



Full wwPDB X-ray Structure Validation Report ⓘ

Sep 7, 2017 – 09:25 AM EDT

PDB ID : 5O4C
Title : From macrocrystals to microcrystals: a strategy for membrane protein serial crystallography
Authors : Dods, R.; Baath, P.; Branden, G.; Neutze, R.
Deposited on : unknown
Resolution : 2.80 Å(reported)

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

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

A user guide is available at

<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 : rb-20029824
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) : rb-20029824

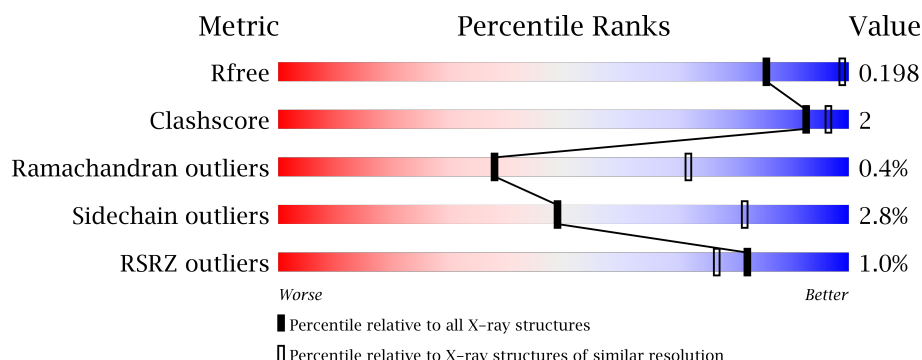
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	100719	2583 (2.80-2.80)
Clashscore	112137	3033 (2.80-2.80)
Ramachandran outliers	110173	2983 (2.80-2.80)
Sidechain outliers	110143	2985 (2.80-2.80)
RSRZ outliers	101464	2610 (2.80-2.80)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments 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	C	336	
2	H	258	
3	L	273	
4	M	323	

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 crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
14	NS5	M	406	-	-	-	X
6	DGA	C	405	-	-	-	X
7	SO4	H	704	-	-	-	X
7	SO4	M	412	-	-	-	X
8	LDA	H	706	-	-	-	X
8	LDA	H	707	-	-	-	X
8	LDA	L	304	-	-	-	X
9	HTO	L	305	-	-	-	X

2 Entry composition

There are 15 unique types of molecules in this entry. The entry contains 10196 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 Photosynthetic reaction center cytochrome c subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	C	332	Total	C	N	O	S	0	0	0
			2602	1640	466	478	18			

- Molecule 2 is a protein called Reaction center protein H chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	H	258	Total	C	N	O	S	0	0	0
			2018	1292	344	380	2			

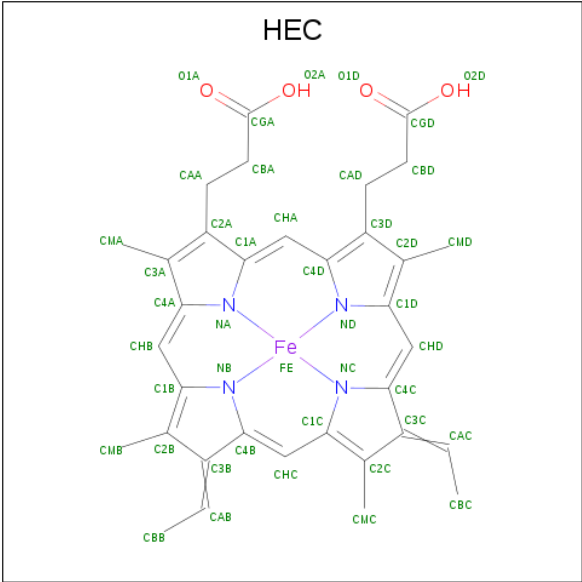
- Molecule 3 is a protein called Reaction center protein L chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	L	273	Total	C	N	O	S	0	1	0
			2172	1460	350	355	7			

- Molecule 4 is a protein called Reaction center protein M chain.

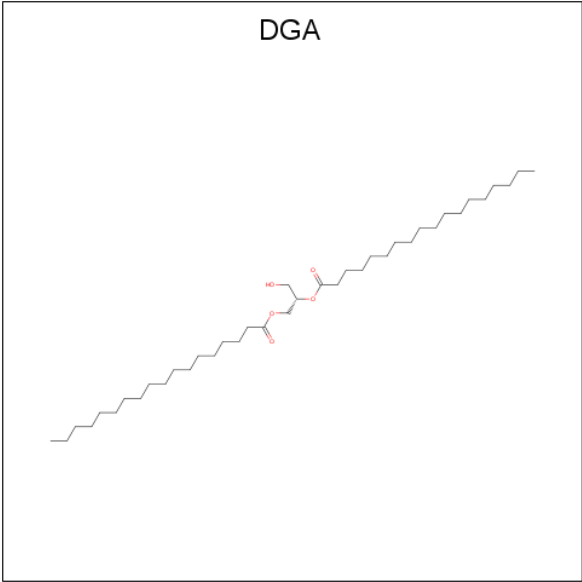
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	M	323	Total	C	N	O	S	0	0	0
			2555	1702	419	423	11			

- Molecule 5 is HEME C (three-letter code: HEC) (formula: $C_{34}H_{34}FeN_4O_4$).



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

- Molecule 6 is DIACYL GLYCEROL (three-letter code: DGA) (formula: C₃₉H₇₆O₅).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	C	1	Total	C	O	0	0
			37	33	4		

- Molecule 7 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



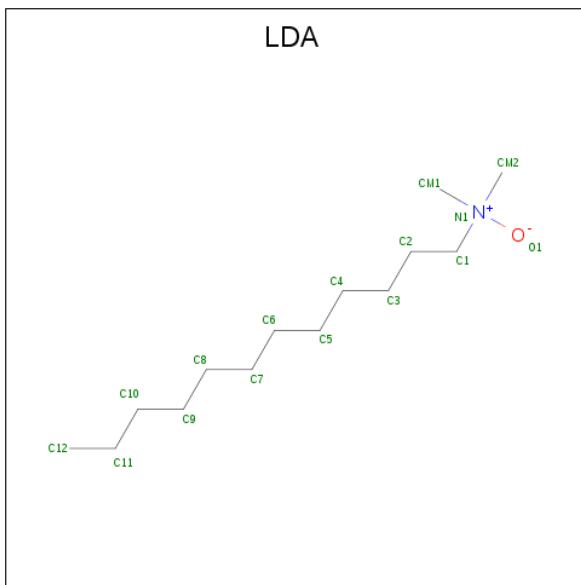
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	C	1	Total	O	S	0	0
			5	4	1		
7	H	1	Total	O	S	0	0
			5	4	1		
7	H	1	Total	O	S	0	0
			5	4	1		
7	H	1	Total	O	S	0	0
			5	4	1		
7	H	1	Total	O	S	0	0
			5	4	1		
7	M	1	Total	O	S	0	0
			5	4	1		
7	M	1	Total	O	S	0	0
			5	4	1		
7	M	1	Total	O	S	0	0
			5	4	1		
7	M	1	Total	O	S	0	0
			5	4	1		
7	M	1	Total	O	S	0	0
			5	4	1		

