



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 4, 2026 – 08:35 PM UTC

PDB ID : 9EFA / pdb_00009efa
Title : Chemical inhibition of the N-acetyltaurine amidohydrolase PTER reduces food intake and obesity
Authors : Fu, S.; Hinshaw, S.M.
Deposited on : 2024-11-20
Resolution : 2.80 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

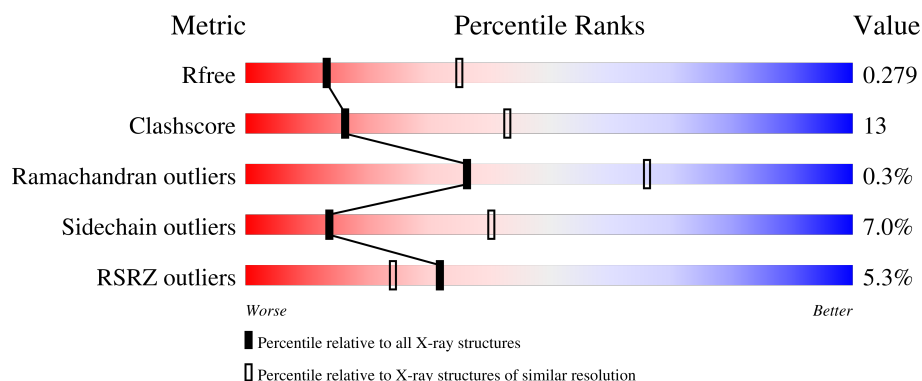
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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	3866 (2.80-2.80)
Clashscore	190562	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)
RSRZ outliers	180081	3869 (2.80-2.80)

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	356	<div> <div>6%</div> <div>67%</div> <div>29%</div> <div>..</div> </div>
1	B	356	<div> <div>4%</div> <div>64%</div> <div>30%</div> <div>..</div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 5440 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 Phosphotriesterase-related protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	350	Total	C	N	O	S	0	1	0
			2717	1727	469	506	15			
1	B	350	Total	C	N	O	S	0	1	0
			2717	1727	469	506	15			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	SER	-	expression tag	UNP A0A1X7VMK4
A	0	ASN	-	expression tag	UNP A0A1X7VMK4
A	1	ALA	-	expression tag	UNP A0A1X7VMK4
B	-1	SER	-	expression tag	UNP A0A1X7VMK4
B	0	ASN	-	expression tag	UNP A0A1X7VMK4
B	1	ALA	-	expression tag	UNP A0A1X7VMK4

- 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	2	Total	Zn	0	0
			2	2		
2	B	2	Total	Zn	0	0
			2	2		

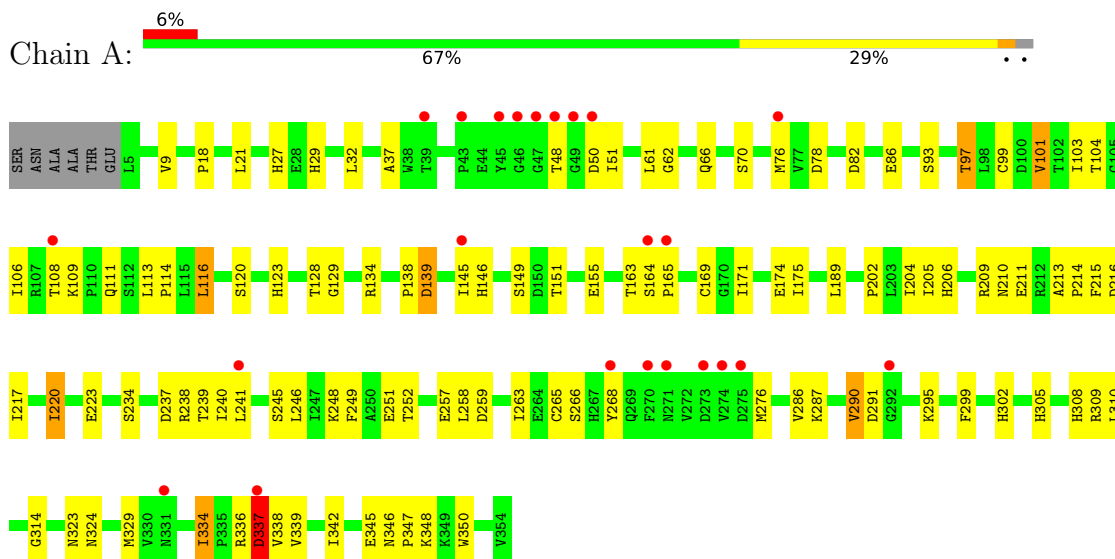
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	O	0	0
			1	1		
3	B	1	Total	O	0	0
			1	1		

