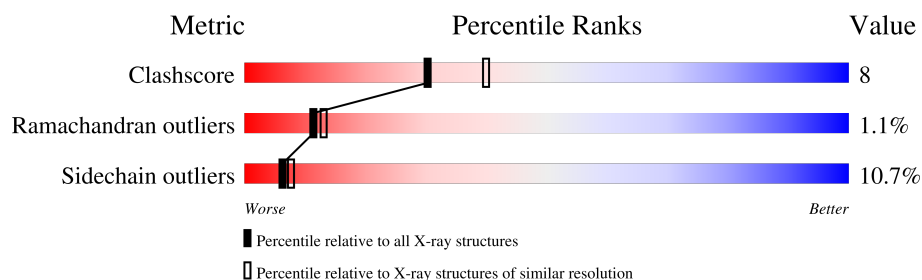
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	190562	6919 (2.30-2.30)
Ramachandran outliers	187476	6854 (2.30-2.30)
Sidechain outliers	187428	6854 (2.30-2.30)

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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	430	71% 25% . .
2	B	352	60% 34% 6%
3	C	385	84% 15% .
4	D	245	84% 14% .
5	E	185	81% 17% .
6	H	74	77% 18% 5%
7	F	125	80% 16% .
8	G	93	76% 20% .

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Mol	Chain	Length	Quality of chain
9	I	55	 84% 15% •
10	X	127	 74% 21% 5% •
11	Y	107	 67% 31% •

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
13	SMA	C	505	X	-	-	-

2 Entry composition

There are 17 unique types of molecules in this entry. The entry contains 17781 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 UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX CORE PROTEIN I.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	430	Total	C	N	O	S	0	0	0
			3338	2106	575	651	6			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	SER	deletion	UNP P07256
A	152	ASP	GLU	conflict	UNP P07256

- Molecule 2 is a protein called UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX CORE PROTEIN 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	352	Total	C	N	O	S	0	0	0
			2735	1747	453	534	1			

- Molecule 3 is a protein called CYTOCHROME B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	385	Total	C	N	O	S	0	0	0
			3089	2080	484	504	21			

- Molecule 4 is a protein called CYTOCHROME C1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	245	Total	C	N	O	S	0	0	0
			1934	1232	333	360	9			

- Molecule 5 is a protein called UBIQUINOL-CYTOCHROME C REDUCTASE IRON-SULFUR SUBUNIT.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	E	185	Total	C	N	O	S	0	0	0
			1411	893	242	266	10			

- Molecule 6 is a protein called UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 17 KD PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	H	74	Total	C	N	O	S	0	0	0
			624	391	108	123	2			

- Molecule 7 is a protein called UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 14 KD PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	F	125	Total	C	N	O	S	0	0	0
			1012	648	172	190	2			

- Molecule 8 is a protein called UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX UBIQUINONE-BINDING PROTEIN QP-C.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	G	93	Total	C	N	O	S	98	0	0
			773	510	131	130	2			

- Molecule 9 is a protein called UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 7.3 KD PROTEIN.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
9	I	55	Total	C	N	O	0	0	0
			449	298	75	76			

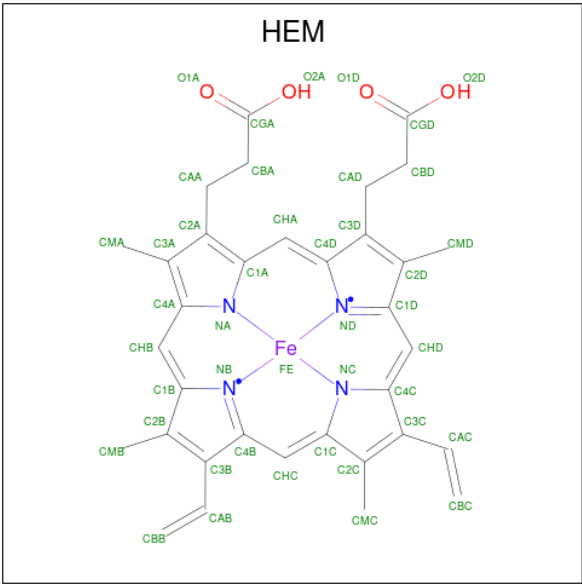
- Molecule 10 is a protein called HEAVY CHAIN (VH) OF FV-FRAGMENT.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	X	127	Total	C	N	O	S	0	0	0
			1015	644	167	201	3			

- Molecule 11 is a protein called LIGHT CHAIN (VL) OF FV-FRAGMENT.

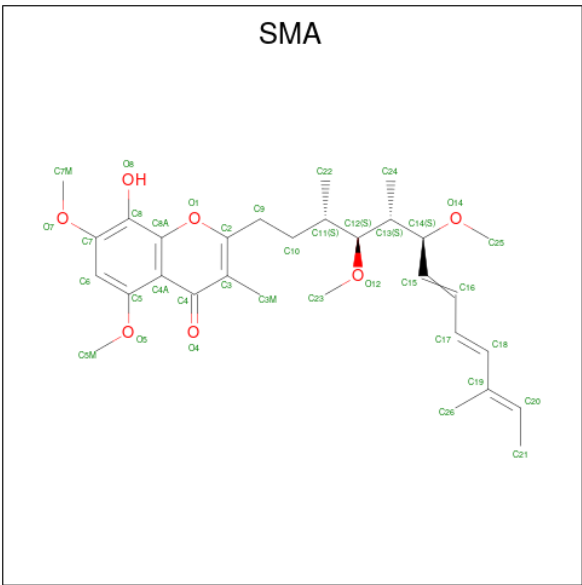
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	Y	107	Total	C	N	O	S	0	0	0
			842	536	141	163	2			

- Molecule 12 is PROTOPORPHYRIN IX CONTAINING FE (CCD ID: HEM) (formula: $C_{34}H_{32}FeN_4O_4$).



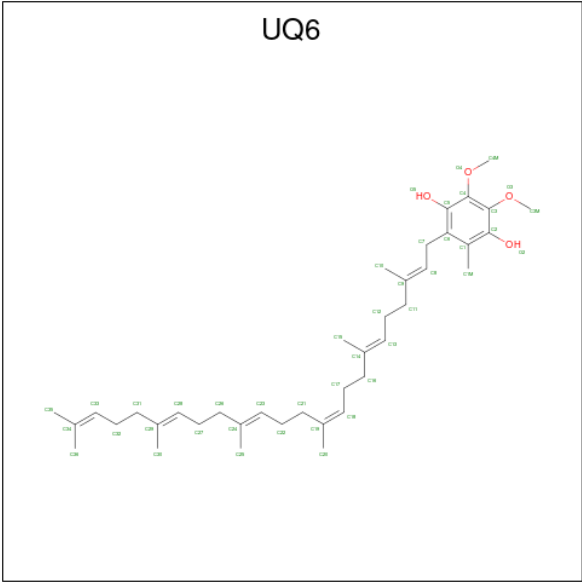
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
12	C	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
12	C	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		

- Molecule 13 is STIGMATELLIN A (CCD ID: SMA) (formula: $C_{30}H_{42}O_7$).



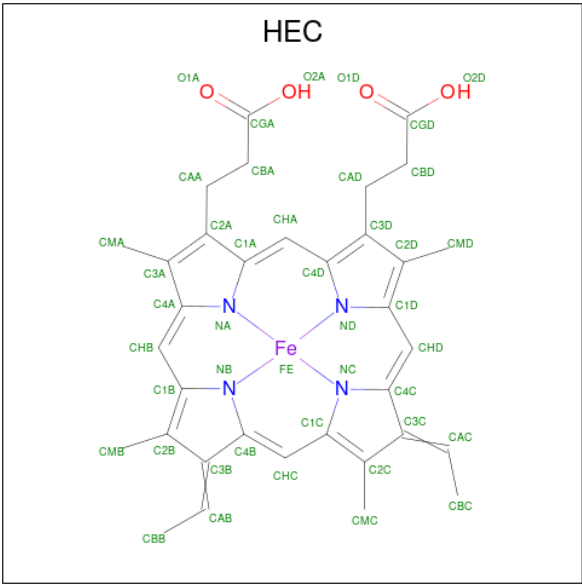
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
13	C	1	Total	C	O	0	0
			37	30	7		

- Molecule 14 is 5-(3,7,11,15,19,23-HEXAMETHYL-TETRACOSA-2,6,10,14,18,22-HEXA ENYL)-2,3-DIMETHOXY-6-METHYL-BENZENE-1,4-DIOL (CCD ID: UQ6) (formula: C₃₉H₆₀O₄).



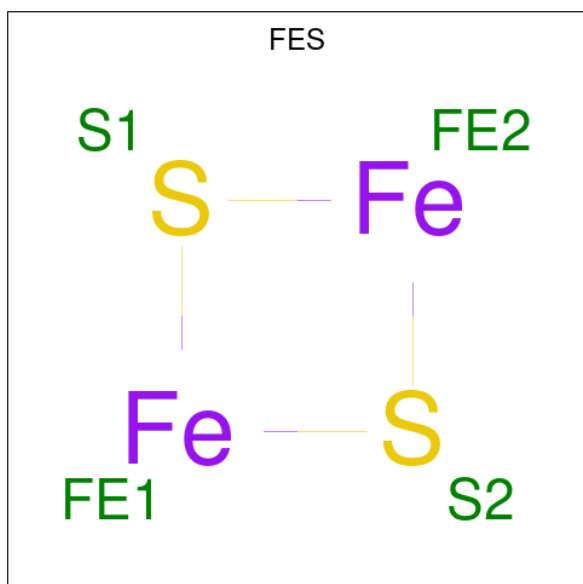
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
14	C	1	Total	C	O	0	0
			43	39	4		

- Molecule 15 is HEME C (CCD ID: HEC) (formula: C₃₄H₃₄FeN₄O₄).



