



Full wwPDB X-ray Structure Validation Report ⓘ

Jun 3, 2025 – 04:09 PM JST

PDB ID : 9LE4 / pdb_00009le4
Title : Crystal structure of the MIT-CD complex of STAMBP
Authors : Chen, Z.; Ding, J.
Deposited on : 2025-01-07
Resolution : 2.60 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:

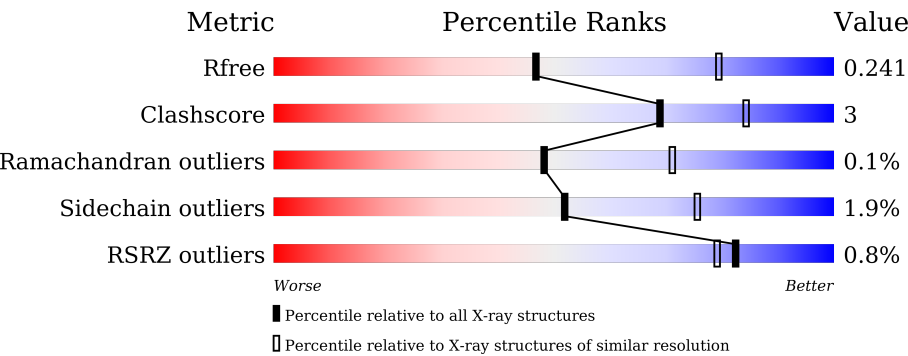
MolProbity : 4-5-2 with Phenix2.0rc1
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 2.0rc1
EDS : 3.0
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4 : 9.0.006 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.43.1

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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}	164625	3775 (2.60-2.60)
Clashscore	180529	4181 (2.60-2.60)
Ramachandran outliers	177936	4129 (2.60-2.60)
Sidechain outliers	177891	4129 (2.60-2.60)
RSRZ outliers	164620	3775 (2.60-2.60)

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	149	<div><div></div><div>79%9%11%</div></div>
1	C	149	<div><div></div><div>83%11%6%</div></div>
1	E	149	<div><div>2%</div><div></div><div>81%14%5%</div></div>
1	G	149	<div><div>2%</div><div></div><div>80%7%9%</div></div>
2	B	184	<div><div></div><div>%</div><div>87%9%.</div></div>

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Mol	Chain	Length	Quality of chain
2	F	184	<div><div>%</div><div><div></div><div>84%</div><div>13%</div><div></div></div><div></div></div>
2	H	184	<div><div>%</div><div><div></div><div>85%</div><div>12%</div><div></div></div><div></div></div>

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 10310 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 STAM-binding protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	132	Total	C	N	O	S	0	0	0
			1090	696	185	207	2			
1	E	142	Total	C	N	O	S	0	0	0
			1174	748	199	225	2			
1	C	140	Total	C	N	O	S	0	0	0
			1156	737	196	221	2			
1	G	135	Total	C	N	O	S	0	0	0
			1112	710	189	211	2			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	GLY	-	expression tag	UNP O95630
A	-1	GLY	-	expression tag	UNP O95630
A	0	SER	-	expression tag	UNP O95630
E	-2	GLY	-	expression tag	UNP O95630
E	-1	GLY	-	expression tag	UNP O95630
E	0	SER	-	expression tag	UNP O95630
C	-2	GLY	-	expression tag	UNP O95630
C	-1	GLY	-	expression tag	UNP O95630
C	0	SER	-	expression tag	UNP O95630
G	-2	GLY	-	expression tag	UNP O95630
G	-1	GLY	-	expression tag	UNP O95630
G	0	SER	-	expression tag	UNP O95630

- Molecule 2 is a protein called STAM-binding protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	179	Total	C	N	O	S	0	0	0
			1393	876	241	264	12			
2	F	179	Total	C	N	O	S	0	0	0
			1393	876	241	264	12			

