



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 14, 2017 – 01:48 pm GMT

PDB ID : 4OGQ
Title : Internal Lipid Architecture of the Hetero-Oligomeric Cytochrome b6f Complex
Authors : Hasan, S.S.; Cramer, W.A.
Deposited on : 2014-01-16
Resolution : 2.50 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

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : trunk28620
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : recalc28949

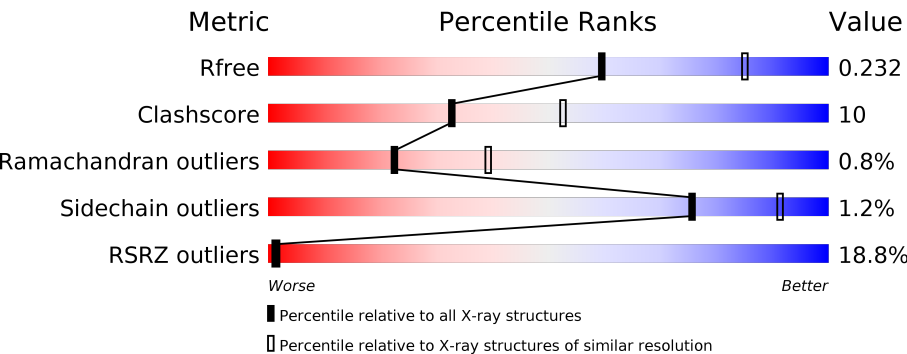
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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}	100719	3846 (2.50-2.50)
Clashscore	112137	4554 (2.50-2.50)
Ramachandran outliers	110173	4463 (2.50-2.50)
Sidechain outliers	110143	4465 (2.50-2.50)
RSRZ outliers	101464	3876 (2.50-2.50)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	215	<div> <div>13%</div> <div> <div>93%</div> <div>7%</div> </div> </div>
2	B	160	<div> <div>14%</div> <div> <div>89%</div> <div>10%</div> <div>•</div> </div> </div>
3	C	333	<div> <div>14%</div> <div> <div>70%</div> <div>14%</div> <div>•</div> <div>16%</div> </div> </div>
4	D	179	<div> <div>36%</div> <div> <div>74%</div> <div>18%</div> <div>7%</div> </div> </div>
5	E	31	<div> <div>16%</div> <div> <div>77%</div> <div>16%</div> <div>•</div> <div>•</div> </div> </div>
6	F	34	<div> <div>3%</div> <div> <div>74%</div> <div>21%</div> <div>6%</div> </div> </div>

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Mol	Chain	Length	Quality of chain
7	G	37	
8	H	29	

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
10	UMQ	B	203[B]	-	-	-	X
10	UMQ	D	201	-	-	-	X
10	UMQ	G	101	-	-	-	X
11	7PH	B	206	-	-	-	X
11	7PH	C	303	-	-	-	X
11	7PH	F	104	-	-	-	X
12	8K6	A	306	-	-	-	X
12	8K6	A	307	-	-	-	X
12	8K6	A	308	-	-	-	X
12	8K6	B	202[A]	-	-	-	X
14	CLA	B	204	X	-	-	-
15	OPC	B	205	-	-	-	X
17	MYS	D	202	-	-	-	X
20	2WD	D	206	-	-	-	X
22	2WA	F	101	-	-	-	X
24	1O2	F	103	X	-	-	X

2 Entry composition

There are 26 unique types of molecules in this entry. The entry contains 8396 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 Cytochrome b6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	214	Total	C	N	O	S	0	0	0
			1708	1139	271	288	10			

- Molecule 2 is a protein called Cytochrome b6-f complex subunit 4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	159	Total	C	N	O	S	0	0	0
			1232	825	194	208	5			

- Molecule 3 is a protein called Apocytochrome f.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	281	Total	C	N	O	S	0	0	0
			2137	1361	355	415	6			

- Molecule 4 is a protein called Cytochrome b6-f complex iron-sulfur subunit 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	166	Total	C	N	O	S	0	0	0
			1250	791	213	240	6			

- Molecule 5 is a protein called Cytochrome b6-f complex subunit 6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	E	31	Total	C	N	O	S	0	0	0
			228	157	35	35	1			

- Molecule 6 is a protein called Cytochrome b6-f complex subunit 7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	F	32	Total	C	N	O	S	0	0	0
			231	156	36	38	1			

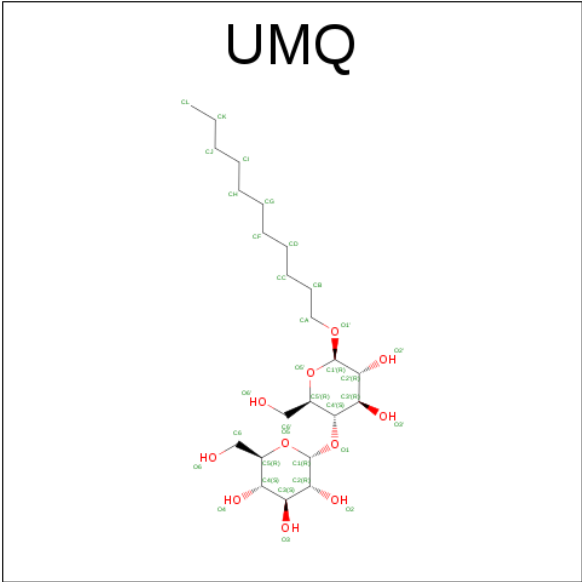
- | Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|---------|-------|
| 7 | G | 37 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 282 | 188 | 44 | 49 | 1 | | | |

- | Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|---------|-------|
| 8 | H | 29 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 228 | 155 | 36 | 35 | 2 | | | |

- # HEM

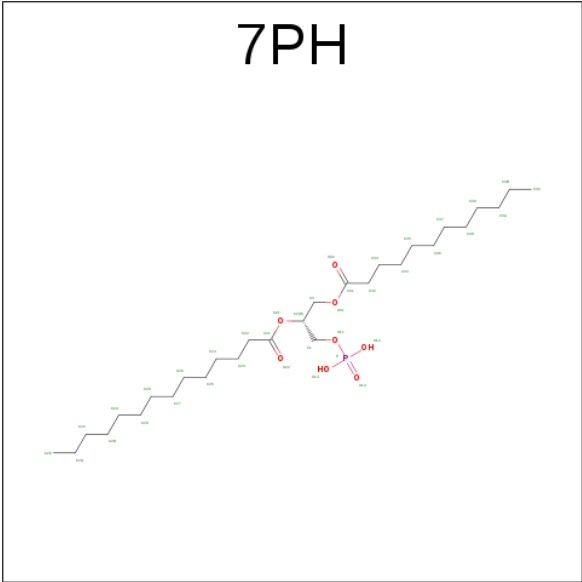
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
9	A	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
9	A	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
9	A	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
9	C	1	Total 43	C 34	Fe 1	N 4	O 4	0	0

- 
- WORLD WIDE
PDB
PROTEIN DATA BANK



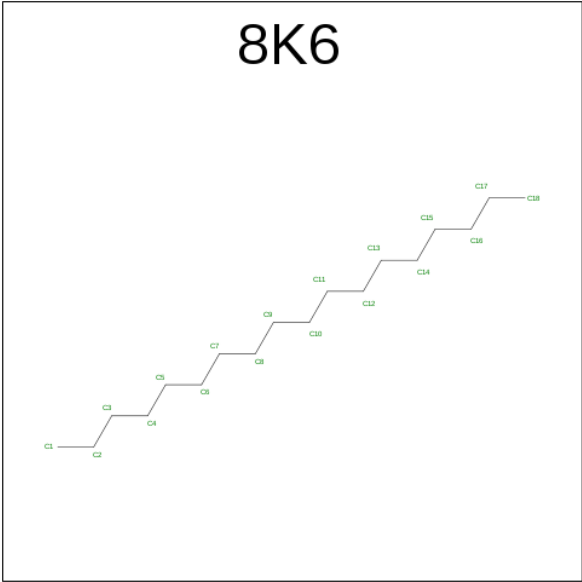
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
10	A	1	Total	C	O	0	0
			34	23	11		
10	B	1	Total	C	O	0	0
			34	23	11		
10	B	1	Total	C	O	0	1
			34	23	11		
10	D	1	Total	C	O	0	0
			34	23	11		
10	G	1	Total	C	O	0	0
			34	23	11		

- Molecule 11 is (1R)-2-(DODECANOYLOXY)-1-[(PHOSPHONOOXY)METHYL]ETHYL TETRADECANOATE (three-letter code: 7PH) (formula: C₂₉H₅₇O₈P).



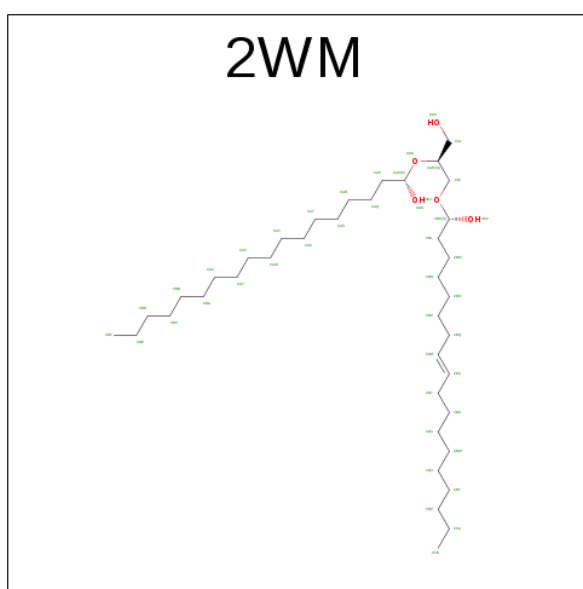
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
11	A	1	Total	C	O	0	0
			32	27	5		
11	B	1	Total	C	O	0	0
			32	27	5		
11	C	1	Total	C	O	0	0
			32	27	5		
11	D	1	Total	C	O	0	0
			32	27	5		
11	F	1	Total	C	O	0	0
			32	27	5		

- Molecule 12 is OCTADECANE (three-letter code: 8K6) (formula: C₁₈H₃₈).



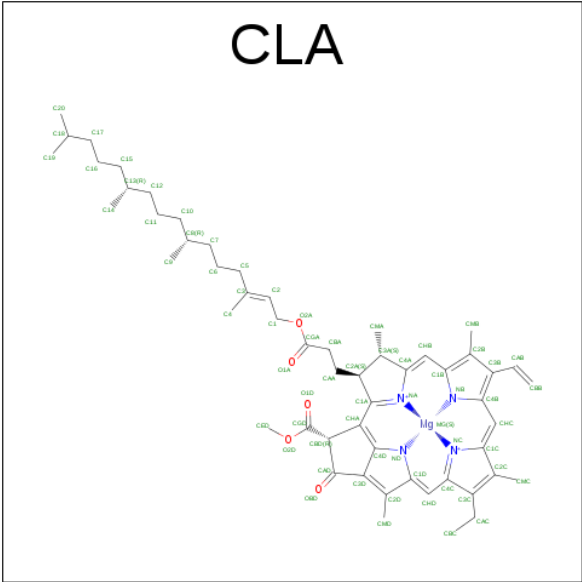
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
12	A	1	Total C 18 18	0	0
12	A	1	Total C 18 18	0	0
12	A	1	Total C 14 14	0	0
12	B	1	Total C 18 18	0	1

- Molecule 13 is (1S,8E)-1-{[(2S)-3-HYDROXY-2-{[(1S)-1-HYDROXYOCTADECYL]OXY}PROPYL]OXY}OCTADEC-8-EN-1-OL (three-letter code: 2WM) (formula: C₃₉H₇₈O₅).