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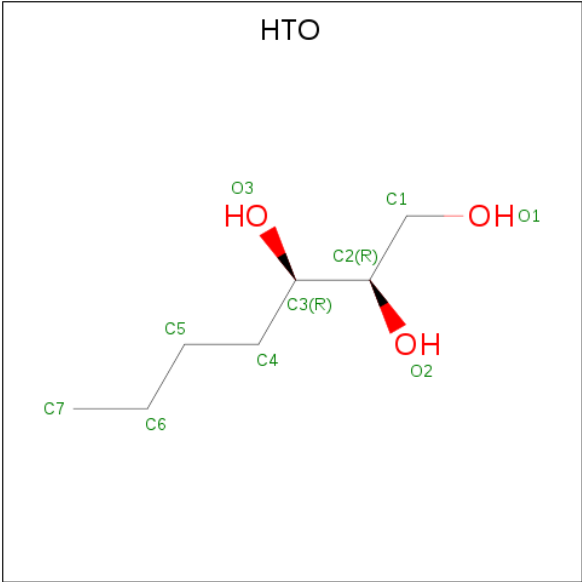
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	M	1	Total	O	S	0	0
			5	4	1		

- Molecule 8 is LAURYL DIMETHYLAMINE-N-OXIDE (three-letter code: LDA) (formula: $C_{14}H_{31}NO$).



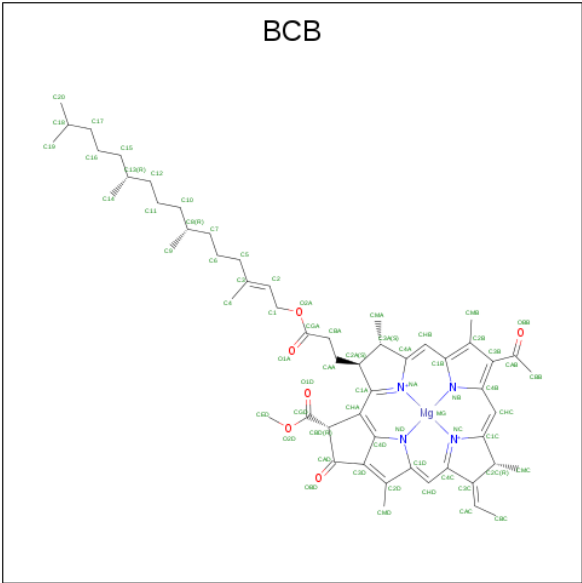
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
8	H	1	Total	C	N	O	0	0
			16	14	1	1		
8	H	1	Total	C	N	O	0	0
			16	14	1	1		
8	H	1	Total	C	N	O	0	0
			16	14	1	1		
8	L	1	Total	C	N	O	0	0
			16	14	1	1		

- Molecule 9 is HEPTANE-1,2,3-TRIOL (three-letter code: HTO) (formula: $C_7H_{16}O_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
9	H	1	Total	C	O		0	0
			10	7	3			
9	L	1	Total	C	O		0	0
			10	7	3			

- Molecule 10 is BACTERIOCHLOROPHYLL B (three-letter code: BCB) (formula: C₅₅H₇₂MgN₄O₆).



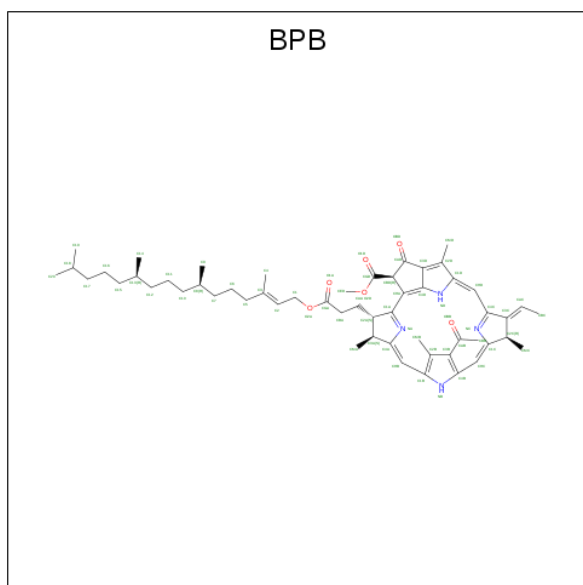
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
10	L	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
10	L	1	Total	C	Mg	N	O	0
			66	55	1	4	6	

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
10	M	1	Total	C	Mg	N	O	0	0
			66	55	1	4	6		
10	M	1	Total	C	Mg	N	O	0	0
			66	55	1	4	6		

- Molecule 11 is BACTERIOPHEOPHYTIN B (three-letter code: BPB) (formula: $C_{55}H_{74}N_4O_6$).

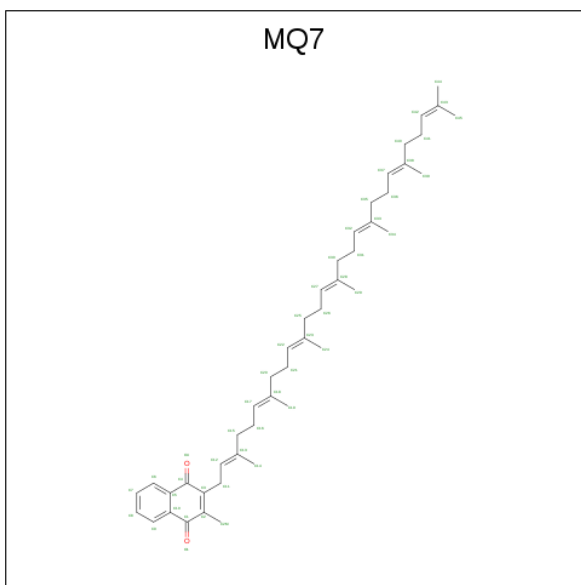


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
11	L	1	Total	C	N	O	0	0
			65	55	4	6		
11	M	1	Total	C	N	O	0	0
			65	55	4	6		

- Molecule 12 is FE (II) ION (three-letter code: FE2) (formula: Fe).

