



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 03:09 PM UTC

PDB ID : 5OKC / pdb_00005okc
Title : Crystal structure of the Ctf18-1-8 module from Ctf18-RFC
Authors : Grabarczyk, D.B.; Kisker, C.
Deposited on : 2017-07-25
Resolution : 2.30 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

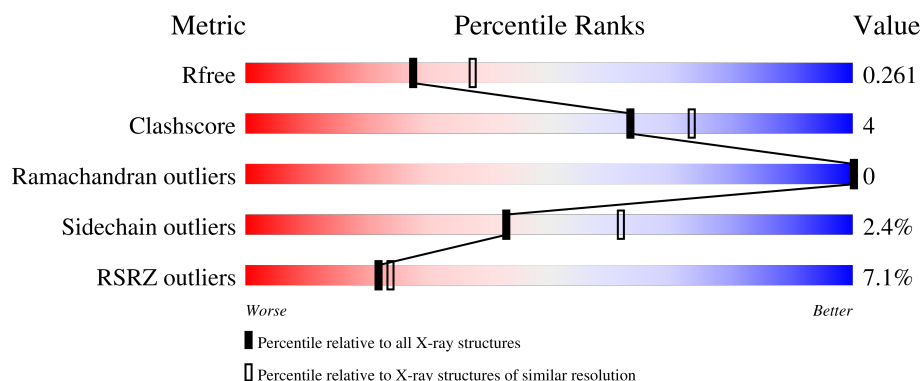
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	6319 (2.30-2.30)
Clashscore	190562	6919 (2.30-2.30)
Ramachandran outliers	187476	6854 (2.30-2.30)
Sidechain outliers	187428	6854 (2.30-2.30)
RSRZ outliers	180081	6325 (2.30-2.30)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. 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	380	8% 87% 9% ..
1	B	380	8% 87% 12% ..
2	F	133	3% 85% 13% ..
2	H	133	3% 86% 10% .
3	G	27	4% 85% 11% .

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Mol	Chain	Length	Quality of chain
3	I	27	11% 81% 19%

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 9018 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 Sister chromatid cohesion protein DCC1.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	369	Total	C	N	O	S	Se	0	0	0
			2999	1933	496	556	4	10			
1	B	377	Total	C	N	O	S	Se	0	1	0
			3082	1983	518	567	4	10			

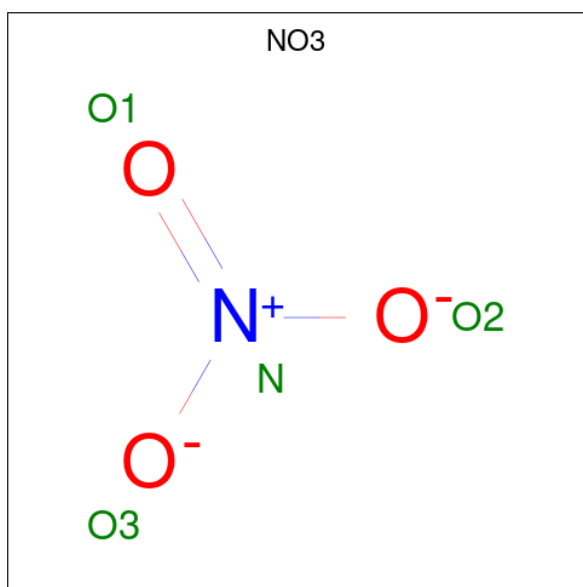
- Molecule 2 is a protein called Chromosome transmission fidelity protein 8.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	F	132	Total	C	N	O	Se	0	0	0
			1053	666	182	198	7			
2	H	128	Total	C	N	O	Se	0	0	0
			1019	646	176	190	7			

- Molecule 3 is a protein called Chromosome transmission fidelity protein 18.