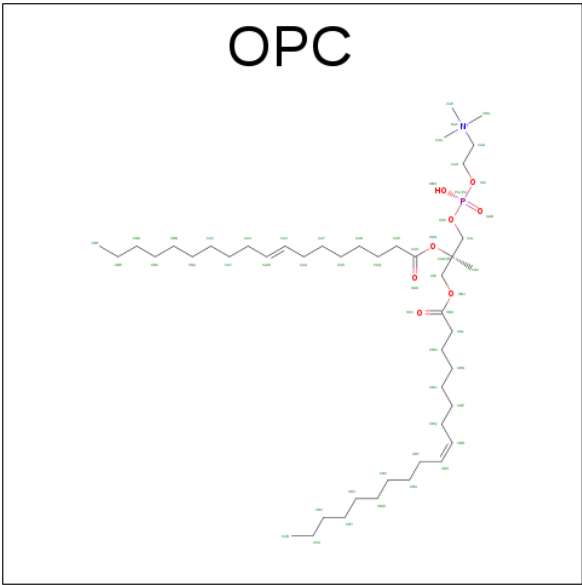
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
13	A	1	Total C O 44 39 5	0	0

- Molecule 14 is CHLOROPHYLL A (three-letter code: CLA) (formula: C₅₅H₇₂MgN₄O₅).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
14	B	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		

- Molecule 15 is (7R,17E)-4-HYDROXY-N,N,N,7-TETRAMETHYL-7-[(8E)-OCTADEC-8-ENOYLOXY]-10-OXO-3,5,9-TRIOXA-4-PHOSPHAHEPTACOS-17-EN-1-AMINIUM 4-OXIDE (three-letter code: OPC) (formula: C₄₅H₈₇NO₈P).

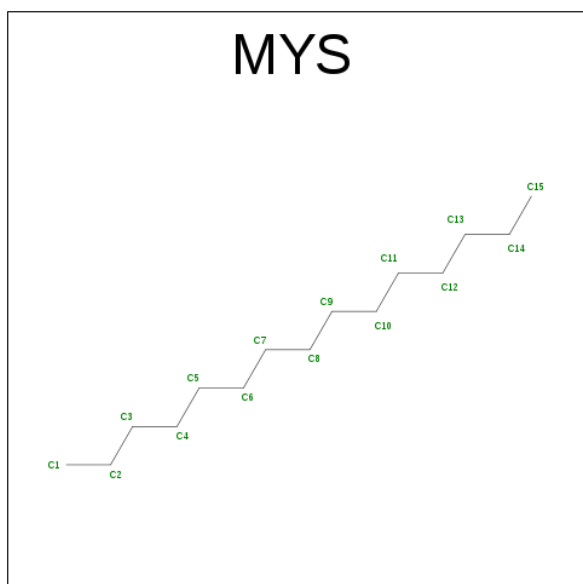


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
15	B	1	Total	C	N	O	P	0	0
			54	44	1	8	1		

- Molecule 16 is CADMIUM ION (three-letter code: CD) (formula: Cd).

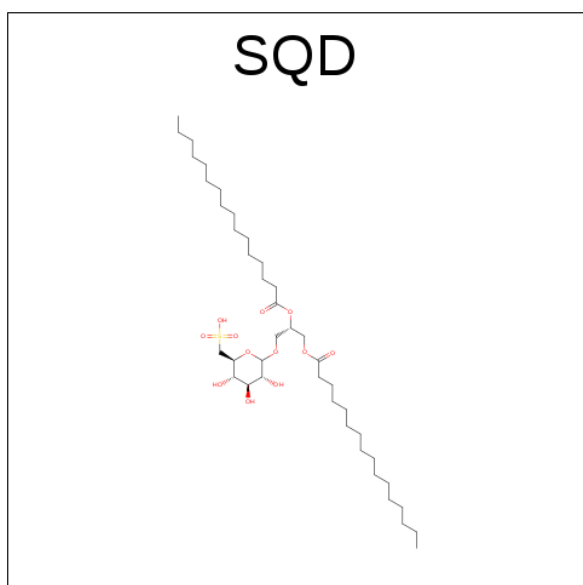
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
16	C	1	Total	Cd	0	0
			1	1		

- Molecule 17 is PENTADECANE (three-letter code: MYS) (formula: $C_{15}H_{32}$).



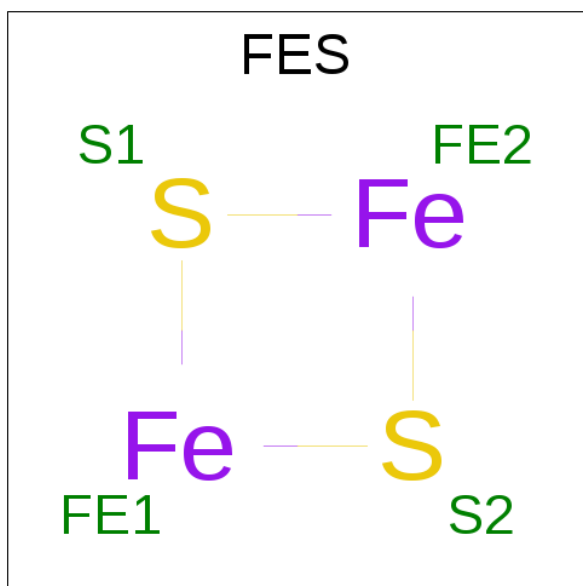
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
17	D	1	Total	C	0	0
			15	15		

- Molecule 18 is 1,2-DI-O-ACYL-3-O-[6-DEOXY-6-SULFO-ALPHA-D-GLUCOPYRANOSYL]-SN-GLYCEROL (three-letter code: SQD) (formula: $C_{41}H_{78}O_{12}S$).



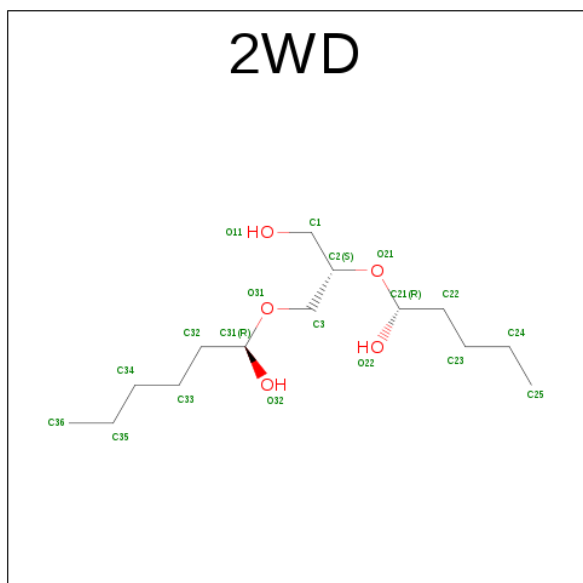
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
18	D	1	Total	C	O	S	0	0
			54	41	12	1		

- Molecule 19 is FE2/S2 (INORGANIC) CLUSTER (three-letter code: FES) (formula: Fe₂S₂).



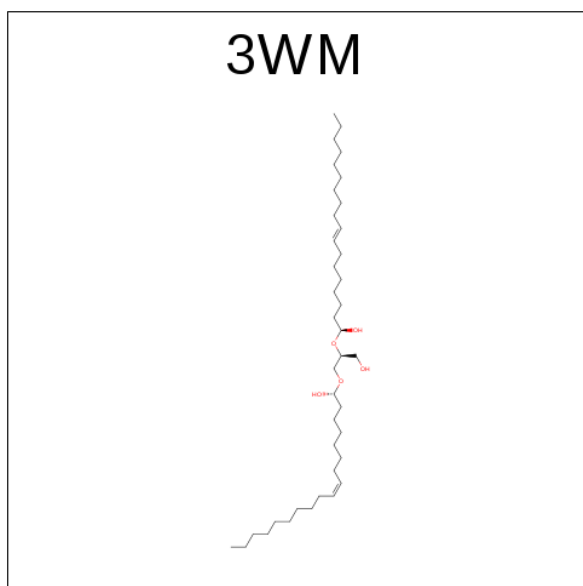
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
19	D	1	Total	Fe	S	0	0
			4	2	2		

- Molecule 20 is (1R)-1-{[(2S)-3-HYDROXY-2-{[(1R)-1-HYDROXYPENTYL]OXY}PROPYL]OXY}HEXAN-1-OL (three-letter code: 2WD) (formula: C₁₄H₃₀O₅).



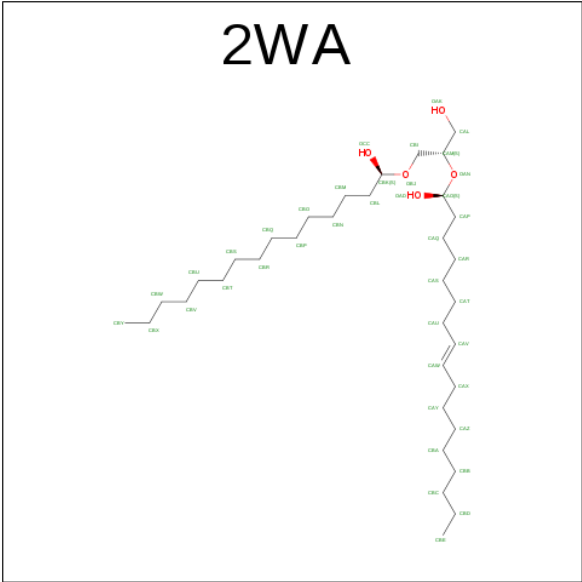
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
20	D	1	Total	C	O	0	0
			19	14	5		

- Molecule 21 is (1S,8E,1'R,8'Z)-1,1'-{[(2S)-3-HYDROXYPROPANE-1,2-DIYL]BIS(OXY)} BIS(OCTADEC-8-EN-1-OL (three-letter code: 3WM) (formula: C₃₉H₇₆O₅).