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

- Molecule 16 is FE2/S2 (INORGANIC) CLUSTER (CCD ID: FES) (formula: Fe_2S_2).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
16	E	1	Total	Fe	S	0	0
			4	2	2		

- Molecule 17 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
17	A	47	Total	O	0	0
			47	47		
17	B	11	Total	O	0	0
			11	11		
17	C	114	Total	O	0	0
			114	114		
17	D	71	Total	O	0	0
			71	71		
17	E	33	Total	O	0	0
			33	33		
17	H	6	Total	O	0	0
			6	6		
17	F	36	Total	O	0	0
			36	36		
17	G	20	Total	O	0	0
			20	20		

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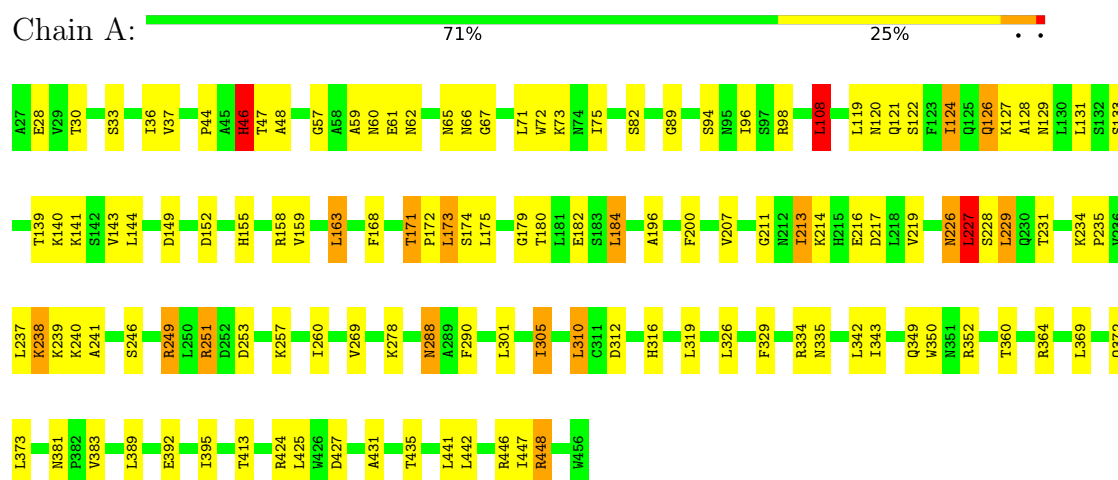
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
17	I	1	Total	O	0	0
			1	1		
17	X	5	Total	O	0	0
			5	5		
17	Y	2	Total	O	0	0
			2	2		

3 Residue-property plots

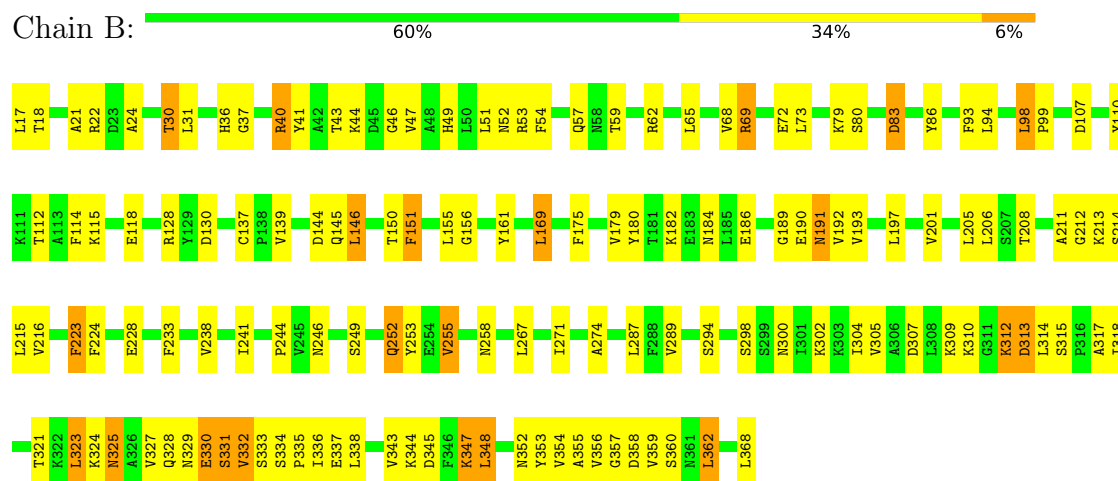
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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. 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.

Note EDS was not executed.

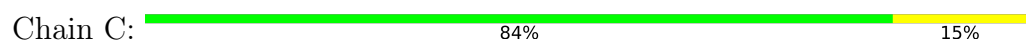
- Molecule 1: UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX CORE PROTEIN I

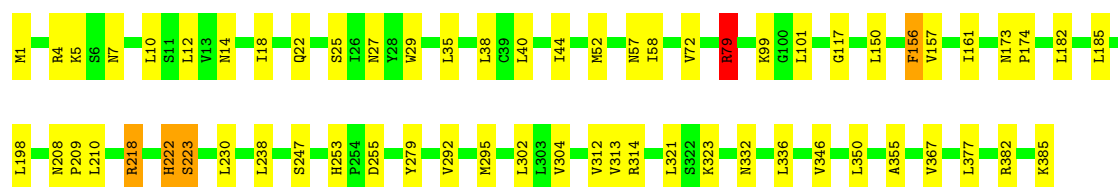


- Molecule 2: UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX CORE PROTEIN 2



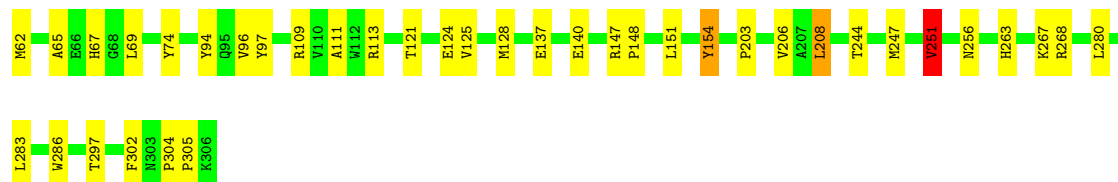
- Molecule 3: CYTOCHROME B





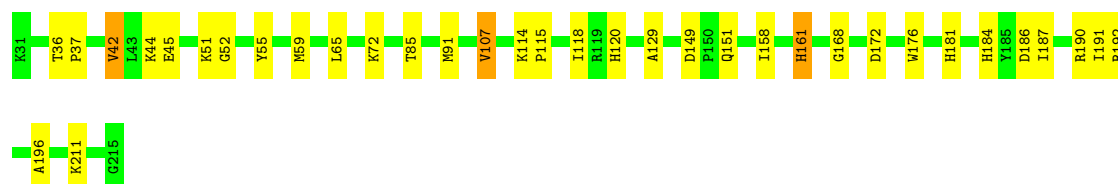
• Molecule 4: CYTOCHROME C1

Chain D: 84% 14% .



• Molecule 5: UBIQUINOL-CYTOCHROME C REDUCTASE IRON-SULFUR SUBUNIT

Chain E: 81% 17% .



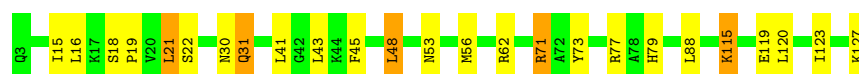
• Molecule 6: UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 17 KD PROTEIN

Chain H: 77% 18% 5% .



• Molecule 7: UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 14 KD PROTEIN

Chain F: 80% 16% .



• Molecule 8: UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX UBIQUINONE-BINDING PROTEIN QP-C

Chain G: 76% 20% .



• Molecule 9: UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 7.3 KD PROTEIN

Chain I:

84%

15%



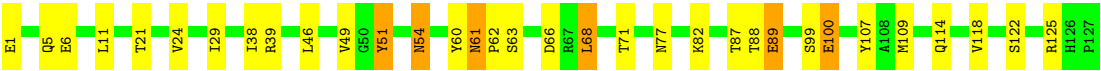
● Molecule 10: HEAVY CHAIN (VH) OF FV-FRAGMENT

Chain X:

74%

21%

5%

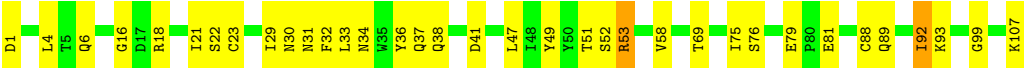


● Molecule 11: LIGHT CHAIN (VL) OF FV-FRAGMENT

Chain Y:

67%

31%



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	214.47Å 163.92Å 147.27Å 90.00° 117.50° 90.00°	Depositor
Resolution (Å)	15.00 – 2.30	Depositor
% Data completeness (in resolution range)	84.7 (15.00-2.30)	Depositor
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS	Depositor
R, R_{free}	0.222 , 0.254	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	17781	wwPDB-VP
Average B, all atoms (Å ²)	70.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: HEM, FES, UQ6, SMA, 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	0.41	0/3399	0.73	2/4606 (0.0%)
2	B	0.37	0/2781	0.74	0/3764
3	C	0.55	1/3191 (0.0%)	0.81	0/4353
4	D	0.42	0/1994	0.77	1/2714 (0.0%)
5	E	0.47	1/1444 (0.1%)	0.83	4/1957 (0.2%)
6	H	0.35	0/638	0.70	0/858
7	F	0.42	0/1032	0.75	0/1397
8	G	0.40	0/804	0.71	0/1088
9	I	0.40	0/462	0.74	0/622
10	X	0.37	0/1043	0.72	0/1422
11	Y	0.38	0/863	0.70	0/1172
All	All	0.43	2/17651 (0.0%)	0.76	7/23953 (0.0%)

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	A	0	4
2	B	0	2
3	C	0	5
4	D	0	4
5	E	0	1
6	H	0	1
7	F	0	1
8	G	0	1
10	X	0	1
11	Y	0	1
All	All	0	21

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	367	VAL	CA-CB	6.71	1.57	1.54
5	E	181	HIS	CE1-NE2	5.24	1.37	1.32

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	E	181	HIS	ND1-CG-CD2	7.13	113.23	106.10
5	E	161	HIS	ND1-CG-CD2	6.81	112.91	106.10
1	A	108	LEU	CA-C-N	5.77	125.44	119.56
1	A	108	LEU	C-N-CA	5.77	125.44	119.56
4	D	251	VAL	CB-CA-C	-5.42	104.83	112.14
5	E	149	ASP	CA-C-N	5.30	124.97	119.56
5	E	149	ASP	C-N-CA	5.30	124.97	119.56

There are no chirality outliers.

