



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 4, 2026 – 09:38 PM UTC

PDB ID : 9XZI / pdb_00009xzi
Title : Crystal Structure of the SUZ12-RBBP4-PHF19-EPOP PRC2.1 Subcomplex
Authors : Yang, X.; Liu, X.
Deposited on : 2025-08-27
Resolution : 2.69 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

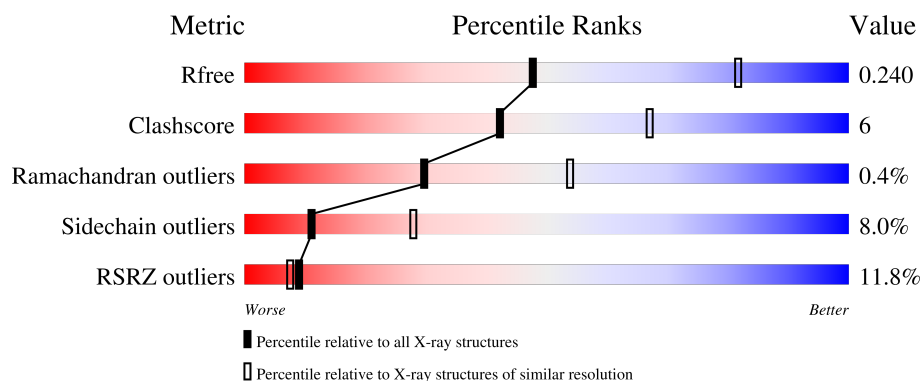
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.69 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	3538 (2.70-2.70)
Clashscore	190562	3843 (2.70-2.70)
Ramachandran outliers	187476	3778 (2.70-2.70)
Sidechain outliers	187428	3778 (2.70-2.70)
RSRZ outliers	180081	3538 (2.70-2.70)

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	473	13% 47% 13% • 37%
2	B	444	5% 75% 11% • 12%
3	C	53	13% 62% 19% • 15%
4	D	78	4% 27% 9% 64%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 6163 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 Polycomb protein SUZ12.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	298	2483	1591	450	427	15	0	0	0

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	73	SER	-	expression tag	UNP Q15022
A	74	ASN	-	expression tag	UNP Q15022
A	75	ALA	-	expression tag	UNP Q15022

- Molecule 2 is a protein called Histone-binding protein RBBP4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	392	3118	1966	531	611	10	0	0	0

There are 19 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-18	MET	-	initiating methionine	UNP Q09028
B	-17	GLY	-	expression tag	UNP Q09028
B	-16	SER	-	expression tag	UNP Q09028
B	-15	SER	-	expression tag	UNP Q09028
B	-14	HIS	-	expression tag	UNP Q09028
B	-13	HIS	-	expression tag	UNP Q09028
B	-12	HIS	-	expression tag	UNP Q09028
B	-11	HIS	-	expression tag	UNP Q09028
B	-10	HIS	-	expression tag	UNP Q09028
B	-9	HIS	-	expression tag	UNP Q09028
B	-8	SER	-	expression tag	UNP Q09028
B	-7	SER	-	expression tag	UNP Q09028
B	-6	GLY	-	expression tag	UNP Q09028

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-5	LEU	-	expression tag	UNP Q09028
B	-4	VAL	-	expression tag	UNP Q09028
B	-3	PRO	-	expression tag	UNP Q09028
B	-2	ARG	-	expression tag	UNP Q09028
B	-1	GLY	-	expression tag	UNP Q09028
B	0	SER	-	expression tag	UNP Q09028

- Molecule 3 is a protein called PHD finger protein 19.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	45	Total	C	N	O	S	0	0	0
			356	227	61	67	1			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	528	SER	-	expression tag	UNP Q5T6S3
C	529	ASN	-	expression tag	UNP Q5T6S3
C	530	ALA	-	expression tag	UNP Q5T6S3

- Molecule 4 is a protein called Elongin BC and Polycomb repressive complex 2-associated protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	28	Total	C	N	O	S	0	0	0
			205	131	34	38	2			

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	310	SER	-	expression tag	UNP A6NHQ4
D	380	ASP	-	expression tag	UNP A6NHQ4
D	381	TYR	-	expression tag	UNP A6NHQ4
D	382	LYS	-	expression tag	UNP A6NHQ4
D	383	ASP	-	expression tag	UNP A6NHQ4
D	384	ASP	-	expression tag	UNP A6NHQ4
D	385	ASP	-	expression tag	UNP A6NHQ4
D	386	ASP	-	expression tag	UNP A6NHQ4
D	387	LYS	-	expression tag	UNP A6NHQ4