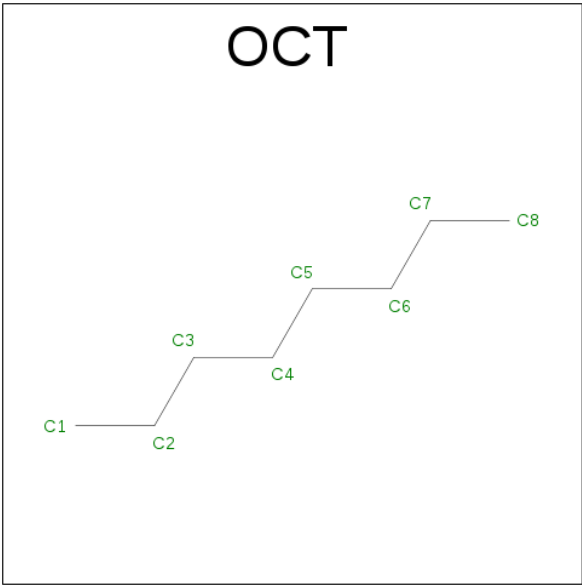
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
21	E	1	Total	C	O	0	0
			44	39	5		

- Molecule 22 is (1S,8E)-1-{[(2S)-1-HYDROXY-3-{[(1S)-1-HYDROXPENTADECYL]OXY}PROPAN-2-YL]OXY}HEPTADEC-8-EN-1-OL (three-letter code: 2WA) (formula: C₃₅H₇₀O₅).



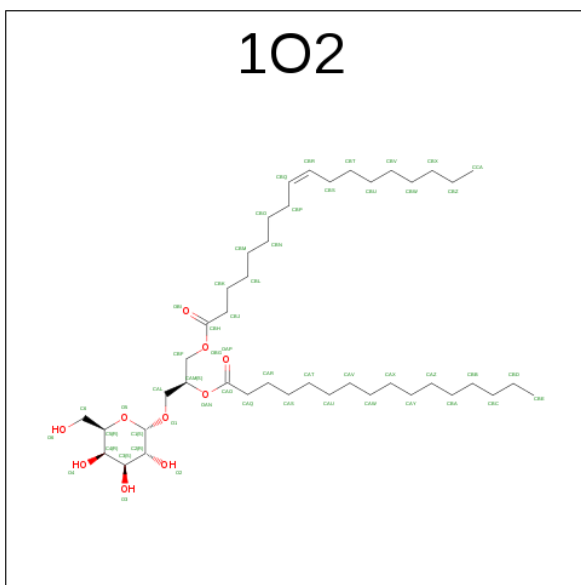
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
22	F	1	Total	C	O	0
			40	35	5	

- Molecule 23 is N-OCTANE (three-letter code: OCT) (formula: C₈H₁₈).



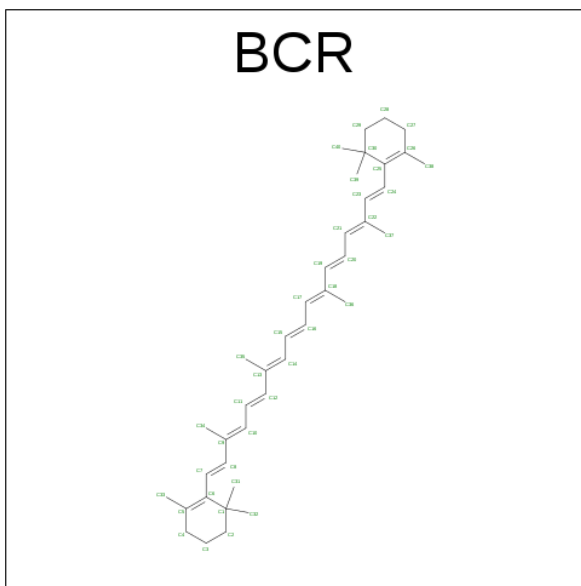
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
23	F	1	Total	C		0
			8	8		

- Molecule 24 is (2S)-3-(ALPHA-D-GALACTOPYRANOSYLOXY)-2-(HEXADECANOYLOXY)PROPYL (9Z)-OCTADEC-9-ENOATE (three-letter code: 1O2) (formula: C₄₃H₈₀O₁₀).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
24	F	1	Total	C	O	0	0
			49	39	10		

- Molecule 25 is BETA-CAROTENE (three-letter code: BCR) (formula: $C_{40}H_{56}$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
25	G	1	Total C 40 40	0	0

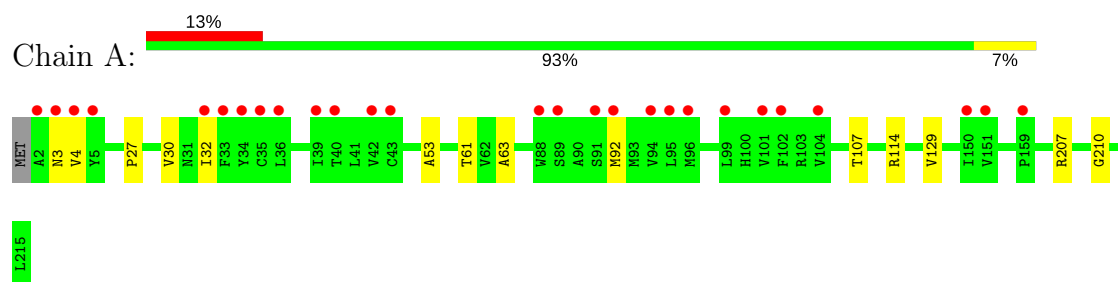
- Molecule 26 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
26	A	21	Total 21	O 21	0	0
26	B	25	Total 25	O 25	0	0
26	C	38	Total 38	O 38	0	0
26	D	1	Total 1	O 1	0	0
26	F	1	Total 1	O 1	0	0
26	G	7	Total 7	O 7	0	0

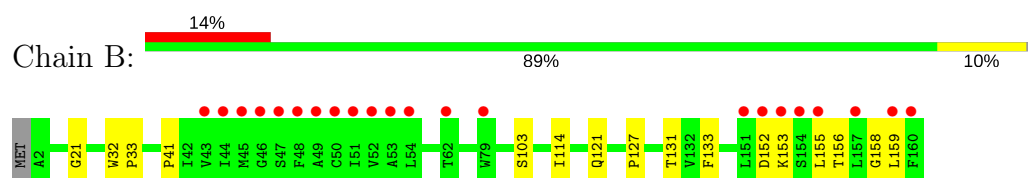
3 Residue-property plots [i](#)

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

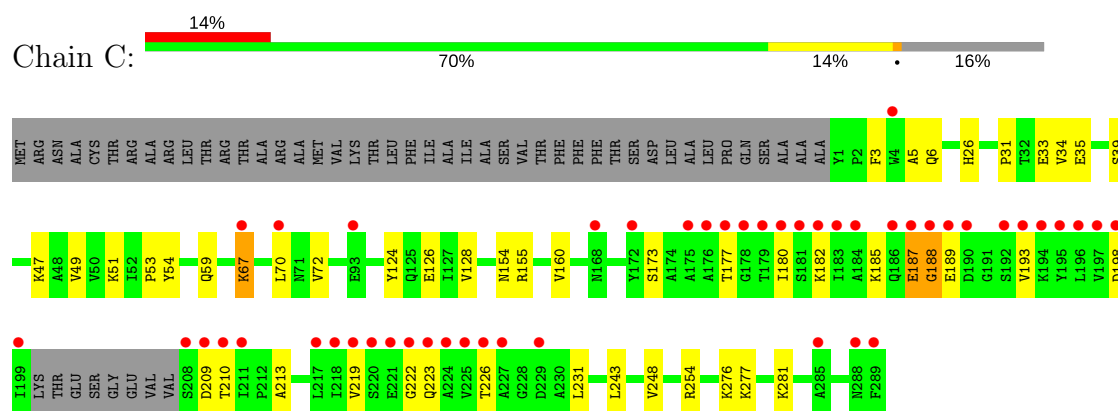
• Molecule 1: Cytochrome b6



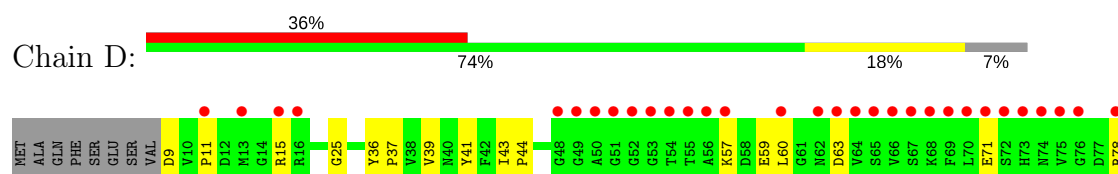
• Molecule 2: Cytochrome b6-f complex subunit 4

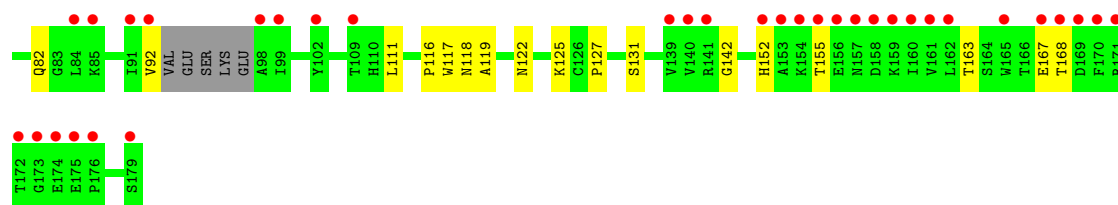


• Molecule 3: Apocytochrome f

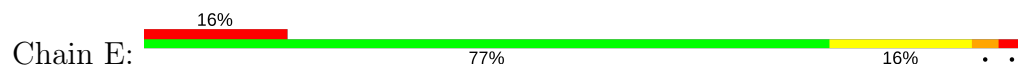


• Molecule 4: Cytochrome b6-f complex iron-sulfur subunit 1

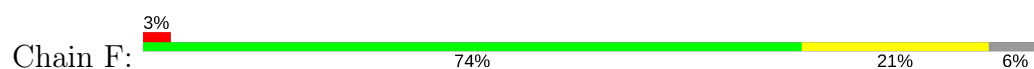




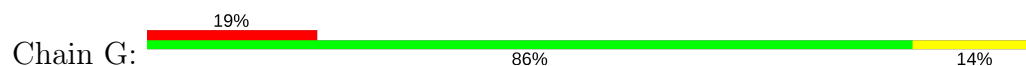
• Molecule 5: Cytochrome b6-f complex subunit 6



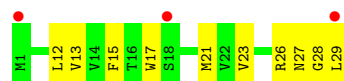
• Molecule 6: Cytochrome b6-f complex subunit 7



