



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 09:12 AM UTC

PDB ID : 6LRD / pdb_00006lrd
Title : Structure of RecJ complexed with a 5'-P-dSpacer-modified ssDNA
Authors : Cheng, K.; Hua, Y.
Deposited on : 2020-01-16
Resolution : 1.90 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

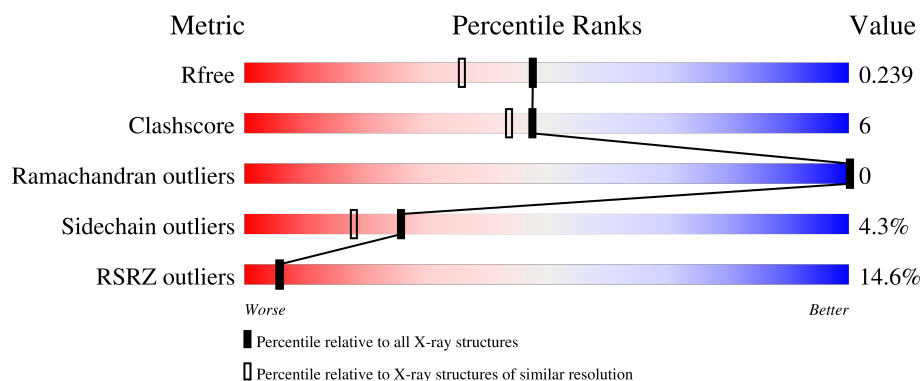
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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	7789 (1.90-1.90)
Clashscore	190562	8410 (1.90-1.90)
Ramachandran outliers	187476	8333 (1.90-1.90)
Sidechain outliers	187428	8333 (1.90-1.90)
RSRZ outliers	180081	7790 (1.90-1.90)

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	705	14% 87% 11% ..
2	C	6	17% 67% 17% 17%
3	B	4	50% 100%

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
2	3DR	C	1	-	-	X	-
5	SO4	A	805	-	-	X	-

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 5922 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 Single-stranded-DNA-specific exonuclease.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	698	Total	C	N	O	S	0	3	0
			5303	3348	967	976	12			

- Molecule 2 is a DNA chain called DNA (5'-D(P*(3DR)P*TP*TP*TP*TP*T)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	6	Total	C	N	O	P	0	0	0
			112	55	10	41	6			

- Molecule 3 is a protein called ASP-LEU-PRO-PHE.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	B	4	Total	C	N	O	0	0	0
			34	24	4	6			

- Molecule 4 is MANGANESE (II) ION (CCD ID: MN) (formula: Mn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	2	Total	Mn	0	0
			2	2		

- Molecule 5 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



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

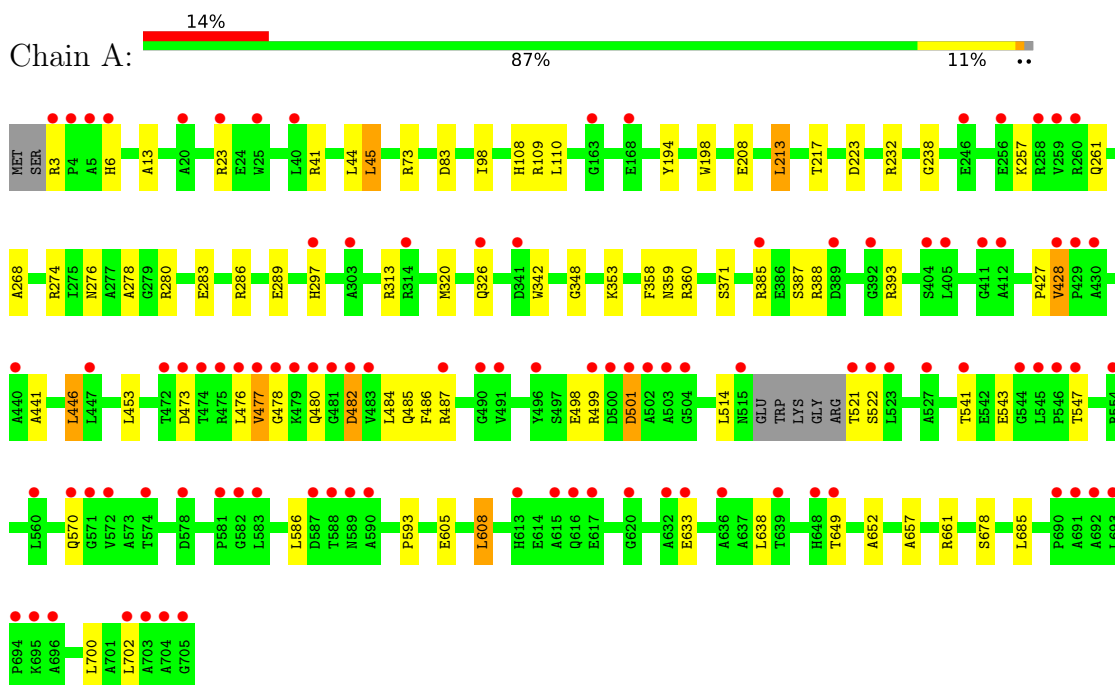
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	441	Total	O	0	0
			441	441		
6	C	8	Total	O	0	0
			8	8		
6	B	2	Total	O	0	0
			2	2		