All (21) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	108	LEU	Peptide
1	A	249	ARG	Sidechain
1	A	446	ARG	Sidechain
1	A	448	ARG	Sidechain
2	B	332	VAL	Peptide
2	B	69	ARG	Sidechain
3	C	218	ARG	Sidechain
3	C	222	HIS	Mainchain
3	C	279	TYR	Sidechain
3	C	314	ARG	Sidechain
3	C	79	ARG	Sidechain
4	D	109	ARG	Sidechain
4	D	154	TYR	Sidechain
4	D	94	TYR	Sidechain
4	D	97	TYR	Sidechain
5	E	192	ARG	Sidechain
7	F	71	ARG	Sidechain
8	G	40	ILE	Peptide
6	H	98	TYR	Sidechain
10	X	60	TYR	Sidechain
11	Y	79	GLU	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	3338	0	3316	67	0
2	B	2735	0	2774	79	0
3	C	3089	0	3125	34	0
4	D	1934	0	1855	18	0
5	E	1411	0	1386	22	0
6	H	624	0	581	9	0
7	F	1012	0	1026	14	0
8	G	773	0	736	8	0
9	I	449	0	445	7	0
10	X	1015	0	959	22	0
11	Y	842	0	820	16	0
12	C	86	0	60	3	0
13	C	37	0	40	7	0
14	C	43	0	58	15	0
15	D	43	0	30	0	0
16	E	4	0	0	0	0
17	A	47	0	0	1	0
17	B	11	0	0	0	0
17	C	114	0	0	1	0
17	D	71	0	0	0	0
17	E	33	0	0	0	0
17	F	36	0	0	2	0
17	G	20	0	0	1	0
17	H	6	0	0	0	0
17	I	1	0	0	0	0
17	X	5	0	0	1	0
17	Y	2	0	0	0	0
All	All	17781	0	17211	290	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 8.