• Molecule 7: Cytochrome b6-f complex subunit 5



• Molecule 8: Cytochrome b6-f complex subunit 8



4 Data and refinement statistics

Property	Value	Source
Space group	P 61 2 2	Depositor
Cell constants a, b, c, α , β , γ	159.23Å 159.23Å 365.88Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	39.57 – 2.50 39.57 – 2.50	Depositor EDS
% Data completeness (in resolution range)	98.2 (39.57-2.50) 89.3 (39.57-2.50)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.79 (at 2.51Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.4_1496)	Depositor
R, R_{free}	0.201 , 0.232 0.200 , 0.232	Depositor DCC
R_{free} test set	4696 reflections (5.03%)	DCC
Wilson B-factor (Å ²)	57.4	Xtriage
Anisotropy	0.005	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 80.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	8396	wwPDB-VP
Average B, all atoms (Å ²)	95.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.69% 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: 2WA, 2WD, 1O2, 3WM, MYS, CLA, 2WM, BCR, 7PH, FES, OPC, UMQ, CD, 8K6, OCT, HEM, SQD

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	0.26	0/1761	0.41	0/2401
2	B	0.23	0/1271	0.38	0/1742
3	C	0.22	0/2182	0.38	0/2972
4	D	0.22	0/1281	0.40	0/1745
5	E	0.25	0/231	0.65	0/309
6	F	0.22	0/234	0.33	0/315
7	G	0.23	0/287	0.34	0/387
8	H	0.26	0/234	0.39	0/319
All	All	0.23	0/7481	0.40	0/10190

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
5	E	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
5	E	10	PHE	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	1708	0	1721	13	0
2	B	1232	0	1278	14	0
3	C	2137	0	2122	28	0
4	D	1250	0	1208	20	0
5	E	228	0	257	9	0
6	F	231	0	252	8	0
7	G	282	0	303	4	0
8	H	228	0	243	9	0
9	A	129	0	90	9	0
9	C	43	0	30	3	0
10	A	34	0	44	9	0
10	B	68	0	87	17	0
10	D	34	0	44	4	0
10	G	34	0	44	4	0
11	A	32	0	45	1	0
11	B	32	0	45	5	0
11	C	32	0	45	4	0
11	D	32	0	45	1	0
11	F	32	0	45	6	0
12	A	50	0	103	8	0
12	B	18	0	38	2	0
13	A	44	0	78	0	0
14	B	65	0	72	4	0
15	B	54	0	83	5	0
16	C	1	0	0	0	0
17	D	15	0	32	1	0
18	D	54	0	77	2	0
19	D	4	0	0	0	0
20	D	19	0	30	2	0
21	E	44	0	76	9	0
22	F	40	0	70	7	0
23	F	8	0	18	0	0
24	F	49	0	69	11	0
25	G	40	0	56	2	0
26	A	21	0	0	0	0
26	B	25	0	0	1	0
26	C	38	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
26	D	1	0	0	0	0
26	F	1	0	0	0	0
26	G	7	0	0	0	0
All	All	8396	0	8750	168	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 10.

All (168) 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)
10:G:101:UMQ:C5'	10:G:101:UMQ:O5'	1.63	1.46
10:A:304:UMQ:C5'	10:A:304:UMQ:O5'	1.63	1.45
10:B:203[B]:UMQ:O5'	10:B:203[B]:UMQ:C5'	1.63	1.44
10:B:201:UMQ:C1'	10:B:201:UMQ:O5'	1.69	1.41
10:B:203[B]:UMQ:O5'	10:B:203[B]:UMQ:C1'	1.69	1.38
10:D:201:UMQ:C1'	10:D:201:UMQ:O5'	1.69	1.38
10:A:304:UMQ:C1'	10:A:304:UMQ:O5'	1.69	1.38
10:G:101:UMQ:O5'	10:G:101:UMQ:C1'	1.69	1.37
10:D:201:UMQ:C1'	10:D:201:UMQ:C5'	2.46	0.93
10:G:101:UMQ:C5'	10:G:101:UMQ:C1'	2.47	0.93
10:B:203[B]:UMQ:C1'	10:B:203[B]:UMQ:C5'	2.47	0.92
10:A:304:UMQ:C1'	10:A:304:UMQ:C5'	2.48	0.92
10:B:201:UMQ:C5'	10:B:201:UMQ:C1'	2.48	0.92
10:A:304:UMQ:H6'2	10:A:304:UMQ:H11	1.59	0.83
3:C:34:VAL:HG23	3:C:243:LEU:HD23	1.70	0.73
9:A:303:HEM:HHD	9:A:303:HEM:HBC2	1.71	0.72
11:C:303:7PH:H25	11:C:303:7PH:H35A	1.70	0.72
5:E:8:ILE:HD11	21:E:101:3WM:H11	1.71	0.71
2:B:41:PRO:HG3	12:B:202[A]:8K6:H92C	1.73	0.71
10:B:201:UMQ:H6'1	10:B:201:UMQ:H51	1.73	0.71
1:A:61:THR:HG22	1:A:63:ALA:H	1.56	0.70
8:H:26:ARG:HE	8:H:29:LEU:HD11	1.57	0.70
3:C:31:PRO:O	3:C:155:ARG:NH2	2.26	0.69
1:A:4:VAL:HG13	11:A:305:7PH:H34	1.74	0.69
4:D:131:SER:HA	4:D:142:GLY:HA3	1.76	0.67
1:A:114:ARG:NH1	1:A:210:GLY:O	2.29	0.66
10:D:201:UMQ:H51	10:D:201:UMQ:H4'1	1.79	0.65
3:C:26:HIS:CG	3:C:154:ASN:HD21	2.14	0.64
3:C:33:GLU:HB2	3:C:51:LYS:HB2	1.81	0.62
10:D:201:UMQ:C5	10:D:201:UMQ:H4'1	2.30	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:C:301:HEM:HBB2	9:C:301:HEM:HMB1	1.81	0.62
24:F:103:1O2:HAZA	24:F:103:1O2:HBSA	1.82	0.60
21:E:101:3WM:H29	21:E:101:3WM:H44	1.83	0.60
24:F:103:1O2:HAY	24:F:103:1O2:HBQ	1.83	0.60
4:D:15:ARG:HH12	5:E:29:LYS:HE3	1.67	0.59
9:A:302:HEM:HBC2	9:A:302:HEM:HMC2	1.84	0.59
3:C:281:LYS:NZ	4:D:9:ASP:O	2.29	0.59
10:B:203[B]:UMQ:O5'	10:B:203[B]:UMQ:C6'	2.47	0.58
24:F:103:1O2:HAY	24:F:103:1O2:CBQ	2.33	0.58
3:C:3:PHE:HA	3:C:6:GLN:HG2	1.84	0.58
2:B:32:TRP:CE2	10:B:201:UMQ:HC2	2.39	0.58
6:F:29:ILE:HG22	24:F:103:1O2:HAS	1.85	0.57
21:E:101:3WM:H53	8:H:12:LEU:HD21	1.86	0.57
10:B:203[B]:UMQ:H6'1	10:B:203[B]:UMQ:H11	1.85	0.57
11:B:206:7PH:H29A	11:B:206:7PH:H24	1.86	0.57
2:B:114:ILE:HD13	15:B:205:OPC:HAT2	1.88	0.56
10:A:304:UMQ:C6'	10:A:304:UMQ:O5'	2.47	0.55
6:F:13:PHE:CD2	22:F:101:2WA:H14	2.41	0.55
3:C:59:GLN:HB3	3:C:67:LYS:HG3	1.89	0.55
2:B:127:PRO:HD2	15:B:205:OPC:HAG1	1.88	0.55
10:G:101:UMQ:O5'	10:G:101:UMQ:C6'	2.48	0.54
3:C:180:ILE:HB	3:C:223:GLN:H	1.73	0.54
3:C:70:LEU:HD13	3:C:155:ARG:HB3	1.90	0.54
5:E:10:PHE:H	5:E:11:LEU:HB2	1.73	0.54
1:A:32:ILE:N	8:H:29:LEU:HD13	2.23	0.54
21:E:101:3WM:H1	24:F:103:1O2:HBEA	1.89	0.53
6:F:26:LEU:HD13	6:F:29:ILE:HD11	1.90	0.53
5:E:10:PHE:CD2	8:H:13:VAL:HG11	2.44	0.53
4:D:11:PRO:HA	4:D:15:ARG:HD2	1.91	0.53
12:A:308:8K6:H112	12:A:308:8K6:H72C	1.90	0.52
4:D:59:GLU:HG2	4:D:60:LEU:HD12	1.90	0.52
7:G:34:GLU:HG2	7:G:35:LEU:HG	1.91	0.52
2:B:133:PHE:HA	14:B:204:CLA:HBB1	1.93	0.51
10:A:304:UMQ:HL3	10:B:201:UMQ:HK2	1.91	0.51
22:F:101:2WA:H2	11:F:104:7PH:H2B	1.92	0.51
12:A:308:8K6:H72C	12:A:308:8K6:C13	2.40	0.51
2:B:33:PRO:HG3	18:D:204:SQD:H4	1.91	0.51
1:A:92:MET:HB3	21:E:101:3WM:H76	1.93	0.50
11:C:303:7PH:C35	11:C:303:7PH:H25	2.39	0.50
21:E:101:3WM:H65	8:H:15:PHE:CD1	2.46	0.50
21:E:101:3WM:H1	24:F:103:1O2:CBE	2.41	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:180:ILE:HG13	3:C:219:VAL:HG11	1.92	0.50
8:H:23:VAL:HG13	8:H:28:GLY:HA2	1.93	0.50
4:D:78:ARG:HD3	4:D:92:VAL:HG22	1.93	0.50
9:A:301:HEM:HBB2	9:A:301:HEM:HMB1	1.92	0.49
4:D:78:ARG:HG3	4:D:117:TRP:CD1	2.47	0.49
9:A:303:HEM:C1A	10:B:203[B]:UMQ:H62	2.47	0.49
20:D:206:2WD:H2	20:D:206:2WD:O22	2.12	0.49
10:A:304:UMQ:CJ	10:A:304:UMQ:HF2	2.42	0.49
14:B:204:CLA:O1D	22:F:101:2WA:H66	2.13	0.48
11:B:206:7PH:H29A	11:B:206:7PH:C24	2.44	0.48
5:E:9:GLY:HA2	5:E:12:ALA:HB3	1.95	0.48
1:A:27:PRO:HG2	1:A:30:VAL:HG23	1.95	0.48
6:F:17:PHE:CE1	11:F:104:7PH:H29	2.49	0.47
3:C:5:ALA:HB2	9:C:301:HEM:HHC	1.97	0.47
12:A:306:8K6:H101	12:A:306:8K6:H61C	1.97	0.47
12:A:308:8K6:H72C	12:A:308:8K6:H131	1.97	0.47
24:F:103:1O2:HAWA	24:F:103:1O2:HBQ	1.97	0.47
1:A:129:VAL:HG21	14:B:204:CLA:H43	1.96	0.46
4:D:39:VAL:HG11	20:D:206:2WD:H19	1.97	0.46
4:D:57:LYS:NZ	4:D:63:ASP:OD1	2.49	0.46
3:C:47:LYS:HG3	3:C:128:VAL:HG13	1.96	0.46
6:F:5:LEU:HD21	7:G:11:LEU:HD12	1.98	0.46
24:F:103:1O2:HBMA	24:F:103:1O2:HBJA	1.74	0.46
4:D:57:LYS:O	4:D:82:GLN:N	2.45	0.46
2:B:153:LYS:HG3	2:B:158:GLY:H	1.81	0.45
2:B:41:PRO:HG3	10:B:203[B]:UMQ:HF1	1.97	0.45
15:B:205:OPC:HAA3	15:B:205:OPC:HAH2	1.61	0.45
4:D:118:ASN:HD22	4:D:125:LYS:HE2	1.80	0.45
22:F:101:2WA:H34	22:F:101:2WA:CBL	2.46	0.45
24:F:103:1O2:HBSA	24:F:103:1O2:CAZ	2.45	0.45
4:D:25:GLY:HA2	18:D:204:SQD:H311	1.99	0.45
5:E:10:PHE:HD2	8:H:13:VAL:HG21	1.81	0.45
11:C:303:7PH:H33A	11:C:303:7PH:H36	1.74	0.45
3:C:209:ASP:OD1	3:C:210:THR:N	2.50	0.45
5:E:11:LEU:HA	5:E:11:LEU:HD22	1.78	0.45
2:B:131:THR:HG23	11:B:206:7PH:H25	1.98	0.45
1:A:53:ALA:HB1	4:D:41:TYR:CE1	2.52	0.45
6:F:27:LEU:HD21	8:H:27:ASN:HA	1.98	0.45
1:A:129:VAL:HG21	14:B:204:CLA:H11	1.99	0.45
3:C:160:VAL:O	9:C:301:HEM:HAC	2.17	0.45
4:D:36:TYR:HB3	4:D:37:PRO:HD3	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:B:206:7PH:H38	11:B:206:7PH:H35A	1.68	0.44
4:D:117:TRP:HE1	4:D:119:ALA:HB2	1.83	0.44
6:F:20:TRP:CD2	11:F:104:7PH:H34A	2.52	0.44
9:A:303:HEM:HBA2	10:B:203[B]:UMQ:H41	2.00	0.44
3:C:182:LYS:HB2	3:C:198:ASP:H	1.82	0.44
11:F:104:7PH:H39A	11:F:104:7PH:H36	1.72	0.44
2:B:156:THR:HG22	2:B:159:LEU:H	1.81	0.44
9:A:302:HEM:HBB2	9:A:302:HEM:HMB1	2.00	0.43
10:A:304:UMQ:HB1	10:A:304:UMQ:H2'1	2.01	0.43
2:B:103:SER:OG	15:B:205:OPC:HBD2	2.18	0.43
3:C:193:VAL:HB	3:C:213:ALA:HB2	2.00	0.43
3:C:54:TYR:HB3	3:C:155:ARG:HD3	1.99	0.43
12:A:308:8K6:H171	12:A:308:8K6:H142	1.68	0.43
3:C:59:GLN:CB	3:C:67:LYS:HG3	2.49	0.43
11:F:104:7PH:H27A	25:G:102:BCR:C22	2.49	0.43
12:B:202[A]:8K6:H142	12:B:202[A]:8K6:H112	1.64	0.43
9:A:303:HEM:HMB1	9:A:303:HEM:HBB2	2.00	0.42
25:G:102:BCR:H361	25:G:102:BCR:H20C	1.80	0.42
22:F:101:2WA:H44	7:G:2:VAL:HG11	2.00	0.42
15:B:205:OPC:HBP1	15:B:205:OPC:HBS	1.79	0.42
5:E:16:GLY:CA	24:F:103:1O2:HBUA	2.49	0.42
4:D:116:PRO:HD2	4:D:127:PRO:HD3	2.01	0.42
12:A:308:8K6:H132	12:A:308:8K6:H62C	2.01	0.42
3:C:177:THR:HG23	3:C:226:THR:HA	2.01	0.42
4:D:167:GLU:HG2	4:D:168:THR:H	1.85	0.42
9:A:301:HEM:HMC1	9:A:301:HEM:HBC2	2.01	0.42
1:A:92:MET:SD	21:E:101:3WM:H71	2.60	0.42
3:C:277:LYS:NZ	26:C:402:HOH:O	2.53	0.42
3:C:51:LYS:HG2	3:C:126:GLU:HG2	2.01	0.42
3:C:53:PRO:HD2	3:C:155:ARG:HH21	1.85	0.42
9:A:303:HEM:C2A	10:B:203[B]:UMQ:H62	2.54	0.41
4:D:152:HIS:HB2	4:D:163:THR:OG1	2.21	0.41
11:B:206:7PH:H35	7:G:22:PHE:CD2	2.54	0.41
12:A:307:8K6:H152	12:A:307:8K6:H121	1.84	0.41
2:B:32:TRP:NE1	10:B:201:UMQ:HA2	2.35	0.41
1:A:207:ARG:NH1	10:B:203[B]:UMQ:O2	2.54	0.41
21:E:101:3WM:H55	21:E:101:3WM:H58	1.74	0.41
12:A:306:8K6:H132	12:A:307:8K6:H81C	2.03	0.41
4:D:122:ASN:ND2	4:D:122:ASN:O	2.54	0.41
6:F:5:LEU:HD22	22:F:101:2WA:H28	2.01	0.41
3:C:187:GLU:HB2	3:C:188:GLY:H	1.72	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:39:SER:HB3	3:C:248:VAL:HB	2.02	0.41
26:B:310:HOH:O	3:C:276:LYS:NZ	2.53	0.41
3:C:35:GLU:HB2	3:C:49:VAL:HB	2.03	0.41
22:F:101:2WA:H42	22:F:101:2WA:H34	2.03	0.41
1:A:114:ARG:NH2	2:B:21:GLY:O	2.54	0.41
3:C:72:VAL:HG21	3:C:124:TYR:O	2.21	0.41
3:C:254:ARG:HA	11:D:203:7PH:H25	2.03	0.41
11:C:303:7PH:O32	11:C:303:7PH:H34	2.15	0.41
10:A:304:UMQ:CL	10:B:201:UMQ:HI2	2.51	0.41
8:H:17:TRP:O	8:H:21:MET:HG2	2.21	0.41
1:A:107:THR:O	2:B:121:GLN:HB3	2.21	0.40
5:E:16:GLY:HA3	24:F:103:1O2:HBUA	2.03	0.40
17:D:202:MYS:H82	17:D:202:MYS:H112	1.64	0.40
4:D:43:ILE:HA	4:D:44:PRO:HD3	1.91	0.40
11:F:104:7PH:H29A	11:F:104:7PH:H2C	1.82	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	212/215 (99%)	202 (95%)	9 (4%)	1 (0%)	32	53
2	B	157/160 (98%)	151 (96%)	6 (4%)	0	100	100
3	C	277/333 (83%)	249 (90%)	23 (8%)	5 (2%)	10	17
4	D	162/179 (90%)	147 (91%)	15 (9%)	0	100	100
5	E	29/31 (94%)	26 (90%)	2 (7%)	1 (3%)	4	5
6	F	30/34 (88%)	30 (100%)	0	0	100	100
7	G	35/37 (95%)	34 (97%)	1 (3%)	0	100	100
8	H	27/29 (93%)	26 (96%)	1 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	929/1018 (91%)	865 (93%)	57 (6%)	7 (1%)	22	39