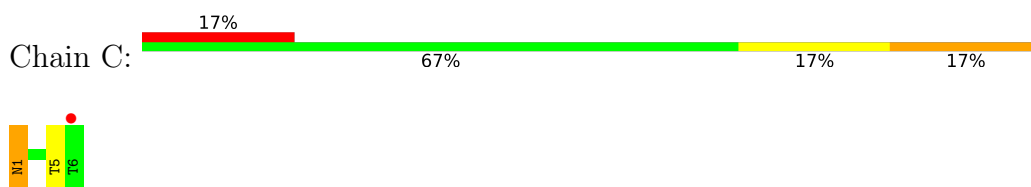
3 Residue-property plots

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

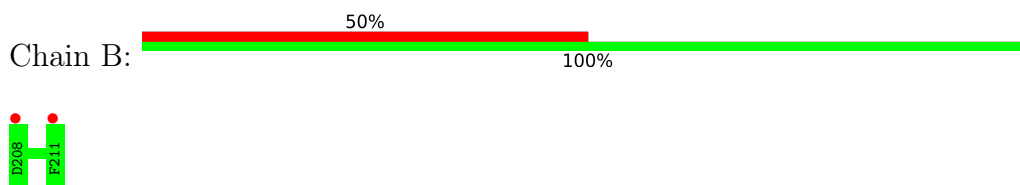
- Molecule 1: Single-stranded-DNA-specific exonuclease



- Molecule 2: DNA (5'-D(P*(3DR)P*TP*TP*TP*TP*T)-3')



- Molecule 3: ASP-LEU-PRO-PHE



4 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α , β , γ	106.14Å 106.14Å 164.56Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	29.35 – 1.90 29.35 – 1.90	Depositor EDS
% Data completeness (in resolution range)	98.3 (29.35-1.90) 98.2 (29.35-1.90)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.87 (at 1.91Å)	Xtriage
Refinement program	PHENIX 1.11.1_2575	Depositor
R, R_{free}	0.208 , 0.234 (Not available) , 0.239	Depositor DCC
R_{free} test set	4134 reflections (4.87%)	wwPDB-VP
Wilson B-factor (Å ²)	35.6	Xtriage
Anisotropy	0.428	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 42.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.024 for -h,-k,l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	5922	wwPDB-VP
Average B, all atoms (Å ²)	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.79% 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: 3DR, SO4, MN

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	0.33	0/5431	0.49	0/7421
2	C	0.42	0/109	0.81	0/166
3	B	0.26	0/35	0.36	0/47
All	All	0.33	0/5575	0.50	0/7634

There are no bond length outliers.

There are no bond angle outliers.