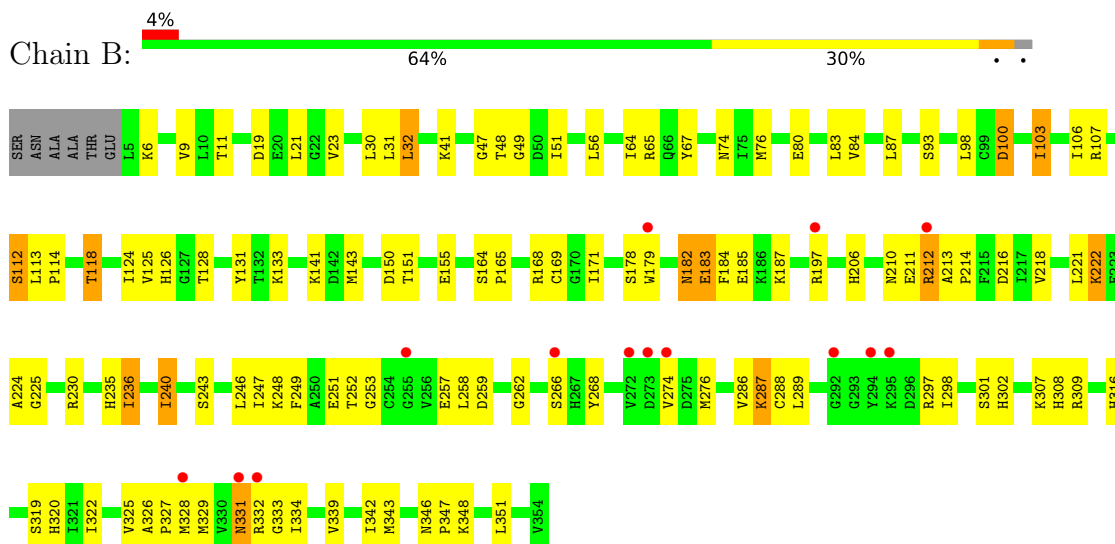
3 Residue-property plots [i](#)

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: Phosphotriesterase-related protein



• Molecule 1: Phosphotriesterase-related protein



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	82.88Å 48.40Å 83.23Å 90.00° 96.98° 90.00°	Depositor
Resolution (Å)	31.12 – 2.80 31.12 – 2.80	Depositor EDS
% Data completeness (in resolution range)	97.0 (31.12-2.80) 97.0 (31.12-2.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.69 (at 2.81Å)	Xtriage
Refinement program	REFMAC 5.8.0430	Depositor
R, R_{free}	0.207 , 0.281 0.209 , 0.279	Depositor DCC
R_{free} test set	777 reflections (3.15%)	wwPDB-VP
Wilson B-factor (Å ²)	24.9	Xtriage
Anisotropy	0.814	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 30.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.022 for l,-k,h	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	5440	wwPDB-VP
Average B, all atoms (Å ²)	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.12% 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	0.62	0/2777	1.19	8/3767 (0.2%)
1	B	0.60	0/2777	1.16	5/3767 (0.1%)
All	All	0.61	0/5554	1.17	13/7534 (0.2%)

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
1	B	0	2

There are no bond length outliers.

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	104	THR	CA-CB-OG1	-7.68	98.09	109.60
1	A	82	ASP	CA-CB-CG	6.61	119.21	112.60
1	A	97	THR	CA-CB-OG1	-5.98	100.63	109.60
1	B	118	THR	CA-CB-OG1	-5.78	100.93	109.60
1	A	50	ASP	CA-CB-CG	5.65	118.25	112.60
1	A	291	ASP	CA-CB-CG	5.45	118.05	112.60
1	B	32	LEU	N-CA-CB	-5.41	101.34	111.13
1	B	183	GLU	N-CA-CB	5.32	117.94	110.12
1	B	11	THR	CA-CB-OG1	-5.17	101.85	109.60
1	A	151	THR	CA-CB-OG1	-5.16	101.85	109.60
1	B	150	ASP	CB-CA-C	-5.03	102.76	110.81
1	A	252	THR	CA-CB-OG1	-5.02	102.07	109.60
1	A	337	ASP	CA-CB-CG	5.02	117.62	112.60

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	168	ARG	Sidechain
1	B	309	ARG	Sidechain

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	2717	0	2743	69	0
1	B	2717	0	2743	76	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
All	All	5440	0	5486	142	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 13.

All (142) 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:116:LEU:O	1:A:120:SER:OG	1.98	0.81
1:A:128:THR:HG23	1:A:169:CYS:SG	2.22	0.79
1:B:125:VAL:HG12	1:B:171:ILE:HG13	1.65	0.79
1:A:290:VAL:HG23	1:A:295:LYS:HB3	1.65	0.78
1:A:76:MET:HE2	1:A:78:ASP:OD2	1.87	0.74
1:A:329:MET:HE2	1:A:339:VAL:HG22	1.73	0.70
1:B:326:ALA:HB3	1:B:327:PRO:HD3	1.75	0.69
1:B:47:GLY:C	1:B:49:GLY:H	2.00	0.69
1:A:346:ASN:HB2	1:A:347:PRO:HD3	1.75	0.69
1:B:47:GLY:O	1:B:49:GLY:N	2.27	0.68
1:A:220:ILE:C	1:A:220:ILE:HD13	2.19	0.67
1:B:230:ARG:HH11	1:B:230:ARG:HG2	1.61	0.65
1:A:216:ASP:O	1:A:220:ILE:HG22	1.96	0.65