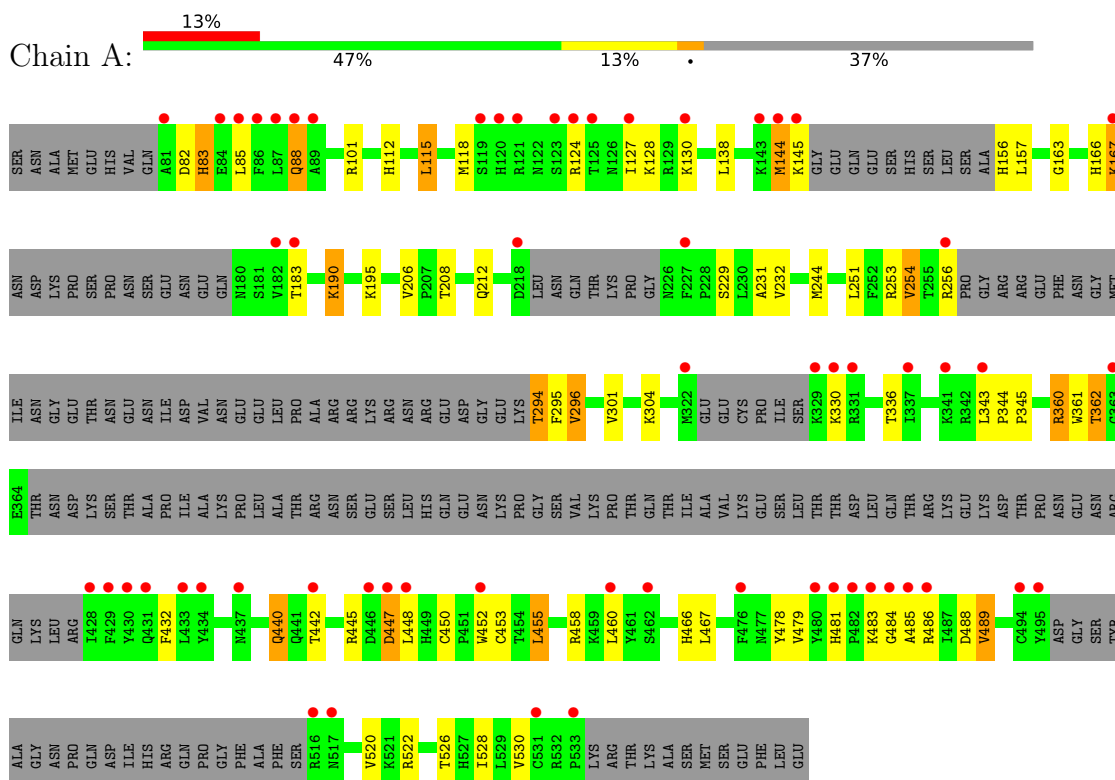
- Molecule 5 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

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

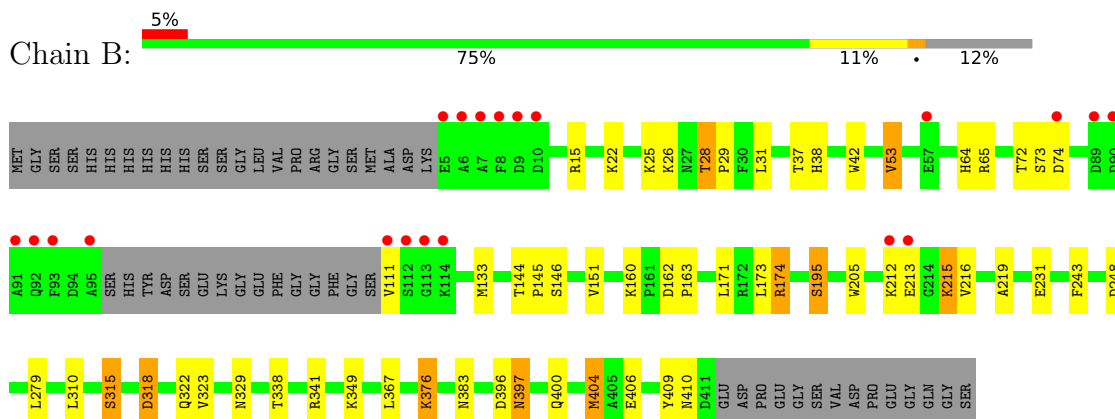
3 Residue-property plots

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.