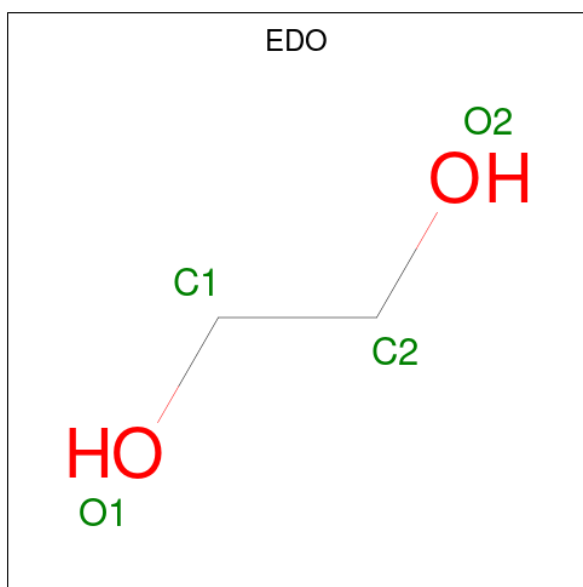
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	G	26	Total	C	N	O	0	0	0
			226	147	40	39			
3	I	27	Total	C	N	O	0	0	0
			234	153	41	40			

- Molecule 4 is NITRATE ION (CCD ID: NO3) (formula: NO₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	N	O	0	0
			4	1	3		
4	A	1	Total	N	O	0	0
			4	1	3		
4	A	1	Total	N	O	0	0
			4	1	3		
4	B	1	Total	N	O	0	0
			4	1	3		
4	F	1	Total	N	O	0	0
			4	1	3		
4	H	1	Total	N	O	0	0
			4	1	3		

- Molecule 5 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	B	1	Total	C	O	0	0
			4	2	2		

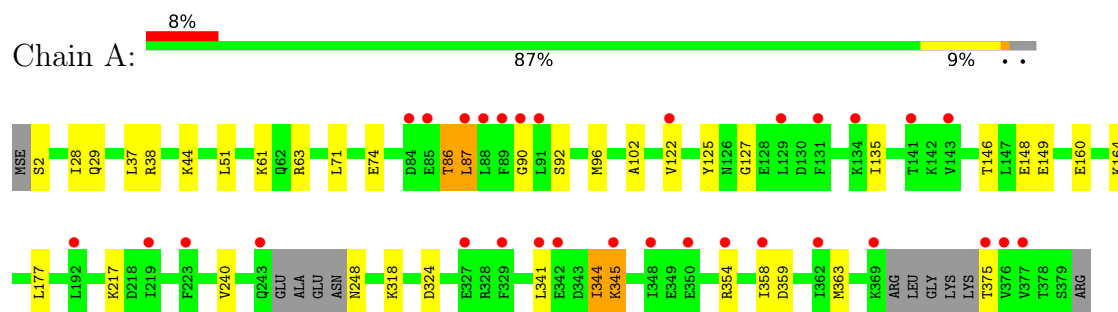
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	105	Total	O	0	0
			105	105		
6	B	144	Total	O	0	0
			144	144		
6	F	52	Total	O	0	0
			52	52		
6	G	14	Total	O	0	0
			14	14		
6	H	50	Total	O	0	0
			50	50		
6	I	12	Total	O	0	0
			12	12		

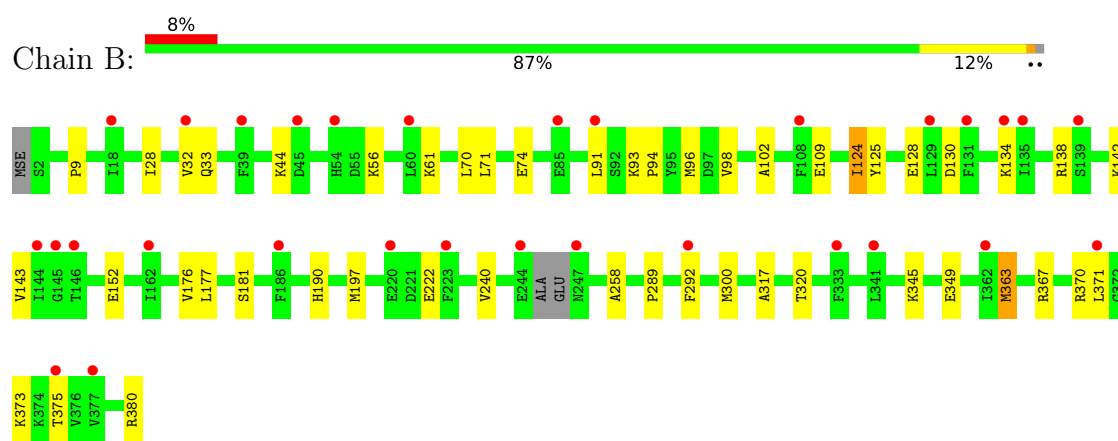
3 Residue-property plots [i](#)