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:9:VAL:HG21	1:B:21:LEU:HD11	1.79	0.64
1:B:100:ASP:OD2	1:B:126:HIS:ND1	2.30	0.64
1:A:128:THR:HG21	1:A:155:GLU:HB3	1.80	0.63
1:B:253:GLY:O	1:B:297:ARG:NH1	2.33	0.62
1:A:128:THR:CG2	1:A:169:CYS:SG	2.87	0.62
1:A:329:MET:CE	1:A:339:VAL:HG22	2.31	0.61
1:B:289:LEU:HB3	1:B:298:ILE:HD11	1.82	0.60
1:A:174:GLU:OE2	1:A:206:HIS:HB2	2.01	0.60
1:B:221:LEU:O	1:B:224:ALA:N	2.33	0.60
1:A:175:ILE:HG21	1:A:189:LEU:HD23	1.83	0.59
1:B:243:SER:HB2	1:B:288:CYS:SG	2.42	0.59
1:B:125:VAL:CG1	1:B:171:ILE:HG13	2.35	0.57
1:B:342:ILE:HA	1:B:346:ASN:HD22	1.68	0.57
1:A:128:THR:HG23	1:A:169:CYS:CB	2.35	0.57
1:B:19:ASP:OD1	1:B:348:LYS:HE3	2.04	0.57
1:B:128:THR:OG1	1:B:155:GLU:OE2	2.15	0.57
1:B:243:SER:HA	1:B:246:LEU:HB3	1.86	0.57
1:B:80:GLU:O	1:B:84:VAL:HG23	2.05	0.56
1:B:289:LEU:CB	1:B:298:ILE:HD11	2.35	0.56
1:B:182:ASN:ND2	1:B:185:GLU:OE1	2.39	0.56
1:B:259:ASP:O	1:B:302:HIS:C	2.48	0.56
1:A:205:ILE:HG21	1:A:217:ILE:HG21	1.88	0.56
1:A:111:GLN:NE2	1:A:111:GLN:HA	2.21	0.55
1:B:128:THR:HB	1:B:169:CYS:SG	2.46	0.54
1:B:179:TRP:NE1	1:B:210:ASN:HD22	2.05	0.54
1:B:236:ILE:HG23	1:B:240:ILE:HD13	1.88	0.54
1:A:103:ILE:HB	1:A:129:GLY:O	2.07	0.54
1:A:128:THR:HG21	1:A:155:GLU:CB	2.37	0.54
1:B:240:ILE:O	1:B:240:ILE:HG12	2.07	0.54
1:A:18:PRO:HB3	1:A:348:LYS:HG2	1.90	0.53
1:B:93:SER:O	1:B:322:ILE:HG21	2.09	0.53
1:B:230:ARG:HG2	1:B:230:ARG:NH1	2.25	0.52
1:A:9:VAL:HG21	1:A:21:LEU:HD11	1.92	0.52
1:B:235:HIS:O	1:B:236:ILE:C	2.53	0.51
1:B:342:ILE:HA	1:B:346:ASN:ND2	2.25	0.51
1:A:111:GLN:OE1	1:A:163:THR:HA	2.10	0.51
1:A:111:GLN:HA	1:A:111:GLN:HE21	1.73	0.51
1:B:141:LYS:HD2	1:B:184:PHE:CG	2.46	0.51
1:A:29:HIS:CD2	1:A:305:HIS:HB3	2.46	0.51
1:A:314:GLY:O	1:B:65[A]:ARG:NH1	2.43	0.51
1:B:113:LEU:N	1:B:114:PRO:CD	2.74	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:238:ARG:NH1	1:A:239:THR:OG1	2.45	0.49
1:B:302:HIS:NE2	1:B:320:HIS:HB3	2.27	0.49
1:A:215:PHE:CZ	1:A:249:PHE:HB2	2.48	0.49
1:B:178:SER:N	1:B:185:GLU:OE2	2.45	0.49
1:B:213:ALA:N	1:B:214:PRO:CD	2.75	0.49
1:A:338:VAL:O	1:A:342:ILE:N	2.39	0.49
1:A:97:THR:OG1	1:A:123:HIS:HB2	2.13	0.48
1:B:41:LYS:HD3	1:B:67:TYR:CD2	2.48	0.48
1:B:325:VAL:O	1:B:329:MET:HG3	2.14	0.48
1:B:76:MET:O	1:B:307:LYS:NZ	2.45	0.48
1:B:212:ARG:C	1:B:214:PRO:HD2	2.39	0.48
1:B:9:VAL:HG22	1:B:351:LEU:C	2.38	0.48
1:B:47:GLY:C	1:B:49:GLY:N	2.67	0.47
1:B:331:ASN:C	1:B:333:GLY:H	2.21	0.47
1:B:197:ARG:NH1	1:B:225:GLY:HA3	2.29	0.47
1:A:257:GLU:HA	1:A:299:PHE:O	2.14	0.47
1:A:287:LYS:HG3	1:A:334:ILE:HG12	1.96	0.47
1:B:30:LEU:HD11	1:B:98:LEU:HD22	1.97	0.47
1:B:346:ASN:N	1:B:347:PRO:HD2	2.30	0.47
1:A:32:LEU:HA	1:A:106:ILE:O	2.15	0.47
1:A:103:ILE:HD13	1:A:174:GLU:O	2.14	0.47
1:B:221:LEU:O	1:B:222:LYS:C	2.58	0.47
1:A:202:PRO:HB3	1:A:350:TRP:O	2.15	0.46
1:A:164:SER:HB3	1:A:165:PRO:HD3	1.97	0.46
1:A:240:ILE:HG21	1:A:246:LEU:HA	1.97	0.46
1:B:98:LEU:HD23	1:B:98:LEU:C	2.40	0.46