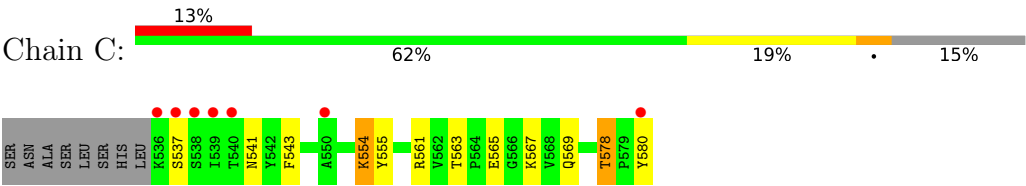
• Molecule 1: Polycomb protein SUZ12



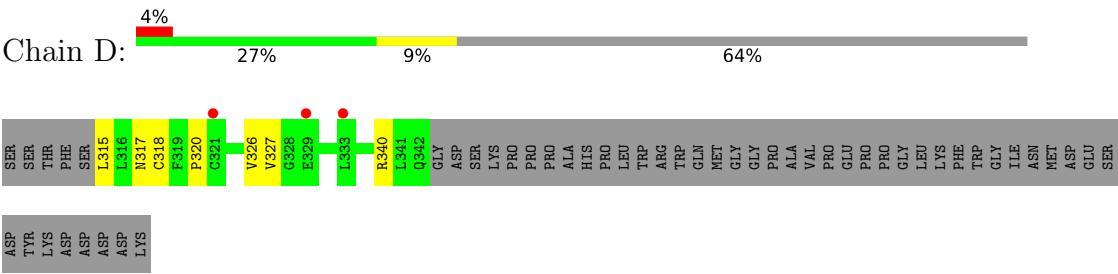
• Molecule 2: Histone-binding protein RBBP4



● Molecule 3: PHD finger protein 19



● Molecule 4: Elongin BC and Polycomb repressive complex 2-associated protein



4 Data and refinement statistics

Property	Value	Source
Space group	H 3 2	Depositor
Cell constants a, b, c, α , β , γ	148.84Å 148.84Å 290.67Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	48.45 – 2.69 48.45 – 2.69	Depositor EDS
% Data completeness (in resolution range)	95.9 (48.45-2.69) 95.9 (48.45-2.69)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.48 (at 2.69Å)	Xtriage
Refinement program	BUSTER 2.10.4 (20-APR-2021)	Depositor
R, R_{free}	0.209 , 0.253 0.205 , 0.240	Depositor DCC
R_{free} test set	1674 reflections (4.83%)	wwPDB-VP
Wilson B-factor (Å ²)	40.8	Xtriage
Anisotropy	0.048	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 57.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	6163	wwPDB-VP
Average B, all atoms (Å ²)	51.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.19% 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	A	0.69	0/2539	1.03	4/3417 (0.1%)
2	B	0.80	2/3203 (0.1%)	1.06	3/4368 (0.1%)
3	C	0.58	0/364	1.03	1/491 (0.2%)
4	D	0.70	0/209	0.98	0/285
All	All	0.74	2/6315 (0.0%)	1.04	8/8561 (0.1%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	133	MET	SD-CE	-6.31	1.63	1.79
2	B	404	MET	SD-CE	-6.13	1.64	1.79

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	163	GLY	N-CA-C	6.43	120.52	111.00
1	A	344	PRO	N-CA-C	6.17	118.23	110.70
1	A	447	ASP	CA-CB-CG	6.02	118.62	112.60
3	C	578	THR	CB-CA-C	5.82	117.24	108.86
2	B	243	PHE	CA-CB-CG	5.46	119.26	113.80
1	A	301	VAL	N-CA-C	-5.37	106.46	111.45
2	B	329	ASN	CA-C-N	5.18	127.74	120.28
2	B	329	ASN	C-N-CA	5.18	127.74	120.28