All (290) 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)
14:C:506:UQ6:C1M	14:C:506:UQ6:H103	1.93	0.98
14:C:506:UQ6:H103	14:C:506:UQ6:H1M3	1.46	0.95
6:H:77:GLN:HE21	6:H:77:GLN:H	1.11	0.91
2:B:347:LYS:H	2:B:347:LYS:HD3	1.43	0.82
1:A:316:HIS:HE1	1:A:350:TRP:HE1	1.29	0.81
2:B:182:LYS:HB2	2:B:211:ALA:HB2	1.64	0.80
3:C:7:ASN:HD22	3:C:10:LEU:H	1.31	0.77
3:C:40:LEU:HD23	14:C:506:UQ6:H18	1.67	0.76
3:C:253:HIS:HD2	3:C:255:ASP:H	1.34	0.76
1:A:108:LEU:HB2	2:B:323:LEU:HD22	1.68	0.76
7:F:31:GLN:HA	7:F:31:GLN:HE21	1.51	0.74
5:E:107:VAL:HG12	5:E:118:ILE:HB	1.68	0.74
10:X:6:GLU:H	10:X:114:GLN:HE21	1.38	0.71
14:C:506:UQ6:H103	14:C:506:UQ6:H1M2	1.71	0.71
3:C:58:ILE:H	3:C:173:ASN:HD22	1.38	0.70
6:H:78:LEU:HD13	6:H:142:LEU:HD22	1.71	0.70
7:F:77:ARG:HD3	7:F:88:LEU:HD11	1.74	0.70
5:E:115:PRO:HD2	5:E:158:ILE:HD11	1.73	0.69
5:E:72:LYS:NZ	9:I:29:GLN:HE22	1.90	0.69
7:F:77:ARG:HD2	17:F:155:HOH:O	1.93	0.69
5:E:44:LYS:NZ	5:E:52:GLY:H	1.91	0.69
10:X:38:ILE:HD12	10:X:46:LEU:HD22	1.75	0.68
1:A:349:GLN:HE22	1:A:352:ARG:HH21	1.41	0.68
1:A:73:LYS:HG3	1:A:94:SER:HB3	1.76	0.68
2:B:325:ASN:HD22	2:B:328:GLN:HE22	1.43	0.67
6:H:77:GLN:HE21	6:H:77:GLN:N	1.91	0.67
2:B:49:HIS:HD2	2:B:161:TYR:H	1.43	0.67
6:H:91:GLY:O	6:H:95:VAL:HG13	1.95	0.66
1:A:155:HIS:HD2	1:A:158:ARG:HH21	1.44	0.66
1:A:257:LYS:HG2	1:A:334:ARG:HG3	1.78	0.66
2:B:258:ASN:HD21	2:B:324:LYS:HG2	1.61	0.66
1:A:120:ASN:HD21	1:A:124:ILE:HD12	1.60	0.65
1:A:98:ARG:HD3	1:A:173:LEU:HD12	1.76	0.65
3:C:22:GLN:HE22	14:C:506:UQ6:H3M3	1.60	0.65
1:A:66:ASN:HD22	1:A:180:THR:HG23	1.62	0.65
5:E:72:LYS:HZ3	9:I:29:GLN:HE22	1.45	0.64
3:C:346:VAL:HG23	17:G:103:HOH:O	1.97	0.64
3:C:218:ARG:HG3	8:G:16:MET:HE3	1.80	0.63
2:B:65:LEU:O	2:B:69:ARG:HG2	1.97	0.63
1:A:216:GLU:HA	1:A:219:VAL:HG12	1.80	0.63
2:B:313:ASP:HB3	2:B:344:LYS:O	1.98	0.63
5:E:44:LYS:HB3	8:G:35:LYS:HA	1.81	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:147:ARG:HG2	4:D:148:PRO:O	1.99	0.62
1:A:62:ASN:HB2	1:A:65:ASN:ND2	2.15	0.62
11:Y:4:LEU:HD22	11:Y:88:CYS:SG	2.40	0.61
2:B:49:HIS:CD2	2:B:161:TYR:H	2.18	0.61
11:Y:29:ILE:HG22	11:Y:92:ILE:HD12	1.81	0.61
4:D:62:MET:HB3	4:D:67:HIS:NE2	2.16	0.60
2:B:255:VAL:HB	2:B:321:THR:HG21	1.84	0.59
3:C:52:MET:HE1	14:C:506:UQ6:H352	1.83	0.59
1:A:72:TRP:CE3	1:A:75:ILE:HD11	2.37	0.59
2:B:150:THR:HG22	2:B:352:ASN:ND2	2.18	0.59
5:E:168:GLY:HA2	5:E:176:TRP:CD1	2.38	0.59
10:X:54:ASN:HD22	10:X:54:ASN:H	1.50	0.59
8:G:52:PHE:O	8:G:56:PHE:HB3	2.02	0.59
1:A:305:ILE:HA	1:A:310:LEU:HD22	1.84	0.59
4:D:113:ARG:HG2	4:D:151:LEU:O	2.03	0.58
1:A:288:ASN:C	1:A:288:ASN:HD22	2.11	0.58
10:X:29:ILE:H	10:X:77:ASN:HD21	1.49	0.58
2:B:315:SER:HB3	2:B:344:LYS:HB2	1.87	0.57
3:C:58:ILE:H	3:C:173:ASN:ND2	2.03	0.57
3:C:157:VAL:O	3:C:161:ILE:HG12	2.05	0.57
2:B:246:ASN:HB2	2:B:249:SER:HB3	1.86	0.57
2:B:155:LEU:H	2:B:155:LEU:HD12	1.70	0.57
5:E:72:LYS:HZ2	9:I:29:GLN:NE2	2.03	0.57
11:Y:34:ASN:HD22	11:Y:49:TYR:HA	1.69	0.57
2:B:317:ALA:O	2:B:321:THR:HG22	2.05	0.56
5:E:72:LYS:NZ	9:I:29:GLN:NE2	2.52	0.56
8:G:56:PHE:O	8:G:60:LEU:HB2	2.05	0.56
10:X:38:ILE:HA	10:X:49:VAL:HG23	1.87	0.56
1:A:62:ASN:HB2	1:A:65:ASN:HD22	1.68	0.56
7:F:43:LEU:HD13	7:F:48:LEU:HD11	1.88	0.56
5:E:172:ASP:H	5:E:184:HIS:HD2	1.53	0.56
11:Y:32:PHE:HB2	11:Y:92:ILE:HG22	1.87	0.56
1:A:66:ASN:ND2	1:A:179:GLY:HA2	2.21	0.56
4:D:203:PRO:HG2	4:D:206:VAL:HG21	1.88	0.56
2:B:238:VAL:HG13	2:B:356:VAL:HB	1.88	0.55
1:A:301:LEU:HB2	1:A:349:GLN:HG3	1.89	0.55
3:C:57:ASN:HA	3:C:173:ASN:HD21	1.71	0.55
11:Y:36:TYR:HE2	11:Y:89:GLN:HG2	1.72	0.55
2:B:325:ASN:HA	2:B:328:GLN:NE2	2.22	0.55
2:B:228:GLU:HA	2:B:353:TYR:O	2.06	0.55
7:F:15:ILE:HG23	7:F:21:LEU:HB3	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:24:ALA:HB3	2:B:191:ASN:ND2	2.23	0.54
4:D:121:THR:OG1	4:D:124:GLU:HG3	2.08	0.54
5:E:172:ASP:H	5:E:184:HIS:CD2	2.25	0.54
2:B:300:ASN:O	2:B:304:ILE:HG12	2.08	0.54
2:B:305:VAL:O	2:B:309:LYS:HB2	2.08	0.53
4:D:96:VAL:HB	4:D:251:VAL:HG13	1.91	0.53
4:D:247:MET:O	4:D:251:VAL:HG22	2.08	0.53
4:D:297:THR:HG21	5:E:42:VAL:HG11	1.89	0.53
11:Y:6:GLN:HG2	11:Y:23:CYS:SG	2.49	0.53
5:E:44:LYS:HZ2	5:E:52:GLY:H	1.54	0.53
5:E:55:TYR:O	5:E:59:MET:HG2	2.08	0.53
3:C:1:MET:N	17:C:585:HOH:O	2.42	0.53
14:C:506:UQ6:H1M3	14:C:506:UQ6:C10	2.29	0.52
11:Y:31:ASN:HD22	11:Y:51:THR:CG2	2.23	0.52
1:A:214:LYS:HB2	1:A:217:ASP:HB2	1.92	0.52
3:C:44:ILE:HD12	14:C:506:UQ6:C20	2.39	0.52
1:A:47:THR:HG21	2:B:327:VAL:HG12	1.92	0.52
1:A:71:LEU:HD13	1:A:143:VAL:HG21	1.90	0.52
3:C:295:MET:HE3	13:C:505:SMA:C23	2.40	0.51
1:A:67:GLY:HA3	1:A:184:LEU:CD1	2.40	0.51
10:X:24:VAL:HG21	10:X:29:ILE:HD11	1.92	0.51
10:X:61:ASN:HD22	10:X:63:SER:H	1.56	0.51
2:B:294:SER:HB3	2:B:358:ASP:HB3	1.93	0.51
2:B:252:GLN:HG3	2:B:253:TYR:N	2.25	0.51
2:B:347:LYS:HG2	2:B:348:LEU:N	2.26	0.51
2:B:68:VAL:O	2:B:72:GLU:HG3	2.10	0.51
7:F:53:ASN:ND2	7:F:56:MET:H	2.09	0.51
2:B:115:LYS:HB2	2:B:118:GLU:HG3	1.93	0.51
3:C:25:SER:OG	7:F:79:HIS:HD2	1.94	0.51
1:A:413:THR:HB	17:A:480:HOH:O	2.11	0.50
2:B:305:VAL:HG11	2:B:368:LEU:HB3	1.93	0.50
3:C:208:ASN:HB2	3:C:209:PRO:HD2	1.93	0.50
10:X:6:GLU:H	10:X:114:GLN:NE2	2.05	0.50
1:A:269:VAL:HG21	1:A:395:ILE:HD13	1.93	0.50
1:A:316:HIS:CE1	1:A:350:TRP:HE1	2.19	0.50
2:B:44:LYS:HB2	2:B:47:VAL:HG21	1.93	0.49
3:C:208:ASN:HD22	3:C:210:LEU:H	1.59	0.49
14:C:506:UQ6:O5	14:C:506:UQ6:H4M3	2.11	0.49
1:A:171:THR:HG23	1:A:241:ALA:HA	1.93	0.49
7:F:71:ARG:NH1	17:F:148:HOH:O	2.43	0.49
11:Y:37:GLN:HB2	11:Y:47:LEU:HD11	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:57:GLY:H	1:A:60:ASN:HD22	1.61	0.49
2:B:241:ILE:HG12	2:B:287:LEU:HB3	1.94	0.49
4:D:74:TYR:CE1	6:H:139:ALA:HA	2.47	0.49
17:X:130:HOH:O	11:Y:49:TYR:HB2	2.12	0.49
10:X:61:ASN:ND2	10:X:63:SER:H	2.11	0.49
2:B:312:LYS:O	2:B:313:ASP:HB2	2.13	0.49
3:C:198:LEU:HD11	14:C:506:UQ6:H153	1.95	0.49
1:A:121:GLN:O	1:A:126:GLN:HB2	2.12	0.48
1:A:122:SER:O	1:A:127:LYS:HD3	2.13	0.48
10:X:61:ASN:HD22	10:X:62:PRO:N	2.11	0.48
3:C:18:ILE:HA	3:C:222:HIS:HB2	1.95	0.48
13:C:505:SMA:H39	13:C:505:SMA:H21	1.94	0.48
2:B:83:ASP:HB2	2:B:86:TYR:H	1.78	0.48
1:A:372:GLN:HG3	1:A:373:LEU:N	2.28	0.48
2:B:46:GLY:O	2:B:49:HIS:HB3	2.13	0.48
6:H:74:VAL:HG12	6:H:75:THR:H	1.77	0.48
10:X:87:THR:HB	10:X:89:GLU:HB2	1.96	0.47
1:A:73:LYS:HB2	1:A:96:ILE:HD11	1.96	0.47
1:A:66:ASN:ND2	1:A:180:THR:HG23	2.27	0.47
1:A:155:HIS:HD2	1:A:158:ARG:NH2	2.10	0.47
1:A:343:ILE:HG21	1:A:447:ILE:HD12	1.96	0.47
2:B:51:LEU:HD21	2:B:180:TYR:CE1	2.49	0.47
2:B:325:ASN:HD22	2:B:328:GLN:NE2	2.08	0.47
1:A:59:ALA:O	1:A:172:PRO:HB3	2.15	0.47
1:A:72:TRP:CZ3	1:A:75:ILE:HD11	2.50	0.47
11:Y:49:TYR:O	11:Y:53:ARG:HB2	2.15	0.47
2:B:146:LEU:HD13	2:B:354:VAL:HG22	1.97	0.46
12:C:401:HEM:HBC2	12:C:401:HEM:HHD	1.97	0.46
5:E:120:HIS:CD2	5:E:151:GLN:HG2	2.50	0.46
3:C:253:HIS:CD2	3:C:255:ASP:H	2.22	0.46
5:E:129:ALA:HB2	5:E:187:ILE:HG23	1.97	0.46
1:A:48:ALA:HA	1:A:211:GLY:HA3	1.97	0.46
4:D:304:PRO:HA	4:D:305:PRO:HD3	1.74	0.46
2:B:197:LEU:O	2:B:201:VAL:HG23	2.15	0.46
1:A:288:ASN:HD22	1:A:290:PHE:H	1.61	0.46
1:A:335:ASN:C	1:A:335:ASN:HD22	2.24	0.46
2:B:98:LEU:N	2:B:99:PRO:HD2	2.30	0.46
6:H:77:GLN:H	6:H:77:GLN:NE2	1.94	0.46
2:B:182:LYS:HB2	2:B:211:ALA:CB	2.41	0.46
10:X:68:LEU:HA	10:X:82:LYS:O	2.16	0.46
3:C:52:MET:CE	14:C:506:UQ6:H352	2.46	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:G:61:ILE:HB	8:G:62:PRO:HD3	1.98	0.46
1:A:349:GLN:NE2	1:A:352:ARG:HH21	2.12	0.45
1:A:381:ASN:OD1	1:A:383:VAL:HG22	2.16	0.45
2:B:274:ALA:HB2	2:B:287:LEU:HD12	1.97	0.45
2:B:287:LEU:HD21	2:B:304:ILE:HG21	1.97	0.45
4:D:125:VAL:HA	4:D:128:MET:HE3	1.98	0.45
7:F:18:SER:HA	7:F:19:PRO:HD3	1.82	0.45
2:B:223:PHE:CD2	2:B:244:PRO:HB3	2.51	0.45
1:A:238:LYS:HB2	1:A:239:LYS:H	1.62	0.45
2:B:40:ARG:HD3	2:B:155:LEU:HG	1.98	0.45
2:B:52:ASN:ND2	2:B:80:SER:OG	2.50	0.45
3:C:7:ASN:ND2	3:C:10:LEU:H	2.05	0.45
4:D:111:ALA:HA	4:D:154:TYR:HA	1.98	0.45
2:B:175:PHE:CZ	2:B:179:VAL:HG21	2.52	0.45
3:C:323:LYS:HE3	8:G:55:GLN:HE22	1.81	0.45
13:C:505:SMA:H39	13:C:505:SMA:C16	2.47	0.45
1:A:75:ILE:HG23	1:A:139:THR:HG21	1.97	0.45
1:A:251:ARG:HD3	1:A:253:ASP:OD1	2.16	0.45
1:A:288:ASN:ND2	1:A:290:PHE:H	2.15	0.45
1:A:312:ASP:OD1	1:A:334:ARG:HD3	2.16	0.45
2:B:271:ILE:HG21	2:B:287:LEU:HD11	1.99	0.45
11:Y:21:ILE:HG22	11:Y:22:SER:N	2.31	0.45
2:B:224:PHE:CD1	2:B:224:PHE:N	2.85	0.44
2:B:321:THR:O	2:B:325:ASN:HB2	2.18	0.44
2:B:59:THR:HA	2:B:112:THR:HA	1.99	0.44
10:X:68:LEU:HD12	10:X:68:LEU:H	1.83	0.44
5:E:120:HIS:HD2	5:E:151:GLN:HG2	1.82	0.44
11:Y:6:GLN:HG3	11:Y:99:GLY:HA3	1.99	0.44
7:F:45:PHE:O	7:F:48:LEU:HB2	2.17	0.44
2:B:214:SER:OG	2:B:216:VAL:HG23	2.18	0.44
10:X:51:TYR:C	10:X:51:TYR:CD2	2.95	0.44
2:B:252:GLN:HE21	2:B:252:GLN:HB2	1.66	0.44
10:X:99:SER:HB3	10:X:109:MET:HG2	1.99	0.44
11:Y:47:LEU:HA	11:Y:58:VAL:HG11	1.99	0.44
1:A:168:PHE:O	1:A:171:THR:HB	2.18	0.44
2:B:37:GLY:HA3	2:B:179:VAL:HG11	2.00	0.44
3:C:79:ARG:C	3:C:79:ARG:HD2	2.43	0.44
1:A:73:LYS:HG3	1:A:94:SER:CB	2.48	0.43
2:B:49:HIS:HE1	2:B:130:ASP:OD1	2.01	0.43
2:B:325:ASN:ND2	2:B:328:GLN:HE22	2.11	0.43
2:B:24:ALA:HB3	2:B:191:ASN:HD21	1.81	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:110:TYR:CD2	2:B:205:LEU:HD23	2.53	0.43
8:G:35:LYS:HA	8:G:36:PRO:HD2	1.76	0.43
10:X:49:VAL:HG12	10:X:68:LEU:HD23	1.99	0.43
1:A:226:ASN:HB3	1:A:227:LEU:H	1.57	0.43
4:D:286:TRP:CE3	5:E:59:MET:HG3	2.53	0.43
1:A:89:GLY:O	2:B:323:LEU:HD23	2.18	0.43
2:B:36:HIS:HB2	2:B:184:ASN:OD1	2.19	0.43
3:C:295:MET:HE3	13:C:505:SMA:H34	2.00	0.43
1:A:126:GLN:C	1:A:128:ALA:H	2.27	0.43
1:A:246:SER:O	1:A:431:ALA:HA	2.18	0.43
1:A:349:GLN:NE2	1:A:352:ARG:HD3	2.34	0.43
2:B:145:GLN:HB3	2:B:354:VAL:HG11	2.01	0.43
3:C:27:ASN:OD1	3:C:29:TRP:HB2	2.19	0.43
13:C:505:SMA:H36	13:C:505:SMA:H14	2.00	0.43
9:I:14:ASN:HD22	9:I:14:ASN:HA	1.56	0.43
10:X:61:ASN:HD22	10:X:61:ASN:C	2.26	0.43
3:C:4:ARG:HE	3:C:14:ASN:ND2	2.17	0.43
4:D:263:HIS:NE2	4:D:267:LYS:HE3	2.33	0.43
2:B:325:ASN:HA	2:B:328:GLN:HE21	1.82	0.42
2:B:334:SER:HA	2:B:335:PRO:HD3	1.90	0.42
2:B:151:PHE:O	2:B:156:GLY:HA3	2.18	0.42
2:B:233:PHE:HB3	2:B:357:GLY:HA2	2.01	0.42
7:F:120:LEU:O	7:F:123:ILE:HG12	2.18	0.42
1:A:127:LYS:HD2	1:A:127:LYS:HA	1.88	0.42
10:X:87:THR:HG22	10:X:88:THR:H	1.85	0.42
2:B:330:GLU:HG3	2:B:331:SER:N	2.33	0.42
11:Y:37:GLN:HB2	11:Y:47:LEU:CD1	2.49	0.42
1:A:159:VAL:CG2	1:A:435:THR:HG22	2.49	0.42
1:A:163:LEU:HD13	1:A:326:LEU:HD13	2.02	0.42
9:I:5:SER:O	9:I:9:THR:HG23	2.20	0.42
1:A:196:ALA:O	1:A:200:PHE:HB2	2.20	0.42
3:C:72:VAL:HA	5:E:85:THR:HG22	2.01	0.42
3:C:332:ASN:HD21	3:C:355:ALA:HA	1.85	0.42
4:D:302:PHE:HB2	7:F:73:TYR:CD1	2.54	0.42
1:A:168:PHE:O	1:A:174:SER:HB3	2.19	0.42
5:E:186:ASP:OD2	5:E:190:ARG:HD2	2.19	0.42
6:H:117:LEU:O	6:H:118:GLU:HG3	2.20	0.42
3:C:52:MET:HE1	14:C:506:UQ6:C35	2.47	0.41
10:X:49:VAL:HG12	10:X:68:LEU:CD2	2.50	0.41
1:A:427:ASP:OD1	1:A:448:ARG:NH1	2.52	0.41
2:B:21:ALA:HA	2:B:189:GLY:O	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:C:401:HEM:HHD	12:C:401:HEM:CBC	2.50	0.41
14:C:506:UQ6:H322	14:C:506:UQ6:H301	1.72	0.41
4:D:65:ALA:HB2	6:H:124:VAL:HG11	2.02	0.41
1:A:47:THR:HG21	2:B:327:VAL:CG1	2.50	0.41
2:B:298:SER:O	2:B:302:LYS:HB2	2.20	0.41
4:D:256:ASN:C	4:D:256:ASN:HD22	2.28	0.41
5:E:36:THR:HA	5:E:37:PRO:HD2	1.92	0.41
7:F:115:LYS:HA	7:F:115:LYS:HD3	1.92	0.41
10:X:29:ILE:HG12	10:X:77:ASN:ND2	2.35	0.41
2:B:114:PHE:O	2:B:169:LEU:HD11	2.20	0.41
11:Y:75:ILE:HG22	11:Y:76:SER:N	2.36	0.41
2:B:30:THR:HG23	2:B:190:GLU:HB3	2.02	0.41
2:B:98:LEU:HD11	2:B:192:VAL:HG22	2.02	0.41
14:C:506:UQ6:O5	14:C:506:UQ6:C4M	2.69	0.41
9:I:23:ALA:O	9:I:27:VAL:HG23	2.21	0.41
1:A:67:GLY:HA3	1:A:184:LEU:HD11	2.02	0.41
2:B:146:LEU:HD12	2:B:146:LEU:HA	1.94	0.41
3:C:218:ARG:CG	8:G:16:MET:HE3	2.46	0.41
3:C:222:HIS:ND1	3:C:223:SER:N	2.66	0.41
1:A:364:ARG:HD2	2:B:72:GLU:OE1	2.20	0.41
2:B:151:PHE:CD2	2:B:155:LEU:HB2	2.56	0.41
2:B:355:ALA:HB1	2:B:362:LEU:HD23	2.03	0.41
3:C:173:ASN:HB3	3:C:174:PRO:HD3	2.02	0.41
4:D:208:LEU:HD12	4:D:208:LEU:HA	1.95	0.41
1:A:61:GLU:OE1	1:A:66:ASN:HA	2.21	0.41
1:A:213:ILE:H	1:A:213:ILE:HG13	1.63	0.41
2:B:137:CYS:SG	2:B:139:VAL:HG22	2.61	0.41
13:C:505:SMA:H36	13:C:505:SMA:C10	2.49	0.41
14:C:506:UQ6:H101	14:C:506:UQ6:H121	1.58	0.41
7:F:19:PRO:HA	7:F:22:SER:HB3	2.03	0.41
5:E:191:ILE:HD13	5:E:196:ALA:HB3	2.04	0.40
1:A:46:HIS:CE1	2:B:332:VAL:HG21	2.55	0.40
2:B:93:PHE:HD1	2:B:94:LEU:O	2.03	0.40
3:C:117:GLY:O	12:C:402:HEM:HMC3	2.20	0.40
10:X:6:GLU:N	10:X:114:GLN:HE21	2.14	0.40
10:X:100:GLU:O	10:X:107:TYR:HA	2.21	0.40
11:Y:34:ASN:ND2	11:Y:49:TYR:HA	2.36	0.40
1:A:171:THR:HG23	1:A:172:PRO:HD2	2.04	0.40
2:B:238:VAL:HA	2:B:289:VAL:O	2.22	0.40
13:C:505:SMA:C16	13:C:505:SMA:C25	3.00	0.40
1:A:228:SER:HB3	1:A:231:THR:HB	2.04	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:249:ARG:NH1	1:A:441:LEU:O	2.55	0.40
2:B:325:ASN:HD22	2:B:325:ASN:HA	1.64	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	428/430 (100%)	396 (92%)	27 (6%)	5 (1%)	10	12
2	B	350/352 (99%)	311 (89%)	31 (9%)	8 (2%)	5	4
3	C	383/385 (100%)	369 (96%)	13 (3%)	1 (0%)	36	46
4	D	243/245 (99%)	238 (98%)	5 (2%)	0	100	100
5	E	183/185 (99%)	174 (95%)	7 (4%)	2 (1%)	11	13
6	H	72/74 (97%)	68 (94%)	4 (6%)	0	100	100
7	F	123/125 (98%)	120 (98%)	3 (2%)	0	100	100
8	G	91/93 (98%)	76 (84%)	10 (11%)	5 (6%)	1	0
9	I	53/55 (96%)	50 (94%)	3 (6%)	0	100	100
10	X	125/127 (98%)	116 (93%)	9 (7%)	0	100	100
11	Y	105/107 (98%)	91 (87%)	11 (10%)	3 (3%)	3	2
All	All	2156/2178 (99%)	2009 (93%)	123 (6%)	24 (1%)	11	13