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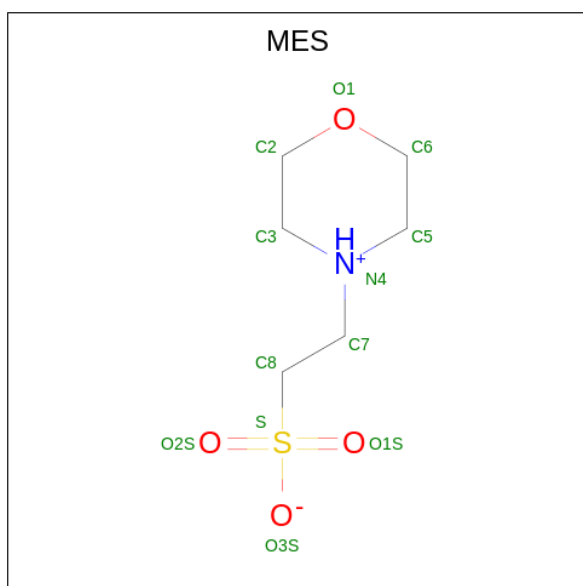
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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	179	Total	C	N	O	S	0	0	0
			1393	876	241	264	12			
2	H	179	Total	C	N	O	S	0	0	0
			1393	876	241	264	12			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	241	GLY	-	expression tag	UNP O95630
B	242	GLY	-	expression tag	UNP O95630
F	241	GLY	-	expression tag	UNP O95630
F	242	GLY	-	expression tag	UNP O95630
D	241	GLY	-	expression tag	UNP O95630
D	242	GLY	-	expression tag	UNP O95630
H	241	GLY	-	expression tag	UNP O95630
H	242	GLY	-	expression tag	UNP O95630

- Molecule 3 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (CCD ID: MES) (formula: $C_6H_{13}NO_4S$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	B	1	Total	C	N	O	S	0	0
			12	6	1	4	1		
3	B	1	Total	C	N	O	S	0	0
			12	6	1	4	1		
3	F	1	Total	C	N	O	S	0	0
			12	6	1	4	1		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	F	1	Total	C	N	O	S	0	0
			12	6	1	4	1		

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	2	Total	Zn	0	0
			2	2		
4	F	2	Total	Zn	0	0
			2	2		
4	D	2	Total	Zn	0	0
			2	2		
4	H	2	Total	Zn	0	0
			2	2		


- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	17	Total	O	0	0
			17	17		
5	B	45	Total	O	0	0
			45	45		
5	E	5	Total	O	0	0
			5	5		
5	F	26	Total	O	0	0
			26	26		
5	C	9	Total	O	0	0
			9	9		
5	D	28	Total	O	0	0
			28	28		
5	G	5	Total	O	0	0
			5	5		
5	H	15	Total	O	0	0
			15	15		

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.

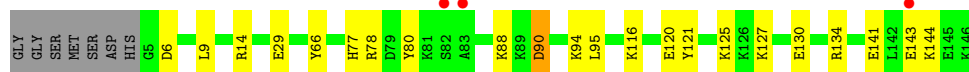
- Molecule 1: STAM-binding protein

Chain A: 




- Molecule 1: STAM-binding protein

Chain E: 




- Molecule 1: STAM-binding protein

Chain C: 




- Molecule 1: STAM-binding protein

Chain G: 

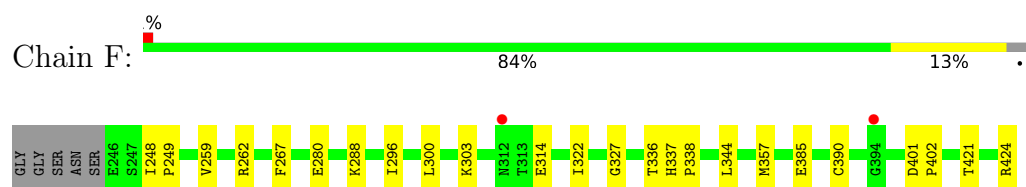


- Molecule 2: STAM-binding protein

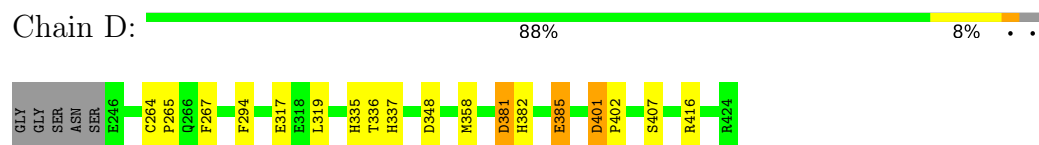
Chain B: 



