



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 06:25 AM UTC

PDB ID : 7TV4 / pdb_00007tv4
Title : Crystal structure of NEMO CoZi in complex with HOIP NZF1 and linear diubiquitin
Authors : Rahighi, S.; Iyer, M.; Oveisi, H.
Deposited on : 2022-02-03
Resolution : 4.20 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
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

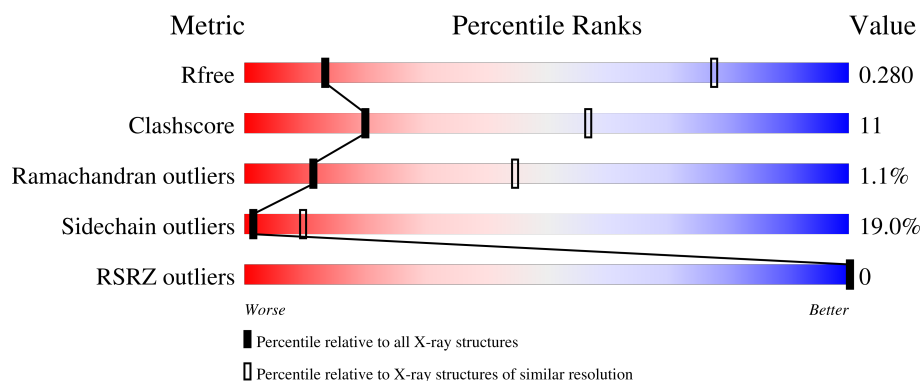
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 4.20 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	1004 (4.52-3.88)
Clashscore	190562	1019 (4.50-3.90)
Ramachandran outliers	187476	1020 (4.56-3.84)
Sidechain outliers	187428	1006 (4.56-3.84)
RSRZ outliers	180081	1001 (4.52-3.88)

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	B	98	
1	D	98	
2	C	156	
2	G	156	
3	K	35	

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 3906 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 NF-kappa-B essential modulator.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	B	81	Total	C	N	O	S	0	0	0
			671	420	115	135	1			
1	D	79	Total	C	N	O	S	0	0	0
			650	406	113	130	1			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	249	GLY	-	expression tag	UNP Q9Y6K9
B	250	PRO	-	expression tag	UNP Q9Y6K9
B	251	LEU	-	expression tag	UNP Q9Y6K9
B	252	GLY	-	expression tag	UNP Q9Y6K9
B	253	SER	-	expression tag	UNP Q9Y6K9
B	254	PRO	-	expression tag	UNP Q9Y6K9
B	255	GLU	-	expression tag	UNP Q9Y6K9
B	256	PHE	-	expression tag	UNP Q9Y6K9
D	249	GLY	-	expression tag	UNP Q9Y6K9
D	250	PRO	-	expression tag	UNP Q9Y6K9
D	251	LEU	-	expression tag	UNP Q9Y6K9
D	252	GLY	-	expression tag	UNP Q9Y6K9
D	253	SER	-	expression tag	UNP Q9Y6K9
D	254	PRO	-	expression tag	UNP Q9Y6K9
D	255	GLU	-	expression tag	UNP Q9Y6K9
D	256	PHE	-	expression tag	UNP Q9Y6K9

- Molecule 2 is a protein called Polyubiquitin-C.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	147	Total	C	N	O	S	0	0	0
			1167	735	202	229	1			
2	G	152	Total	C	N	O	S	0	0	0
			1198	754	207	235	2			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	-3	GLY	-	expression tag	UNP P0CG48
C	-2	SER	-	expression tag	UNP P0CG48
C	-1	GLY	-	expression tag	UNP P0CG48
C	0	SER	-	expression tag	UNP P0CG48
G	-3	GLY	-	expression tag	UNP P0CG48
G	-2	SER	-	expression tag	UNP P0CG48
G	-1	GLY	-	expression tag	UNP P0CG48
G	0	SER	-	expression tag	UNP P0CG48

