



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 26, 2026 – 11:30 AM EDT

PDB ID : 8AVZ / pdb_00008avz
Title : Crystal structure of PksD, the trans-acting acyl hydrolase domain from the bacillaene trans-AT PKS (SeMet derivative)
Authors : Fage, C.D.; Challis, G.L.; Lewandowski, J.; Jenner, M.
Deposited on : 2022-08-28
Resolution : 1.96 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

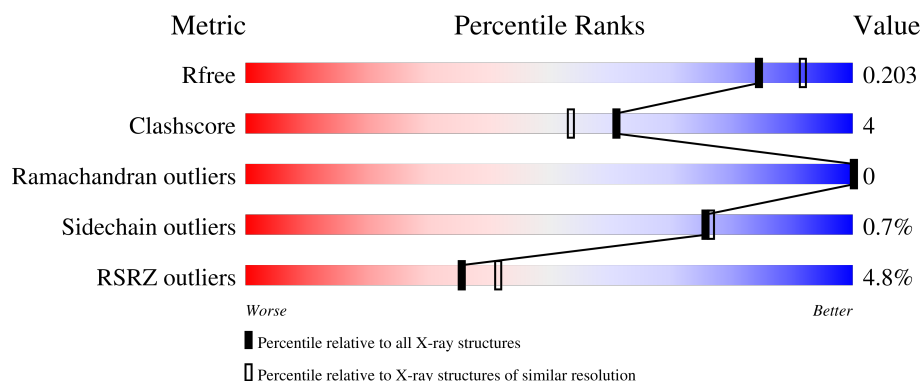
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.96 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	3494 (1.96-1.96)
Clashscore	190562	3612 (1.96-1.96)
Ramachandran outliers	187476	3587 (1.96-1.96)
Sidechain outliers	187428	3587 (1.96-1.96)
RSRZ outliers	180081	3495 (1.96-1.96)

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	327	4% 87% 10% .
1	B	327	5% 85% 11% .
1	C	327	3% 86% 10% ..
1	D	327	5% 85% 11% .

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 10968 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 Polyketide biosynthesis acyltransferase homolog PksD.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	317	Total	C	N	O	S	Se	0	9	0
			2594	1654	429	491	9	11			
1	B	315	Total	C	N	O	S	Se	0	10	0
			2585	1646	430	489	9	11			
1	C	315	Total	C	N	O	S	Se	0	6	0
			2551	1628	420	484	8	11			
1	D	315	Total	C	N	O	S	Se	0	7	0
			2565	1636	427	483	8	11			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	GLY	-	expression tag	UNP O34877
A	-1	SER	-	expression tag	UNP O34877
A	0	HIS	-	expression tag	UNP O34877
B	-2	GLY	-	expression tag	UNP O34877
B	-1	SER	-	expression tag	UNP O34877
B	0	HIS	-	expression tag	UNP O34877
C	-2	GLY	-	expression tag	UNP O34877
C	-1	SER	-	expression tag	UNP O34877
C	0	HIS	-	expression tag	UNP O34877
D	-2	GLY	-	expression tag	UNP O34877
D	-1	SER	-	expression tag	UNP O34877
D	0	HIS	-	expression tag	UNP O34877

- Molecule 2 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Zn	0	0
			1	1		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	1	Total 1	Zn 1	0	0

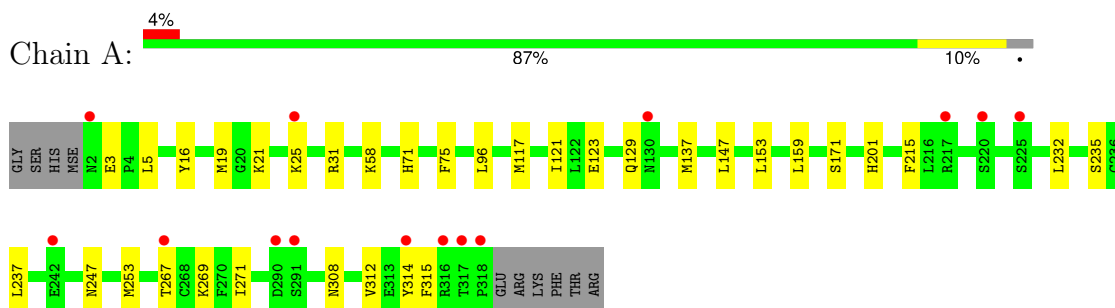
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	194	Total 194	O 194	0	0
3	B	196	Total 196	O 196	0	0
3	C	151	Total 151	O 151	0	0
3	D	130	Total 130	O 130	0	0