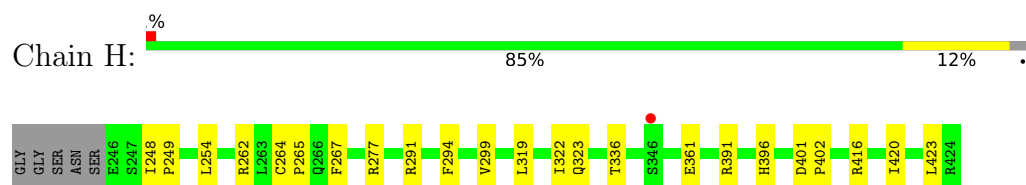
- Molecule 2: STAM-binding protein



- Molecule 2: STAM-binding protein



- Molecule 2: STAM-binding protein



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	58.35Å 110.55Å 270.46Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	22.43 – 2.60 22.43 – 2.60	Depositor EDS
% Data completeness (in resolution range)	99.9 (22.43-2.60) 99.7 (22.43-2.60)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.94 (at 2.60Å)	Xtriage
Refinement program	PHENIX 1.21.2_5419	Depositor
R, R_{free}	0.218 , 0.241 0.218 , 0.241	Depositor DCC
R_{free} test set	52607 reflections (3.66%)	wwPDB-VP
Wilson B-factor (Å ²)	53.2	Xtriage
Anisotropy	0.402	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 42.9	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	0.94	EDS
Total number of atoms	10310	wwPDB-VP
Average B, all atoms (Å ²)	55.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.36% 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: MES, 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	0.88	0/1110	1.21	0/1490
1	C	0.88	0/1176	1.17	0/1578
1	E	0.87	0/1194	1.21	0/1601
1	G	0.88	0/1132	1.18	0/1520
2	B	0.91	0/1425	1.29	6/1935 (0.3%)
2	D	0.94	1/1425 (0.1%)	1.26	3/1935 (0.2%)
2	F	0.91	0/1425	1.26	1/1935 (0.1%)
2	H	0.91	0/1425	1.25	2/1935 (0.1%)
All	All	0.90	1/10312 (0.0%)	1.23	12/13929 (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
1	A	0	2
1	C	0	3
1	E	0	3
1	G	0	3
2	B	0	2
2	D	0	1
2	F	0	1
2	H	0	5
All	All	0	20

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	385	GLU	C-N	9.20	1.47	1.33

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	337	HIS	CB-CA-C	8.29	118.78	110.33
2	B	337	HIS	CB-CA-C	7.95	117.59	110.44
2	H	396	HIS	CA-CB-CG	6.49	120.29	113.80
2	B	335	HIS	CA-CB-CG	6.08	119.88	113.80
2	B	394	GLY	CA-C-O	-5.74	117.99	122.52
2	B	402	PRO	N-CA-C	-5.73	103.71	110.70
2	B	403	PRO	CB-CA-C	5.61	118.68	111.56
2	D	335	HIS	CA-CB-CG	5.51	119.31	113.80
2	D	337	HIS	CB-CA-C	5.12	115.98	110.65
2	D	294	PHE	CA-CB-CG	5.09	118.89	113.80
2	H	294	PHE	CA-CB-CG	5.09	118.89	113.80
2	B	396	HIS	CA-CB-CG	5.03	118.83	113.80

There are no chirality outliers.

All (20) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	14	ARG	Sidechain
1	A	45	ARG	Sidechain
2	B	291	ARG	Sidechain
2	B	416	ARG	Sidechain
1	C	134	ARG	Sidechain
1	C	45	ARG	Sidechain
1	C	78	ARG	Sidechain
2	D	416	ARG	Sidechain
1	E	134	ARG	Sidechain
1	E	14	ARG	Sidechain
1	E	78	ARG	Sidechain
2	F	262	ARG	Sidechain
1	G	113	ARG	Sidechain
1	G	134	ARG	Sidechain
1	G	78	ARG	Sidechain
2	H	262	ARG	Sidechain
2	H	277	ARG	Sidechain
2	H	291	ARG	Sidechain
2	H	391	ARG	Sidechain
2	H	416	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	1090	0	1110	6	0
1	C	1156	0	1178	7	0
1	E	1174	0	1197	10	0
1	G	1112	0	1134	8	0
2	B	1393	0	1367	8	0
2	D	1393	0	1367	12	0
2	F	1393	0	1367	10	0
2	H	1393	0	1367	10	0
3	B	24	0	26	1	0
3	F	24	0	26	0	0
4	B	2	0	0	1	0
4	D	2	0	0	1	0
4	F	2	0	0	0	0
4	H	2	0	0	0	0
5	A	17	0	0	0	0
5	B	45	0	0	0	0
5	C	9	0	0	0	0
5	D	28	0	0	1	0
5	E	5	0	0	0	0
5	F	26	0	0	0	0
5	G	5	0	0	0	0
5	H	15	0	0	0	0
All	All	10310	0	10139	69	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 3.