- Molecule 3 is a protein called E3 ubiquitin-protein ligase RNF31.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	K	27	Total	C	N	O	S	0	0	0
			208	127	39	38	4			

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
K	345	GLY	-	expression tag	UNP Q96EP0
K	346	PRO	-	expression tag	UNP Q96EP0
K	347	LEU	-	expression tag	UNP Q96EP0
K	348	GLY	-	expression tag	UNP Q96EP0
K	349	SER	-	expression tag	UNP Q96EP0

- Molecule 4 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	K	1	Total	Zn	0	0
			1	1		

- Molecule 5 is water.

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

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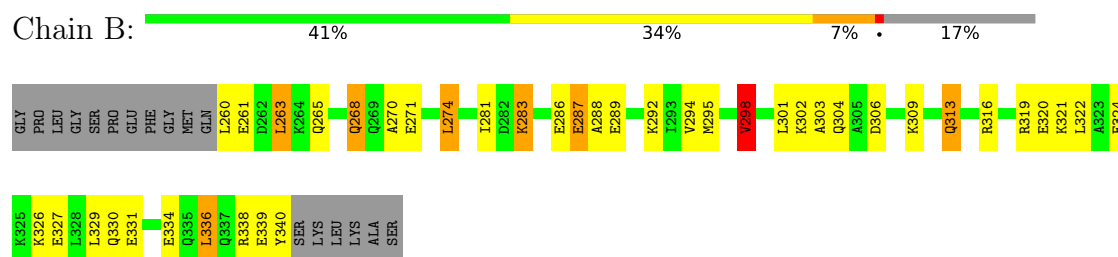
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	K	1	Total	O	0	0
			1	1		

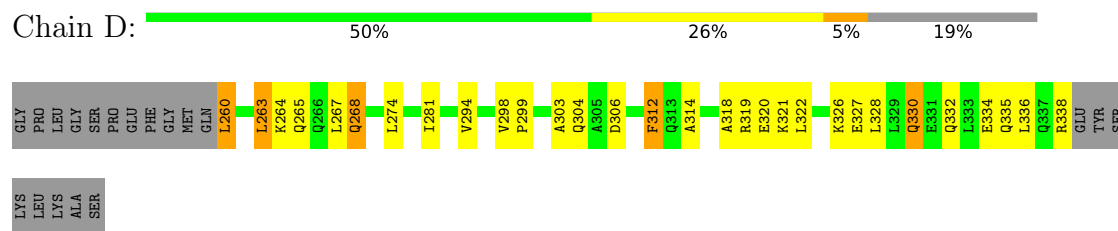
3 Residue-property plots

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.

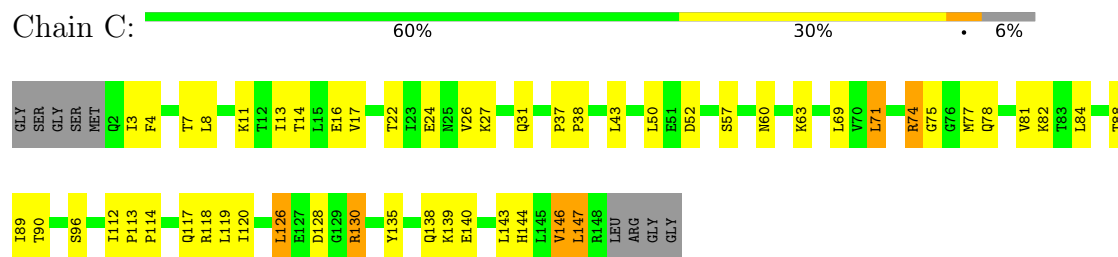
• Molecule 1: NF-kappa-B essential modulator