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

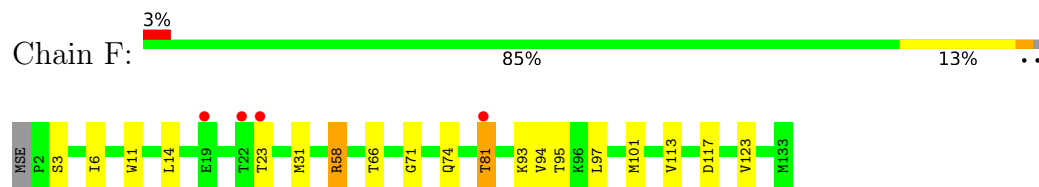
- Molecule 1: Sister chromatid cohesion protein DCC1



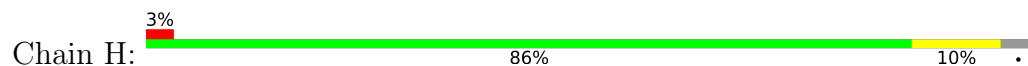
- Molecule 1: Sister chromatid cohesion protein DCC1



- Molecule 2: Chromosome transmission fidelity protein 8

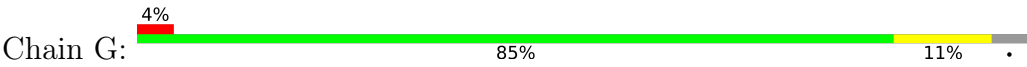


- Molecule 2: Chromosome transmission fidelity protein 8

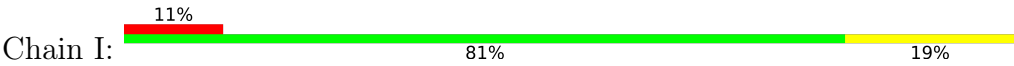




● Molecule 3: Chromosome transmission fidelity protein 18



● Molecule 3: Chromosome transmission fidelity protein 18



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	58.52Å 164.18Å 59.61Å 90.00° 90.50° 90.00°	Depositor
Resolution (Å)	48.23 – 2.30 48.23 – 2.30	Depositor EDS
% Data completeness (in resolution range)	99.9 (48.23-2.30) 99.9 (48.23-2.30)	Depositor EDS
R_{merge}	0.24	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.54 (at 2.29Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.200 , 0.260 0.203 , 0.261	Depositor DCC
R_{free} test set	2460 reflections (4.32%)	wwPDB-VP
Wilson B-factor (Å ²)	37.8	Xtriage
Anisotropy	0.733	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 43.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.003 for l,k,-h 0.116 for h,-k,-l 0.030 for l,-k,h	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	9018	wwPDB-VP
Average B, all atoms (Å ²)	55.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.96% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: EDO, NO3

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	0.27	0/3058	0.69	3/4118 (0.1%)
1	B	0.28	0/3145	0.70	0/4231
2	F	0.26	0/1062	0.71	1/1411 (0.1%)
2	H	0.26	0/1027	0.70	1/1363 (0.1%)
3	G	0.21	0/233	0.58	0/315
3	I	0.21	0/241	0.55	0/328
All	All	0.27	0/8766	0.69	5/11766 (0.0%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	90	GLY	N-CA-C	-5.67	107.43	115.43
1	A	324	ASP	CA-C-N	5.63	125.09	119.24
1	A	324	ASP	C-N-CA	5.63	125.09	119.24
2	F	71	GLY	N-CA-C	5.17	118.10	110.80
2	H	71	GLY	N-CA-C	5.08	117.96	110.80

There are no chirality outliers.

There are no planarity outliers.

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	2999	0	2998	27	0
1	B	3082	0	3108	28	0
2	F	1053	0	1087	11	0
2	H	1019	0	1052	8	0
3	G	226	0	212	3	0
3	I	234	0	226	6	0
4	A	12	0	0	0	0
4	B	4	0	0	0	0
4	F	4	0	0	0	0
4	H	4	0	0	0	0
5	B	4	0	6	0	0
6	A	105	0	0	9	0
6	B	144	0	0	4	0
6	F	52	0	0	1	0
6	G	14	0	0	0	0
6	H	50	0	0	1	0
6	I	12	0	0	0	0
All	All	9018	0	8689	69	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 4.