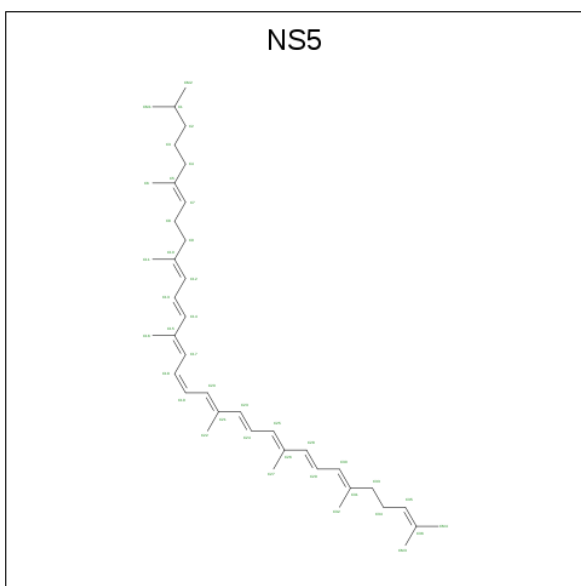
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
12	M	1	Total	Fe	0	0
			1	1		

- Molecule 13 is MENAQUINONE-7 (three-letter code: MQ7) (formula: $C_{46}H_{64}O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
13	M	1	Total	C	O	0	0
			48	46	2		

- Molecule 14 is 15-cis-1,2-dihydroneurosporene (three-letter code: NS5) (formula: C₄₀H₆₀).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
14	M	1	Total	C	0	0
			40	40		

- Molecule 15 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
15	C	3	Total 3	O 3	0	0
15	H	2	Total 2	O 2	0	0
15	L	4	Total 4	O 4	0	0
15	M	4	Total 4	O 4	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: Photosynthetic reaction center cytochrome c subunit

Chain C:  95% ..



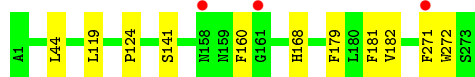
- Molecule 2: Reaction center protein H chain

Chain H:  93% 6% .



- Molecule 3: Reaction center protein L chain

Chain L:  96% .



- Molecule 4: Reaction center protein M chain

Chain M:  94% 6%



4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	226.40 Å 226.40 Å 113.70 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	36.90 – 2.80 36.88 – 2.80	Depositor EDS
% Data completeness (in resolution range)	99.9 (36.90-2.80) 100.0 (36.88-2.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.42 (at 2.81 Å)	Xtriage
Refinement program	REFMAC 5.8.0158	Depositor
R, R_{free}	0.165 , 0.196 0.172 , 0.198	Depositor DCC
R_{free} test set	3626 reflections (5.23%)	DCC
Wilson B-factor (Å ²)	102.2	Xtriage
Anisotropy	0.021	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 67.9	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	0.96	EDS
Total number of atoms	10196	wwPDB-VP
Average B, all atoms (Å ²)	98.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.91% 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: LDA, DGA, HTO, BCB, BPB, FE2, SO4, MQ7, HEC, FME, NS5

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	C	0.46	0/2669	0.70	0/3637
2	H	0.50	0/2055	0.75	1/2807 (0.0%)
3	L	0.50	0/2267	0.67	0/3095
4	M	0.50	0/2659	0.66	0/3637
All	All	0.49	0/9650	0.70	1/13176 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	86	ARG	NE-CZ-NH1	5.50	123.05	120.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	2602	0	2578	5	0
2	H	2018	0	2020	5	0
3	L	2172	0	2097	5	0
4	M	2555	0	2452	10	0
5	C	172	0	120	4	0
6	C	37	0	58	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	C	5	0	0	0	0
7	H	20	0	0	0	0
7	M	35	0	0	0	0
8	H	48	0	93	0	0
8	L	16	0	31	0	0
9	H	10	0	16	0	0
9	L	10	0	16	0	0
10	L	132	0	144	5	0
10	M	132	0	144	6	0
11	L	65	0	74	2	0
11	M	65	0	74	3	0
12	M	1	0	0	0	0
13	M	48	0	64	0	0
14	M	40	0	60	4	0
15	C	3	0	0	0	0
15	H	2	0	0	0	0
15	L	4	0	0	0	0
15	M	4	0	0	0	0
All	All	10196	0	10041	37	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 2.

All (37) 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)
11:L:303:BPB:HBBB	11:L:303:BPB:HMB	1.74	0.70
4:M:159:GLY:HA3	14:M:406:NS5:H272	1.80	0.63
11:M:405:BPB:HBBB	11:M:405:BPB:HHC	1.82	0.61
10:L:302:BCB:HBB2	10:L:302:BCB:HMB1	1.84	0.59
10:M:403:BCB:HBB2	10:M:403:BCB:HHC	1.84	0.59
5:C:402:HEC:HMC1	5:C:402:HEC:HBC3	1.86	0.57
3:L:124:PRO:HD3	11:L:303:BPB:HAC	1.87	0.55
4:M:184:LEU:CD2	10:M:403:BCB:HBC3	2.37	0.54
5:C:402:HEC:HMB1	5:C:402:HEC:HBB3	1.88	0.54
4:M:121:THR:HG23	4:M:156:LEU:HD21	1.90	0.53
10:L:302:BCB:CBB	10:L:302:BCB:HMB1	2.38	0.53
4:M:184:LEU:HD21	10:M:403:BCB:HBC3	1.89	0.53
5:C:401:HEC:HMB1	5:C:401:HEC:HBB3	1.93	0.51
3:L:168:HIS:CE1	10:L:301:BCB:HMC2	2.45	0.51
2:H:180:PHE:CE2	4:M:12:ALA:HB2	2.47	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:278:ASN:HB3	1:C:302:GLN:HE21	1.77	0.50
5:C:403:HEC:HBC1	5:C:404:HEC:HMA1	1.94	0.50
10:L:302:BCB:HMD2	10:M:404:BCB:HBB3	1.94	0.49
1:C:102:TYR:CG	1:C:103:PRO:HD3	2.49	0.48
2:H:117:TYR:HB2	2:H:236:ASP:HB3	1.97	0.46
3:L:181:PHE:HB3	11:M:405:BPB:CBB	2.46	0.46
2:H:20:GLN:HG2	4:M:202:PHE:CE2	2.51	0.46
4:M:157:CYS:HA	4:M:161:ILE:HB	1.97	0.45
3:L:181:PHE:CD2	11:M:405:BPB:HBB	2.51	0.45
2:H:136:PRO:HA	2:H:172:TRP:HA	1.98	0.45
1:C:102:TYR:CD2	1:C:103:PRO:HD3	2.53	0.44
2:H:45:GLU:HG3	2:H:46:PRO:HD2	1.99	0.44
3:L:179:PHE:HA	3:L:182:VAL:HG12	2.00	0.44
10:M:404:BCB:HMB1	10:M:404:BCB:CBB	2.47	0.43
10:M:403:BCB:HBB3	10:M:404:BCB:H62	1.99	0.43
1:C:163:VAL:HA	1:C:168:THR:HG21	2.01	0.43
10:L:301:BCB:HMB1	10:L:301:BCB:HBB3	2.00	0.42
14:M:406:NS5:H111	14:M:406:NS5:H13	1.89	0.42
1:C:217:GLY:HA2	4:M:167:GLY:O	2.21	0.41
14:M:406:NS5:H29	14:M:406:NS5:H271	1.86	0.41
4:M:132:TYR:CE2	4:M:142:THR:HG21	2.56	0.41
4:M:114:LEU:HD11	14:M:406:NS5:H351	2.02	0.41

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	C	330/336 (98%)	316 (96%)	14 (4%)	0	100	100
2	H	256/258 (99%)	244 (95%)	9 (4%)	3 (1%)	15	44
3	L	272/273 (100%)	259 (95%)	12 (4%)	1 (0%)	38	72