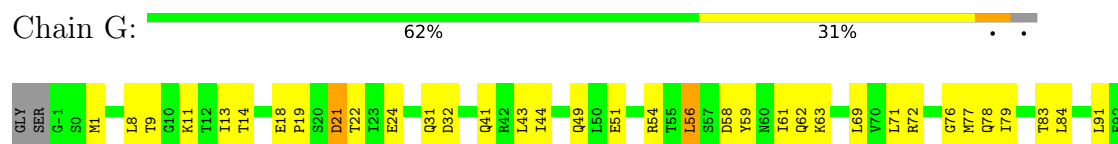
• Molecule 1: NF-kappa-B essential modulator

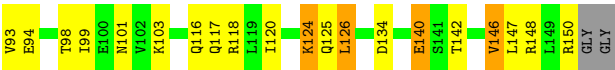


• Molecule 2: Polyubiquitin-C

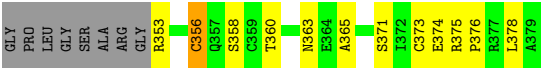


• Molecule 2: Polyubiquitin-C





● Molecule 3: E3 ubiquitin-protein ligase RNF31



4 Data and refinement statistics

Property	Value	Source
Space group	P 2 21 21	Depositor
Cell constants a, b, c, α , β , γ	55.95Å 69.56Å 180.05Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	56.01 – 4.20 56.01 – 4.20	Depositor EDS
% Data completeness (in resolution range)	99.8 (56.01-4.20) 99.8 (56.01-4.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.25 (at 4.14Å)	Xtriage
Refinement program	REFMAC 5.8.0238	Depositor
R, R_{free}	0.222 , 0.286 0.224 , 0.280	Depositor DCC
R_{free} test set	286 reflections (5.17%)	wwPDB-VP
Wilson B-factor (Å ²)	93.1	Xtriage
Anisotropy	0.314	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.27 , 76.7	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	0.92	EDS
Total number of atoms	3906	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 5.11% 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: 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	B	1.02	0/675	1.56	1/902 (0.1%)
1	D	1.04	0/653	1.57	0/872
2	C	1.05	0/1180	1.46	2/1590 (0.1%)
2	G	1.08	0/1211	1.44	2/1631 (0.1%)
3	K	1.01	0/211	1.42	0/285
All	All	1.05	0/3930	1.49	5/5280 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
2	C	0	1

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	298	VAL	N-CA-CB	7.20	116.07	110.45
2	C	52	ASP	CA-C-N	5.56	126.11	120.00
2	C	52	ASP	C-N-CA	5.56	126.11	120.00
2	G	124	LYS	CA-C-N	5.12	128.82	121.50
2	G	124	LYS	C-N-CA	5.12	128.82	121.50

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	C	75	GLY	Peptide

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	671	0	684	24	0
1	D	650	0	669	24	0
2	C	1167	0	1214	35	0
2	G	1198	0	1247	21	0
3	K	208	0	196	6	0
4	K	1	0	0	0	0
5	B	4	0	0	1	0
5	C	1	0	0	0	0
5	G	5	0	0	0	0
5	K	1	0	0	0	0
All	All	3906	0	4010	90	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 11.