All (24) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	336	ILE
8	G	52	PHE
8	G	93	ASN
2	B	313	ASP

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Mol	Chain	Res	Type
2	B	329	ASN
2	B	333	SER
3	C	156	PHE
5	E	45	GLU
11	Y	16	GLY
11	Y	30	ASN
11	Y	52	SER
1	A	227	LEU
2	B	57	GLN
8	G	4	PRO
8	G	41	PHE
1	A	229	LEU
2	B	22	ARG
5	E	161	HIS
1	A	44	PRO
1	A	235	PRO
1	A	46	HIS
2	B	79	LYS
2	B	212	GLY
8	G	45	VAL

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	369/369 (100%)	320 (87%)	49 (13%)	4	4
2	B	301/301 (100%)	253 (84%)	48 (16%)	2	2
3	C	338/338 (100%)	312 (92%)	26 (8%)	12	16
4	D	203/203 (100%)	194 (96%)	9 (4%)	25	38
5	E	151/151 (100%)	144 (95%)	7 (5%)	24	36
6	H	67/67 (100%)	58 (87%)	9 (13%)	4	4
7	F	109/109 (100%)	99 (91%)	10 (9%)	8	11
8	G	77/77 (100%)	67 (87%)	10 (13%)	4	4

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
9	I	45/45 (100%)	41 (91%)	4 (9%)	9	12
10	X	112/112 (100%)	96 (86%)	16 (14%)	3	3
11	Y	93/93 (100%)	82 (88%)	11 (12%)	5	6
All	All	1865/1865 (100%)	1666 (89%)	199 (11%)	6	8

All (199) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	28	GLU
1	A	30	THR
1	A	33	SER
1	A	36	ILE
1	A	37	VAL
1	A	46	HIS
1	A	82	SER
1	A	119	LEU
1	A	124	ILE
1	A	126	GLN
1	A	129	ASN
1	A	131	LEU
1	A	133	SER
1	A	140	LYS
1	A	141	LYS
1	A	144	LEU
1	A	149	ASP
1	A	152	ASP
1	A	163	LEU
1	A	171	THR
1	A	173	LEU
1	A	175	LEU
1	A	182	GLU
1	A	184	LEU
1	A	207	VAL
1	A	213	ILE
1	A	226	ASN
1	A	227	LEU
1	A	229	LEU
1	A	234	LYS
1	A	237	LEU
1	A	238	LYS
1	A	240	LYS

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Mol	Chain	Res	Type
1	A	251	ARG
1	A	260	ILE
1	A	278	LYS
1	A	288	ASN
1	A	305	ILE
1	A	310	LEU
1	A	319	LEU
1	A	329	PHE
1	A	342	LEU
1	A	360	THR
1	A	369	LEU
1	A	389	LEU
1	A	392	GLU
1	A	424	ARG
1	A	425	LEU
1	A	442	LEU
2	B	17	LEU
2	B	18	THR
2	B	30	THR
2	B	31	LEU
2	B	40	ARG
2	B	41	TYR
2	B	43	THR
2	B	53	ARG
2	B	54	PHE
2	B	62	ARG
2	B	73	LEU
2	B	83	ASP
2	B	98	LEU
2	B	107	ASP
2	B	128	ARG
2	B	144	ASP
2	B	146	LEU
2	B	151	PHE
2	B	169	LEU
2	B	186	GLU
2	B	191	ASN
2	B	193	VAL
2	B	206	LEU
2	B	208	THR
2	B	213	LYS
2	B	215	LEU