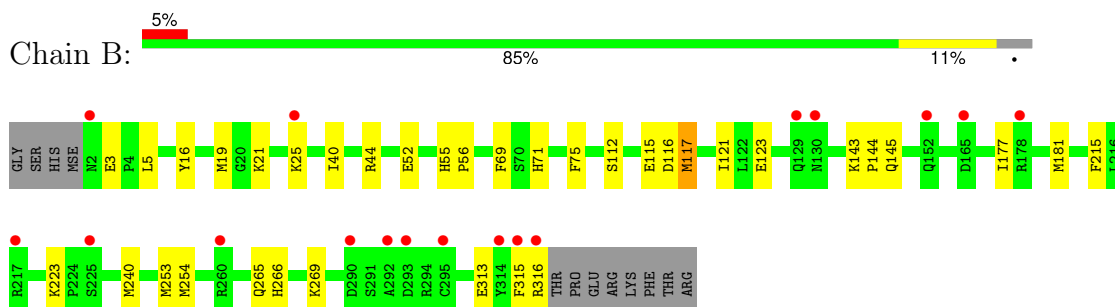
3 Residue-property plots [i](#)

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.

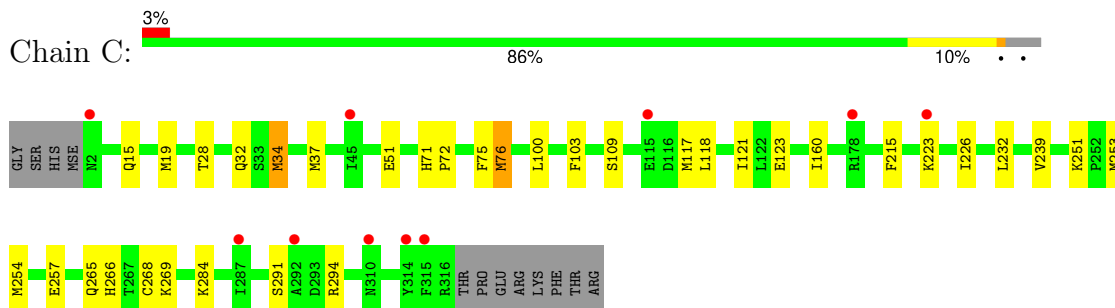
- Molecule 1: Polyketide biosynthesis acyltransferase homolog PksD



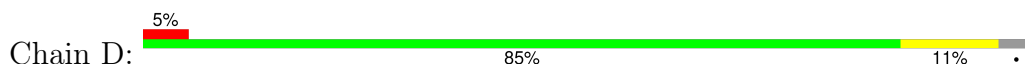
- Molecule 1: Polyketide biosynthesis acyltransferase homolog PksD

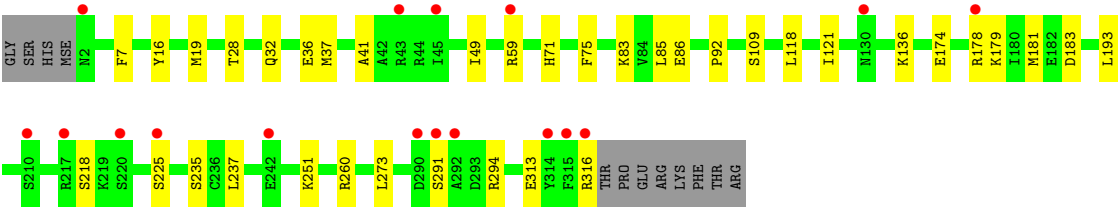


- Molecule 1: Polyketide biosynthesis acyltransferase homolog PksD



- Molecule 1: Polyketide biosynthesis acyltransferase homolog PksD





4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	207.71Å 83.56Å 145.74Å 90.00° 119.71° 90.00°	Depositor
Resolution (Å)	59.79 – 1.96 59.79 – 1.96	Depositor EDS
% Data completeness (in resolution range)	99.8 (59.79-1.96) 100.0 (59.79-1.96)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.68 (at 1.95Å)	Xtriage
Refinement program	PHENIX 1.19.2-4158	Depositor
R, R_{free}	0.179 , 0.203 0.180 , 0.203	Depositor DCC
R_{free} test set	7706 reflections (4.96%)	wwPDB-VP
Wilson B-factor (Å ²)	35.4	Xtriage
Anisotropy	0.722	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 40.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	10968	wwPDB-VP
Average B, all atoms (Å ²)	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 44.71 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.4672e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: ZN