1:B:80:GLU:HG2	1:B:112:SER:HB3	1.96	0.46
1:A:210:ASN:OD1	1:A:211:GLU:N	2.49	0.46
1:A:308:HIS:CE1	1:A:309:ARG:HG3	2.51	0.46
1:B:87:LEU:HD21	1:B:98:LEU:HD13	1.98	0.46
1:A:99:CYS:HB3	1:A:171:ILE:CD1	2.47	0.45
1:A:205:ILE:O	1:A:234:SER:HB2	2.17	0.45
1:B:211:GLU:O	1:B:240:ILE:HG22	2.15	0.45
1:B:249:PHE:O	1:B:252:THR:OG1	2.18	0.45
1:B:164:SER:HA	1:B:165:PRO:C	2.41	0.45
1:A:337:ASP:O	1:A:338:VAL:HB	2.17	0.45
1:A:27:HIS:HD1	1:A:204:ILE:HD11	1.82	0.44
1:A:259:ASP:O	1:A:302:HIS:C	2.60	0.44
1:B:30:LEU:HB3	1:B:83:LEU:HD13	1.98	0.44
1:A:86:GLU:HG3	1:A:310:LEU:HD22	1.99	0.44
1:B:103:ILE:HD13	1:B:103:ILE:H	1.82	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:143:MET:O	1:B:187:LYS:NZ	2.43	0.44
1:A:146:HIS:O	1:A:149:SER:HB3	2.17	0.44
1:B:131:TYR:OH	1:B:206:HIS:CE1	2.71	0.44
1:A:51:ILE:HD11	1:A:70:SER:HB2	2.00	0.44
1:B:31:LEU:HD11	1:B:112:SER:HB2	2.00	0.44
1:A:61:LEU:O	1:A:62:GLY:C	2.60	0.43
1:A:29:HIS:CE1	1:A:174:GLU:OE1	2.71	0.43
1:B:257:GLU:HG2	1:B:259:ASP:HB3	2.00	0.43
1:A:66:GLN:OE1	1:B:328:MET:HE1	2.18	0.43
1:B:327:PRO:O	1:B:328:MET:C	2.61	0.43
1:B:184:PHE:HA	1:B:187:LYS:HD3	1.99	0.43
1:A:93:SER:OG	1:A:323:ASN:OD1	2.37	0.43
1:A:268:TYR:CD1	1:A:276:MET:HE1	2.53	0.43
1:B:262:GLY:HA3	1:B:316:HIS:NE2	2.34	0.43
1:B:268:TYR:CG	1:B:276:MET:HE2	2.54	0.43
1:A:103:ILE:CD1	1:A:174:GLU:O	2.67	0.43
1:B:98:LEU:O	1:B:124:ILE:HA	2.19	0.43
1:B:218:VAL:HG11	1:B:252:THR:HB	2.01	0.42
1:A:238:ARG:C	1:A:238:ARG:HD2	2.44	0.42
1:B:333:GLY:O	1:B:334:ILE:C	2.62	0.42
1:B:248:LYS:O	1:B:251:GLU:HB2	2.19	0.42
1:A:113:LEU:HB2	1:A:114:PRO:HD3	2.01	0.42
1:A:336:ARG:C	1:A:337:ASP:O	2.63	0.42
1:A:138:PRO:O	1:A:139:ASP:C	2.61	0.42
1:A:324:ASN:OD1	1:B:67:TYR:OH	2.29	0.42
1:A:336:ARG:O	1:A:337:ASP:OD2	2.38	0.42
1:A:345:GLU:O	1:A:346:ASN:C	2.63	0.42
1:A:37:ALA:HA	1:A:134:ARG:NH1	2.34	0.42
1:B:236:ILE:HD13	1:B:236:ILE:HA	1.82	0.41
1:A:248:LYS:O	1:A:251:GLU:HB2	2.20	0.41
1:A:111:GLN:HE21	1:A:111:GLN:CA	2.30	0.41
1:B:287:LYS:O	1:B:288:CYS:C	2.63	0.41
1:B:319:SER:O	1:B:320:HIS:C	2.63	0.41
1:A:213:ALA:HB3	1:A:214:PRO:HD3	2.03	0.41
1:A:263:ILE:HG13	1:A:309:ARG:CZ	2.50	0.41
1:A:240:ILE:HG23	1:A:245:SER:HB2	2.03	0.41
1:A:101:VAL:O	1:A:101:VAL:HG23	2.21	0.40
1:B:56:LEU:HG	1:B:64:ILE:HD13	2.04	0.40
1:B:65[A]:ARG:HH11	1:B:65[A]:ARG:HD3	1.76	0.40
1:B:286:VAL:HG11	1:B:329:MET:CE	2.52	0.40
1:A:211:GLU:HB3	1:A:239:THR:O	2.21	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:23:VAL:CG1	1:B:343:MET:HE2	2.51	0.40
1:B:74:ASN:OD1	1:B:308:HIS:N	2.47	0.40
1:A:145:ILE:N	1:A:145:ILE:HD12	2.36	0.40
1:A:237:ASP:OD1	1:A:237:ASP:N	2.54	0.40
1:A:258:LEU:HD12	1:A:286:VAL:CG2	2.52	0.40
1:B:240:ILE:O	1:B:240:ILE:CG1	2.69	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	349/356 (98%)	322 (92%)	25 (7%)	2 (1%)	21	51
1	B	349/356 (98%)	314 (90%)	35 (10%)	0	100	100
All	All	698/712 (98%)	636 (91%)	60 (9%)	2 (0%)	36	66