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Mol	Chain	Res	Type
2	B	223	PHE
2	B	252	GLN
2	B	255	VAL
2	B	267	LEU
2	B	307	ASP
2	B	310	LYS
2	B	312	LYS
2	B	314	LEU
2	B	318	ILE
2	B	323	LEU
2	B	325	ASN
2	B	330	GLU
2	B	331	SER
2	B	337	GLU
2	B	338	LEU
2	B	343	VAL
2	B	345	ASP
2	B	347	LYS
2	B	348	LEU
2	B	359	VAL
2	B	360	SER
2	B	362	LEU
3	C	5	LYS
3	C	12	LEU
3	C	35	LEU
3	C	38	LEU
3	C	79	ARG
3	C	99	LYS
3	C	101	LEU
3	C	150	LEU
3	C	156	PHE
3	C	182	LEU
3	C	185	LEU
3	C	223	SER
3	C	230	LEU
3	C	238	LEU
3	C	247	SER
3	C	292	VAL
3	C	302	LEU
3	C	304	VAL
3	C	312	VAL
3	C	313	VAL

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Mol	Chain	Res	Type
3	C	321	LEU
3	C	336	LEU
3	C	350	LEU
3	C	377	LEU
3	C	382	ARG
3	C	385	LYS
4	D	69	LEU
4	D	137	GLU
4	D	140	GLU
4	D	208	LEU
4	D	244	THR
4	D	251	VAL
4	D	268	ARG
4	D	280	LEU
4	D	283	LEU
5	E	42	VAL
5	E	51	LYS
5	E	65	LEU
5	E	91	MET
5	E	107	VAL
5	E	114	LYS
5	E	211	LYS
6	H	74	VAL
6	H	77	GLN
6	H	79	GLU
6	H	89	GLU
6	H	94	LEU
6	H	99	GLU
6	H	117	LEU
6	H	118	GLU
6	H	130	LEU
7	F	16	LEU
7	F	21	LEU
7	F	30	ASN
7	F	31	GLN
7	F	41	LEU
7	F	48	LEU
7	F	62	ARG
7	F	115	LYS
7	F	119	GLU
7	F	127	LYS
8	G	35	LYS

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Mol	Chain	Res	Type
8	G	38	GLN
8	G	43	ASN
8	G	48	SER
8	G	60	LEU
8	G	68	TYR
8	G	71	LYS
8	G	88	GLU
8	G	89	LEU
8	G	94	VAL
9	I	13	ARG
9	I	14	ASN
9	I	18	VAL
9	I	48	LEU
10	X	1	GLU
10	X	5	GLN
10	X	11	LEU
10	X	21	THR
10	X	39	ARG
10	X	51	TYR
10	X	54	ASN
10	X	61	ASN
10	X	66	ASP
10	X	68	LEU
10	X	71	THR
10	X	89	GLU
10	X	100	GLU
10	X	118	VAL
10	X	122	SER
10	X	125	ARG
11	Y	1	ASP
11	Y	18	ARG
11	Y	33	LEU
11	Y	38	GLN
11	Y	41	ASP
11	Y	53	ARG
11	Y	69	THR
11	Y	81	GLU
11	Y	92	ILE
11	Y	93	LYS
11	Y	107	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (68) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	60	ASN
1	A	62	ASN
1	A	65	ASN
1	A	66	ASN
1	A	81	ASN
1	A	101	GLN
1	A	120	ASN
1	A	155	HIS
1	A	157	ASN
1	A	169	GLN
1	A	170	ASN
1	A	199	HIS
1	A	230	GLN
1	A	282	GLN
1	A	288	ASN
1	A	304	ASN
1	A	316	HIS
1	A	335	ASN
1	A	349	GLN
1	A	375	GLN
1	A	384	ASN
1	A	428	GLN
2	B	49	HIS
2	B	52	ASN
2	B	55	ASN
2	B	103	ASN
2	B	191	ASN
2	B	252	GLN
2	B	258	ASN
2	B	325	ASN
2	B	328	GLN
3	C	7	ASN
3	C	14	ASN
3	C	22	GLN
3	C	57	ASN
3	C	173	ASN
3	C	177	GLN
3	C	208	ASN
3	C	253	HIS
3	C	332	ASN
4	D	78	HIS
4	D	79	ASN
4	D	127	ASN

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Mol	Chain	Res	Type
5	E	38	ASN
5	E	106	ASN
5	E	124	HIS
5	E	151	GLN
5	E	184	HIS
6	H	77	GLN
7	F	31	GLN
7	F	53	ASN
7	F	79	HIS
7	F	91	ASN
7	F	97	GLN
9	I	14	ASN
9	I	29	GLN
9	I	42	ASN
10	X	54	ASN
10	X	59	ASN
10	X	61	ASN
10	X	77	ASN
10	X	78	GLN
10	X	114	GLN
11	Y	31	ASN
11	Y	34	ASN
11	Y	77	ASN
11	Y	89	GLN
11	Y	91	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

6 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
12	HEM	C	401	3	50,50,50	1.38	10 (20%)	67,82,82	1.02	3 (4%)
16	FES	E	4	5	0,4,4	-	-	-	-	-
14	UQ6	C	506	-	43,43,43	2.55	16 (37%)	54,55,55	2.09	13 (24%)
13	SMA	C	505	-	38,38,38	1.59	7 (18%)	47,52,52	2.12	11 (23%)
12	HEM	C	402	3	50,50,50	1.29	7 (14%)	67,82,82	0.71	0
15	HEC	D	3	4	46,50,50	1.38	2 (4%)	58,82,82	1.67	2 (3%)

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
12	HEM	C	401	3	-	5/14/54/54	-
16	FES	E	4	5	-	-	0/1/1/1
14	UQ6	C	506	-	-	13/39/39/39	0/1/1/1
13	SMA	C	505	-	2/2/5/10	21/34/34/34	0/2/2/2
12	HEM	C	402	3	-	4/14/54/54	-
15	HEC	D	3	4	-	6/14/54/54	-

All (42) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
14	C	506	UQ6	O5-C5	-7.05	1.20	1.36
14	C	506	UQ6	O2-C2	-5.88	1.23	1.36
14	C	506	UQ6	C7-C6	5.76	1.58	1.51
14	C	506	UQ6	C2-C3	5.75	1.48	1.39
15	D	3	HEC	CAB-C3B	5.42	1.52	1.35
15	D	3	HEC	CAC-C3C	5.09	1.51	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
14	C	506	UQ6	C13-C14	3.86	1.41	1.33
14	C	506	UQ6	C11-C9	3.78	1.59	1.51
13	C	505	SMA	C4A-C5	3.76	1.47	1.40
13	C	505	SMA	C20-C19	3.71	1.36	1.33
12	C	402	HEM	FE-NB	3.68	2.06	1.94
13	C	505	SMA	C4A-C8A	3.65	1.48	1.40
12	C	401	HEM	CMC-C2C	3.60	1.58	1.50
13	C	505	SMA	C13-C12	3.34	1.62	1.54
14	C	506	UQ6	C16-C14	3.28	1.58	1.51
12	C	401	HEM	CAB-C3B	-3.19	1.38	1.47
14	C	506	UQ6	C2-C1	3.06	1.46	1.40
12	C	401	HEM	CMB-C2B	2.80	1.56	1.50
14	C	506	UQ6	C18-C19	2.80	1.39	1.33
12	C	402	HEM	CBC-CAC	2.79	1.43	1.30
12	C	401	HEM	CAC-C3C	-2.77	1.40	1.47
14	C	506	UQ6	C5-C4	2.77	1.44	1.39
12	C	402	HEM	FE-NC	2.75	2.04	1.95
12	C	402	HEM	FE-NA	2.67	2.04	1.95
12	C	401	HEM	FE-NB	2.65	2.03	1.94
14	C	506	UQ6	C33-C34	2.54	1.40	1.32
12	C	401	HEM	FE-NC	2.51	2.03	1.95
12	C	401	HEM	FE-ND	2.50	2.02	1.94
12	C	401	HEM	CBC-CAC	2.41	1.42	1.30
13	C	505	SMA	O12-C12	-2.40	1.36	1.42
14	C	506	UQ6	C4-C3	-2.35	1.35	1.39
13	C	505	SMA	C6-C7	2.32	1.42	1.38
12	C	402	HEM	CAB-C3B	-2.30	1.41	1.47
12	C	402	HEM	CBB-CAB	2.27	1.41	1.30
14	C	506	UQ6	C5-C6	2.21	1.43	1.40
12	C	401	HEM	CBB-CAB	2.15	1.40	1.30
14	C	506	UQ6	C23-C24	2.14	1.38	1.33
14	C	506	UQ6	C7-C8	2.07	1.55	1.50
13	C	505	SMA	O7-C7	2.06	1.40	1.37
12	C	402	HEM	CMA-C3A	2.05	1.55	1.50
14	C	506	UQ6	C6-C1	-2.03	1.37	1.40
12	C	401	HEM	O2A-CGA	-2.00	1.24	1.30

All (29) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
15	D	3	HEC	CBB-CAB-C3B	-8.41	110.61	127.43
15	D	3	HEC	CBC-CAC-C3C	-7.77	111.91	127.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
14	C	506	UQ6	C3M-O3-C3	7.25	134.43	114.74
13	C	505	SMA	C26-C19-C18	-6.48	108.19	118.09
13	C	505	SMA	O14-C14-C15	6.42	129.71	111.05
13	C	505	SMA	O14-C14-C13	5.08	118.45	107.97
14	C	506	UQ6	C4M-O4-C4	4.64	127.35	114.74
14	C	506	UQ6	C17-C18-C19	4.52	137.96	127.62
13	C	505	SMA	O12-C12-C13	4.07	113.98	107.97
13	C	505	SMA	O7-C7-C8	3.88	118.59	114.53
14	C	506	UQ6	C17-C16-C14	3.87	126.00	113.19
12	C	401	HEM	CMC-C2C-C1C	3.73	131.30	124.73
14	C	506	UQ6	C1M-C1-C2	-3.42	114.83	120.52
14	C	506	UQ6	C22-C23-C24	3.35	135.29	127.62
13	C	505	SMA	C18-C19-C20	2.92	126.32	118.55
14	C	506	UQ6	C11-C9-C8	2.92	127.72	121.17
14	C	506	UQ6	C3-C2-C1	-2.77	117.99	121.59
14	C	506	UQ6	C7-C6-C5	-2.74	116.52	120.85
12	C	401	HEM	CMC-C2C-C3C	-2.74	121.81	128.43
14	C	506	UQ6	C1M-C1-C6	2.63	124.23	120.43
14	C	506	UQ6	C11-C12-C13	2.56	124.69	112.02
14	C	506	UQ6	C10-C9-C11	-2.53	110.84	115.23
13	C	505	SMA	O7-C7-C6	-2.52	119.73	124.08
13	C	505	SMA	O5-C5-C4A	2.25	119.03	115.84
13	C	505	SMA	C4A-C4-C3	-2.22	115.51	118.78
12	C	401	HEM	CAC-C3C-C4C	2.22	130.12	124.82
13	C	505	SMA	O5-C5-C6	-2.13	120.41	124.08
14	C	506	UQ6	C7-C6-C1	2.10	123.99	120.79
13	C	505	SMA	C11-C12-C13	-2.09	108.70	114.29