All (69) 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)
2:D:401:ASP:HB3	2:D:402:PRO:HD3	1.54	0.89
2:H:401:ASP:HB3	2:H:402:PRO:HD3	1.62	0.82
2:B:401:ASP:HB3	2:B:402:PRO:HD3	1.62	0.79
2:F:401:ASP:HB3	2:F:402:PRO:HD3	1.65	0.78
2:D:348:ASP:OD2	4:D:501:ZN:ZN	1.37	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:6:ASP:HB2	1:C:9:LEU:HD23	1.74	0.68
2:H:267:PHE:HE2	2:H:336:THR:HG23	1.59	0.68
2:F:267:PHE:HE2	2:F:336:THR:HG23	1.63	0.63
2:H:322:ILE:HD12	2:H:423:LEU:HD11	1.82	0.60
1:A:94:LYS:HG3	1:A:98:ILE:HD12	1.84	0.58
1:G:78:ARG:HG3	1:G:79:ASP:OD1	2.04	0.58
2:B:348:ASP:OD2	4:B:503:ZN:ZN	1.51	0.58
2:B:267:PHE:HE2	2:B:336:THR:HG23	1.69	0.57
1:E:6:ASP:HB3	1:E:9:LEU:HG	1.88	0.56
1:E:127:LYS:O	1:E:130:GLU:HG2	2.06	0.55
2:D:381:ASP:N	2:D:381:ASP:OD1	2.40	0.54
2:F:267:PHE:CE2	2:F:336:THR:HG23	2.43	0.54
2:H:267:PHE:CE2	2:H:336:THR:HG23	2.40	0.53
1:G:71:ILE:HG22	1:G:72:GLU:HG3	1.89	0.53
1:E:29:GLU:HA	1:E:77:HIS:NE2	2.25	0.52
1:C:31:ILE:HG21	2:D:358:MET:CE	2.40	0.51
2:D:402:PRO:HD2	5:D:615:HOH:O	2.10	0.51
1:E:121:TYR:O	1:E:125:LYS:HG2	2.11	0.51
2:F:357:MET:HA	2:F:357:MET:HE2	1.92	0.51
1:A:98:ILE:O	1:A:102:LYS:HB2	2.12	0.49
1:A:29:GLU:HA	1:A:77:HIS:NE2	2.27	0.49
2:B:267:PHE:CE2	2:B:336:THR:HG23	2.47	0.49
1:G:113:ARG:HH11	1:G:113:ARG:HG3	1.77	0.49
2:H:322:ILE:HD11	2:H:423:LEU:HD21	1.94	0.49
2:B:381:ASP:N	2:B:381:ASP:OD1	2.45	0.48
1:G:131:GLU:HA	1:G:134:ARG:HE	1.78	0.47
2:D:401:ASP:HB3	2:D:402:PRO:CD	2.34	0.47
1:E:80:TYR:OH	1:E:88:LYS:NZ	2.48	0.47
2:F:280:GLU:HG2	2:F:338:PRO:HD3	1.96	0.46
1:C:31:ILE:HG21	2:D:358:MET:HE3	1.97	0.46
1:E:143:GLU:O	1:E:144:LYS:C	2.58	0.46
2:D:264:CYS:HB2	2:D:265:PRO:HD3	1.98	0.46
2:D:267:PHE:HE2	2:D:336:THR:HG23	1.80	0.46
1:G:29:GLU:HA	1:G:77:HIS:NE2	2.30	0.46
1:A:18:LEU:HD22	1:A:61:ILE:HD11	1.97	0.45