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	A	5303	0	5284	60	0
2	C	112	0	69	12	0
3	B	34	0	30	0	0
4	A	2	0	0	0	0
5	A	20	0	0	5	0
6	A	441	0	0	8	0
6	B	2	0	0	0	0
6	C	8	0	0	0	0
All	All	5922	0	5383	61	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 6.

All (61) 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:348:GLY:H	2:C:1:3DR:H1'2	1.15	1.06
1:A:109:ARG:HE	2:C:1:3DR:H4'1	1.31	0.94
1:A:286:ARG:NH2	1:A:289:GLU:OE1	2.10	0.82
1:A:348:GLY:H	2:C:1:3DR:C1'	1.95	0.78
1:A:348:GLY:N	2:C:1:3DR:H1'2	1.96	0.77
1:A:482:ASP:OD1	1:A:499:ARG:NH2	2.20	0.73
1:A:109:ARG:NE	2:C:1:3DR:H4'1	2.02	0.72
1:A:73[B]:ARG:NH2	6:A:902:HOH:O	2.24	0.70
1:A:649:THR:HG23	1:A:652:ALA:H	1.58	0.68
1:A:477:VAL:HG12	1:A:478:GLY:H	1.60	0.66
1:A:326:GLN:NE2	6:A:906:HOH:O	2.30	0.64
1:A:484:LEU:HD12	1:A:498:GLU:HG2	1.81	0.62
1:A:257:LYS:HE3	1:A:274:ARG:NH2	2.17	0.59
1:A:198:TRP:NE1	1:A:208:GLU:HG2	2.18	0.58
1:A:232:ARG:NH2	1:A:453:LEU:O	2.39	0.55
1:A:261:GLN:NE2	6:A:916:HOH:O	2.40	0.55
1:A:268:ALA:HB1	2:C:5:DT:H72	1.87	0.55
1:A:605:GLU:OE2	1:A:661:ARG:NH1	2.40	0.55
1:A:441:ALA:HB1	1:A:446:LEU:HD13	1.88	0.55
1:A:388:ARG:NH2	5:A:805:SO4:S	2.76	0.54
1:A:73[B]:ARG:NH1	6:A:917:HOH:O	2.40	0.54
1:A:393:ARG:NH1	6:A:909:HOH:O	2.35	0.54
1:A:276:ASN:O	1:A:280:ARG:HG3	2.08	0.54
1:A:194:TYR:CZ	1:A:213:LEU:HD13	2.43	0.53
1:A:109:ARG:HH21	2:C:1:3DR:H4'1	1.73	0.52
1:A:13:ALA:O	1:A:661:ARG:NH2	2.39	0.52
1:A:547:THR:HB	1:A:678:SER:OG	2.10	0.52
1:A:6[B]:HIS:CE1	1:A:428:VAL:HG11	2.44	0.52
1:A:388:ARG:NH2	5:A:805:SO4:O2	2.42	0.51
1:A:359:ASN:O	1:A:427:PRO:HB2	2.10	0.51
1:A:385:ARG:NH1	5:A:805:SO4:O1	2.45	0.50
1:A:482:ASP:HB3	6:A:1016:HOH:O	2.10	0.50
1:A:476:LEU:CD1	1:A:501:ASP:HB3	2.41	0.49
1:A:608:LEU:HD13	1:A:685:LEU:HD11	1.94	0.49
1:A:320:MET:HG2	1:A:342:TRP:CD1	2.48	0.49
1:A:586:LEU:HD11	1:A:593:PRO:HD3	1.95	0.48
1:A:480:GLN:HG2	1:A:499:ARG:NH2	2.28	0.48
1:A:23:ARG:NH1	6:A:923:HOH:O	2.46	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:371:SER:OG	2:C:1:3DR:H2'	2.16	0.46
1:A:657:ALA:O	1:A:661:ARG:HG3	2.16	0.46
1:A:108:HIS:CE1	1:A:110:LEU:HB2	2.51	0.46
1:A:109:ARG:NH2	2:C:1:3DR:H4'1	2.30	0.45
1:A:109:ARG:HE	2:C:1:3DR:C4'	2.16	0.45
2:C:1:3DR:OP3	2:C:1:3DR:H3'	2.17	0.45
1:A:484:LEU:HD22	1:A:486:PHE:HD2	1.82	0.45
1:A:41:ARG:HH21	1:A:44:LEU:HD11	1.83	0.44
1:A:108:HIS:HE1	1:A:110:LEU:HB2	1.82	0.44
1:A:6[B]:HIS:ND1	1:A:428:VAL:HG11	2.32	0.44
1:A:257:LYS:HD3	1:A:257:LYS:HA	1.70	0.44
1:A:480:GLN:HG2	1:A:499:ARG:HH22	1.81	0.44
1:A:83:ASP:HB3	6:A:928:HOH:O	2.18	0.44
1:A:388:ARG:NH2	5:A:805:SO4:O3	2.48	0.43
1:A:297:HIS:ND1	5:A:803:SO4:O1	2.52	0.43
1:A:109:ARG:CZ	2:C:1:3DR:H4'1	2.48	0.43
1:A:217:THR:OG1	1:A:238:GLY:HA3	2.18	0.43
1:A:473:ASP:OD2	1:A:487:ARG:HD3	2.20	0.41
1:A:358:PHE:HB3	1:A:360:ARG:HD2	2.02	0.41
1:A:514:LEU:HD23	1:A:514:LEU:HA	1.85	0.41
1:A:477:VAL:HG21	1:A:485:GLN:CD	2.46	0.41
1:A:45:LEU:HD12	1:A:45:LEU:HA	1.92	0.41
1:A:278:ALA:HB1	1:A:283:GLU:O	2.21	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	697/705 (99%)	689 (99%)	8 (1%)	0	100	100
3	B	2/4 (50%)	2 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	699/709 (99%)	691 (99%)	8 (1%)	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	536/543 (99%)	513 (96%)	23 (4%)	26	18
3	B	4/4 (100%)	4 (100%)	0	100	100
All	All	540/547 (99%)	517 (96%)	23 (4%)	26	18