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
13	C	505	SMA	C12
13	C	505	SMA	C14

All (49) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
13	C	505	SMA	C11-C12-C13-C24
13	C	505	SMA	O12-C12-C13-C14
13	C	505	SMA	O12-C12-C13-C24
13	C	505	SMA	C13-C14-C15-C16
13	C	505	SMA	C15-C14-O14-C25

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Mol	Chain	Res	Type	Atoms
13	C	505	SMA	C14-C15-C16-C17
13	C	505	SMA	C15-C16-C17-C18
13	C	505	SMA	C16-C17-C18-C19
15	D	3	HEC	C2B-C3B-CAB-CBB
15	D	3	HEC	C4B-C3B-CAB-CBB
15	D	3	HEC	C2C-C3C-CAC-CBC
15	D	3	HEC	C4C-C3C-CAC-CBC
13	C	505	SMA	C9-C10-C11-C22
14	C	506	UQ6	C12-C11-C9-C10
14	C	506	UQ6	C15-C14-C16-C17
14	C	506	UQ6	C12-C11-C9-C8
14	C	506	UQ6	C13-C14-C16-C17
14	C	506	UQ6	C30-C29-C31-C32
14	C	506	UQ6	C28-C29-C31-C32
14	C	506	UQ6	C24-C26-C27-C28
13	C	505	SMA	C6-C5-O5-C5M
13	C	505	SMA	C17-C18-C19-C26
13	C	505	SMA	C17-C18-C19-C20
13	C	505	SMA	C4A-C5-O5-C5M
14	C	506	UQ6	C3-C4-O4-C4M
13	C	505	SMA	C24-C13-C14-O14
13	C	505	SMA	C22-C11-C12-O12
14	C	506	UQ6	C19-C21-C22-C23
14	C	506	UQ6	C5-C4-O4-C4M
13	C	505	SMA	C11-C12-C13-C14
14	C	506	UQ6	C4-C3-O3-C3M
12	C	401	HEM	C3D-CAD-CBD-CGD
13	C	505	SMA	C24-C13-C14-C15
13	C	505	SMA	C12-C13-C14-C15
13	C	505	SMA	C9-C10-C11-C12
14	C	506	UQ6	C2-C3-O3-C3M
13	C	505	SMA	C12-C13-C14-O14
12	C	402	HEM	CAA-CBA-CGA-O1A
15	D	3	HEC	CAA-CBA-CGA-O2A
15	D	3	HEC	CAA-CBA-CGA-O1A
12	C	401	HEM	CAD-CBD-CGD-O2D
14	C	506	UQ6	C20-C19-C21-C22
12	C	402	HEM	CAA-CBA-CGA-O2A
12	C	402	HEM	CAD-CBD-CGD-O2D
12	C	401	HEM	CAD-CBD-CGD-O1D
13	C	505	SMA	C10-C11-C12-O12
12	C	401	HEM	CAA-CBA-CGA-O1A

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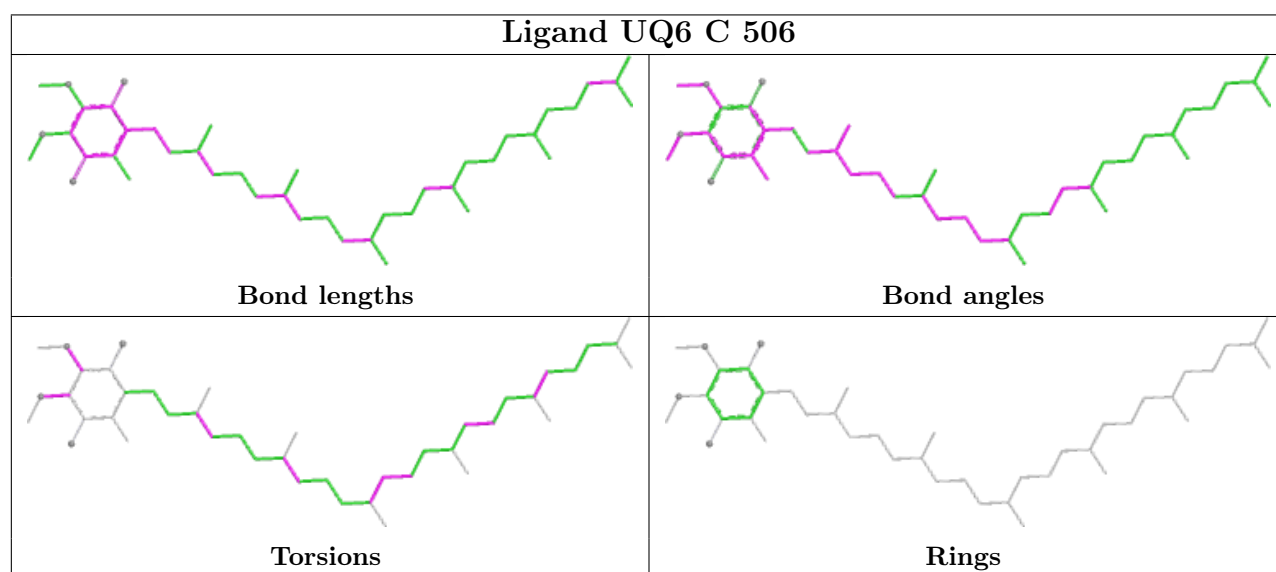
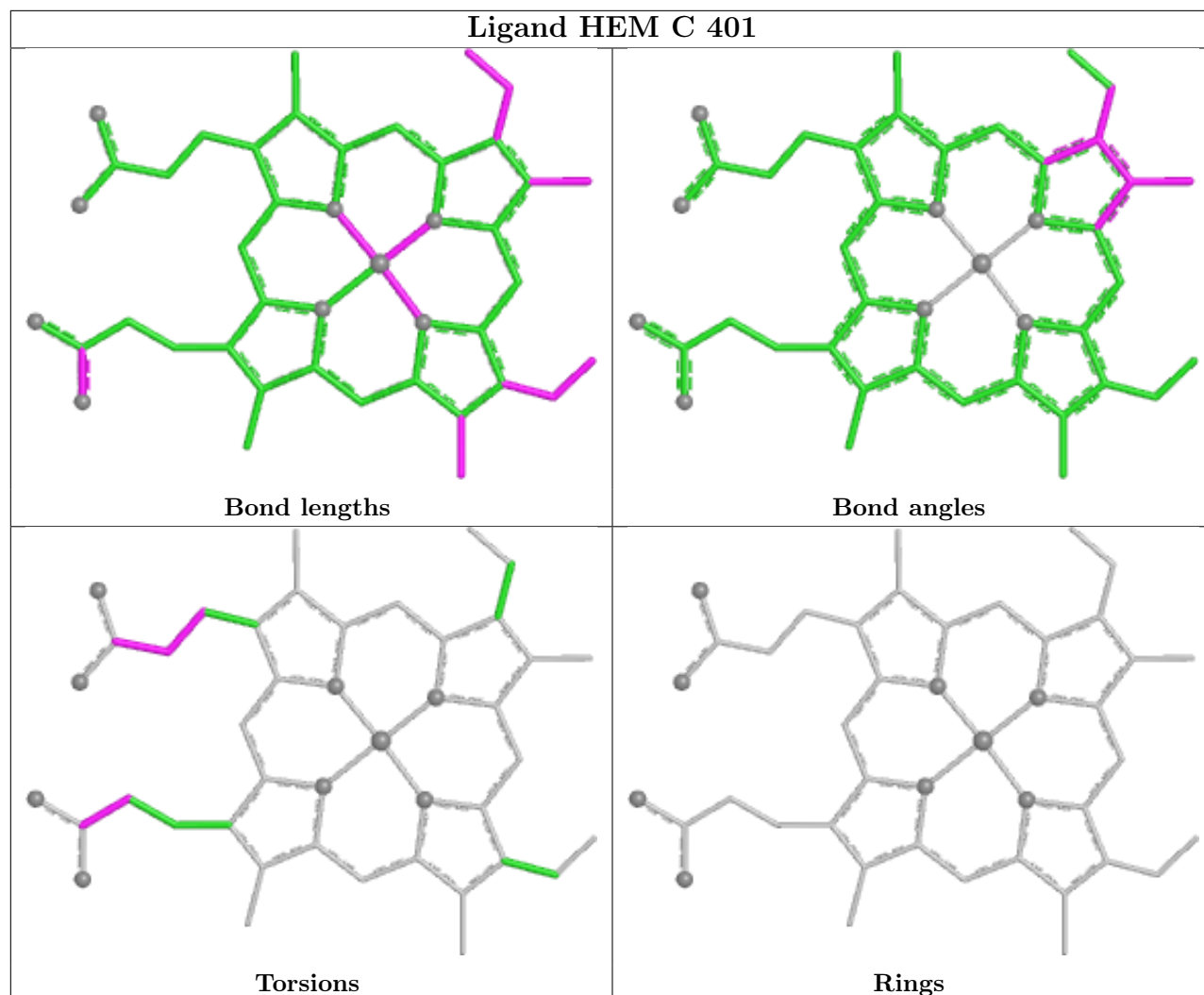
Mol	Chain	Res	Type	Atoms
12	C	401	HEM	CAA-CBA-CGA-O2A
12	C	402	HEM	CAD-CBD-CGD-O1D