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	2483	0	2513	40	0
2	B	3118	0	2959	37	0
3	C	356	0	350	7	0
4	D	205	0	210	2	0
5	A	1	0	0	0	0
All	All	6163	0	6032	77	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 (77) 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:145:LYS:HA	1:A:156:HIS:N	1.91	0.85
2:B:215:LYS:N	2:B:215:LYS:HD3	2.05	0.72
3:C:554:LYS:HZ2	3:C:555:TYR:H	1.39	0.70
2:B:215:LYS:HD3	2:B:215:LYS:H	1.56	0.70
2:B:144:THR:HG22	2:B:146:SER:H	1.60	0.67
1:A:183:THR:HG22	1:A:212:GLN:HE22	1.60	0.67
1:A:256:ARG:NE	1:A:294:THR:HG21	2.12	0.65
2:B:144:THR:HG23	2:B:145:PRO:HD2	1.78	0.65
1:A:254:VAL:HG22	1:A:295:PHE:HB2	1.78	0.64
1:A:256:ARG:HE	1:A:294:THR:HG21	1.65	0.61
1:A:256:ARG:H	1:A:256:ARG:HD3	1.66	0.61
3:C:554:LYS:NZ	3:C:555:TYR:H	1.98	0.61
1:A:479:VAL:HG23	1:A:486:ARG:HB3	1.84	0.59
1:A:360:ARG:HE	1:A:362:THR:HG23	1.68	0.58
1:A:528:ILE:HG12	2:B:111:VAL:HG21	1.85	0.58
2:B:397:ASN:HD22	2:B:397:ASN:N	2.02	0.57
1:A:530:VAL:CG2	2:B:28:THR:HG23	2.34	0.57
1:A:112:HIS:HA	1:A:115:LEU:HD22	1.86	0.56
2:B:28:THR:HG22	2:B:29:PRO:HD3	1.87	0.56
2:B:338:THR:HA	2:B:376:LYS:HB2	1.86	0.56
1:A:166:HIS:CD2	1:A:167:LYS:NZ	2.75	0.55
1:A:208:THR:HG21	1:A:232:VAL:HG22	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:215:LYS:H	2:B:215:LYS:CD	2.20	0.54
2:B:42:TRP:CG	2:B:72:THR:HG22	2.43	0.53
2:B:174:ARG:HG3	2:B:216:VAL:HG13	1.92	0.52
2:B:25:LYS:HB3	2:B:26:LYS:HE2	1.90	0.52
2:B:318:ASP:HB3	2:B:338:THR:OG1	2.10	0.52
1:A:256:ARG:HD3	1:A:256:ARG:N	2.24	0.51
1:A:166:HIS:CD2	1:A:167:LYS:HZ2	2.29	0.51
1:A:440:GLN:HE22	1:A:442:THR:HB	1.76	0.50
2:B:195:SER:HB3	2:B:205:TRP:HZ3	1.76	0.50
2:B:322:GLN:HE21	2:B:323:VAL:H	1.59	0.50
1:A:88:GLN:HE21	1:A:88:GLN:HA	1.76	0.50
1:A:478:TYR:HE1	1:A:485:ALA:HB1	1.76	0.50
1:A:101:ARG:HD3	1:A:453:CYS:HB2	1.94	0.50
1:A:304:LYS:NZ	3:C:580:TYR:CD2	2.79	0.50
3:C:561:ARG:HH21	3:C:569:GLN:NE2	2.10	0.50
1:A:256:ARG:H	1:A:256:ARG:CD	2.24	0.49
1:A:450:CYS:SG	1:A:452:TRP:HD1	2.35	0.49
2:B:37:THR:HG22	2:B:400:GLN:HG2	1.95	0.49
2:B:215:LYS:HE2	2:B:216:VAL:HG23	1.93	0.49
2:B:231:GLU:OE2	2:B:248:ASP:OD1	2.31	0.48
2:B:22:LYS:O	2:B:26:LYS:HG2	2.14	0.48
2:B:396:ASP:C	2:B:397:ASN:HD22	2.22	0.47
2:B:215:LYS:N	2:B:215:LYS:CD	2.77	0.47
1:A:115:LEU:HD13	2:B:31:LEU:HD21	1.98	0.46
4:D:318:CYS:O	4:D:320:PRO:HD3	2.16	0.46
1:A:190:LYS:HE2	1:A:206:VAL:HG21	1.98	0.45
1:A:343:LEU:HD22	1:A:345:PRO:HD2	1.98	0.45
2:B:151:VAL:HB	2:B:171:LEU:HB2	1.99	0.44
1:A:253:ARG:HG2	1:A:296:VAL:HG23	2.00	0.44
1:A:85:LEU:HG	4:D:340:ARG:HG2	1.98	0.44
3:C:563:THR:HG22	3:C:565:GLU:H	1.83	0.44
3:C:541:ASN:HD22	3:C:543:PHE:H	1.66	0.43
1:A:481:HIS:O	1:A:484:GLY:O	2.35	0.43
1:A:244:MET:HE3	1:A:244:MET:HB3	1.91	0.43
1:A:124:ARG:HH21	2:B:349:LYS:HD3	1.83	0.42
1:A:156:HIS:CD2	1:A:231:ALA:HB1	2.54	0.42
3:C:563:THR:HB	3:C:567:LYS:HB3	2.01	0.42
1:A:455:LEU:HD21	1:A:466:HIS:CE1	2.55	0.42
2:B:53:VAL:HG22	2:B:64:HIS:CD2	2.54	0.42
1:A:522:ARG:HD3	2:B:397:ASN:HB2	2.01	0.42
1:A:526:THR:OG1	2:B:38:HIS:HD2	2.03	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:157:LEU:HD13	1:A:361:TRP:CE2	2.55	0.41
1:A:138:LEU:HD13	2:B:310:LEU:HD11	2.02	0.41
1:A:83:HIS:ND1	1:A:83:HIS:C	2.78	0.41
1:A:251:LEU:HD11	1:A:296:VAL:HG22	2.01	0.41
2:B:173:LEU:HB3	2:B:205:TRP:CE2	2.56	0.41
2:B:162:ASP:OD1	2:B:163:PRO:HD2	2.19	0.41
2:B:404:MET:HE2	2:B:409:TYR:HB3	2.03	0.41
2:B:205:TRP:CD1	2:B:219:ALA:HA	2.55	0.41
2:B:406:GLU:O	2:B:410:ASN:HB3	2.20	0.41
1:A:118:MET:HE3	1:A:118:MET:HB3	1.97	0.41
2:B:367:LEU:CD2	2:B:404:MET:HE1	2.52	0.40
2:B:64:HIS:CD2	2:B:383:ASN:HD21	2.39	0.40
1:A:432:PHE:HA	1:A:489:VAL:HG22	2.03	0.40
2:B:42:TRP:CD1	2:B:72:THR:HG22	2.57	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	282/473 (60%)	269 (95%)	11 (4%)	2 (1%)	18	41
2	B	388/444 (87%)	375 (97%)	12 (3%)	1 (0%)	36	60
3	C	43/53 (81%)	43 (100%)	0	0	100	100
4	D	26/78 (33%)	24 (92%)	2 (8%)	0	100	100
All	All	739/1048 (70%)	711 (96%)	25 (3%)	3 (0%)	30	54