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	337	ASP
1	A	101	VAL

5.3.2 Protein sidechains [i](#)

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	303/306 (99%)	289 (95%)	14 (5%)	24	58
1	B	303/306 (99%)	275 (91%)	28 (9%)	8	27
All	All	606/612 (99%)	564 (93%)	42 (7%)	14	41

All (42) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	48	THR
1	A	108	THR
1	A	109	LYS
1	A	116	LEU
1	A	139	ASP
1	A	209	ARG
1	A	220	ILE
1	A	223	GLU
1	A	241	LEU
1	A	265	CYS
1	A	266	SER
1	A	290	VAL
1	A	334	ILE
1	A	337	ASP
1	B	6	LYS
1	B	32	LEU
1	B	48	THR
1	B	51	ILE
1	B	100	ASP
1	B	103	ILE
1	B	106	ILE
1	B	107	ARG
1	B	112	SER
1	B	118	THR
1	B	133	LYS
1	B	151	THR
1	B	182	ASN
1	B	183	GLU
1	B	212	ARG
1	B	216	ASP
1	B	222	LYS
1	B	236	ILE
1	B	240	ILE
1	B	247	ILE
1	B	258	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	266	SER
1	B	274	VAL
1	B	287	LYS
1	B	301	SER
1	B	331	ASN
1	B	332	ARG
1	B	339	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	123	HIS
1	A	267	HIS
1	A	281	GLN
1	A	331	ASN
1	B	331	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 4 ligands modelled in this entry, 4 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	350/356 (98%)	0.31	23 (6%)	24 18	4, 22, 62, 84	1 (0%)
1	B	350/356 (98%)	0.40	14 (4%)	42 33	5, 28, 62, 94	1 (0%)
All	All	700/712 (98%)	0.36	37 (5%)	32 24	4, 25, 62, 94	2 (0%)

All (37) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	46	GLY	4.8
1	A	275	ASP	4.0
1	B	274	VAL	3.7
1	A	43	PRO	3.6
1	A	292	GLY	3.6
1	A	270	PHE	3.5
1	A	108	THR	3.3
1	B	328	MET	3.2
1	A	271	ASN	3.1
1	A	164	SER	3.0
1	A	273	ASP	2.9
1	A	268	TYR	2.8
1	A	47	GLY	2.8
1	B	331	ASN	2.7
1	B	272	VAL	2.7
1	B	266	SER	2.7
1	B	294	TYR	2.6
1	A	331	ASN	2.6
1	B	179	TRP	2.6
1	B	212	ARG	2.6
1	A	45	TYR	2.6
1	A	241	LEU	2.4
1	A	48	THR	2.4
1	A	49	GLY	2.4

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	B	273	ASP	2.4
1	A	165	PRO	2.3
1	B	197	ARG	2.3
1	B	332	ARG	2.3
1	A	39	THR	2.2
1	A	337	ASP	2.2
1	A	145	ILE	2.2
1	B	292	GLY	2.2
1	B	255	GLY	2.1
1	A	76	MET	2.1
1	B	295	LYS	2.0
1	A	274	VAL	2.0
1	A	50	ASP	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](#)