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	0.54	0/2642	0.71	2/3549 (0.1%)
1	B	0.57	1/2632 (0.0%)	0.70	3/3534 (0.1%)
1	C	0.52	0/2598	0.65	2/3490 (0.1%)
1	D	0.48	0/2612	0.65	0/3507
All	All	0.53	1/10484 (0.0%)	0.68	7/14080 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	253	MSE	CB-CG	6.30	1.71	1.52

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	117	MSE	N-CA-C	-7.38	102.61	111.69
1	B	254	MSE	N-CA-C	-5.84	101.70	110.06
1	C	34	MSE	CG-SE-CE	5.71	111.50	98.92
1	C	76	MSE	N-CA-C	-5.57	105.13	111.14
1	A	314	TYR	CA-CB-CG	-5.51	103.98	113.90
1	A	129	GLN	CA-CB-CG	-5.28	103.53	114.10
1	B	253	MSE	CB-CG-SE	-5.27	96.89	112.70

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	2594	0	2537	20	0
1	B	2585	0	2526	22	0
1	C	2551	0	2493	22	0
1	D	2565	0	2514	23	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	194	0	0	3	0
3	B	196	0	0	2	0
3	C	151	0	0	3	0
3	D	130	0	0	2	0
All	All	10968	0	10070	86	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 (86) 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:D:32:GLN:O	1:D:36:GLU:HG3	1.76	0.84
1:B:40:ILE:HD13	1:B:115:GLU:HG3	1.61	0.83
1:B:116:ASP:OD2	3:B:501:HOH:O	1.98	0.82
1:C:223:LYS:HE2	1:C:239:VAL:HG22	1.64	0.79
1:D:260:ARG:NH1	3:D:401:HOH:O	2.18	0.77
1:B:21:LYS:O	1:B:25:LYS:HD3	1.91	0.71
1:B:313:GLU:OE2	1:B:316:ARG:NH2	2.24	0.70
1:C:15:GLN:HB2	1:C:19:MSE:HE1	1.73	0.68
1:B:112:SER:HB3	1:B:117:MSE:HG2	1.75	0.67
1:B:143:LYS:HD2	1:B:144:PRO:HD2	1.77	0.66
1:C:284:LYS:NZ	3:C:402:HOH:O	2.31	0.61
1:B:3:GLU:OE1	1:B:269:LYS:HE2	2.00	0.61
1:C:123:GLU:HG2	1:C:215:PHE:CD1	2.35	0.61
1:C:51:GLU:OE1	3:C:401:HOH:O	2.17	0.60
1:C:103:PHE:CD2	1:C:117:MSE:HE2	2.38	0.58
1:C:291:SER:HB3	1:C:294:ARG:HE	1.69	0.58
1:B:16:TYR:O	1:B:19:MSE:HG2	2.04	0.57
1:B:143:LYS:HE3	1:B:145:GLN:H	1.68	0.57
1:B:44[B]:ARG:NH2	1:B:123:GLU:OE1	2.35	0.55
1:A:3:GLU:HG2	1:A:267:THR:O	2.05	0.55
1:D:291:SER:HB3	1:D:294:ARG:HE	1.71	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:223:LYS:O	3:B:502:HOH:O	2.18	0.55
1:A:21:LYS:O	1:A:25[A]:LYS:HG3	2.07	0.55
1:B:177:ILE:O	1:B:181:MSE:HG3	2.07	0.54
1:D:174:GLU:HG3	3:D:433:HOH:O	2.08	0.53
1:C:160:ILE:HD12	1:C:253:MSE:HE1	1.90	0.52
1:C:37:MSE:HG2	1:C:118:LEU:HD22	1.93	0.51
1:A:308:ASN:O	1:A:312:VAL:HG23	2.11	0.51
1:B:112:SER:HB3	1:B:117:MSE:CG	2.41	0.50
1:C:72:PRO:O	1:C:76:MSE:HG3	2.11	0.50
1:A:16:TYR:O	1:A:19:MSE:HG2	2.11	0.50
1:B:5:LEU:HD23	1:B:269:LYS:HB2	1.93	0.49
1:B:52[A]:GLU:HG2	1:B:69:PHE:CD2	2.48	0.49
1:A:58:LYS:NZ	3:A:506:HOH:O	2.45	0.49
1:D:291:SER:HB3	1:D:294:ARG:NE	2.28	0.49
1:D:83:LYS:NZ	1:D:86:GLU:OE1	2.37	0.48
1:D:28:THR:O	1:D:32:GLN:HG3	2.14	0.48
1:D:179:LYS:HE3	1:D:183:ASP:OD2	2.13	0.48