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	C	173	SER
1	A	3	ASN
3	C	185	LYS
5	E	11	LEU
3	C	189	GLU
3	C	222	GLY
3	C	188	GLY

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	183/184 (100%)	183 (100%)	0	100	100
2	B	133/134 (99%)	131 (98%)	2 (2%)	70	89
3	C	231/272 (85%)	228 (99%)	3 (1%)	73	90
4	D	133/145 (92%)	130 (98%)	3 (2%)	56	81
5	E	21/21 (100%)	20 (95%)	1 (5%)	30	53
6	F	22/24 (92%)	22 (100%)	0	100	100
7	G	29/29 (100%)	29 (100%)	0	100	100
8	H	24/24 (100%)	24 (100%)	0	100	100
All	All	776/833 (93%)	767 (99%)	9 (1%)	75	91

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	152	ASP
2	B	155	LEU
3	C	67	LYS

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Mol	Chain	Res	Type
3	C	187	GLU
3	C	231	LEU
4	D	71	GLU
4	D	111	LEU
4	D	155	THR
5	E	11	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
3	C	154	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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 31 ligands modelled in this entry, 1 is monoatomic - leaving 30 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	$\# Z > 2$
9	HEM	A	301	1	28,50,50	2.17	7 (25%)	17,82,82	1.53	5 (29%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
9	HEM	A	302	1	28,50,50	2.14	6 (21%)	17,82,82	1.49	4 (23%)
9	HEM	A	303	1,26	28,50,50	2.27	6 (21%)	17,82,82	1.47	2 (11%)
10	UMQ	A	304	-	35,35,35	3.77	17 (48%)	46,46,46	2.19	8 (17%)
11	7PH	A	305	-	31,31,37	1.25	2 (6%)	33,33,42	1.22	2 (6%)
12	8K6	A	306	-	17,17,17	0.09	0	16,16,16	0.84	0
12	8K6	A	307	-	17,17,17	0.08	0	16,16,16	0.87	0
12	8K6	A	308	-	13,13,17	0.10	0	12,12,16	0.78	0
13	2WM	A	309	-	43,43,43	0.65	2 (4%)	43,45,45	0.50	0
10	UMQ	B	201	-	35,35,35	3.76	17 (48%)	46,46,46	2.21	7 (15%)
12	8K6	B	202[A]	-	17,17,17	0.09	0	16,16,16	0.85	0
10	UMQ	B	203[B]	-	35,35,35	3.77	17 (48%)	46,46,46	2.21	9 (19%)
14	CLA	B	204	26	56,73,73	1.10	4 (7%)	65,113,113	1.22	7 (10%)
15	OPC	B	205	-	53,53,54	1.03	2 (3%)	58,61,64	1.03	2 (3%)
11	7PH	B	206	-	31,31,37	1.26	2 (6%)	33,33,42	1.18	2 (6%)
9	HEM	C	301	3	28,50,50	2.14	6 (21%)	17,82,82	1.49	3 (17%)
11	7PH	C	303	-	31,31,37	1.26	2 (6%)	33,33,42	1.23	2 (6%)
10	UMQ	D	201	-	35,35,35	3.78	17 (48%)	46,46,46	2.25	9 (19%)
17	MYS	D	202	-	14,14,14	0.09	0	13,13,13	0.83	0
11	7PH	D	203	-	31,31,37	1.26	2 (6%)	33,33,42	1.15	2 (6%)
18	SQD	D	204	-	53,54,54	0.96	5 (9%)	63,65,65	1.70	10 (15%)
19	FES	D	205	4	0,4,4	0.00	-	0,4,4	0.00	-
20	2WD	D	206	-	18,18,18	1.14	1 (5%)	18,20,20	0.55	0
21	3WM	E	101	-	43,43,43	0.76	1 (2%)	43,45,45	0.53	0
22	2WA	F	101	-	39,39,39	0.89	1 (2%)	39,41,41	0.53	0
23	OCT	F	102	-	7,7,7	0.13	0	6,6,6	0.70	0
24	1O2	F	103	-	49,49,53	1.46	5 (10%)	57,57,61	1.15	6 (10%)
11	7PH	F	104	-	31,31,37	1.26	2 (6%)	33,33,42	1.21	2 (6%)
10	UMQ	G	101	-	35,35,35	3.77	17 (48%)	46,46,46	2.23	8 (17%)
25	BCR	G	102	-	41,41,41	1.05	2 (4%)	56,56,56	1.14	4 (7%)