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
4	M	321/323 (99%)	311 (97%)	9 (3%)	1 (0%)	44 77
All	All	1179/1190 (99%)	1130 (96%)	44 (4%)	5 (0%)	38 72

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	H	47	LEU
3	L	271	PHE
2	H	46	PRO
2	H	50	VAL
4	M	177	ILE

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	C	281/282 (100%)	274 (98%)	7 (2%)	53 84
2	H	212/212 (100%)	203 (96%)	9 (4%)	34 68
3	L	219/218 (100%)	214 (98%)	5 (2%)	56 86
4	M	249/249 (100%)	243 (98%)	6 (2%)	54 85
All	All	961/961 (100%)	934 (97%)	27 (3%)	49 82

All (27) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	38	TYR
1	C	123	GLN
1	C	146	ARG
1	C	159	THR
1	C	252	THR
1	C	322	LEU
1	C	332	LYS
2	H	47	LEU
2	H	52	LEU

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Mol	Chain	Res	Type
2	H	102	GLN
2	H	178	HIS
2	H	185	LEU
2	H	193	THR
2	H	205	LYS
2	H	212	SER
2	H	236	ASP
3	L	44	LEU
3	L	119	LEU
3	L	141	SER
3	L	160	PHE
3	L	272	TRP
4	M	40	LYS
4	M	51	LEU
4	M	194	PHE
4	M	214	PHE
4	M	257	ASN
4	M	290	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	C	123	GLN
1	C	206	GLN
1	C	302	GLN
1	C	310	GLN
2	H	102	GLN
2	H	106	ASN
4	M	147	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

1 non-standard protein/DNA/RNA residue is 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	$\# Z > 2$
2	FME	H	1	2	9,9,10	0.84	0	7,9,11	3.47	3 (42%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	FME	H	1	2	-	0/6/9/11	0/0/0/0

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
2	H	1	FME	CA-N-CN	-8.07	110.41	122.82
2	H	1	FME	O-C-CA	-2.19	120.03	125.15
2	H	1	FME	CE-SD-CG	2.80	110.40	100.35

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates

There are no carbohydrates in this entry.

5.6 Ligand geometry

Of 32 ligands modelled in this entry, 1 is monoatomic - leaving 31 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
5	HEC	C	401	1	28,50,50	1.50	2 (7%)	16,82,82	2.21	5 (31%)
5	HEC	C	402	1	28,50,50	1.41	2 (7%)	16,82,82	1.91	5 (31%)
5	HEC	C	403	1	28,50,50	1.68	3 (10%)	16,82,82	1.84	4 (25%)
5	HEC	C	404	1	28,50,50	1.51	3 (10%)	16,82,82	2.21	6 (37%)
6	DGA	C	405	1	36,36,43	1.27	2 (5%)	38,38,45	1.47	5 (13%)
7	SO4	C	406	-	4,4,4	0.47	0	6,6,6	0.30	0
8	LDA	H	701	-	13,15,15	2.26	1 (7%)	14,17,17	0.76	0
7	SO4	H	702	-	4,4,4	0.43	0	6,6,6	0.48	0
7	SO4	H	703	-	4,4,4	0.43	0	6,6,6	0.17	0
7	SO4	H	704	-	4,4,4	0.37	0	6,6,6	0.26	0
7	SO4	H	705	-	4,4,4	0.41	0	6,6,6	0.21	0
8	LDA	H	706	-	13,15,15	2.37	1 (7%)	14,17,17	0.96	1 (7%)
8	LDA	H	707	-	13,15,15	2.36	1 (7%)	14,17,17	1.16	1 (7%)
9	HTO	H	708	-	9,9,9	0.55	0	9,10,10	0.48	0
10	BCB	L	301	-	63,74,74	3.42	25 (39%)	50,115,115	2.28	17 (34%)
10	BCB	L	302	-	63,74,74	3.34	27 (42%)	50,115,115	2.08	14 (28%)
11	BPB	L	303	-	63,70,70	2.78	17 (26%)	67,101,101	2.06	13 (19%)
8	LDA	L	304	-	13,15,15	2.32	1 (7%)	14,17,17	0.45	0
9	HTO	L	305	-	9,9,9	0.70	0	9,10,10	0.91	0
13	MQ7	M	402	-	49,49,49	1.39	2 (4%)	61,63,63	1.20	5 (8%)
10	BCB	M	403	-	63,74,74	3.35	26 (41%)	50,115,115	1.99	11 (22%)
10	BCB	M	404	-	63,74,74	3.13	23 (36%)	50,115,115	2.24	15 (30%)
11	BPB	M	405	-	63,70,70	2.84	18 (28%)	67,101,101	2.13	18 (26%)
14	NS5	M	406	-	39,39,39	1.48	2 (5%)	44,46,46	1.83	11 (25%)
7	SO4	M	407	-	4,4,4	0.38	0	6,6,6	0.49	0
7	SO4	M	408	-	4,4,4	0.37	0	6,6,6	0.18	0
7	SO4	M	409	-	4,4,4	0.42	0	6,6,6	0.30	0
7	SO4	M	410	-	4,4,4	0.49	0	6,6,6	0.31	0
7	SO4	M	411	-	4,4,4	0.48	0	6,6,6	0.23	0
7	SO4	M	412	-	4,4,4	0.46	0	6,6,6	0.32	0
7	SO4	M	413	-	4,4,4	0.42	0	6,6,6	0.14	0

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
5	HEC	C	401	1	-	0/6/54/54	0/0/8/8
5	HEC	C	402	1	-	0/6/54/54	0/0/8/8
5	HEC	C	403	1	-	0/6/54/54	0/0/8/8
5	HEC	C	404	1	-	0/6/54/54	0/0/8/8
6	DGA	C	405	1	-	0/37/37/45	0/0/0/0
7	SO4	C	406	-	-	0/0/0/0	0/0/0/0
8	LDA	H	701	-	-	0/13/13/13	0/0/0/0
7	SO4	H	702	-	-	0/0/0/0	0/0/0/0
7	SO4	H	703	-	-	0/0/0/0	0/0/0/0
7	SO4	H	704	-	-	0/0/0/0	0/0/0/0
7	SO4	H	705	-	-	0/0/0/0	0/0/0/0
8	LDA	H	706	-	-	0/13/13/13	0/0/0/0
8	LDA	H	707	-	-	0/13/13/13	0/0/0/0
9	HTO	H	708	-	-	0/10/10/10	0/0/0/0
10	BCB	L	301	-	-	0/41/177/177	0/0/9/9
10	BCB	L	302	-	-	0/41/177/177	0/0/9/9
11	BPB	L	303	-	-	1/47/105/105	0/1/6/6
8	LDA	L	304	-	-	0/13/13/13	0/0/0/0
9	HTO	L	305	-	-	0/10/10/10	0/0/0/0
13	MQ7	M	402	-	-	0/41/61/61	0/2/2/2
10	BCB	M	403	-	-	1/41/177/177	0/0/9/9
10	BCB	M	404	-	-	0/41/177/177	0/0/9/9
11	BPB	M	405	-	-	0/47/105/105	0/1/6/6
14	NS5	M	406	-	-	0/43/43/43	0/0/0/0
7	SO4	M	407	-	-	0/0/0/0	0/0/0/0
7	SO4	M	408	-	-	0/0/0/0	0/0/0/0
7	SO4	M	409	-	-	0/0/0/0	0/0/0/0
7	SO4	M	410	-	-	0/0/0/0	0/0/0/0
7	SO4	M	411	-	-	0/0/0/0	0/0/0/0
7	SO4	M	412	-	-	0/0/0/0	0/0/0/0
7	SO4	M	413	-	-	0/0/0/0	0/0/0/0