1:D:41:ALA:CB	1:D:49:ILE:HD12	2.44	0.47
1:C:34:MSE:CE	1:C:76:MSE:HE2	2.44	0.47
1:D:41:ALA:HB1	1:D:49:ILE:HD12	1.96	0.47
1:A:31[A]:ARG:NH2	3:A:501:HOH:O	2.15	0.47
1:C:269:LYS:NZ	3:C:403:HOH:O	2.41	0.46
1:D:37:MSE:HG2	1:D:118:LEU:HD22	1.97	0.46
1:B:265:GLN:NE2	1:D:235[B]:SER:OG	2.45	0.46
1:C:15:GLN:HB2	1:C:19:MSE:CE	2.44	0.46
1:B:123:GLU:HG2	1:B:215:PHE:CD1	2.51	0.46
1:B:143:LYS:HE3	1:B:143:LYS:HB3	1.55	0.46
1:C:34:MSE:HE3	1:C:76:MSE:HE2	1.98	0.46
1:C:109:SER:HA	1:C:226:ILE:HB	1.97	0.45
1:D:237:LEU:C	1:D:237:LEU:HD23	2.41	0.45
1:D:136:LYS:HE3	1:D:178[A]:ARG:NH2	2.33	0.44
1:A:123:GLU:HG2	1:A:215:PHE:CG	2.52	0.44
1:C:28:THR:O	1:C:32:GLN:HG3	2.18	0.44
1:C:254:MSE:HE2	1:C:257:GLU:HG2	1.99	0.44
1:A:75:PHE:HB2	1:A:121:ILE:HD13	2.00	0.43
1:A:5:LEU:HD21	1:A:269:LYS:HE3	1.99	0.43
1:C:75:PHE:HB2	1:C:121:ILE:HD13	2.00	0.43
1:D:75:PHE:HB2	1:D:121:ILE:HD13	2.01	0.42
1:B:75:PHE:HB2	1:B:121:ILE:HD13	2.00	0.42
1:D:16:TYR:CE2	1:D:19:MSE:HA	2.54	0.42
1:A:137:MSE:HG2	1:A:171:SER:HB2	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:201:HIS:CE1	1:A:253:MSE:HE2	2.54	0.42
1:D:251:LYS:HA	1:D:251:LYS:HD2	1.82	0.42
1:A:117:MSE:HE3	1:A:117:MSE:HA	2.00	0.42
1:A:237:LEU:HD12	1:A:237:LEU:HA	1.93	0.42
1:A:312:VAL:O	1:A:315:PHE:HB2	2.19	0.42
1:A:235:SER:HB3	3:A:572:HOH:O	2.19	0.42
1:A:147:LEU:HD11	1:A:159:LEU:HD13	2.01	0.42
1:A:153:LEU:HA	1:A:153:LEU:HD23	1.76	0.41
1:C:268:CYS:O	1:C:294:ARG:HD2	2.20	0.41
1:D:109:SER:O	1:D:225:SER:HB2	2.19	0.41
1:C:265:GLN:HB2	1:C:266:HIS:CD2	2.55	0.41
1:D:7:PHE:CG	1:D:92:PRO:HB3	2.55	0.41
1:A:232:LEU:HD21	1:A:247:ASN:HB3	2.00	0.41
1:D:59[A]:ARG:HE	1:D:59[A]:ARG:HB2	1.66	0.41
1:D:85:LEU:HD12	1:D:273:LEU:HD21	2.02	0.41
1:D:181:MSE:SE	1:D:193:LEU:HG	2.71	0.41
1:D:313:GLU:OE2	1:D:316:ARG:NH2	2.54	0.41
1:A:271:ILE:HD13	1:A:312:VAL:HG13	2.03	0.41
1:B:240:MSE:HE2	1:B:240:MSE:HB3	1.83	0.40
1:C:232:LEU:HD13	1:C:251:LYS:HB2	2.03	0.40
1:A:96:LEU:C	1:A:96:LEU:HD23	2.46	0.40
1:C:117:MSE:HE3	1:C:117:MSE:HA	2.04	0.40
1:B:44[B]:ARG:NH1	1:B:123:GLU:OE1	2.51	0.40
1:B:55:HIS:HA	1:B:56:PRO:HD3	1.98	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	324/327 (99%)	318 (98%)	6 (2%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	323/327 (99%)	319 (99%)	4 (1%)	0	100	100
1	C	319/327 (98%)	311 (98%)	8 (2%)	0	100	100
1	D	320/327 (98%)	312 (98%)	8 (2%)	0	100	100
All	All	1286/1308 (98%)	1260 (98%)	26 (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	290/278 (104%)	289 (100%)	1 (0%)	86	87
1	B	289/278 (104%)	286 (99%)	3 (1%)	68	67
1	C	285/278 (102%)	283 (99%)	2 (1%)	76	76
1	D	286/278 (103%)	284 (99%)	2 (1%)	76	76
All	All	1150/1112 (103%)	1142 (99%)	8 (1%)	76	76