2:F:288:LYS:HE2	2:F:327:GLY:O	2.17	0.45
1:C:48:SER:O	1:C:52:GLU:HG3	2.17	0.44
2:F:259:VAL:HG22	2:F:296:ILE:HD12	1.99	0.44
2:F:300:LEU:HD13	2:F:421:THR:HB	1.99	0.44
2:D:382:HIS:O	2:D:385:GLU:HG2	2.17	0.43
1:G:12:GLU:H	1:G:12:GLU:CD	2.25	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:254:LEU:HB3	2:H:361:GLU:HG3	2.01	0.43
2:D:401:ASP:CB	2:D:402:PRO:HD3	2.38	0.42
1:C:12:GLU:O	1:C:16:ARG:HG3	2.19	0.42
1:E:66:TYR:CE2	1:E:95:LEU:HG	2.54	0.42
2:H:264:CYS:HB2	2:H:265:PRO:HD3	2.01	0.42
2:H:319:LEU:O	2:H:323:GLN:HG3	2.20	0.42
3:B:501:MES:H32	2:D:407:SER:HB2	2.00	0.42
1:G:123:GLU:O	1:G:127:LYS:HG2	2.20	0.42
1:E:90:ASP:OD2	1:E:94:LYS:HE2	2.20	0.41
1:C:111:LEU:HD12	1:C:111:LEU:HA	1.80	0.41
2:B:307:GLY:HA3	2:B:310:TYR:CE2	2.55	0.41
1:E:116:LYS:O	1:E:120:GLU:HG3	2.20	0.41
2:H:248:ILE:HA	2:H:249:PRO:HD3	1.96	0.41
2:F:248:ILE:HA	2:F:249:PRO:HD3	1.93	0.41
1:A:100:PHE:HB2	1:A:101:PRO:HD3	2.02	0.41
2:F:303:LYS:HG2	2:F:424:ARG:HA	2.03	0.41
2:B:423:LEU:O	2:B:424:ARG:C	2.64	0.41
1:C:10:PRO:HA	1:C:11:PRO:HD3	1.96	0.40
2:B:259:VAL:HG22	2:B:296:ILE:HD12	2.03	0.40
1:A:32:PRO:HA	1:A:33:PRO:HD3	1.91	0.40
1:E:29:GLU:HA	1:E:77:HIS:CD2	2.56	0.40
2:H:299:VAL:HB	2:H:420:ILE:HG12	2.03	0.40
1:G:93:LYS:HA	1:G:93:LYS:HD3	1.85	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	130/149 (87%)	129 (99%)	1 (1%)	0	100	100
1	C	138/149 (93%)	135 (98%)	3 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	E	140/149 (94%)	137 (98%)	3 (2%)	0	100	100
1	G	133/149 (89%)	130 (98%)	3 (2%)	0	100	100
2	B	177/184 (96%)	172 (97%)	5 (3%)	0	100	100
2	D	177/184 (96%)	173 (98%)	3 (2%)	1 (1%)	22	43
2	F	177/184 (96%)	173 (98%)	4 (2%)	0	100	100
2	H	177/184 (96%)	171 (97%)	6 (3%)	0	100	100
All	All	1249/1332 (94%)	1220 (98%)	28 (2%)	1 (0%)	48	71