All (156) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
10	L	302	BCB	C3D-C4D	-13.73	1.39	1.54
10	L	301	BCB	C3D-C4D	-13.48	1.39	1.54
10	M	403	BCB	C3D-C4D	-13.33	1.39	1.54
10	M	404	BCB	C3D-C4D	-12.09	1.40	1.54
10	L	301	BCB	C1D-ND	-8.63	1.31	1.50
8	H	706	LDA	O1-N1	-8.47	1.25	1.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	H	707	LDA	O1-N1	-8.41	1.25	1.42
8	L	304	LDA	O1-N1	-8.17	1.26	1.42
10	M	403	BCB	CHB-C4A	-8.11	1.33	1.52
8	H	701	LDA	O1-N1	-8.04	1.26	1.42
10	M	403	BCB	C1D-ND	-7.98	1.33	1.50
10	M	404	BCB	C1D-ND	-7.78	1.33	1.50
10	L	301	BCB	CHB-C4A	-7.65	1.34	1.52
10	L	302	BCB	C1D-ND	-7.64	1.33	1.50
10	L	302	BCB	CHB-C4A	-7.58	1.34	1.52
10	M	404	BCB	CHB-C4A	-7.25	1.35	1.52
10	L	301	BCB	C1B-NB	-7.21	1.34	1.50
10	M	403	BCB	C1B-NB	-7.16	1.34	1.50
10	M	403	BCB	C4B-NB	-6.72	1.35	1.50
10	L	302	BCB	C1B-NB	-6.66	1.36	1.50
10	M	404	BCB	C1B-NB	-6.63	1.36	1.50
10	L	302	BCB	C4B-NB	-6.32	1.36	1.50
10	L	301	BCB	C4D-ND	-6.24	1.36	1.50
5	C	403	HEC	C3B-C2B	-6.24	1.34	1.40
10	L	302	BCB	C4D-ND	-6.23	1.36	1.50
10	L	301	BCB	CHD-C1D	-6.20	1.43	1.53
10	M	404	BCB	C4D-ND	-6.08	1.37	1.50
10	M	404	BCB	C4B-NB	-6.04	1.37	1.50
10	L	301	BCB	C4B-NB	-6.02	1.37	1.50
10	M	403	BCB	C4D-ND	-5.72	1.38	1.50
10	M	403	BCB	C3B-C4B	-5.18	1.48	1.54
10	M	404	BCB	CHD-C1D	-5.14	1.45	1.53
5	C	401	HEC	C3B-C2B	-5.12	1.35	1.40
11	L	303	BPB	C1A-NA	-5.11	1.26	1.36
10	L	301	BCB	CHD-C4C	-5.05	1.44	1.53
5	C	404	HEC	C3B-C2B	-5.03	1.35	1.40
10	L	302	BCB	CHD-C1D	-4.86	1.45	1.53
10	M	403	BCB	CHD-C1D	-4.86	1.45	1.53
11	M	405	BPB	C4C-NC	-4.80	1.26	1.36
11	M	405	BPB	C1A-NA	-4.78	1.27	1.36
10	L	301	BCB	CHB-C1B	-4.72	1.46	1.53
10	L	302	BCB	C3B-C4B	-4.68	1.49	1.54
5	C	402	HEC	C3B-C2B	-4.63	1.35	1.40
10	M	403	BCB	CHD-C4C	-4.45	1.45	1.53
10	L	302	BCB	CHD-C4C	-4.22	1.45	1.53
10	M	404	BCB	CHB-C1B	-4.16	1.47	1.53
10	M	403	BCB	CHB-C1B	-4.14	1.47	1.53
11	L	303	BPB	C4C-NC	-4.11	1.27	1.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
10	M	404	BCB	CHD-C4C	-4.07	1.45	1.53
5	C	404	HEC	C3C-C2C	-4.00	1.36	1.40
10	L	301	BCB	C3B-C4B	-3.97	1.49	1.54
10	L	301	BCB	C2D-C1D	-3.91	1.45	1.53
5	C	403	HEC	C3C-C2C	-3.88	1.36	1.40
5	C	401	HEC	C3C-C2C	-3.83	1.36	1.40
10	L	302	BCB	CHB-C1B	-3.79	1.47	1.53
10	L	302	BCB	C1A-CHA	-3.59	1.48	1.53
10	M	404	BCB	C2D-C1D	-3.59	1.46	1.53
10	L	302	BCB	C2D-C1D	-3.58	1.46	1.53
10	M	404	BCB	C3B-C4B	-3.58	1.50	1.54
10	L	302	BCB	CHC-C4B	-3.50	1.48	1.53
10	L	301	BCB	C4A-C3A	-3.30	1.49	1.53
10	M	403	BCB	C3B-C2B	-3.24	1.46	1.55
5	C	402	HEC	C3C-C2C	-3.19	1.37	1.40
10	M	404	BCB	CBD-CAD	-3.18	1.48	1.53
10	M	403	BCB	C1A-CHA	-3.16	1.48	1.53
11	L	303	BPB	C1C-NC	-3.12	1.32	1.38
10	M	403	BCB	C4A-C3A	-3.09	1.50	1.53
11	M	405	BPB	C1C-NC	-3.08	1.32	1.38
10	L	302	BCB	C3B-CAB	-3.08	1.48	1.52
10	L	301	BCB	C1A-CHA	-3.08	1.49	1.53
10	L	301	BCB	C3D-C2D	-3.05	1.47	1.55
10	M	403	BCB	CHC-C4B	-3.03	1.48	1.53
10	M	404	BCB	CHC-C4B	-2.99	1.48	1.53
10	L	302	BCB	C3B-C2B	-2.98	1.47	1.55
10	L	301	BCB	CBD-CAD	-2.96	1.48	1.53
10	M	403	BCB	C2D-C1D	-2.95	1.47	1.53
10	L	302	BCB	CBD-CGD	-2.93	1.47	1.52