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	445	ARG

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Mol	Chain	Res	Type
2	B	315	SER
1	A	144	MET

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	281/436 (64%)	251 (89%)	30 (11%)	6	16
2	B	349/391 (89%)	331 (95%)	18 (5%)	21	47
3	C	36/43 (84%)	33 (92%)	3 (8%)	10	26
4	D	24/67 (36%)	20 (83%)	4 (17%)	2	6
All	All	690/937 (74%)	635 (92%)	55 (8%)	11	28

All (55) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	82	ASP
1	A	83	HIS
1	A	88	GLN
1	A	115	LEU
1	A	127	ILE
1	A	128	LYS
1	A	130	LYS
1	A	144	MET
1	A	167	LYS
1	A	190	LYS
1	A	195	LYS
1	A	229	SER
1	A	254	VAL
1	A	294	THR
1	A	296	VAL
1	A	330	LYS
1	A	336	THR
1	A	360	ARG
1	A	362	THR

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Mol	Chain	Res	Type
1	A	440	GLN
1	A	447	ASP
1	A	448	LEU
1	A	455	LEU
1	A	458	ARG
1	A	460	LEU
1	A	467	LEU
1	A	483	LYS
1	A	488	ASP
1	A	489	VAL
1	A	520	VAL
2	B	15	ARG
2	B	28	THR
2	B	53	VAL
2	B	65	ARG
2	B	73	SER
2	B	74	ASP
2	B	160	LYS
2	B	174	ARG
2	B	195	SER
2	B	212	LYS
2	B	213	GLU
2	B	215	LYS
2	B	279	LEU
2	B	315	SER
2	B	318	ASP
2	B	341	ARG
2	B	376	LYS
2	B	397	ASN
3	C	537	SER
3	C	554	LYS
3	C	578	THR
4	D	315	LEU
4	D	317	ASN
4	D	326	VAL
4	D	327	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (27) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	88	GLN
1	A	112	HIS