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

Mol	Chain	Res	Type
1	A	3	ARG
1	A	45	LEU
1	A	98	ILE
1	A	213	LEU
1	A	223	ASP
1	A	313	ARG
1	A	353	LYS
1	A	387	SER
1	A	428	VAL
1	A	446	LEU
1	A	477	VAL
1	A	482	ASP
1	A	501	ASP
1	A	521	THR
1	A	522	SER
1	A	541	THR
1	A	543	GLU
1	A	570	GLN
1	A	608	LEU
1	A	633	GLU

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Mol	Chain	Res	Type
1	A	638	LEU
1	A	700	LEU
1	A	702	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	359	ASN
1	A	382	GLN

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	3DR	C	1	2	12,12,12	0.62	0	14,17,17	2.15	4 (28%)

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	3DR	C	1	2	-	4/6/16/16	0/1/1/1

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	1	3DR	OP2-P-O5'	-4.33	95.38	106.67
2	C	1	3DR	O3'-C3'-C4'	3.91	124.89	110.07
2	C	1	3DR	C1'-C2'-C3'	2.97	106.44	103.26
2	C	1	3DR	OP3-P-OP2	2.95	118.87	107.80

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	C	1	3DR	C5'-O5'-P-OP3
2	C	1	3DR	O4'-C4'-C5'-O5'
2	C	1	3DR	C5'-O5'-P-OP1
2	C	1	3DR	C5'-O5'-P-OP2

There are no ring outliers.

1 monomer is involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	1	3DR	11	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 6 ligands modelled in this entry, 2 are monoatomic - leaving 4 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	SO4	A	803	-	4,4,4	0.26	0	6,6,6	0.15	0
5	SO4	A	804	-	4,4,4	0.24	0	6,6,6	0.27	0
5	SO4	A	806	-	4,4,4	0.24	0	6,6,6	0.06	0
5	SO4	A	805	-	4,4,4	0.24	0	6,6,6	0.09	0

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.