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	D	401	ASP

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	118/132 (89%)	117 (99%)	1 (1%)	79	91
1	C	125/132 (95%)	121 (97%)	4 (3%)	34	60
1	E	127/132 (96%)	125 (98%)	2 (2%)	58	79
1	G	120/132 (91%)	115 (96%)	5 (4%)	25	50
2	B	161/164 (98%)	160 (99%)	1 (1%)	84	94
2	D	161/164 (98%)	158 (98%)	3 (2%)	52	75
2	F	161/164 (98%)	156 (97%)	5 (3%)	35	62
2	H	161/164 (98%)	161 (100%)	0	100	100
All	All	1134/1184 (96%)	1113 (98%)	21 (2%)	52	75

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	109	GLU

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Mol	Chain	Res	Type
2	B	381	ASP
1	E	90	ASP
1	E	141	GLU
2	F	314	GLU
2	F	322	ILE
2	F	344	LEU
2	F	385	GLU
2	F	390	CYS
1	C	20	GLN
1	C	21	LEU
1	C	25	VAL
1	C	84	VAL
2	D	317	GLU
2	D	319	LEU
2	D	381	ASP
1	G	9	LEU
1	G	38	ARG
1	G	71	ILE
1	G	131	GLU
1	G	132	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	55	ASN
1	A	58	HIS
2	B	323	GLN
2	B	326	GLN
2	F	325	GLN
2	F	326	GLN
2	F	352	HIS
1	C	139	GLN
2	D	266	GLN
2	H	266	GLN
2	H	312	ASN

5.3.3 RNA ⓘ

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 12 ligands modelled in this entry, 8 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	$\# Z > 2$
3	MES	B	502	-	12,12,12	0.93	1 (8%)	14,16,16	1.66	1 (7%)
3	MES	B	501	-	12,12,12	1.21	1 (8%)	14,16,16	2.70	4 (28%)
3	MES	F	501	-	12,12,12	0.71	0	14,16,16	0.40	0
3	MES	F	502	-	12,12,12	1.17	1 (8%)	14,16,16	2.91	8 (57%)

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
3	MES	B	502	-	-	0/6/14/14	0/1/1/1
3	MES	B	501	-	-	2/6/14/14	0/1/1/1
3	MES	F	501	-	-	0/6/14/14	0/1/1/1
3	MES	F	502	-	-	5/6/14/14	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	501	MES	C8-S	2.96	1.81	1.77

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	F	502	MES	C8-S	2.93	1.81	1.77
3	B	502	MES	C8-S	2.38	1.80	1.77

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	501	MES	C6-C5-N4	5.77	118.85	110.10
3	F	502	MES	O1S-S-C8	-5.76	99.98	106.92
3	B	501	MES	O2S-S-C8	-5.62	100.15	106.92
3	F	502	MES	C7-N4-C3	-5.07	98.27	111.23
3	B	502	MES	O1S-S-C8	-4.82	101.11	106.92
3	F	502	MES	C2-C3-N4	-4.51	103.27	110.10
3	B	501	MES	O1-C6-C5	3.86	120.29	111.80
3	F	502	MES	C6-C5-N4	3.19	114.94	110.10
3	F	502	MES	O1-C6-C5	2.78	117.92	111.80
3	B	501	MES	C7-N4-C5	-2.65	104.45	111.23
3	F	502	MES	O2S-S-O1S	2.37	122.17	113.95
3	F	502	MES	O3S-S-O2S	-2.30	105.66	111.27
3	F	502	MES	O3S-S-O1S	2.08	116.35	111.27

There are no chirality outliers.

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	F	502	MES	C7-C8-S-O2S
3	F	502	MES	C7-C8-S-O3S
3	B	501	MES	C8-C7-N4-C3
3	B	501	MES	C8-C7-N4-C5
3	F	502	MES	C8-C7-N4-C3
3	F	502	MES	C8-C7-N4-C5
3	F	502	MES	C7-C8-S-O1S

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	501	MES	1	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 [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	A	132/149 (88%)	-0.10	0 100 100	30, 50, 72, 85	0
1	C	140/149 (93%)	0.17	0 100 100	37, 66, 86, 92	0
1	E	142/149 (95%)	0.28	3 (2%) 63 58	37, 64, 88, 94	0
1	G	135/149 (90%)	0.20	3 (2%) 62 57	41, 68, 93, 102	0
2	B	179/184 (97%)	-0.25	1 (0%) 85 83	24, 39, 69, 83	0
2	D	179/184 (97%)	-0.13	0 100 100	26, 45, 77, 88	0
2	F	179/184 (97%)	-0.01	2 (1%) 77 74	27, 47, 84, 93	0
2	H	179/184 (97%)	0.00	1 (0%) 85 83	31, 53, 83, 91	0
All	All	1265/1332 (94%)	0.01	10 (0%) 82 79	24, 53, 86, 102	0

All (10) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	F	312	ASN	3.4
1	E	83	ALA	3.0
2	F	394	GLY	2.5
1	G	5	GLY	2.5
1	E	82	SER	2.4
2	B	309	ASP	2.4
1	G	129	ALA	2.3
1	G	133	ALA	2.2
2	H	346	SER	2.1
1	E	143	GLU	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 ⓘ

There are no monosaccharides in this entry.