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Mol	Chain	Res	Type
1	A	120	HIS
1	A	122	ASN
1	A	126	ASN
1	A	156	HIS
1	A	166	HIS
1	A	212	GLN
1	A	235	ASN
1	A	351	GLN
1	A	356	GLN
1	A	440	GLN
1	A	477	ASN
1	A	481	HIS
2	B	18	ASN
2	B	38	HIS
2	B	64	HIS
2	B	122	ASN
2	B	188	ASN
2	B	260	ASN
2	B	267	HIS
2	B	322	GLN
2	B	324	GLN
2	B	397	ASN
3	C	541	ASN
3	C	569	GLN
4	D	317	ASN

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 ⓘ

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	298/473 (63%)	0.97	60 (20%) 3 2	25, 63, 100, 115	0
2	B	392/444 (88%)	-0.04	20 (5%) 33 29	12, 31, 74, 109	0
3	C	45/53 (84%)	0.89	7 (15%) 5 4	50, 69, 106, 108	0
4	D	28/78 (35%)	1.03	3 (10%) 11 9	59, 79, 107, 114	0
All	All	763/1048 (72%)	0.45	90 (11%) 9 7	12, 47, 97, 115	0

All (90) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	91	ALA	6.7
2	B	8	PHE	6.2
2	B	93	PHE	5.3
2	B	111	VAL	5.3
3	C	536	LYS	5.2
1	A	81	ALA	5.2
1	A	484	GLY	5.1
1	A	447	ASP	4.9
1	A	89	ALA	4.8
1	A	480	TYR	4.5
1	A	495	TYR	4.5
2	B	5	GLU	4.5
1	A	330	LYS	4.4
2	B	7	ALA	4.3
1	A	123	SER	4.2
3	C	580	TYR	4.2
1	A	87	LEU	4.1
2	B	213	GLU	4.1
1	A	86	PHE	4.0
2	B	95	ALA	3.9
2	B	9	ASP	3.7

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Mol	Chain	Res	Type	RSRZ
2	B	6	ALA	3.7
2	B	92	GLN	3.7
1	A	85	LEU	3.6
1	A	533	PRO	3.5
1	A	120	HIS	3.5
1	A	428	ILE	3.5
2	B	112	SER	3.5
2	B	57	GLU	3.3
1	A	429	PHE	3.3
1	A	125	THR	3.2
1	A	483	LYS	3.1
3	C	537	SER	3.1
1	A	144	MET	3.1
1	A	494	CYS	3.0
1	A	322	MET	3.0
1	A	167	LYS	3.0
1	A	84	GLU	2.9
1	A	482	PRO	2.9
1	A	446	ASP	2.9
1	A	452	TRP	2.9
1	A	218	ASP	2.9
1	A	434	TYR	2.9
1	A	256	ARG	2.8
1	A	88	GLN	2.8
1	A	437	ASN	2.8
1	A	430	TYR	2.7
3	C	539	ILE	2.7
1	A	145	LYS	2.7
2	B	89	ASP	2.6
1	A	442	THR	2.5
2	B	10	ASP	2.5
1	A	341	LYS	2.5
1	A	227	PHE	2.5
1	A	124	ARG	2.5
1	A	485	ALA	2.5
1	A	517	ASN	2.4
2	B	90	ASP	2.4
1	A	486	ARG	2.4
1	A	337	ILE	2.4
3	C	538	SER	2.4
4	D	321	CYS	2.4
1	A	127	ILE	2.4

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Mol	Chain	Res	Type	RSRZ
2	B	113	GLY	2.4
1	A	460	LEU	2.3
1	A	431	GLN	2.3
3	C	540	THR	2.3
1	A	329	LYS	2.3
1	A	462	SER	2.3
1	A	143	LYS	2.3
1	A	481	HIS	2.3
1	A	130	LYS	2.3
2	B	74	ASP	2.2
1	A	183	THR	2.2
1	A	516	ARG	2.2
1	A	363	GLY	2.2
4	D	329	GLU	2.2
2	B	114	LYS	2.2
1	A	476	PHE	2.2
3	C	550	ALA	2.1
1	A	531	CYS	2.1
2	B	212	LYS	2.1
1	A	433	LEU	2.1
1	A	448	LEU	2.1
1	A	331	ARG	2.1
1	A	182	VAL	2.1
1	A	121	ARG	2.1
1	A	343	LEU	2.1
4	D	333	LEU	2.1
1	A	119	SER	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,