All (90) 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:319:ARG:NH1	2:G:140:GLU:OE2	2.05	0.89
1:D:298:VAL:HB	1:D:299:PRO:HD3	1.65	0.78
2:C:147:LEU:HD13	2:C:147:LEU:N	2.03	0.74
1:D:298:VAL:HB	1:D:299:PRO:CD	2.20	0.72
2:C:81:VAL:HB	2:C:89:ILE:CG2	2.22	0.70
2:C:8:LEU:HD11	1:D:304:GLN:NE2	2.10	0.66
1:D:328:LEU:O	1:D:332:GLN:NE2	2.29	0.65
1:D:268:GLN:HE21	1:D:268:GLN:HA	1.61	0.64
1:B:329:LEU:HD11	1:D:330:GLN:HG2	1.81	0.63
1:B:330:GLN:O	1:B:334:GLU:HG2	1.99	0.62
1:B:320:GLU:HG3	2:C:90:THR:HG23	1.83	0.61
2:G:1:MET:HE3	2:G:63:LYS:HA	1.80	0.61
2:C:71:LEU:HD22	2:C:71:LEU:H	1.67	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:270:ALA:O	1:B:274:LEU:HD12	2.03	0.59
1:B:327:GLU:CD	2:C:144:HIS:HE2	2.12	0.58
2:G:44:ILE:HD13	2:G:49:GLN:HA	1.86	0.58
5:B:402:HOH:O	1:D:326:LYS:HG3	2.04	0.57
1:B:271:GLU:OE2	1:B:274:LEU:HD13	2.03	0.57
2:C:74:ARG:NH1	1:D:314:ALA:HB1	2.20	0.56
1:B:313:GLN:O	1:B:316:ARG:N	2.38	0.56
3:K:373:CYS:HB3	3:K:375:ARG:HG3	1.88	0.56
2:C:119:LEU:O	2:C:120:ILE:HD13	2.07	0.55
1:B:324:GLU:OE1	2:C:88:THR:OG1	2.23	0.55
1:B:327:GLU:OE2	2:C:144:HIS:NE2	2.39	0.55
3:K:353:ARG:N	3:K:365:ALA:HB2	2.22	0.54
1:B:303:ALA:O	1:B:306:ASP:N	2.40	0.54
2:G:21:ASP:OD1	2:G:21:ASP:N	2.41	0.53
2:G:77:MET:HB2	2:G:93:VAL:HG23	1.90	0.52
2:C:4:PHE:CD1	2:C:14:THR:HG22	2.44	0.52
2:C:140:GLU:OE1	1:D:322:LEU:HD13	2.10	0.51
2:C:112:ILE:O	2:C:117:GLN:NE2	2.44	0.51
2:G:146:VAL:C	2:G:147:LEU:HD12	2.36	0.51
2:G:126:LEU:N	2:G:126:LEU:HD23	2.26	0.50
2:C:81:VAL:HB	2:C:89:ILE:HG23	1.92	0.50
2:C:82:LYS:HD3	2:C:144:HIS:NE2	2.26	0.50
1:B:336:LEU:HD12	1:D:336:LEU:HD22	1.94	0.49
2:C:43:LEU:HB2	2:C:50:LEU:HD12	1.94	0.49
1:D:274:LEU:HB3	3:K:376:PRO:HG3	1.94	0.49
2:C:147:LEU:N	2:C:147:LEU:CD1	2.73	0.49
2:G:18:GLU:HB3	2:G:19:PRO:HD2	1.95	0.49
2:G:99:ILE:HG22	2:G:103:LYS:HD2	1.96	0.48
3:K:353:ARG:HA	3:K:363:ASN:O	2.14	0.48
2:C:8:LEU:HD11	1:D:304:GLN:HE22	1.78	0.48
2:G:43:LEU:HD21	2:G:69:LEU:HD13	1.95	0.47
1:B:339:GLU:OE2	1:D:338:ARG:HD3	2.15	0.47
2:C:81:VAL:HB	2:C:89:ILE:HG22	1.93	0.47
2:C:126:LEU:N	2:C:126:LEU:HD23	2.30	0.47
2:G:116:GLN:NE2	2:G:150:ARG:O	2.48	0.47