10	M	404	BCB	C1A-CHA	-2.88	1.49	1.53
10	L	301	BCB	C3B-CAB	-2.88	1.49	1.52
10	M	403	BCB	C2B-C1B	-2.81	1.47	1.53
10	L	302	BCB	C3D-C2D	-2.81	1.47	1.55
10	M	404	BCB	C3D-C2D	-2.77	1.47	1.55
10	M	404	BCB	CHA-CBD	-2.71	1.47	1.53
10	L	301	BCB	C3B-C2B	-2.68	1.48	1.55
10	L	302	BCB	CHA-CBD	-2.62	1.47	1.53
10	L	301	BCB	C2B-C1B	-2.59	1.48	1.53
10	L	302	BCB	CHC-C1C	-2.57	1.46	1.52
10	L	301	BCB	CHC-C4B	-2.57	1.49	1.53
10	L	302	BCB	C4A-C3A	-2.54	1.50	1.53
10	L	302	BCB	CBD-CAD	-2.52	1.49	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
10	M	404	BCB	C3B-C2B	-2.51	1.48	1.55
10	M	403	BCB	C3D-C2D	-2.50	1.48	1.55
10	M	403	BCB	CBD-CAD	-2.49	1.49	1.53
10	M	403	BCB	CHC-C1C	-2.48	1.46	1.52
10	L	301	BCB	CHA-CBD	-2.47	1.47	1.53
11	M	405	BPB	C1D-ND	-2.41	1.33	1.38
10	M	403	BCB	C3B-CAB	-2.33	1.49	1.52
10	M	403	BCB	CBD-CGD	-2.27	1.48	1.52
10	L	302	BCB	C2B-C1B	-2.21	1.48	1.53
10	L	301	BCB	C3D-CAD	-2.20	1.47	1.51
10	L	302	BCB	C3D-CAD	-2.19	1.47	1.51
11	M	405	BPB	C4A-NA	-2.17	1.32	1.37
11	L	303	BPB	C4A-NA	-2.17	1.32	1.37
10	M	403	BCB	CHA-CBD	-2.08	1.48	1.53
11	L	303	BPB	C1D-ND	-2.08	1.33	1.38
10	M	404	BCB	CHC-C1C	-2.04	1.47	1.52
10	M	404	BCB	C3D-CAD	-2.01	1.47	1.51
11	M	405	BPB	C4C-C3C	2.00	1.50	1.45
11	L	303	BPB	C4C-C3C	2.02	1.50	1.45
14	M	406	NS5	C30-C31	2.04	1.36	1.34
11	L	303	BPB	C1B-CHB	2.06	1.48	1.40
5	C	404	HEC	C3C-C4C	2.09	1.46	1.43
11	M	405	BPB	C2-C3	2.15	1.38	1.33
11	M	405	BPB	C4B-CHC	2.16	1.48	1.40
11	L	303	BPB	C4B-CHC	2.24	1.48	1.40
11	M	405	BPB	CHD-C4C	2.26	1.45	1.40
5	C	403	HEC	C3C-C4C	2.35	1.47	1.43
11	L	303	BPB	CHD-C4C	2.39	1.46	1.40
11	M	405	BPB	C1B-CHB	2.56	1.50	1.40
11	L	303	BPB	C3D-C2D	3.15	1.47	1.38
11	M	405	BPB	C3B-C2B	3.39	1.47	1.39
11	L	303	BPB	C3B-C2B	3.44	1.47	1.39
10	M	404	BCB	O2A-CGA	3.57	1.43	1.33
10	L	302	BCB	O2A-CGA	3.59	1.43	1.33
11	M	405	BPB	C3D-C2D	3.72	1.48	1.38
11	L	303	BPB	O2A-CGA	3.74	1.44	1.33
10	L	301	BCB	O2A-CGA	3.74	1.44	1.33
11	M	405	BPB	OBD-CAD	3.74	1.29	1.22
11	L	303	BPB	OBD-CAD	3.98	1.29	1.22
10	M	403	BCB	OBD-CAD	3.99	1.28	1.21
11	L	303	BPB	CHD-C1D	4.07	1.46	1.38
10	M	403	BCB	O2D-CGD	4.11	1.43	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
10	M	404	BCB	OBD-CAD	4.11	1.28	1.21
10	M	403	BCB	CAC-C3C	4.23	1.47	1.33
11	M	405	BPB	CHD-C1D	4.28	1.47	1.38
10	L	302	BCB	O2D-CGD	4.31	1.44	1.33
10	L	302	BCB	OBD-CAD	4.34	1.28	1.21
10	M	403	BCB	O2A-CGA	4.36	1.46	1.33
11	L	303	BPB	O2D-CGD	4.38	1.44	1.33
10	L	302	BCB	CAC-C3C	4.38	1.47	1.33
11	M	405	BPB	O2D-CGD	4.45	1.44	1.33
10	L	301	BCB	OBD-CAD	4.59	1.29	1.21
10	M	404	BCB	O2D-CGD	4.60	1.44	1.33
6	C	405	DGA	OG2-CB1	4.63	1.47	1.34
10	L	301	BCB	CAC-C3C	4.79	1.49	1.33
11	L	303	BPB	C3B-C4B	4.81	1.47	1.41
10	L	301	BCB	O2D-CGD	4.85	1.45	1.33
6	C	405	DGA	OG1-CA1	4.88	1.47	1.33
11	M	405	BPB	C3B-C4B	4.91	1.47	1.41
10	M	404	BCB	CAC-C3C	4.98	1.49	1.33
13	M	402	MQ7	C10-C5	5.17	1.49	1.40
11	M	405	BPB	O2A-CGA	5.19	1.48	1.33
13	M	402	MQ7	C3-C2	6.61	1.49	1.35
14	M	406	NS5	C35-C36	7.39	1.54	1.32
11	M	405	BPB	CAC-C3C	16.24	1.52	1.33
11	L	303	BPB	CAC-C3C	16.32	1.52	1.33