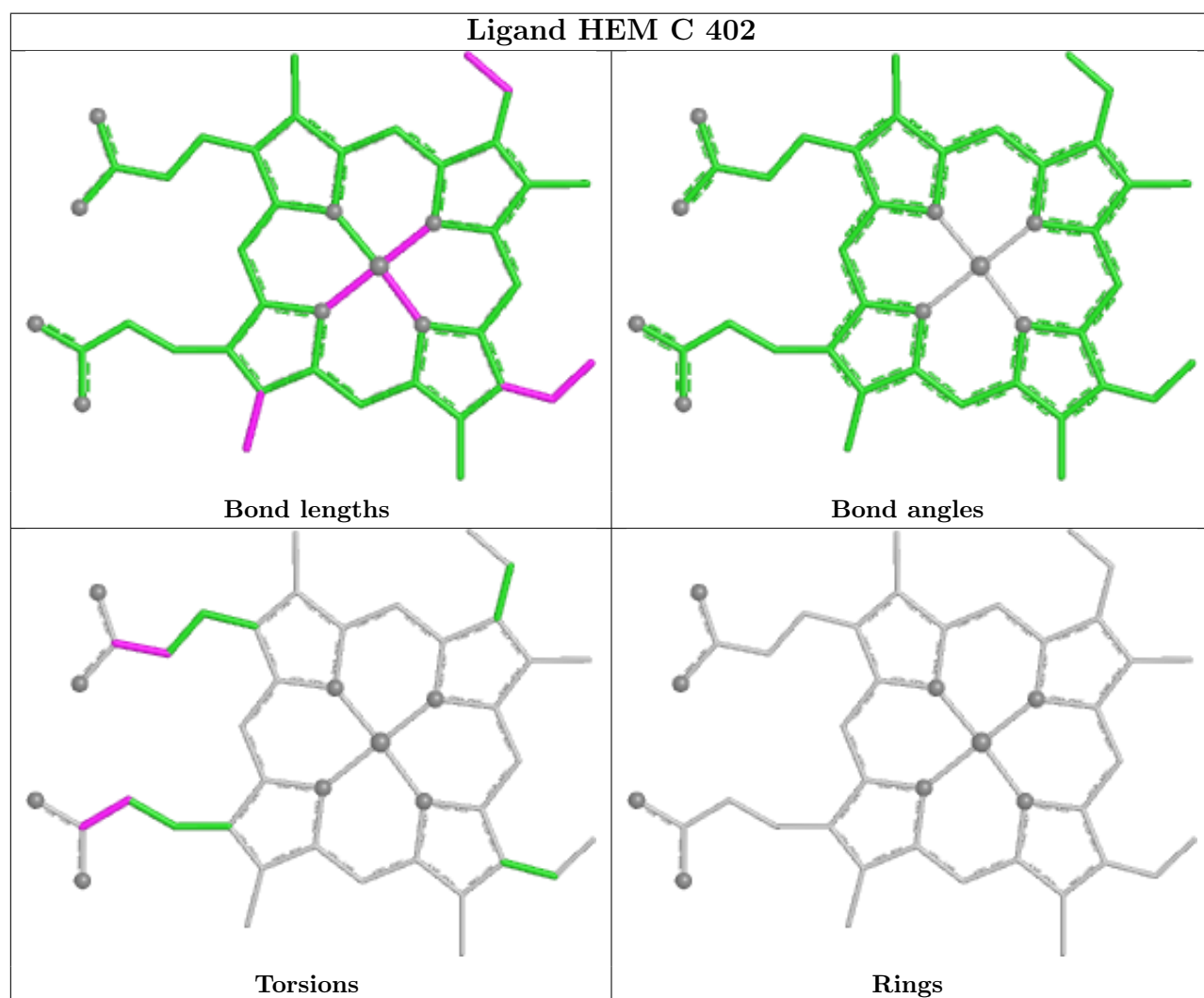
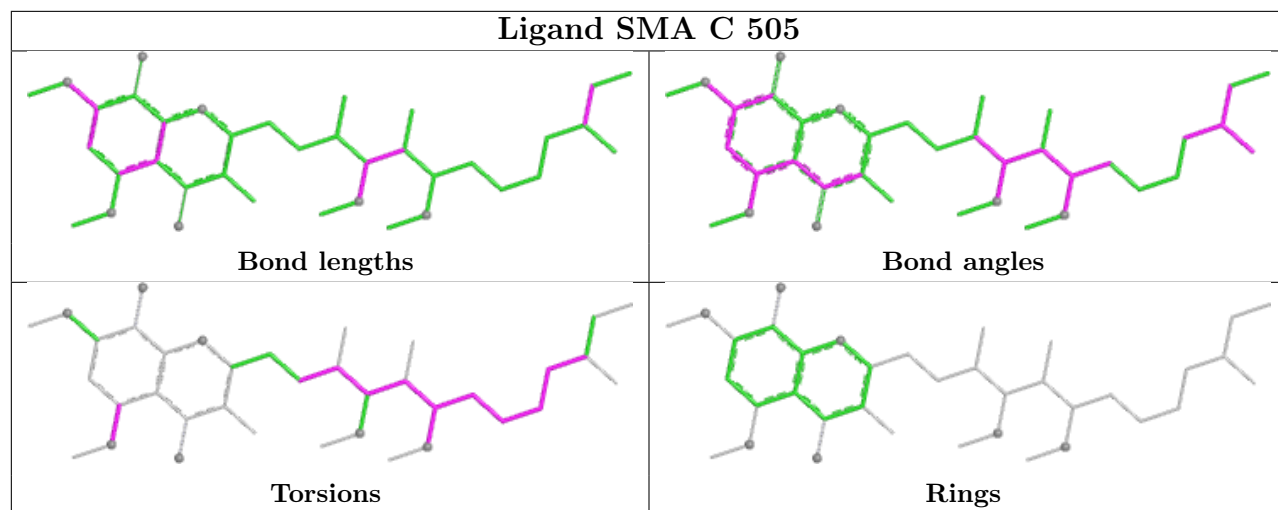
There are no ring outliers.

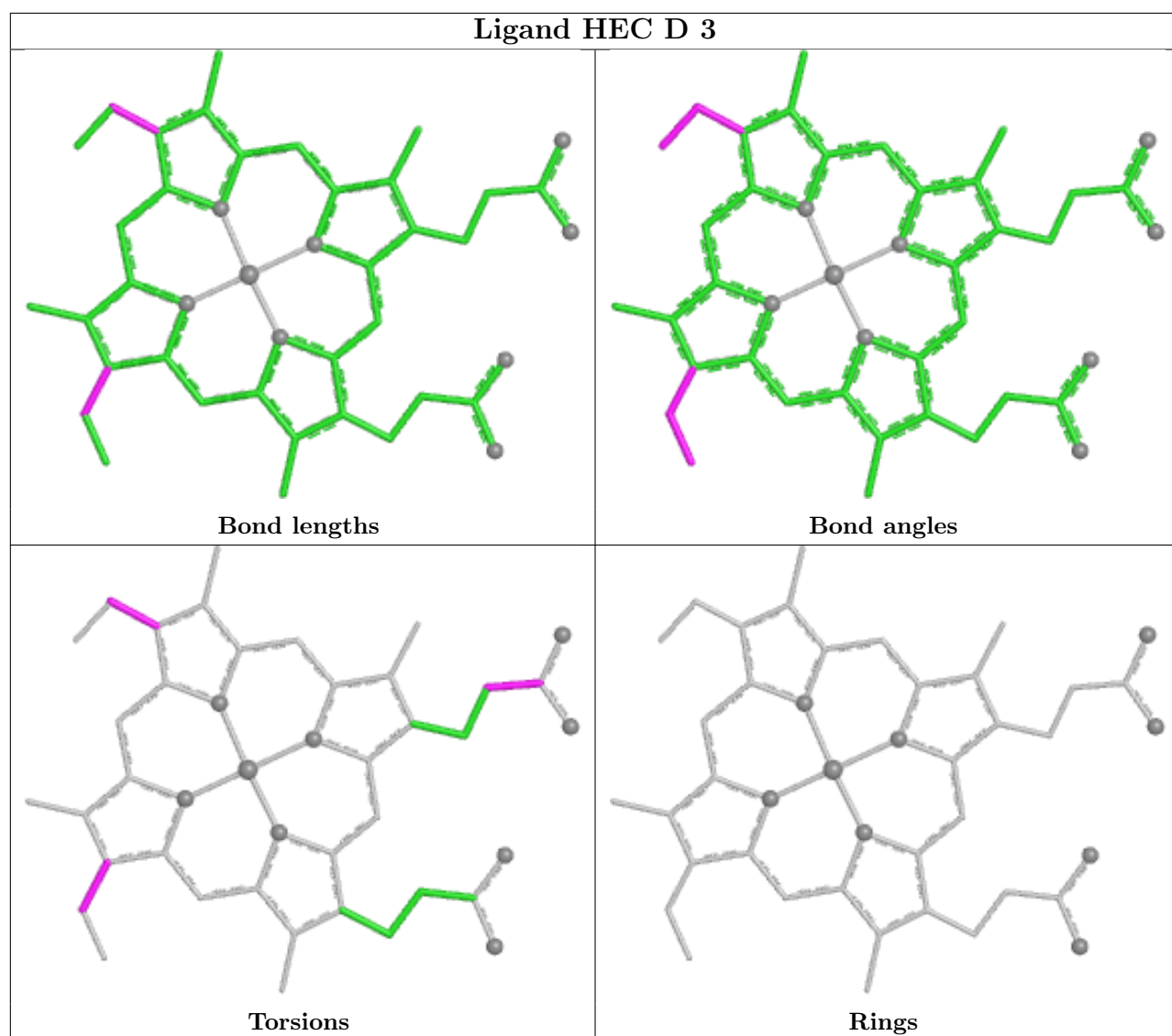
4 monomers are involved in 25 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
12	C	401	HEM	2	0
14	C	506	UQ6	15	0
13	C	505	SMA	7	0
12	C	402	HEM	1	0

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







5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates ⓘ

EDS was not executed - this section is therefore empty.

6.4 Ligands ⓘ

EDS was not executed - this section is therefore empty.

6.5 Other polymers ⓘ

EDS was not executed - this section is therefore empty.