1:D:312:PHE:C	1:D:312:PHE:CD1	2.89	0.46
2:G:79:ILE:HD12	2:G:79:ILE:C	2.41	0.46
1:B:268:GLN:HE21	1:B:268:GLN:HA	1.80	0.46
3:K:356:CYS:C	3:K:358:SER:H	2.23	0.46
1:B:319:ARG:NH2	1:D:318:ALA:HB1	2.31	0.46
1:B:295:MET:O	1:B:298:VAL:HG13	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:327:GLU:OE2	2:C:82:LYS:NZ	2.30	0.45
2:G:51:GLU:OE1	2:G:51:GLU:HA	2.16	0.45
2:C:77:MET:HG3	2:C:139:LYS:HD2	1.98	0.45
2:G:118:ARG:HD2	2:G:148:ARG:HG3	1.98	0.45
2:C:77:MET:HA	2:C:139:LYS:HE3	1.97	0.44
1:D:332:GLN:O	1:D:335:GLN:NE2	2.46	0.44
2:G:84:LEU:HD11	2:G:146:VAL:CG1	2.48	0.44
1:B:287:GLU:O	1:B:288:ALA:C	2.60	0.44
2:C:22:THR:O	2:C:26:VAL:HG23	2.18	0.44
2:C:37:PRO:O	2:C:38:PRO:C	2.60	0.43
2:G:56:LEU:N	2:G:56:LEU:HD23	2.33	0.43
2:C:130:ARG:HG2	2:C:135:TYR:CZ	2.53	0.43
1:B:283:LYS:HD3	1:B:283:LYS:HA	1.78	0.43
1:D:327:GLU:HG3	2:G:142:THR:HG21	2.01	0.43
2:G:59:TYR:O	2:G:61:ILE:HG12	2.19	0.43
1:D:303:ALA:O	1:D:304:GLN:C	2.62	0.42
1:B:286:GLU:O	1:B:289:GLU:HB3	2.19	0.42
2:C:146:VAL:C	2:C:147:LEU:HD13	2.44	0.42
1:B:327:GLU:OE2	2:C:144:HIS:CE1	2.72	0.42
1:B:303:ALA:O	1:B:304:GLN:C	2.62	0.42
2:C:126:LEU:HB3	2:C:135:TYR:CE2	2.55	0.42
1:D:274:LEU:HB3	3:K:376:PRO:CG	2.50	0.42
1:B:260:LEU:HB2	1:D:260:LEU:HG	2.02	0.42
2:C:17:VAL:O	2:C:17:VAL:HG23	2.19	0.41
1:B:321:LYS:O	1:B:324:GLU:HB3	2.19	0.41
2:C:119:LEU:C	2:C:120:ILE:HD13	2.45	0.41
1:D:319:ARG:O	1:D:320:GLU:C	2.63	0.41
2:G:78:GLN:HA	2:G:91:LEU:O	2.20	0.41
1:B:263:LEU:HD12	1:D:263:LEU:HB3	2.03	0.41
2:C:82:LYS:HD3	2:C:144:HIS:HE2	1.86	0.41
2:G:98:THR:O	2:G:101:ASN:HB3	2.20	0.41
2:G:13:ILE:HG22	2:G:14:THR:N	2.36	0.41
2:C:112:ILE:HA	2:C:113:PRO:HD3	1.94	0.40
1:D:303:ALA:O	1:D:306:ASP:N	2.54	0.40
2:C:7:THR:OG1	2:C:69:LEU:HD23	2.21	0.40
2:C:113:PRO:HA	2:C:114:PRO:HD3	1.90	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	B	79/98 (81%)	62 (78%)	15 (19%)	2 (2%)	4	27
1	D	77/98 (79%)	61 (79%)	16 (21%)	0	100	100
2	C	145/156 (93%)	128 (88%)	17 (12%)	0	100	100
2	G	150/156 (96%)	136 (91%)	11 (7%)	3 (2%)	6	32
3	K	25/35 (71%)	18 (72%)	7 (28%)	0	100	100
All	All	476/543 (88%)	405 (85%)	66 (14%)	5 (1%)	11	45