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
9	HEM	A	301	1	-	0/6/54/54	0/0/8/8

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
9	HEM	A	302	1	-	0/6/54/54	0/0/8/8
9	HEM	A	303	1,26	-	0/6/54/54	0/0/8/8
10	UMQ	A	304	-	-	0/20/60/60	0/2/2/2
11	7PH	A	305	-	-	0/33/33/39	0/0/0/0
12	8K6	A	306	-	-	0/15/15/15	0/0/0/0
12	8K6	A	307	-	-	0/15/15/15	0/0/0/0
12	8K6	A	308	-	-	0/11/11/15	0/0/0/0
13	2WM	A	309	-	-	0/44/45/45	0/0/0/0
10	UMQ	B	201	-	-	0/20/60/60	0/2/2/2
12	8K6	B	202[A]	-	-	0/15/15/15	0/0/0/0
10	UMQ	B	203[B]	-	-	1/20/60/60	0/2/2/2
14	CLA	B	204	26	3/3/20/25	0/37/135/135	0/0/9/9
15	OPC	B	205	-	-	0/57/57/60	0/0/0/0
11	7PH	B	206	-	-	0/33/33/39	0/0/0/0
9	HEM	C	301	3	-	0/6/54/54	0/0/8/8
11	7PH	C	303	-	-	0/33/33/39	0/0/0/0
10	UMQ	D	201	-	-	0/20/60/60	0/2/2/2
17	MYS	D	202	-	-	0/12/12/12	0/0/0/0
11	7PH	D	203	-	-	0/33/33/39	0/0/0/0
18	SQD	D	204	-	-	0/49/69/69	0/1/1/1
19	FES	D	205	4	-	0/0/4/4	0/1/1/1
20	2WD	D	206	-	-	0/19/20/20	0/0/0/0
21	3WM	E	101	-	-	0/44/45/45	0/0/0/0
22	2WA	F	101	-	-	0/40/41/41	0/0/0/0
23	OCT	F	102	-	-	0/5/5/5	0/0/0/0
24	1O2	F	103	-	1/1/8/10	0/44/64/68	0/1/1/1
11	7PH	F	104	-	-	0/33/33/39	0/0/0/0
10	UMQ	G	101	-	-	0/20/60/60	0/2/2/2
25	BCR	G	102	-	-	0/29/63/63	0/2/2/2

All (143) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
10	B	203[B]	UMQ	C6-C5	-5.78	1.32	1.51
10	B	201	UMQ	C6-C5	-5.75	1.32	1.51
10	D	201	UMQ	C6-C5	-5.74	1.32	1.51
10	A	304	UMQ	C6-C5	-5.73	1.32	1.51
10	G	101	UMQ	C6-C5	-5.70	1.32	1.51
9	A	303	HEM	C3C-C2C	-5.02	1.33	1.40
10	A	304	UMQ	C3'-C4'	-4.64	1.39	1.52
10	B	201	UMQ	O1'-C1'	-4.62	1.32	1.40
10	B	201	UMQ	C3'-C4'	-4.61	1.39	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
10	A	304	UMQ	O1'-C1'	-4.61	1.32	1.40
10	D	201	UMQ	O1'-C1'	-4.60	1.32	1.40
10	G	101	UMQ	C3'-C4'	-4.59	1.40	1.52
10	D	201	UMQ	C3'-C4'	-4.58	1.40	1.52
10	G	101	UMQ	O1'-C1'	-4.58	1.32	1.40
10	B	203[B]	UMQ	C3'-C4'	-4.57	1.40	1.52
10	B	203[B]	UMQ	O1'-C1'	-4.54	1.32	1.40
10	D	201	UMQ	C3-C2	-4.39	1.41	1.52
10	G	101	UMQ	C3-C2	-4.37	1.41	1.52
10	B	203[B]	UMQ	C3-C2	-4.34	1.41	1.52
10	A	304	UMQ	C3-C2	-4.30	1.41	1.52
10	B	201	UMQ	C3-C2	-4.28	1.41	1.52
9	A	303	HEM	C3B-C2B	-4.04	1.35	1.40
9	A	301	HEM	C3C-C2C	-4.00	1.35	1.40
9	A	302	HEM	C3B-C2B	-3.99	1.35	1.40
9	C	301	HEM	C3C-C2C	-3.99	1.35	1.40
9	A	301	HEM	C3B-C2B	-3.95	1.35	1.40
9	C	301	HEM	C3B-C2B	-3.89	1.35	1.40
9	A	302	HEM	C3C-C2C	-3.88	1.35	1.40
10	A	304	UMQ	C3'-C2'	-3.68	1.43	1.52
10	B	201	UMQ	C3'-C2'	-3.62	1.43	1.52
10	G	101	UMQ	C3'-C2'	-3.61	1.43	1.52
10	B	203[B]	UMQ	C3'-C2'	-3.60	1.43	1.52
10	D	201	UMQ	C3'-C2'	-3.57	1.43	1.52
20	D	206	2WD	O21-C2	-3.46	1.39	1.44
25	G	102	BCR	C1-C6	-3.35	1.49	1.53
10	B	203[B]	UMQ	C6'-C5'	-3.01	1.41	1.51
10	G	101	UMQ	C6'-C5'	-2.95	1.41	1.51
10	D	201	UMQ	C6'-C5'	-2.93	1.41	1.51
10	B	201	UMQ	C6'-C5'	-2.93	1.41	1.51
10	A	304	UMQ	C6'-C5'	-2.91	1.42	1.51
13	A	309	2WM	CAW-CAV	-2.82	1.35	1.51
25	G	102	BCR	C30-C25	-2.77	1.50	1.53
10	B	203[B]	UMQ	C1-C2	-2.62	1.45	1.52
10	G	101	UMQ	C1-C2	-2.60	1.45	1.52
10	D	201	UMQ	C1-C2	-2.60	1.45	1.52
10	B	201	UMQ	C1-C2	-2.58	1.45	1.52
14	B	204	CLA	CMB-C2B	-2.50	1.46	1.51
10	A	304	UMQ	C1-C2	-2.49	1.45	1.52
13	A	309	2WM	OAN-CAM	-2.35	1.41	1.44
21	E	101	3WM	OAN-CAM	-2.32	1.41	1.44
14	B	204	CLA	CMD-C2D	-2.32	1.46	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
18	D	204	SQD	O2-C2	-2.21	1.37	1.43
22	F	101	2WA	CBS-CBR	-2.16	1.39	1.51
18	D	204	SQD	O3-C3	-2.11	1.38	1.43
18	D	204	SQD	O4-C4	-2.05	1.38	1.43
9	A	301	HEM	CAA-C2A	2.02	1.55	1.52
10	B	201	UMQ	O5-C1	2.11	1.47	1.41
10	G	101	UMQ	O5-C1	2.15	1.47	1.41
10	B	203[B]	UMQ	O5-C1	2.20	1.47	1.41
10	A	304	UMQ	O5-C1	2.25	1.47	1.41
10	D	201	UMQ	O5-C1	2.30	1.47	1.41
9	A	302	HEM	C4D-ND	2.33	1.39	1.36
9	C	301	HEM	C4D-ND	2.33	1.39	1.36
9	A	301	HEM	C4D-ND	2.40	1.39	1.36
10	B	203[B]	UMQ	O2'-C2'	2.51	1.48	1.43
10	A	304	UMQ	O2'-C2'	2.53	1.48	1.43
10	D	201	UMQ	O2'-C2'	2.59	1.48	1.43
10	B	201	UMQ	O2'-C2'	2.60	1.48	1.43
10	G	101	UMQ	O2'-C2'	2.60	1.48	1.43
14	B	204	CLA	CHC-C1C	2.72	1.43	1.35
9	A	303	HEM	C4D-ND	2.76	1.40	1.36
18	D	204	SQD	O47-C7	2.77	1.42	1.34
24	F	103	1O2	CAQ-CAO	2.89	1.59	1.50
10	B	201	UMQ	O1-C4'	2.97	1.51	1.43
15	B	205	OPC	OAN-CAO	2.97	1.42	1.34
10	D	201	UMQ	O1-C4'	3.06	1.51	1.43
10	G	101	UMQ	O1-C4'	3.07	1.51	1.43
10	B	203[B]	UMQ	O1-C4'	3.14	1.51	1.43
10	A	304	UMQ	O1-C4'	3.16	1.51	1.43
18	D	204	SQD	O48-C23	3.20	1.42	1.33
10	A	304	UMQ	O3-C3	3.40	1.50	1.43
10	D	201	UMQ	O3-C3	3.41	1.50	1.43
10	B	201	UMQ	O3-C3	3.43	1.50	1.43
10	G	101	UMQ	O3-C3	3.45	1.50	1.43
24	F	103	1O2	O5-C1	3.45	1.50	1.41
10	B	203[B]	UMQ	O3-C3	3.46	1.50	1.43
10	A	304	UMQ	C4-C5	3.62	1.60	1.53
10	B	203[B]	UMQ	C4-C5	3.63	1.60	1.53
10	B	201	UMQ	C4-C5	3.64	1.60	1.53
10	D	201	UMQ	C4-C5	3.68	1.60	1.53
10	G	101	UMQ	C4-C5	3.70	1.60	1.53
15	B	205	OPC	OBJ-CBK	3.77	1.44	1.33
9	A	303	HEM	C3C-CAC	3.82	1.55	1.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	C	301	HEM	C3B-CAB	3.86	1.55	1.47
9	A	302	HEM	C3B-CAB	3.89	1.55	1.47
9	A	303	HEM	C3B-CAB	3.94	1.55	1.47
9	A	302	HEM	C3C-CAC	3.95	1.55	1.47
9	C	301	HEM	C3C-CAC	3.96	1.55	1.47
14	B	204	CLA	CHB-C4A	3.98	1.38	1.33
9	A	301	HEM	C3B-CAB	4.00	1.55	1.47
11	A	305	7PH	O21-C21	4.03	1.46	1.34
11	B	206	7PH	O21-C21	4.03	1.46	1.34
11	F	104	7PH	O21-C21	4.04	1.46	1.34
11	C	303	7PH	O21-C21	4.05	1.46	1.34
11	D	203	7PH	O21-C21	4.06	1.46	1.34
9	A	301	HEM	C3C-CAC	4.06	1.55	1.47
24	F	103	1O2	OAN-CAO	4.06	1.46	1.34
11	A	305	7PH	O31-C31	4.16	1.45	1.33
11	B	206	7PH	O31-C31	4.21	1.45	1.33
11	F	104	7PH	O31-C31	4.22	1.45	1.33
11	D	203	7PH	O31-C31	4.24	1.45	1.33
11	C	303	7PH	O31-C31	4.25	1.45	1.33
24	F	103	1O2	OBG-CBH	4.35	1.46	1.33
24	F	103	1O2	CBQ-CBR	4.51	1.57	1.31
10	G	101	UMQ	O2-C2	4.55	1.53	1.43
10	B	201	UMQ	O2-C2	4.55	1.53	1.43
10	D	201	UMQ	O2-C2	4.57	1.53	1.43
10	B	203[B]	UMQ	O2-C2	4.58	1.53	1.43
10	A	304	UMQ	O2-C2	4.61	1.53	1.43
9	A	302	HEM	C3D-C2D	5.38	1.53	1.37
9	A	301	HEM	C3D-C2D	5.38	1.53	1.37
9	A	303	HEM	C3D-C2D	5.47	1.53	1.37
9	C	301	HEM	C3D-C2D	5.50	1.54	1.37
10	G	101	UMQ	O5-C5	5.98	1.58	1.44
10	B	201	UMQ	O5-C5	5.98	1.58	1.44
10	B	203[B]	UMQ	O5-C5	6.05	1.59	1.44
10	A	304	UMQ	O5-C5	6.05	1.59	1.44
10	D	201	UMQ	O5-C5	6.24	1.59	1.44
10	B	201	UMQ	O5'-C5'	7.76	1.63	1.44
10	D	201	UMQ	O5'-C5'	7.82	1.63	1.44
10	B	203[B]	UMQ	O5'-C5'	7.87	1.63	1.44
10	G	101	UMQ	O5'-C5'	7.88	1.63	1.44
10	A	304	UMQ	O5'-C5'	7.91	1.63	1.44
10	D	201	UMQ	O3'-C3'	8.62	1.62	1.43
10	A	304	UMQ	O3'-C3'	8.64	1.62	1.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
10	B	203[B]	UMQ	O3'-C3'	8.67	1.62	1.43
10	G	101	UMQ	O3'-C3'	8.70	1.63	1.43
10	B	201	UMQ	O3'-C3'	8.74	1.63	1.43
10	B	201	UMQ	O5'-C1'	11.03	1.69	1.41
10	G	101	UMQ	O5'-C1'	11.07	1.69	1.41
10	A	304	UMQ	O5'-C1'	11.07	1.69	1.41
10	D	201	UMQ	O5'-C1'	11.07	1.69	1.41
10	B	203[B]	UMQ	O5'-C1'	11.08	1.69	1.41