6.4 Ligands ⓘ

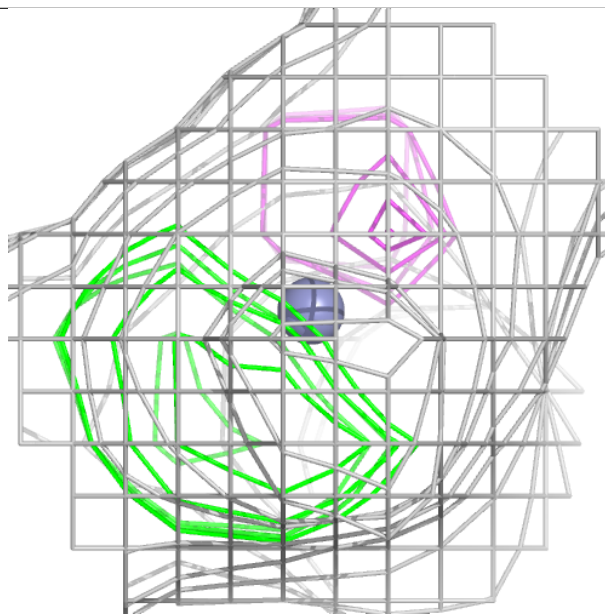
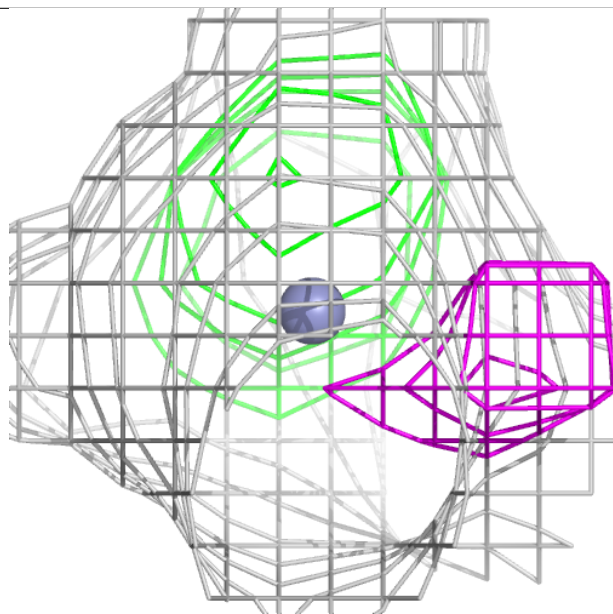
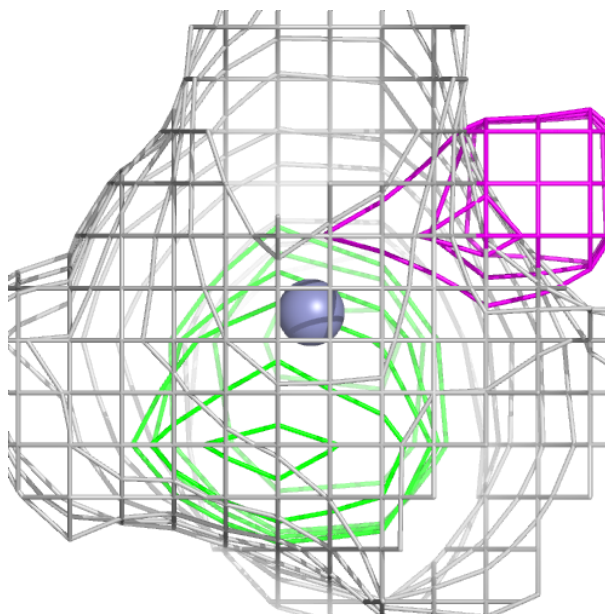
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	MES	B	501	12/12	0.90	0.10	44,50,63,66	0
4	ZN	D	501	1/1	0.91	0.08	47,47,47,47	0
3	MES	F	501	12/12	0.92	0.10	42,50,63,64	0
4	ZN	F	504	1/1	0.94	0.11	127,127,127,127	0
3	MES	F	502	12/12	0.95	0.09	50,61,75,85	0
3	MES	B	502	12/12	0.97	0.07	34,39,56,65	0
4	ZN	F	503	1/1	0.99	0.03	47,47,47,47	0
4	ZN	B	503	1/1	0.99	0.02	34,34,34,34	0
4	ZN	B	504	1/1	0.99	0.02	39,39,39,39	0
4	ZN	H	501	1/1	0.99	0.02	47,47,47,47	0
4	ZN	H	502	1/1	0.99	0.03	57,57,57,57	0
4	ZN	D	502	1/1	1.00	0.01	56,56,56,56	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.