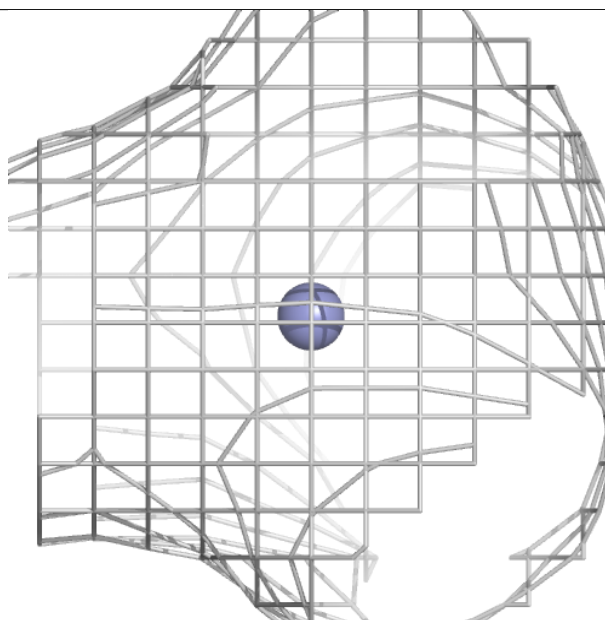
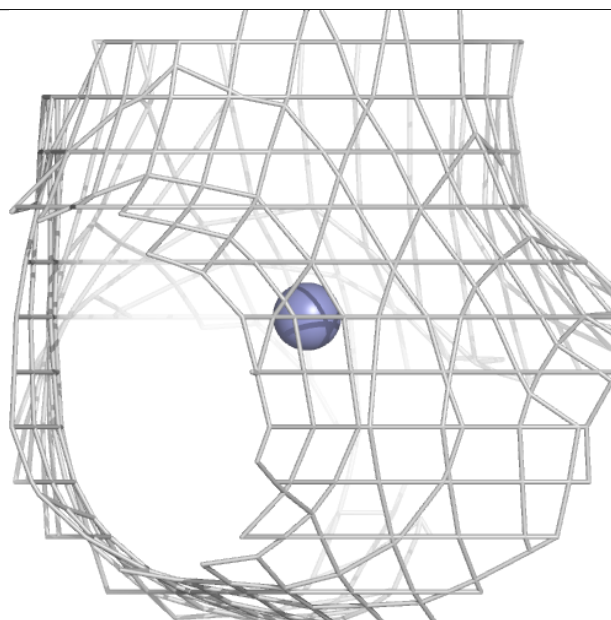
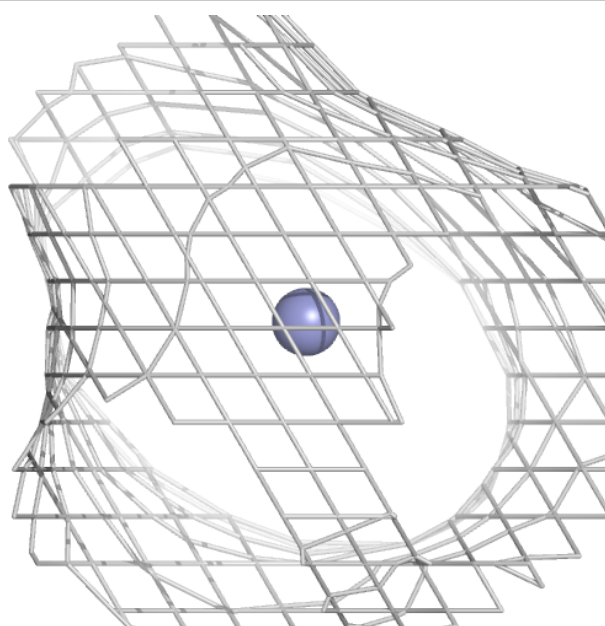
median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
5	ZN	A	1001	1/1	1.00	0.04	70,70,70,70	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 1001:

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 [i](#)

There are no such residues in this entry.