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	71	HIS
1	B	71	HIS
1	B	266	HIS
1	B	315	PHE
1	C	71	HIS
1	C	100	LEU
1	D	71	HIS
1	D	218	SER

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

Mol	Chain	Res	Type
1	A	310	ASN
1	C	12	GLN
1	C	124	GLN
1	C	145	GLN
1	C	310	ASN
1	D	130	ASN
1	D	310	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](#)

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

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	306/327 (93%)	0.36	14 (4%) 37 43	16, 41, 61, 90	9 (2%)
1	B	304/327 (92%)	0.42	17 (5%) 30 35	15, 41, 64, 100	10 (3%)
1	C	304/327 (92%)	0.64	10 (3%) 49 55	19, 48, 71, 102	6 (1%)
1	D	304/327 (92%)	0.63	17 (5%) 30 35	19, 47, 73, 106	7 (2%)
All	All	1218/1308 (93%)	0.51	58 (4%) 35 41	15, 44, 69, 106	32 (2%)

All (58) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	314	TYR	4.5
1	A	25[A]	LYS	4.4
1	D	314	TYR	4.3
1	A	318	PRO	3.8
1	B	315	PHE	3.8
1	B	316	ARG	3.7
1	A	2	ASN	3.5
1	D	220	SER	3.2
1	D	43[A]	ARG	3.2
1	D	290	ASP	3.1
1	B	314	TYR	3.0
1	A	267	THR	3.0
1	A	314	TYR	2.9
1	B	2	ASN	2.9
1	C	315	PHE	2.8
1	D	178[A]	ARG	2.8
1	C	223	LYS	2.8
1	A	225	SER	2.7
1	C	178[A]	ARG	2.7
1	C	45	ILE	2.7
1	D	292	ALA	2.6

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Mol	Chain	Res	Type	RSRZ
1	C	115[A]	GLU	2.6
1	A	317	THR	2.6
1	B	165[A]	ASP	2.6
1	B	290	ASP	2.6
1	C	287	ILE	2.5
1	A	130	ASN	2.5
1	D	59[A]	ARG	2.4
1	D	217	ARG	2.4
1	B	292	ALA	2.4
1	D	2	ASN	2.4
1	A	220	SER	2.4
1	D	316	ARG	2.3
1	C	292	ALA	2.3
1	C	2	ASN	2.3
1	A	291	SER	2.3
1	A	217[A]	ARG	2.3
1	B	260	ARG	2.3
1	D	225	SER	2.3
1	D	315	PHE	2.2
1	D	45	ILE	2.2
1	B	129	GLN	2.2
1	D	130	ASN	2.2
1	B	295[A]	CYS	2.2
1	A	290	ASP	2.2
1	A	242	GLU	2.2
1	B	217	ARG	2.1
1	B	130	ASN	2.1
1	B	25	LYS	2.1
1	D	242	GLU	2.1
1	C	310	ASN	2.1
1	B	178[A]	ARG	2.1
1	B	225	SER	2.1
1	B	293	ASP	2.1
1	D	291	SER	2.0
1	B	152	GLN	2.0
1	D	210	SER	2.0
1	A	316	ARG	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 [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