All (69) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:341:LEU:O	6:A:501:HOH:O	2.01	0.77
1:B:124:ILE:HD11	1:B:181:SER:HB3	1.72	0.70
2:F:74:GLN:HB3	2:F:81:THR:HG23	1.73	0.70
1:A:63:ARG:HH11	3:I:152:ARG:HG3	1.58	0.67
2:H:48:LEU:HD13	3:I:137:VAL:HG12	1.76	0.66
1:A:71:LEU:HB2	1:A:102:ALA:HB3	1.79	0.64
1:B:367:ARG:NH1	6:B:506:HOH:O	2.31	0.63
2:F:93:LYS:HE2	2:F:95:THR:HB	1.80	0.62
1:B:363:MSE:O	1:B:380:ARG:NH1	2.33	0.62
1:A:38:ARG:NE	2:H:3:SER:OG	2.34	0.60
1:A:375:THR:N	6:A:509:HOH:O	2.36	0.59
1:A:44:LYS:HA	3:I:157:TRP:HB3	1.85	0.57
1:B:370:ARG:NH1	1:B:373:LYS:O	2.37	0.57
2:F:94:VAL:HG22	2:F:123:VAL:HG22	1.88	0.56
1:B:61:LYS:NZ	3:G:154:ASN:OD1	2.36	0.56
1:B:222:GLU:OE1	6:B:501:HOH:O	2.18	0.55
1:B:71:LEU:HB2	1:B:102:ALA:HB3	1.88	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:93:LYS:HD2	1:B:94:PRO:HD2	1.89	0.54
1:A:61:LYS:NZ	3:I:154:ASN:OD1	2.38	0.53
1:A:248:ASN:N	6:A:513:HOH:O	2.41	0.53
1:A:146:THR:HG23	1:A:149:GLU:H	1.74	0.53
1:B:98:VAL:HG21	2:F:31:MSE:HE2	1.91	0.52
1:B:345:LYS:O	1:B:349:GLU:HG3	2.09	0.52
1:A:344:ILE:N	6:A:501:HOH:O	2.42	0.51
1:A:2:SER:N	1:A:92:SER:HG	2.10	0.50
1:A:29:GLN:NE2	6:A:516:HOH:O	2.44	0.50
1:A:37:LEU:HB3	1:A:51:LEU:HD11	1.92	0.50
1:A:44:LYS:NZ	6:A:518:HOH:O	2.45	0.50
1:A:318:LYS:NZ	6:A:520:HOH:O	2.46	0.49
1:A:63:ARG:NE	6:A:521:HOH:O	2.46	0.49
1:A:63:ARG:NH1	3:I:152:ARG:HG3	2.27	0.49
1:B:143:VAL:HG11	1:B:176:VAL:HG22	1.95	0.48
1:B:371:LEU:H	1:B:371:LEU:HD23	1.78	0.48
2:H:32:MSE:HE3	2:H:119:MSE:HG3	1.95	0.48
1:B:44:LYS:HA	3:G:157:TRP:HB3	1.96	0.48
1:B:44:LYS:NZ	6:B:508:HOH:O	2.36	0.47
1:B:109:GLU:OE1	3:G:152:ARG:NE	2.37	0.47
1:A:359:ASP:O	1:A:363:MSE:HG2	2.15	0.46
2:F:58:ARG:NH1	6:F:302:HOH:O	2.36	0.46
1:A:74:GLU:HB2	1:A:96:MSE:HE3	1.98	0.46
1:B:317:ALA:O	1:B:320:THR:HG22	2.17	0.45
1:A:146:THR:OG1	1:A:148:GLU:OE1	2.33	0.45