All (94) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	D	201	UMQ	C1'-O5'-C5'	-9.70	95.44	113.72
10	G	101	UMQ	C1'-O5'-C5'	-9.35	96.10	113.72
10	B	203[B]	UMQ	C1'-O5'-C5'	-9.19	96.41	113.72
10	A	304	UMQ	C1'-O5'-C5'	-9.14	96.50	113.72
10	B	201	UMQ	C1'-O5'-C5'	-9.10	96.57	113.72
10	B	201	UMQ	O5-C5-C4	-4.10	102.11	109.66
10	G	101	UMQ	O5-C5-C4	-3.97	102.35	109.66
10	A	304	UMQ	O5-C5-C4	-3.94	102.40	109.66
18	D	204	SQD	C5-C6-S	-3.86	108.96	114.34
10	B	201	UMQ	C1-O1-C4'	-3.84	108.65	118.00
10	G	101	UMQ	C1-O1-C4'	-3.78	108.79	118.00
18	D	204	SQD	O9-S-O7	-3.71	101.02	113.86
14	B	204	CLA	CMB-C2B-C1B	-3.57	122.97	128.46
10	B	203[B]	UMQ	C1-O1-C4'	-3.49	109.50	118.00
10	B	203[B]	UMQ	O5-C5-C4	-3.31	103.56	109.66
10	A	304	UMQ	C1-O1-C4'	-3.20	110.21	118.00
10	D	201	UMQ	O5-C5-C4	-2.97	104.19	109.66
9	A	302	HEM	CBD-CAD-C3D	-2.94	106.85	112.47
14	B	204	CLA	O2D-CGD-O1D	-2.82	118.15	123.82
25	G	102	BCR	C33-C5-C6	-2.58	121.62	124.51
9	A	301	HEM	C1D-C2D-C3D	-2.56	105.22	107.00
9	A	301	HEM	CBD-CAD-C3D	-2.49	107.72	112.47
14	B	204	CLA	C1B-CHB-C4A	-2.46	125.24	130.12
9	A	302	HEM	C1D-C2D-C3D	-2.39	105.33	107.00
9	C	301	HEM	C1D-C2D-C3D	-2.37	105.35	107.00
9	A	303	HEM	CAD-CBD-CGD	-2.35	108.65	112.66
10	D	201	UMQ	C1-O1-C4'	-2.32	112.34	118.00
25	G	102	BCR	C7-C8-C9	-2.26	122.81	126.21
10	D	201	UMQ	O3'-C3'-C2'	-2.25	105.47	110.36
10	B	201	UMQ	O3'-C3'-C2'	-2.17	105.63	110.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	G	102	BCR	C24-C23-C22	-2.17	122.95	126.21
10	A	304	UMQ	O3'-C3'-C2'	-2.08	105.82	110.36
10	B	203[B]	UMQ	O3'-C3'-C2'	-2.08	105.83	110.36
10	G	101	UMQ	O3'-C3'-C2'	-2.07	105.86	110.36
10	B	203[B]	UMQ	C6'-C5'-C4'	-2.02	107.72	113.24
9	A	302	HEM	CMB-C2B-C3B	2.01	128.61	124.89
9	A	301	HEM	CMB-C2B-C3B	2.01	128.62	124.89
9	C	301	HEM	CMC-C2C-C3C	2.03	128.66	124.89
10	B	201	UMQ	O5-C5-C6	2.03	111.28	106.41
9	A	301	HEM	CMC-C2C-C3C	2.06	128.71	124.89
24	F	103	1O2	C3-C4-C5	2.06	113.85	110.22
10	D	201	UMQ	C3-C4-C5	2.08	113.89	110.22
24	F	103	1O2	C4-C3-C2	2.09	114.52	110.84
10	A	304	UMQ	O5-C5-C6	2.09	111.43	106.41
9	A	301	HEM	C4A-C3A-C2A	2.10	108.45	107.00
9	A	303	HEM	CMB-C2B-C3B	2.16	128.89	124.89
10	G	101	UMQ	O5-C1-C2	2.16	114.47	110.30
14	B	204	CLA	CHB-C4A-NA	2.22	127.58	124.51
10	B	203[B]	UMQ	O5'-C5'-C4'	2.23	114.31	109.75
18	D	204	SQD	O5-C5-C4	2.25	113.81	109.66
10	A	304	UMQ	O5-C1-C2	2.26	114.66	110.30
10	G	101	UMQ	C3-C4-C5	2.26	114.21	110.22
9	A	302	HEM	CMC-C2C-C3C	2.28	129.12	124.89
9	C	301	HEM	CMB-C2B-C3B	2.28	129.12	124.89
14	B	204	CLA	C4A-NA-C1A	2.28	109.28	106.45
14	B	204	CLA	CMD-C2D-C3D	2.30	129.16	124.89
24	F	103	1O2	O5-C1-C2	2.31	114.75	110.30
10	B	201	UMQ	C1-C2-C3	2.34	114.32	109.98
10	D	201	UMQ	C1-O5-C5	2.35	118.14	113.72
10	B	203[B]	UMQ	O5-C5-C6	2.36	112.06	106.41
24	F	103	1O2	C1-C2-C3	2.41	114.46	109.98
11	D	203	7PH	O31-C31-C32	2.44	118.99	111.90
25	G	102	BCR	C27-C26-C25	2.48	126.38	122.74
18	D	204	SQD	C44-O6-C1	2.53	118.95	113.76
10	B	203[B]	UMQ	C1-C2-C3	2.55	114.72	109.98
11	A	305	7PH	O31-C31-C32	2.71	119.78	111.90
10	D	201	UMQ	C1-C2-C3	2.72	115.04	109.98
10	G	101	UMQ	C1-C2-C3	2.74	115.07	109.98
14	B	204	CLA	CMB-C2B-C3B	2.76	130.01	124.89
11	F	104	7PH	O31-C31-C32	2.77	119.95	111.90
11	B	206	7PH	O31-C31-C32	2.78	119.97	111.90
18	D	204	SQD	O48-C23-C24	2.78	119.99	111.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
15	B	205	OPC	OBJ-CBK-CBL	2.79	120.03	111.90
11	C	303	7PH	O31-C31-C32	2.80	120.05	111.90
10	A	304	UMQ	C1-C2-C3	2.81	115.20	109.98
24	F	103	1O2	OBG-CBH-CBJ	2.85	120.20	111.90
10	D	201	UMQ	O5-C1-C2	2.94	115.97	110.30
18	D	204	SQD	O6-C1-C2	2.98	113.10	108.23
11	D	203	7PH	O21-C21-C22	3.23	118.26	111.55
11	B	206	7PH	O21-C21-C22	3.63	119.10	111.55
18	D	204	SQD	O8-S-C6	3.64	110.45	106.01
18	D	204	SQD	O47-C7-C8	3.80	119.44	111.55
11	A	305	7PH	O21-C21-C22	3.88	119.60	111.55
11	F	104	7PH	O21-C21-C22	3.89	119.62	111.55
15	B	205	OPC	OAN-CAO-CAP	3.94	119.74	111.55
11	C	303	7PH	O21-C21-C22	4.00	119.86	111.55
24	F	103	1O2	OAN-CAO-CAQ	4.15	120.17	111.55
18	D	204	SQD	O7-S-C6	5.19	111.26	106.83
18	D	204	SQD	O9-S-C6	5.37	111.42	106.83
10	G	101	UMQ	C2'-C3'-C4'	7.48	125.12	109.61
10	A	304	UMQ	C2'-C3'-C4'	7.50	125.15	109.61
10	B	201	UMQ	C2'-C3'-C4'	7.52	125.20	109.61
10	D	201	UMQ	C2'-C3'-C4'	7.65	125.47	109.61
10	B	203[B]	UMQ	C2'-C3'-C4'	7.70	125.58	109.61

All (4) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
24	F	103	1O2	C1
14	B	204	CLA	NC
14	B	204	CLA	ND
14	B	204	CLA	NA

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
10	B	203[B]	UMQ	CA-O1'-C1'-O5'

There are no ring outliers.