2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	803	SO4	1	0
5	A	805	SO4	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	A	698/705 (99%)	0.84	100 (14%) 6 6	20, 40, 71, 88	3 (0%)
2	C	5/6 (83%)	0.59	1 (20%) 3 2	38, 39, 42, 78	0
3	B	4/4 (100%)	1.68	2 (50%) 0 0	47, 51, 55, 65	0
All	All	707/715 (98%)	0.84	103 (14%) 6 6	20, 41, 71, 88	3 (0%)

All (103) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	692	ALA	7.8
1	A	475	ARG	5.8
1	A	691	ALA	5.8
1	A	545	LEU	5.5
1	A	546	PRO	5.0
1	A	693	LEU	4.8
1	A	544	GLY	4.8
1	A	4	PRO	4.7
1	A	474	THR	4.7
1	A	649	THR	4.6
1	A	481	GLY	4.5
1	A	477	VAL	4.4
1	A	703	ALA	4.4
1	A	574	THR	4.2
1	A	482	ASP	4.2
1	A	705	GLY	4.1
1	A	694	PRO	4.0
1	A	3	ARG	3.9
1	A	502	ALA	3.8
1	A	478	GLY	3.7
1	A	440	ALA	3.6
1	A	620	GLY	3.6
1	A	428	VAL	3.6

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Mol	Chain	Res	Type	RSRZ
1	A	521	THR	3.6
1	A	5	ALA	3.6
1	A	430	ALA	3.6
1	A	547	THR	3.6
1	A	590	ALA	3.4
1	A	479	LYS	3.3
1	A	702	LEU	3.3
1	A	500	ASP	3.3
1	A	503	ALA	3.1
1	A	40	LEU	3.1
1	A	429	PRO	3.0
1	A	589	ASN	2.9
1	A	615	ALA	2.9
1	A	616	GLN	2.9
2	C	6	DT	2.8
1	A	583	LEU	2.8
1	A	617	GLU	2.8
1	A	392	GLY	2.7
1	A	633	GLU	2.7
1	A	541	THR	2.7
1	A	522	SER	2.7
1	A	571	GLY	2.7
1	A	578	ASP	2.7
1	A	389	ASP	2.6
1	A	496	TYR	2.6
1	A	476	LEU	2.6
1	A	515	ASN	2.6
1	A	25	TRP	2.6
1	A	326	GLN	2.6
1	A	554	ARG	2.5
1	A	480	GLN	2.5
1	A	491	VAL	2.5
1	A	490	GLY	2.5
1	A	412	ALA	2.5
1	A	704	ALA	2.5
1	A	639	THR	2.5
1	A	560	LEU	2.4
1	A	20	ALA	2.4
1	A	695	LYS	2.4
1	A	163	GLY	2.4
1	A	570	GLN	2.4
1	A	404	SER	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	527	ALA	2.4
1	A	587	ASP	2.3
1	A	696	ALA	2.3
1	A	523	LEU	2.3
1	A	6[A]	HIS	2.3
1	A	472	THR	2.3
3	B	211	PHE	2.3
1	A	613	HIS	2.3
1	A	405	LEU	2.3
1	A	385	ARG	2.2
1	A	246	GLU	2.2
1	A	504	GLY	2.2
1	A	581	PRO	2.2
3	B	208	ASP	2.2
1	A	447	LEU	2.2
1	A	582	GLY	2.2
1	A	648	HIS	2.2
1	A	23	ARG	2.2
1	A	259	VAL	2.2
1	A	632	ALA	2.2
1	A	258	ARG	2.2
1	A	690	PRO	2.2
1	A	303	ALA	2.2
1	A	636	ALA	2.2
1	A	501	ASP	2.1
1	A	588	THR	2.1
1	A	260	ARG	2.1
1	A	473	ASP	2.1
1	A	499	ARG	2.1
1	A	341	ASP	2.1
1	A	168	GLU	2.1
1	A	411	GLY	2.1
1	A	314	ARG	2.1
1	A	487	ARG	2.1
1	A	256	GLU	2.0
1	A	483	VAL	2.0
1	A	572	VAL	2.0
1	A	297	HIS	2.0

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

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	3DR	C	1	12/12	0.71	0.33	35,47,62,68	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