All (131) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	M	405	BPB	C2C-C3C-C4C	-7.61	99.98	107.35
11	L	303	BPB	C2C-C3C-C4C	-7.04	100.53	107.35
11	L	303	BPB	CBC-CAC-C3C	-6.74	112.14	127.00
11	M	405	BPB	CBC-CAC-C3C	-6.48	112.73	127.00
10	M	404	BCB	CHA-CBD-CGD	-5.40	102.47	115.00
10	L	302	BCB	OBD-CAD-C3D	-5.07	117.92	126.75
10	M	403	BCB	OBD-CAD-C3D	-4.74	118.50	126.75
5	C	404	HEC	CAD-CBD-CGD	-4.42	105.11	112.66
5	C	401	HEC	CBD-CAD-C3D	-4.29	104.28	112.48
14	M	406	NS5	C19-C20-C21	-4.26	121.23	127.31
14	M	406	NS5	CM4-C36-C35	-4.06	110.39	122.65
10	L	301	BCB	OBD-CAD-C3D	-4.05	119.70	126.75
5	C	401	HEC	CBA-CAA-C2A	-4.00	104.83	112.47
11	L	303	BPB	CMD-C2D-C3D	-3.88	118.46	127.86

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	L	301	BCB	CHA-CBD-CGD	-3.84	106.10	115.00
5	C	402	HEC	CMB-C2B-C1B	-3.81	122.61	128.46
10	M	403	BCB	CBC-CAC-C3C	-3.77	118.05	126.49
14	M	406	NS5	CM3-C36-C35	-3.75	111.32	122.65
14	M	406	NS5	C34-C35-C36	-3.75	114.42	127.80
5	C	404	HEC	CMC-C2C-C1C	-3.67	122.82	128.46
10	M	404	BCB	O2D-CGD-O1D	-3.63	116.51	123.82
5	C	403	HEC	CBA-CAA-C2A	-3.57	105.66	112.47
14	M	406	NS5	C18-C17-C15	-3.56	122.24	127.31
10	L	302	BCB	O1D-CGD-CBD	-3.44	117.43	124.53
5	C	403	HEC	CMC-C2C-C1C	-3.42	123.21	128.46
5	C	402	HEC	CBA-CAA-C2A	-3.32	106.13	112.47
11	M	405	BPB	CMD-C2D-C3D	-3.32	119.82	127.86
5	C	401	HEC	CMC-C2C-C1C	-3.29	123.40	128.46
5	C	404	HEC	CMB-C2B-C1B	-3.28	123.42	128.46
10	L	302	BCB	CBC-CAC-C3C	-3.24	119.24	126.49
10	M	404	BCB	OBD-CAD-C3D	-3.21	121.17	126.75
11	L	303	BPB	OBD-CAD-C3D	-3.11	120.78	128.43
10	M	403	BCB	C4A-C3A-C2A	-3.07	99.17	103.86
5	C	402	HEC	CMC-C2C-C1C	-3.06	123.76	128.46
6	C	405	DGA	OG1-CA1-OA1	-3.02	116.06	123.55
10	L	301	BCB	O2D-CGD-O1D	-2.80	118.19	123.82
5	C	402	HEC	CMD-C2D-C1D	-2.80	124.16	128.46
10	L	302	BCB	C4A-C3A-C2A	-2.77	99.63	103.86
5	C	401	HEC	CMB-C2B-C1B	-2.76	124.23	128.46
11	M	405	BPB	OBD-CAD-C3D	-2.68	121.84	128.43
10	L	301	BCB	C4A-C3A-C2A	-2.68	99.76	103.86
11	L	303	BPB	CHD-C4C-C3C	-2.63	121.00	125.26
13	M	402	MQ7	O4-C4-C3	-2.61	116.67	120.63
10	L	301	BCB	C5-C3-C2	-2.58	115.83	121.10
14	M	406	NS5	C14-C15-C17	-2.55	115.02	118.94
14	M	406	NS5	C6-C5-C7	-2.54	116.91	123.69
11	L	303	BPB	O1D-CGD-CBD	-2.52	120.08	124.60
13	M	402	MQ7	C12-C11-C3	-2.48	104.88	111.85
10	M	404	BCB	O2A-CGA-O1A	-2.45	117.46	123.55
11	M	405	BPB	O1D-CGD-CBD	-2.40	120.28	124.60
10	L	301	BCB	O2A-CGA-O1A	-2.40	117.60	123.55
11	M	405	BPB	O2D-CGD-O1D	-2.29	119.21	123.82
5	C	404	HEC	CBA-CAA-C2A	-2.27	108.14	112.47
5	C	403	HEC	CMD-C2D-C1D	-2.23	125.03	128.46
11	M	405	BPB	O2A-CGA-O1A	-2.18	118.15	123.55
11	L	303	BPB	CBA-CAA-C2A	-2.14	107.39	113.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	M	405	BPB	C3A-C2A-C1A	-2.09	98.21	101.34
14	M	406	NS5	C8-C9-C10	-2.08	105.90	112.93
10	M	404	BCB	OBB-CAB-CBB	-2.07	117.28	121.09
10	L	301	BCB	C1-C2-C3	-2.06	122.15	125.96
11	M	405	BPB	CBB-CAB-C3B	-2.04	114.47	120.39
5	C	402	HEC	C1D-C2D-C3D	2.03	108.41	107.00
5	C	404	HEC	C1D-C2D-C3D	2.03	108.41	107.00
11	M	405	BPB	C3D-C4D-ND	2.04	116.90	110.81
10	M	404	BCB	CHD-C1D-C2D	2.04	122.64	116.99
10	L	302	BCB	C1-O2A-CGA	2.09	121.79	116.77
10	M	403	BCB	C4-C3-C5	2.13	118.98	115.29
10	M	404	BCB	C1-O2A-CGA	2.16	121.95	116.77
11	M	405	BPB	C3C-C4C-NC	2.17	113.25	109.60
14	M	406	NS5	C11-C10-C9	2.18	119.07	115.29
10	L	302	BCB	CMD-C2D-C3D	2.19	119.82	114.27
10	L	302	BCB	CBB-CAB-C3B	2.24	119.11	116.82
6	C	405	DGA	CG1-OG1-CA1	2.24	123.87	117.13
10	M	404	BCB	CHB-C1B-C2B	2.30	123.36	116.99
10	L	302	BCB	CHB-C1B-C2B	2.30	123.37	116.99
10	L	301	BCB	CHC-C4B-C3B	2.45	124.15	118.09
10	M	403	BCB	CHD-C1D-C2D	2.48	123.85	116.99
13	M	402	MQ7	C29-C28-C30	2.50	119.63	115.29
11	M	405	BPB	C1-O2A-CGA	2.51	122.78	116.77
10	L	302	BCB	CED-O2D-CGD	2.51	121.86	115.97
13	M	402	MQ7	C2M-C2-C1	2.53	120.48	116.23
8	H	706	LDA	CM2-N1-C1	2.57	115.63	110.23
13	M	402	MQ7	C39-C38-C40	2.58	119.76	115.29
10	L	302	BCB	CHD-C1D-C2D	2.60	124.18	116.99
11	L	303	BPB	CMB-C2B-C3B	2.61	129.73	124.89
10	M	403	BCB	O2A-CGA-CBA	2.64	119.57	111.90
10	M	403	BCB	CMD-C2D-C3D	2.70	121.09	114.27
5	C	401	HEC	CAD-CBD-CGD	2.73	117.32	112.66
10	M	403	BCB	O2D-CGD-CBD	2.75	117.91	111.20
11	M	405	BPB	C5-C3-C2	2.76	126.75	121.10
11	L	303	BPB	CAD-C3D-C2D	2.79	154.25	140.80
10	L	301	BCB	CMD-C2D-C3D	2.80	121.35	114.27
10	L	301	BCB	O2D-CGD-CBD	2.82	118.09	111.20
10	L	301	BCB	CED-O2D-CGD	2.86	122.68	115.97
10	M	404	BCB	CMD-C2D-C3D	2.87	121.53	114.27
11	L	303	BPB	C3C-C4C-NC	3.01	114.67	109.60
11	M	405	BPB	CAD-C3D-C2D	3.02	155.35	140.80
10	L	301	BCB	CBB-CAB-C3B	3.07	119.97	116.82