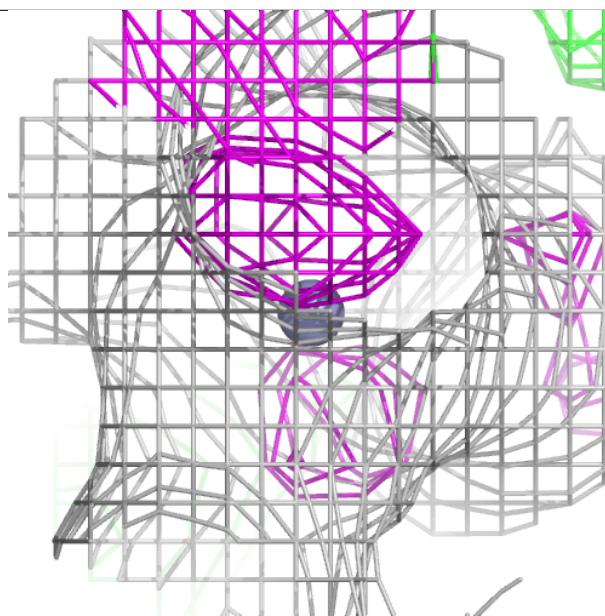
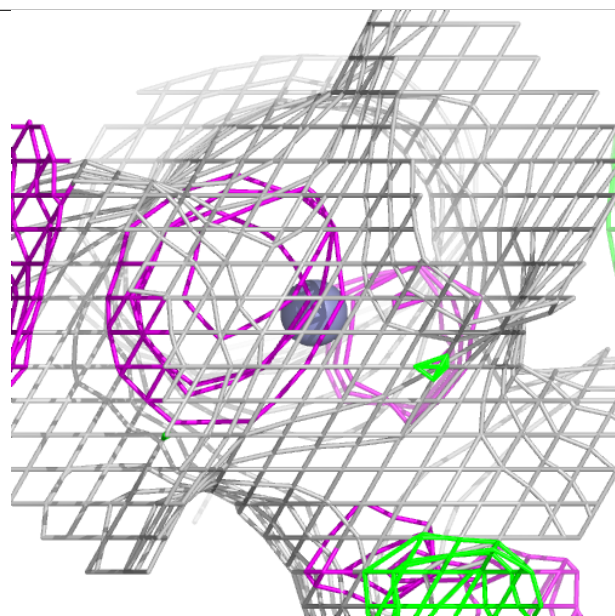
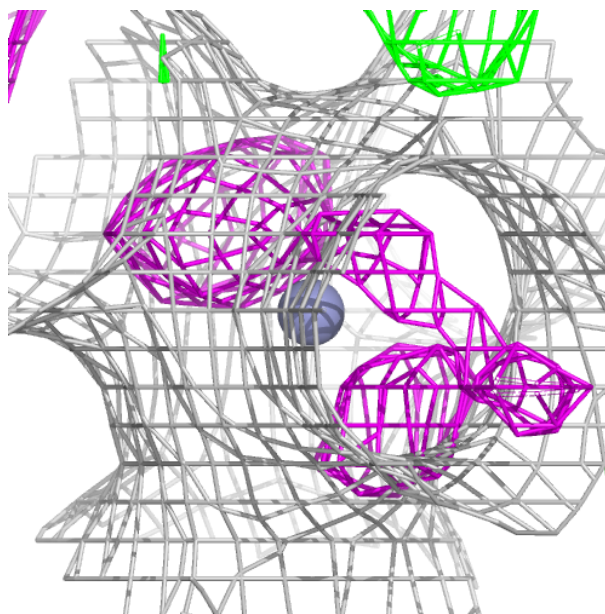
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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
2	ZN	A	401	1/1	0.99	0.04	44,44,44,44	0
2	ZN	B	401	1/1	0.99	0.05	46,46,46,46	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.