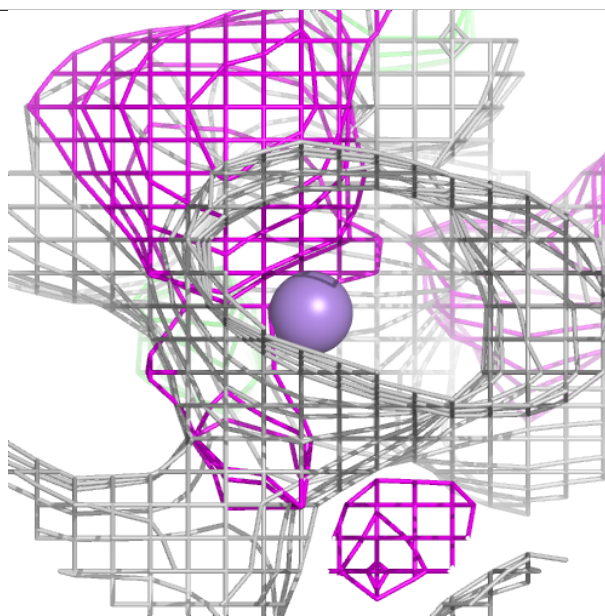
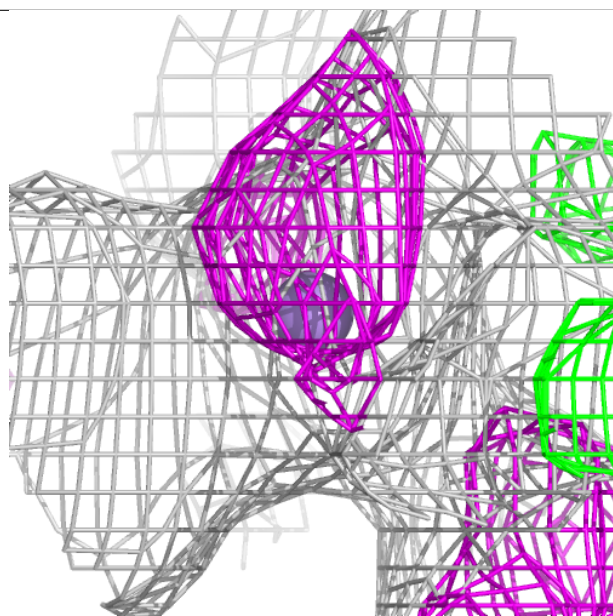
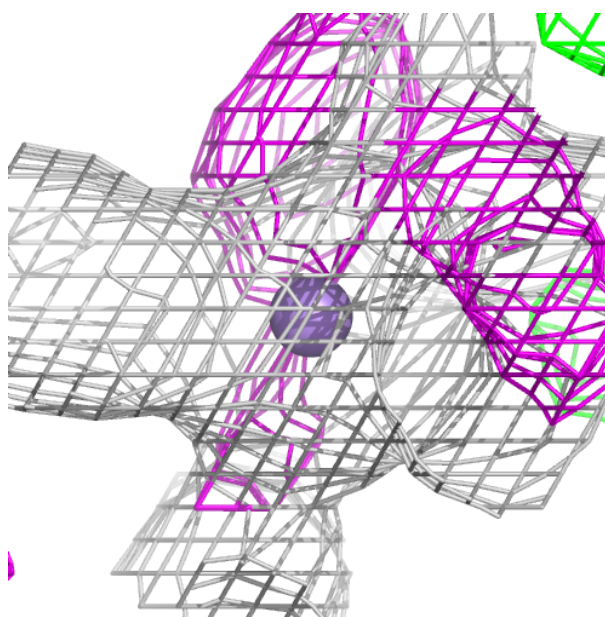
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
5	SO4	A	803	5/5	0.79	0.17	61,63,74,79	0
5	SO4	A	806	5/5	0.84	0.16	117,119,124,129	0
5	SO4	A	804	5/5	0.89	0.14	66,67,71,72	0
5	SO4	A	805	5/5	0.90	0.18	104,108,111,111	0
4	MN	A	802	1/1	0.99	0.09	41,41,41,41	0
4	MN	A	801	1/1	1.00	0.07	37,37,37,37	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