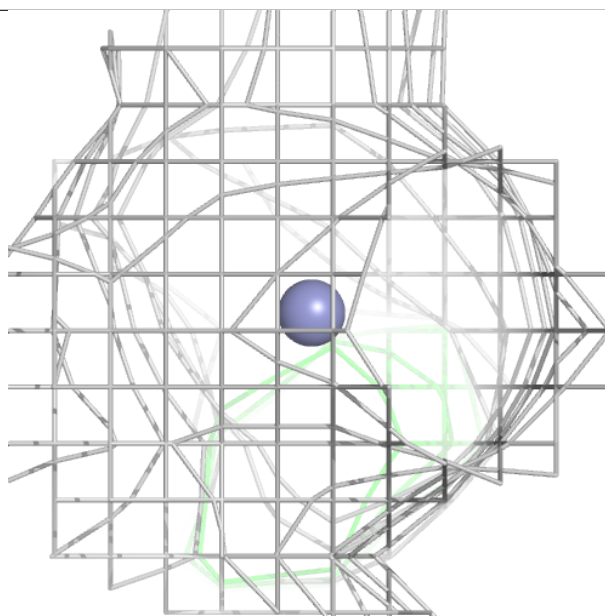
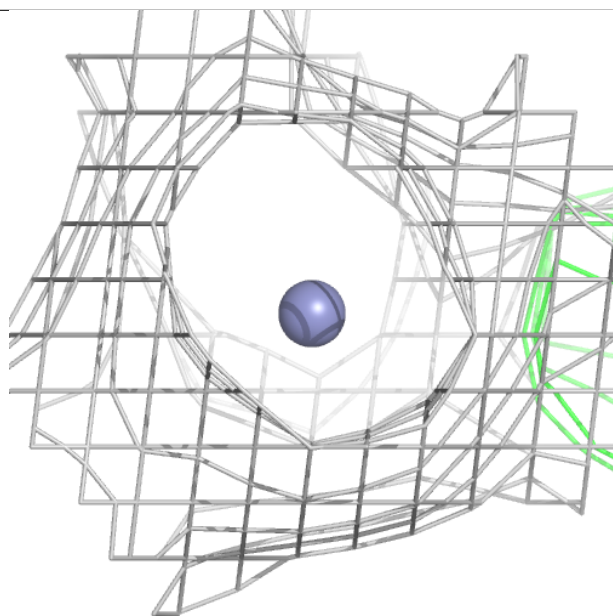
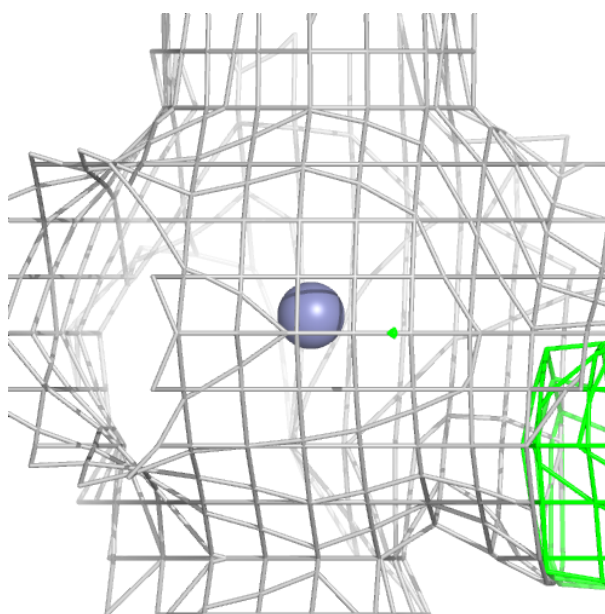
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	ZN	B	401	1/1	0.98	0.03	37,37,37,37	0
2	ZN	A	401	1/1	0.99	0.02	23,23,23,23	0
2	ZN	A	402	1/1	1.00	0.01	9,9,9,9	0
2	ZN	B	402	1/1	1.00	0.04	12,12,12,12	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.