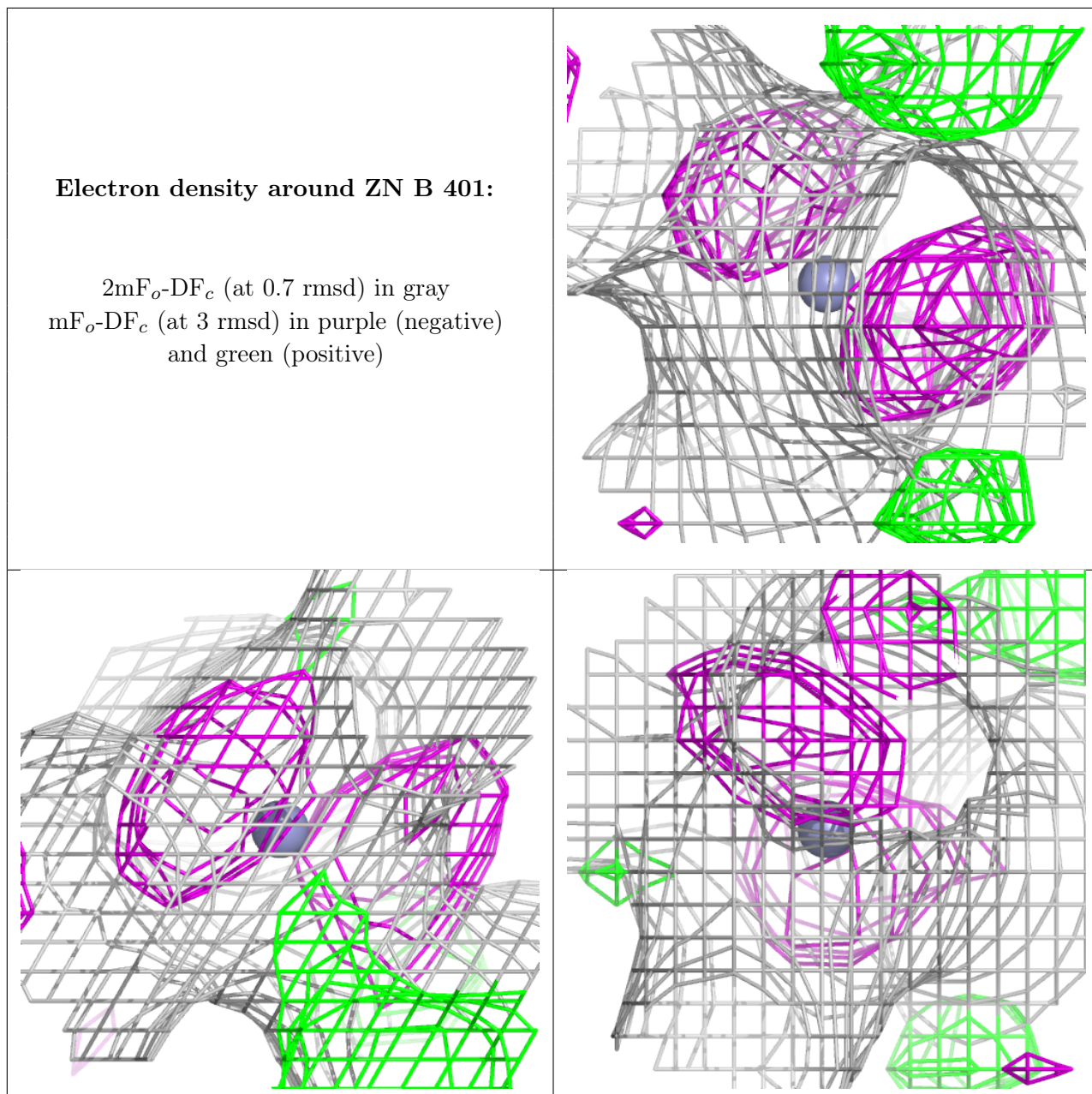
Electron density around ZN A 401:

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



Electron density around ZN B 401:

$2mF_o-DF_c$ (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.