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	G	11	LYS
1	B	309	LYS
2	G	9	THR
1	B	313	GLN
2	G	76	GLY

5.3.2 Protein sidechains

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	71/84 (84%)	52 (73%)	19 (27%)	0	3
1	D	69/84 (82%)	57 (83%)	12 (17%)	2	12
2	C	133/138 (96%)	110 (83%)	23 (17%)	2	12
2	G	136/138 (99%)	113 (83%)	23 (17%)	2	12

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	K	22/26 (85%)	17 (77%)	5 (23%)	1	6
All	All	431/470 (92%)	349 (81%)	82 (19%)	1	10

All (82) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	261	GLU
1	B	263	LEU
1	B	265	GLN
1	B	268	GLN
1	B	274	LEU
1	B	281	ILE
1	B	283	LYS
1	B	287	GLU
1	B	292	LYS
1	B	294	VAL
1	B	298	VAL
1	B	301	LEU
1	B	302	LYS
1	B	322	LEU
1	B	326	LYS
1	B	331	GLU
1	B	336	LEU
1	B	338	ARG
1	B	340	TYR
2	C	3	ILE
2	C	11	LYS
2	C	13	ILE
2	C	16	GLU
2	C	24	GLU
2	C	27	LYS
2	C	31	GLN
2	C	57	SER
2	C	60	ASN
2	C	63	LYS
2	C	71	LEU
2	C	74	ARG
2	C	78	GLN
2	C	84	LEU
2	C	96	SER
2	C	118	ARG
2	C	126	LEU

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Mol	Chain	Res	Type
2	C	128	ASP
2	C	130	ARG
2	C	138	GLN
2	C	143	LEU
2	C	146	VAL
2	C	147	LEU
1	D	260	LEU
1	D	263	LEU
1	D	264	LYS
1	D	265	GLN
1	D	267	LEU
1	D	268	GLN
1	D	281	ILE
1	D	294	VAL
1	D	312	PHE
1	D	321	LYS
1	D	330	GLN
1	D	334	GLU
2	G	8	LEU
2	G	21	ASP
2	G	22	THR
2	G	24	GLU
2	G	31	GLN
2	G	32	ASP
2	G	41	GLN
2	G	54	ARG
2	G	56	LEU
2	G	58	ASP
2	G	62	GLN
2	G	71	LEU
2	G	72	ARG
2	G	83	THR
2	G	94	GLU
2	G	117	GLN
2	G	120	ILE
2	G	124	LYS
2	G	125	GLN
2	G	126	LEU
2	G	134	ASP
2	G	140	GLU
2	G	146	VAL
3	K	356	CYS

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Mol	Chain	Res	Type
3	K	360	THR
3	K	371	SER
3	K	374	GLU
3	K	378	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	265	GLN
1	B	266	GLN
1	B	268	GLN
1	B	269	GLN
1	B	317	GLN
1	B	337	GLN
2	C	2	GLN
2	C	60	ASN
2	C	62	GLN
2	C	68	HIS
2	C	117	GLN
2	C	136	ASN
1	D	268	GLN
1	D	278	GLN
1	D	337	GLN
2	G	107	GLN
2	G	136	ASN
3	K	357	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 1 ligands modelled in this entry, 1 is 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

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	B	81/98 (82%)	-0.42	0 100 100	76, 98, 108, 108	0
1	D	79/98 (80%)	-0.37	0 100 100	76, 100, 108, 108	0
2	C	147/156 (94%)	-0.41	0 100 100	78, 101, 108, 108	0
2	G	152/156 (97%)	-0.34	0 100 100	75, 102, 108, 108	0
3	K	27/35 (77%)	-0.51	0 100 100	89, 100, 107, 108	0
All	All	486/543 (89%)	-0.39	0 100 100	75, 101, 108, 108	0

There are no RSRZ outliers to report.

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.