1:A:86:THR:HG22	1:A:87:LEU:HD22	1.98	0.44
1:B:56:LYS:NZ	6:B:511:HOH:O	2.50	0.44
1:A:354:ARG:HD2	1:A:354:ARG:HA	1.82	0.44
1:B:197:MSE:SE	1:B:292:PHE:HA	2.68	0.44
1:A:96:MSE:HE1	2:H:25:ILE:HG21	2.00	0.43
2:H:94:VAL:HG22	2:H:123:VAL:HG22	2.01	0.43
1:B:32:VAL:HG12	1:B:33:GLN:HG3	2.00	0.43
1:A:160:GLU:O	1:A:164:LYS:HD3	2.19	0.43
1:B:152:GLU:OE1	2:F:3:SER:OG	2.25	0.43
1:B:9:PRO:HD3	2:F:66:THR:O	2.19	0.42
1:B:258:ALA:HB3	1:B:300:MSE:HE1	2.00	0.42
1:B:190:HIS:CE1	1:B:289:PRO:HG3	2.54	0.42
1:A:375:THR:N	6:A:531:HOH:O	2.53	0.42
1:B:143:VAL:HG13	1:B:176:VAL:HG13	2.00	0.42
2:H:96:LYS:NZ	6:H:313:HOH:O	2.52	0.42
1:B:134:LYS:O	1:B:138:ARG:HG3	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:124:ILE:HD13	1:B:125:TYR:N	2.35	0.41
2:F:11:TRP:CD1	2:F:117:ASP:HA	2.54	0.41
2:F:6:ILE:HA	2:F:113:VAL:HG13	2.03	0.41
1:B:128:GLU:C	1:B:130:ASP:H	2.28	0.41
2:F:14:LEU:HD12	2:F:14:LEU:HA	1.90	0.41
1:A:125:TYR:CZ	1:A:127:GLY:HA2	2.56	0.41
1:B:74:GLU:HB2	1:B:96:MSE:HE3	2.03	0.41
1:A:345:LYS:HD3	1:A:358:ILE:HG12	2.02	0.41
2:H:11:TRP:CD1	2:H:117:ASP:HA	2.55	0.40
2:H:70:PHE:HA	3:I:139:ILE:HD13	2.03	0.40
2:F:97:LEU:HD13	2:F:101:MSE:HG2	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	363/380 (96%)	351 (97%)	12 (3%)	0	100	100
1	B	374/380 (98%)	364 (97%)	10 (3%)	0	100	100
2	F	130/133 (98%)	129 (99%)	1 (1%)	0	100	100
2	H	124/133 (93%)	124 (100%)	0	0	100	100
3	G	24/27 (89%)	24 (100%)	0	0	100	100
3	I	25/27 (93%)	25 (100%)	0	0	100	100
All	All	1040/1080 (96%)	1017 (98%)	23 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	339/341 (99%)	329 (97%)	10 (3%)	37	55
1	B	349/341 (102%)	340 (97%)	9 (3%)	40	59
2	F	119/112 (106%)	116 (98%)	3 (2%)	42	60
2	H	115/112 (103%)	114 (99%)	1 (1%)	70	84
3	G	23/25 (92%)	23 (100%)	0	100	100
3	I	25/25 (100%)	25 (100%)	0	100	100
All	All	970/956 (102%)	947 (98%)	23 (2%)	43	62