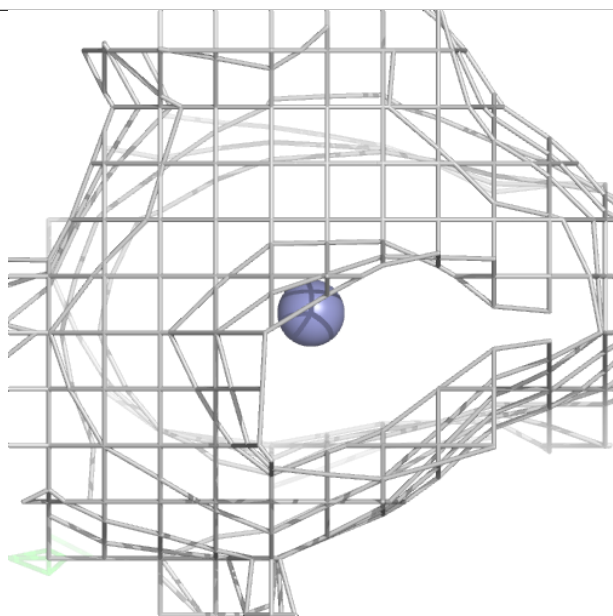
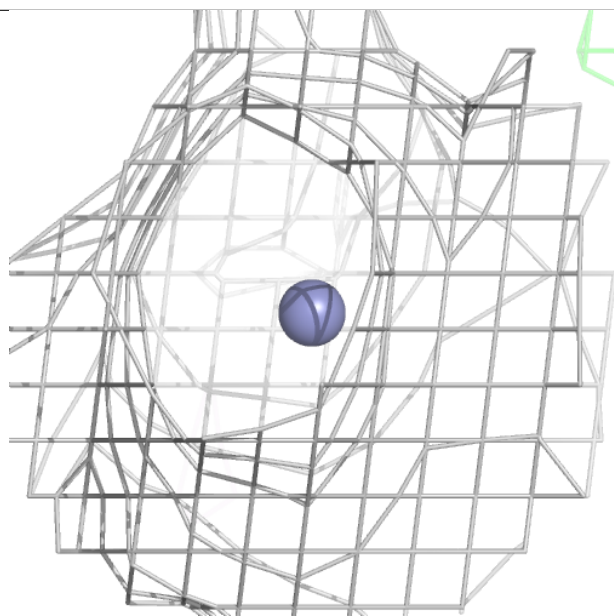
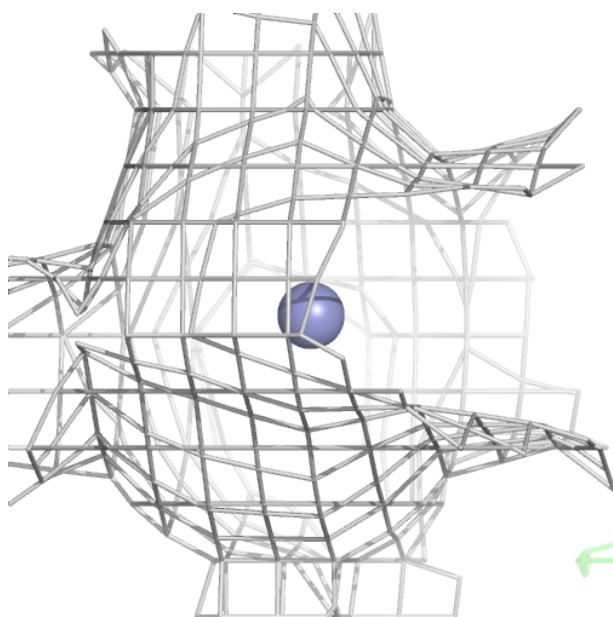
Electron density around ZN B 401:

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



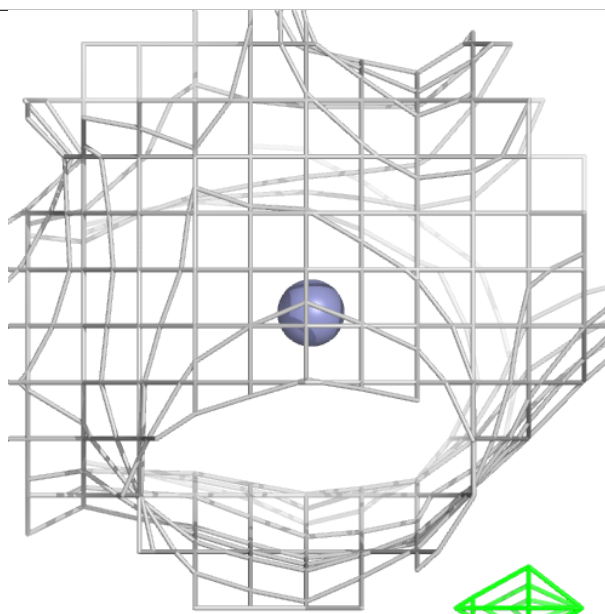
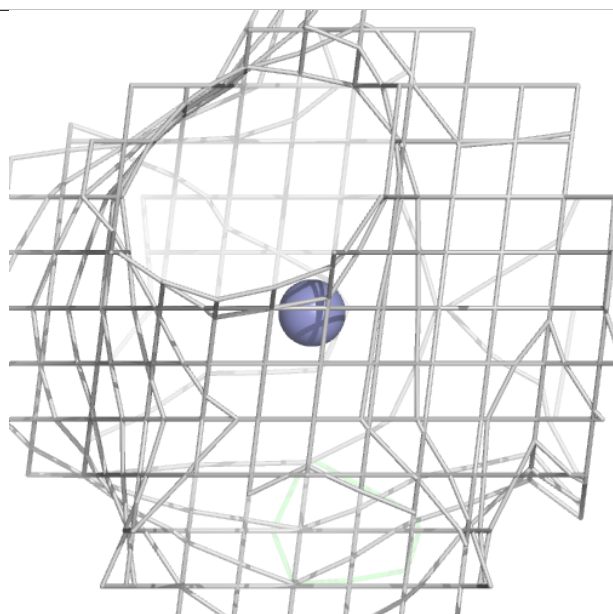
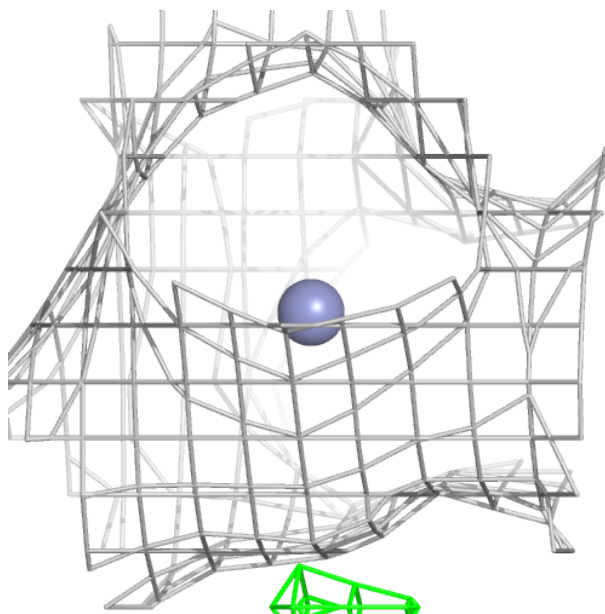
Electron density around ZN A 401:

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



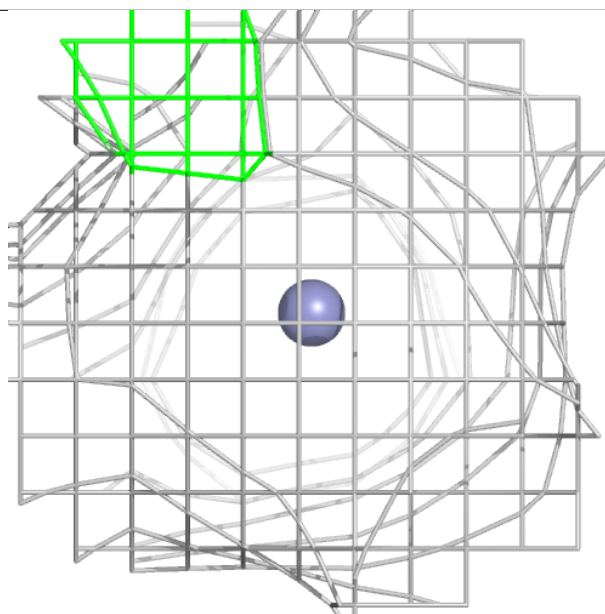
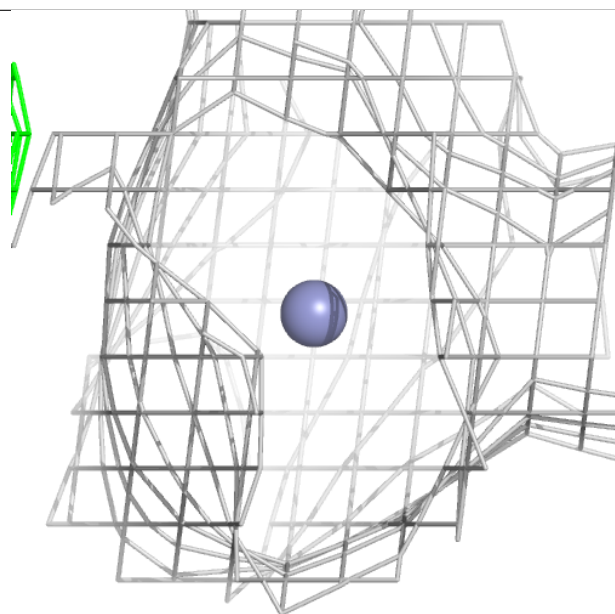
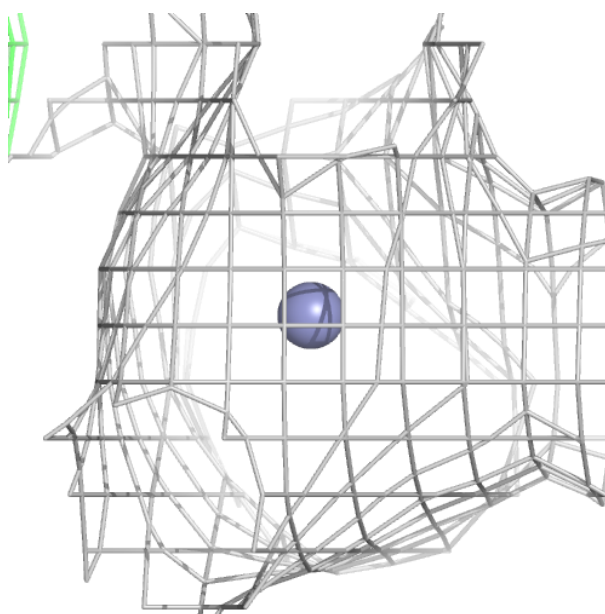
Electron density around ZN A 402:

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



Electron density around ZN B 402:

$2mF_o-DF_c$ (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.