27 monomers are involved in 106 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
9	A	301	HEM	2	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
9	A	302	HEM	2	0
9	A	303	HEM	5	0
10	A	304	UMQ	9	0
11	A	305	7PH	1	0
12	A	306	8K6	2	0
12	A	307	8K6	2	0
12	A	308	8K6	5	0
10	B	201	UMQ	7	0
12	B	202[A]	8K6	2	0
10	B	203[B]	UMQ	10	0
14	B	204	CLA	4	0
15	B	205	OPC	5	0
11	B	206	7PH	5	0
9	C	301	HEM	3	0
11	C	303	7PH	4	0
10	D	201	UMQ	4	0
17	D	202	MYS	1	0
11	D	203	7PH	1	0
18	D	204	SQD	2	0
20	D	206	2WD	2	0
21	E	101	3WM	9	0
22	F	101	2WA	7	0
24	F	103	1O2	11	0
11	F	104	7PH	6	0
10	G	101	UMQ	4	0
25	G	102	BCR	2	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	214/215 (99%)	0.47	27 (12%) 4 3	43, 59, 97, 186	0
2	B	159/160 (99%)	0.54	22 (13%) 3 3	52, 77, 124, 195	0
3	C	281/333 (84%)	0.89	48 (17%) 2 1	57, 85, 191, 249	0
4	D	166/179 (92%)	2.12	65 (39%) 0 0	50, 145, 205, 239	0
5	E	31/31 (100%)	0.43	5 (16%) 2 2	81, 98, 123, 153	0
6	F	32/34 (94%)	0.13	1 (3%) 49 52	69, 87, 131, 169	0
7	G	37/37 (100%)	1.08	7 (18%) 1 1	57, 74, 144, 155	0
8	H	29/29 (100%)	1.10	3 (10%) 7 6	59, 71, 100, 144	0
All	All	949/1018 (93%)	0.93	178 (18%) 1 1	43, 81, 185, 249	0

All (178) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	C	199	ILE	12.1
2	B	160	PHE	11.6
4	D	69	PHE	9.7
3	C	183	ILE	9.2
3	C	196	LEU	9.2
4	D	70	LEU	8.6
4	D	56	ALA	8.3
3	C	176	ALA	7.9
4	D	75	VAL	7.6
4	D	67	SER	7.5
4	D	160	ILE	7.3
3	C	188	GLY	7.3
4	D	64	VAL	7.3
3	C	189	GLU	7.1
3	C	192	SER	7.1
2	B	159	LEU	6.8

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Mol	Chain	Res	Type	RSRZ
3	C	197	VAL	6.7
3	C	225	VAL	6.7
4	D	66	VAL	6.5
3	C	193	VAL	6.4
4	D	161	VAL	6.4
4	D	49	GLY	6.4
4	D	92	VAL	6.3
4	D	159	LYS	6.2
4	D	172	THR	6.2
4	D	50	ALA	6.1
4	D	102	TYR	6.1
1	A	2	ALA	6.0
4	D	55	THR	5.9
3	C	190	ASP	5.8
3	C	186	GLN	5.8
7	G	37	GLY	5.6
3	C	198	ASP	5.6
4	D	173	GLY	5.6
4	D	156	GLU	5.5
3	C	220	SER	5.5
4	D	85	LYS	5.4
3	C	224	ALA	5.3
3	C	180	ILE	5.3
4	D	51	GLY	5.3
4	D	62	ASN	5.3
4	D	157	ASN	5.2
4	D	171	ARG	5.1
3	C	184	ALA	5.1
3	C	219	VAL	5.0
4	D	72	SER	4.9
4	D	168	THR	4.9
4	D	174	GLU	4.9
3	C	218	ILE	4.9
4	D	48	GLY	4.8
4	D	57	LYS	4.8
4	D	71	GLU	4.8
4	D	76	GLY	4.8
4	D	60	LEU	4.7
3	C	177	THR	4.7
4	D	63	ASP	4.7
4	D	53	GLY	4.7
2	B	153	LYS	4.6

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Mol	Chain	Res	Type	RSRZ
3	C	182	LYS	4.6
3	C	289	PHE	4.6
2	B	47	SER	4.5
4	D	179	SER	4.5
2	B	157	LEU	4.5
5	E	31	LEU	4.5
3	C	221	GLU	4.5
4	D	162	LEU	4.5
3	C	288	ASN	4.4
4	D	98	ALA	4.4
4	D	158	ASP	4.4
4	D	73	HIS	4.4
2	B	50	CYS	4.3
4	D	140	VAL	4.2
3	C	179	THR	4.2
4	D	52	GLY	4.1
3	C	195	TYR	4.1
4	D	175	GLU	4.0
4	D	99	ILE	3.9
4	D	154	LYS	3.9
3	C	285	ALA	3.9
3	C	208	SER	3.9
4	D	65	SER	3.8
1	A	92	MET	3.8
4	D	141	ARG	3.7
2	B	46	GLY	3.7
4	D	165	TRP	3.7
3	C	209	ASP	3.6
3	C	181	SER	3.5
4	D	170	PHE	3.5
1	A	95	LEU	3.5
3	C	211	ILE	3.5
3	C	226	THR	3.4
4	D	155	THR	3.4
1	A	35	CYS	3.4
1	A	99	LEU	3.4
4	D	169	ASP	3.4
6	F	1	MET	3.4
1	A	96	MET	3.4
8	H	1	MET	3.3
2	B	151	LEU	3.3
4	D	54	THR	3.2

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Mol	Chain	Res	Type	RSRZ
4	D	13	MET	3.2
2	B	154	SER	3.2
1	A	151	VAL	3.2
2	B	152	ASP	3.1
4	D	91	ILE	3.1
5	E	27	SER	3.1
3	C	223	GLN	3.1
3	C	194	LYS	3.1
1	A	43	CYS	3.1
1	A	36	LEU	3.0
2	B	155	LEU	3.0
1	A	39	ILE	3.0
2	B	51	ILE	3.0
4	D	74	ASN	3.0
3	C	210	THR	3.0
4	D	15	ARG	3.0
4	D	176	PRO	2.9
2	B	44	ILE	2.9
3	C	4	TRP	2.9
4	D	16	ARG	2.9
1	A	150	ILE	2.8
5	E	29	LYS	2.8
4	D	68	LYS	2.8
3	C	187	GLU	2.8
2	B	54	LEU	2.8
2	B	62	THR	2.7
5	E	10	PHE	2.7
1	A	33	PHE	2.7
3	C	222	GLY	2.7
3	C	172	TYR	2.7
7	G	1	MET	2.7
2	B	49	ALA	2.6
3	C	175	ALA	2.6
3	C	178	GLY	2.6
1	A	4	VAL	2.6
1	A	32	ILE	2.6
2	B	79	TRP	2.6
1	A	88	TRP	2.6
3	C	229	ASP	2.6
3	C	217	LEU	2.6
4	D	167	GLU	2.5
1	A	101	VAL	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	34	TYR	2.5
4	D	84	LEU	2.4
4	D	153	ALA	2.4
4	D	78	ARG	2.4
1	A	94	VAL	2.4
2	B	43	VAL	2.4
7	G	26	TYR	2.4
4	D	11	PRO	2.3
4	D	152	HIS	2.3
2	B	48	PHE	2.3
1	A	89	SER	2.3
8	H	29	LEU	2.3
3	C	93	GLU	2.3
3	C	227	ALA	2.3
7	G	10	VAL	2.3
3	C	168	ASN	2.2
1	A	91	SER	2.2
1	A	40	THR	2.2
4	D	139	VAL	2.2
1	A	102	PHE	2.2
2	B	45	MET	2.1
2	B	53	ALA	2.1
1	A	5	TYR	2.1
5	E	30	ILE	2.1
7	G	13	LEU	2.1
7	G	17	THR	2.1
3	C	67	LYS	2.1
1	A	42	VAL	2.1
8	H	18	SER	2.1
2	B	52	VAL	2.1
1	A	3	ASN	2.0
1	A	159	PRO	2.0
4	D	109	THR	2.0
7	G	30	LYS	2.0
1	A	104	VAL	2.0
3	C	70	LEU	2.0

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

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

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q < 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
11	7PH	B	206	32/38	0.56	0.71	18.50	77,132,182,184	0
20	2WD	D	206	19/19	0.63	0.67	18.26	75,123,142,145	0
24	1O2	F	103	49/53	0.65	0.63	10.23	80,127,216,220	0
17	MYS	D	202	15/15	0.56	0.39	8.09	93,107,121,126	0
12	8K6	A	307	18/18	0.67	0.36	7.01	76,108,124,127	0
10	UMQ	G	101	34/34	0.51	0.69	6.08	81,173,199,284	0
10	UMQ	D	201	34/34	0.59	0.66	5.78	102,210,248,264	0
12	8K6	A	306	18/18	0.63	0.30	5.47	93,113,147,148	0
11	7PH	C	303	32/38	0.67	0.40	4.28	73,117,149,150	0
12	8K6	B	202[A]	18/18	0.64	0.46	3.60	47,102,122,122	18
10	UMQ	B	203[B]	34/34	0.77	0.41	3.54	80,103,132,144	34
12	8K6	A	308	14/18	0.77	0.30	3.45	62,82,95,99	0
11	7PH	F	104	32/38	0.81	0.28	3.27	81,101,172,175	0
22	2WA	F	101	40/40	0.63	0.38	2.80	70,111,169,182	0
15	OPC	B	205	54/55	0.95	0.23	2.40	55,92,121,137	0
13	2WM	A	309	44/44	0.77	0.29	1.68	70,96,152,158	0
11	7PH	D	203	32/38	0.65	0.25	1.57	54,81,153,157	0
11	7PH	A	305	32/38	0.71	0.37	1.41	93,126,189,190	0
18	SQD	D	204	54/54	0.92	0.27	1.30	73,116,159,177	0
21	3WM	E	101	44/44	0.62	0.35	1.28	60,97,122,125	0
10	UMQ	B	201	34/34	0.86	0.30	0.86	64,114,151,224	0
25	BCR	G	102	40/40	0.66	0.35	0.85	49,74,116,122	0
14	CLA	B	204	65/65	0.93	0.21	0.53	59,79,107,117	0
9	HEM	A	302	43/43	0.99	0.23	0.24	34,57,71,76	0
9	HEM	A	301	43/43	0.98	0.18	-0.10	31,50,65,78	0
9	HEM	C	301	43/43	0.98	0.17	-0.19	46,69,96,113	0
9	HEM	A	303	43/43	0.97	0.21	-0.21	47,66,85,95	0
19	FES	D	205	4/4	0.99	0.06	-1.84	96,97,100,102	0
23	OCT	F	102	8/8	0.75	0.48	-	101,106,110,116	0
10	UMQ	A	304	34/34	0.67	0.46	-	127,146,201,254	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
16	CD	C	302	1/1	0.67	0.11	-	136,136,136,136	1

6.5 Other polymers [i](#)

There are no such residues in this entry.