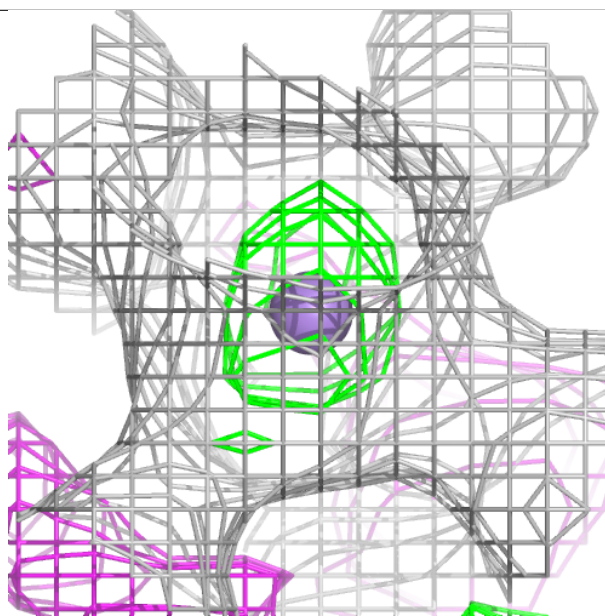
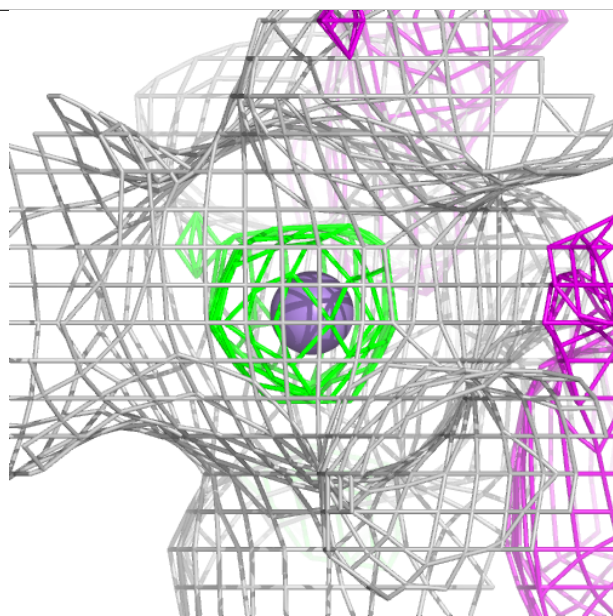
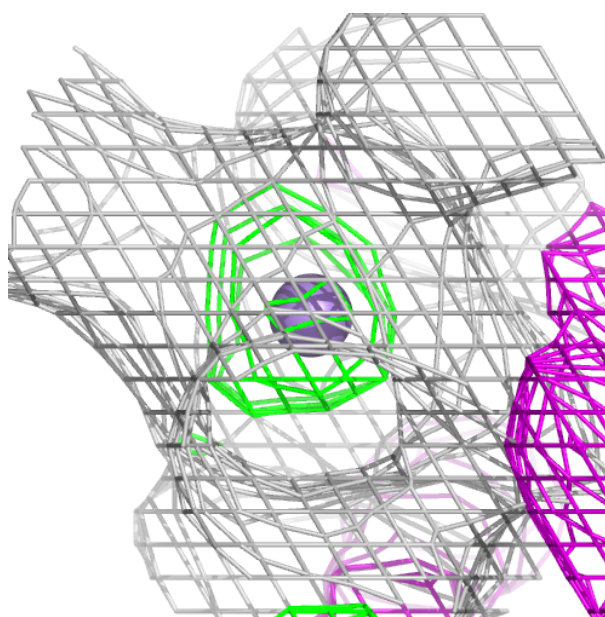
Electron density around MN A 802:

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



Electron density around MN A 801:

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



6.5 Other polymers ⓘ

There are no such residues in this entry.