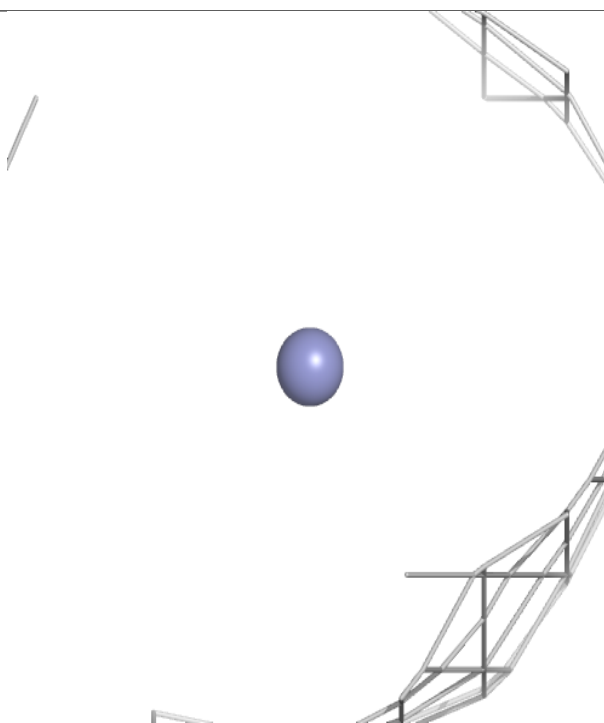
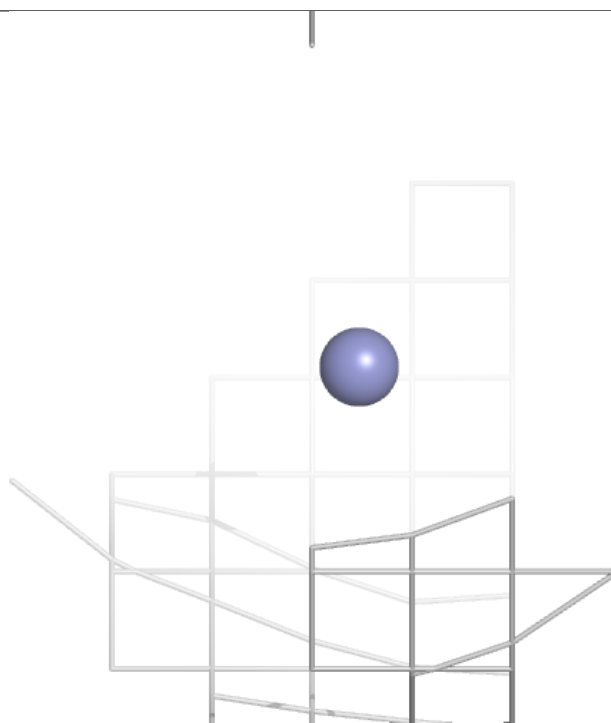
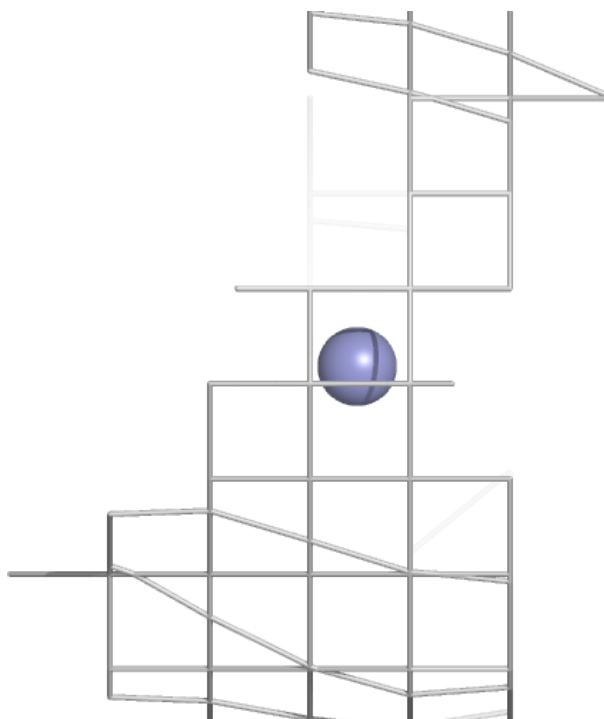
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	ZN	K	401	1/1	0.99	0.03	87,87,87,87	0

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 K 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.