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	M	404	BCB	CED-O2D-CGD	3.12	123.27	115.97
5	C	403	HEC	C1D-C2D-C3D	3.14	109.18	107.00
14	M	406	NS5	C18-C19-C20	3.18	130.26	123.46
14	M	406	NS5	C16-C15-C14	3.18	123.17	118.10
10	L	301	BCB	O2A-CGA-CBA	3.41	121.81	111.90
11	M	405	BPB	O2A-CGA-CBA	3.45	121.93	111.90
5	C	404	HEC	CBD-CAD-C3D	3.52	119.22	112.48
10	L	302	BCB	O2D-CGD-CBD	3.55	119.87	111.20
8	H	707	LDA	CM1-N1-C1	3.61	117.83	110.23
6	C	405	DGA	OG1-CA1-CA2	3.69	122.64	111.90
10	M	404	BCB	C1D-CHD-C4C	3.79	120.45	112.37
10	M	404	BCB	CBB-CAB-C3B	3.82	120.73	116.82
6	C	405	DGA	OG2-CG2-CG1	3.85	114.42	105.88
10	L	301	BCB	C4-C3-C5	3.85	121.97	115.29
10	M	404	BCB	O2D-CGD-CBD	3.88	120.66	111.20
11	L	303	BPB	O2D-CGD-CBD	4.00	118.44	111.30
10	L	302	BCB	C1D-CHD-C4C	4.29	121.50	112.37
10	L	301	BCB	C1D-CHD-C4C	4.47	121.91	112.37
11	L	303	BPB	C2A-C1A-NA	4.75	111.85	107.83
10	L	301	BCB	C3B-C4B-NB	4.83	112.33	103.57
10	M	403	BCB	C3B-C4B-NB	4.85	112.36	103.57
10	M	403	BCB	C1D-CHD-C4C	4.88	122.77	112.37
11	M	405	BPB	CMD-C2D-C1D	4.99	132.82	125.04
10	L	302	BCB	C3B-C4B-NB	5.09	112.80	103.57
11	M	405	BPB	O2D-CGD-CBD	5.14	120.49	111.30
6	C	405	DGA	OG2-CB1-CB2	5.43	122.82	111.55
10	M	404	BCB	C3B-C4B-NB	5.44	113.42	103.57
11	M	405	BPB	C2A-C1A-NA	5.91	112.83	107.83
11	L	303	BPB	CMD-C2D-C1D	6.03	134.44	125.04
10	M	403	BCB	CMB-C2B-C3B	6.34	130.31	114.27
10	L	302	BCB	CMB-C2B-C3B	6.38	130.41	114.27
10	M	404	BCB	CMB-C2B-C3B	6.43	130.54	114.27
10	L	301	BCB	CMB-C2B-C3B	7.70	133.77	114.27

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
10	M	403	BCB	CBC-CAC-C3C-C2C
11	L	303	BPB	CBC-CAC-C3C-C2C

There are no ring outliers.

11 monomers are involved in 23 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	C	401	HEC	1	0
5	C	402	HEC	2	0
5	C	403	HEC	1	0
5	C	404	HEC	1	0
10	L	301	BCB	2	0
10	L	302	BCB	3	0
11	L	303	BPB	2	0
10	M	403	BCB	4	0
10	M	404	BCB	3	0
11	M	405	BPB	3	0
14	M	406	NS5	4	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	C	332/336 (98%)	-0.48	1 (0%) 93 92	73, 92, 119, 156	0
2	H	257/258 (99%)	-0.35	6 (2%) 61 51	80, 104, 152, 211	0
3	L	273/273 (100%)	-0.53	3 (1%) 80 74	75, 91, 117, 139	0
4	M	323/323 (100%)	-0.32	2 (0%) 89 86	73, 90, 117, 149	0
All	All	1185/1190 (99%)	-0.42	12 (1%) 82 77	73, 93, 128, 211	0

All (12) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	H	46	PRO	2.8
3	L	161	GLY	2.5
2	H	257	LEU	2.4
2	H	49	LEU	2.4
4	M	37	TRP	2.4
2	H	258	LEU	2.3
3	L	271	PHE	2.3
2	H	93	THR	2.2
4	M	319	PRO	2.2
1	C	54	GLN	2.1
2	H	189	GLY	2.1
3	L	158	ASN	2.1

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

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(\AA^2)	Q<0.9
2	FME	H	1	10/11	0.98	0.17	-	93,105,115,130	0

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. 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(\AA^2)	Q<0.9
9	HTO	L	305	10/10	0.72	0.56	30.56	109,132,143,144	0
7	SO4	H	704	5/5	0.85	0.58	25.65	90,94,108,109	5
6	DGA	C	405	37/44	0.66	0.52	6.90	112,146,180,185	0
7	SO4	M	412	5/5	0.78	0.50	6.47	158,161,185,212	0
8	LDA	H	706	16/16	0.71	0.41	4.45	106,123,191,192	0
8	LDA	H	707	16/16	0.95	0.35	3.09	108,126,144,147	0
8	LDA	L	304	16/16	0.82	0.37	2.70	120,143,167,172	0
14	NS5	M	406	40/40	0.83	0.27	2.54	84,100,141,143	0
8	LDA	H	701	16/16	0.94	0.26	1.81	89,103,119,119	0
9	HTO	H	708	10/10	0.89	0.15	1.56	116,128,142,144	0
11	BPB	L	303	65/65	0.98	0.21	1.54	78,84,92,98	0
13	MQ7	M	402	48/48	0.94	0.25	1.28	80,88,125,148	0
11	BPB	M	405	65/65	0.97	0.18	1.14	82,95,176,184	0
10	BCB	M	403	66/66	0.95	0.22	0.66	78,88,170,180	0
7	SO4	C	406	5/5	0.83	0.25	0.30	145,159,166,179	0
5	HEC	C	402	43/43	0.98	0.15	0.23	83,95,105,131	0
10	BCB	L	301	66/66	0.98	0.22	0.22	67,77,93,111	0
10	BCB	M	404	66/66	0.98	0.19	0.05	61,76,107,113	0
5	HEC	C	401	43/43	0.98	0.15	-0.01	88,96,110,124	0
10	BCB	L	302	66/66	0.98	0.20	-0.09	72,80,112,115	0
5	HEC	C	403	43/43	0.98	0.17	-0.11	70,79,90,93	0
5	HEC	C	404	43/43	0.99	0.13	-0.50	75,84,101,123	0
7	SO4	M	407	5/5	0.97	0.10	-0.76	98,111,122,123	0
12	FE2	M	401	1/1	1.00	0.16	-0.82	91,91,91,91	0
7	SO4	H	702	5/5	0.96	0.10	-0.90	105,115,122,126	0
7	SO4	H	703	5/5	0.90	0.42	-	182,184,190,202	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
7	SO4	M	408	5/5	0.94	0.13	-	121,121,131,153	0
7	SO4	M	413	5/5	0.73	0.38	-	222,237,243,256	0
7	SO4	H	705	5/5	0.97	0.06	-	115,115,127,127	5
7	SO4	M	410	5/5	0.80	0.31	-	148,154,167,181	0
7	SO4	M	409	5/5	0.98	0.08	-	85,93,99,100	0
7	SO4	M	411	5/5	0.78	0.35	-	148,174,187,192	0

6.5 Other polymers [i](#)

There are no such residues in this entry.