All (23) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	28	ILE
1	A	86	THR
1	A	87	LEU
1	A	122	VAL
1	A	135	ILE
1	A	177	LEU
1	A	217	LYS
1	A	240	VAL
1	A	344	ILE
1	A	345	LYS
1	B	28	ILE
1	B	70	LEU
1	B	91	LEU
1	B	124	ILE
1	B	142	LYS
1	B	177	LEU
1	B	240	VAL
1	B	363	MSE
1	B	375	THR
2	F	23	THR
2	F	58	ARG
2	F	81	THR

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Mol	Chain	Res	Type
2	H	58	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	33	GLN
1	A	36	GLN
1	A	166	HIS
1	A	213	HIS
1	B	33	GLN
1	B	35	HIS
1	B	36	GLN
1	B	212	HIS
2	F	111	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

7 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	NO3	F	201	-	1,3,3	0.55	0	0,3,3	-	-
4	NO3	A	403	-	1,3,3	0.53	0	0,3,3	-	-
4	NO3	A	402	-	1,3,3	0.53	0	0,3,3	-	-
4	NO3	A	401	-	1,3,3	0.55	0	0,3,3	-	-
4	NO3	B	401	-	1,3,3	0.52	0	0,3,3	-	-
4	NO3	H	201	-	1,3,3	0.54	0	0,3,3	-	-
5	EDO	B	402	-	3,3,3	0.43	0	2,2,2	0.33	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	EDO	B	402	-	-	0/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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	359/380 (94%)	0.73	31 (8%)	16 17	26, 53, 100, 131	0
1	B	367/380 (96%)	0.65	30 (8%)	17 19	22, 49, 101, 134	1 (0%)
2	F	125/133 (93%)	0.44	4 (3%)	50 52	31, 48, 77, 107	0
2	H	121/133 (90%)	0.44	4 (3%)	49 51	29, 47, 79, 116	0
3	G	26/27 (96%)	0.24	1 (3%)	44 46	35, 44, 61, 81	0
3	I	27/27 (100%)	0.55	3 (11%)	10 11	32, 45, 76, 91	0
All	All	1025/1080 (94%)	0.61	73 (7%)	22 24	22, 49, 94, 134	1 (0%)

All (73) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	341	LEU	6.1
1	A	141	THR	4.4
1	B	129	LEU	3.9
1	A	129	LEU	3.4
3	I	161	TRP	3.4
1	A	243	GLN	3.4
1	A	89	PHE	3.1
1	B	377	VAL	3.1
1	B	375	THR	3.0
1	A	84	ASP	3.0
1	B	85	GLU	3.0
1	A	345	LYS	2.9
1	B	18	ILE	2.9
1	B	131	PHE	2.9
1	B	223	PHE	2.9
3	G	161	TRP	2.9
1	A	192	LEU	2.9
1	A	87	LEU	2.9
1	A	143	VAL	2.9

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Mol	Chain	Res	Type	RSRZ
1	A	377	VAL	2.9
1	A	88	LEU	2.8
1	B	162	ILE	2.7
1	B	247	ASN	2.7
1	A	369	LYS	2.7
1	B	244	GLU	2.7
2	H	17	SER	2.7
1	B	333	PHE	2.7
1	A	375	THR	2.7
2	H	23	THR	2.7
1	B	341	LEU	2.7
1	A	90	GLY	2.6
1	B	60	LEU	2.6
1	B	145	GLY	2.5
1	A	329	PHE	2.5
3	I	137	VAL	2.5
3	I	136	THR	2.5
1	A	131	PHE	2.5
1	A	350	GLU	2.4
1	B	108	PHE	2.4
2	F	22	THR	2.4
1	A	223	PHE	2.4
1	A	358	ILE	2.4
1	A	342	GLU	2.4
1	B	139	SER	2.3
1	B	362	ILE	2.3
1	A	91	LEU	2.3
1	A	85	GLU	2.3
1	A	122	VAL	2.3
1	A	219	ILE	2.3
2	H	132	ILE	2.2
1	B	292	PHE	2.2
2	H	24	VAL	2.2
1	B	371	LEU	2.2
1	A	354	ARG	2.2
1	A	327	GLU	2.2
1	B	146	THR	2.2
2	F	23	THR	2.2
1	A	134	LYS	2.2
1	B	91	LEU	2.1
1	B	186	PHE	2.1
1	B	134	LYS	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	32	VAL	2.1
2	F	81	THR	2.1
1	B	220	GLU	2.1
1	A	348	ILE	2.1
1	B	135	ILE	2.1
1	B	39	PHE	2.1
1	B	45	ASP	2.1
1	B	144	ILE	2.1
1	A	362	ILE	2.0
1	A	376	VAL	2.0
2	F	19	GLU	2.0
1	B	54	HIS	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	NO3	F	201	4/4	0.83	0.10	79,82,82,84	0
4	NO3	A	403	4/4	0.84	0.15	68,72,73,76	0
5	EDO	B	402	4/4	0.85	0.12	46,47,47,53	0
4	NO3	B	401	4/4	0.86	0.19	80,81,82,82	0
4	NO3	H	201	4/4	0.89	0.10	67,74,74,77	0
4	NO3	A	401	4/4	0.89	0.14	79,79,81,82	0
4	NO3	A	402	4/4	0.91	0.09	70,70,72,72	0

6.5 Other polymers [i](#)

There are no such residues in this entry.