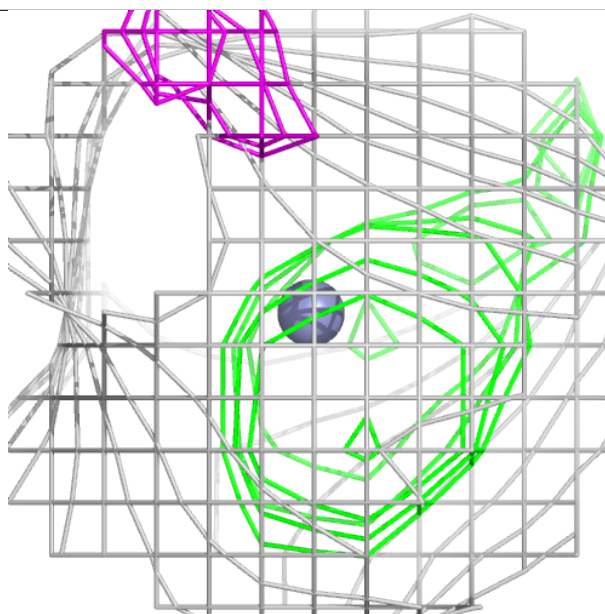
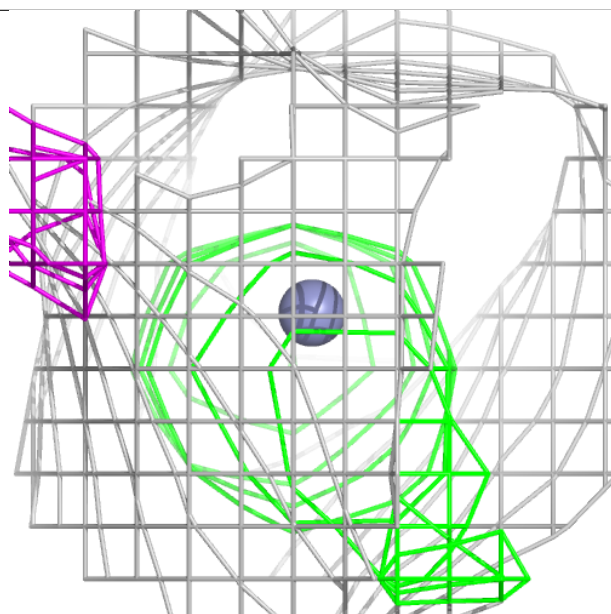
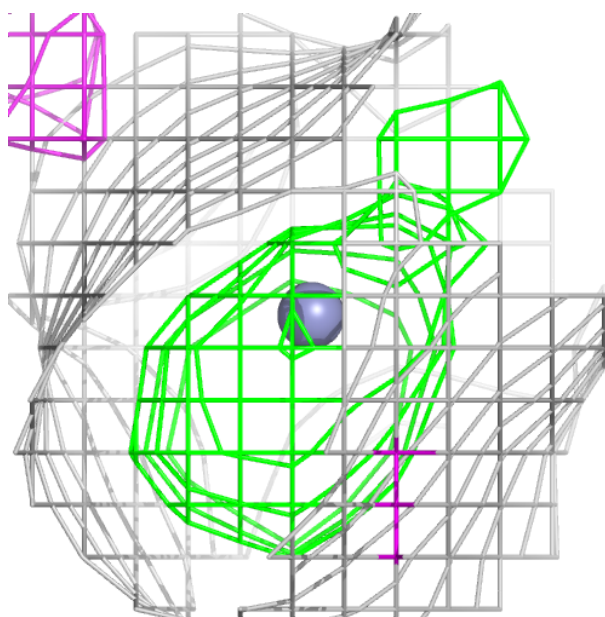
Electron density around ZN D 501:

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



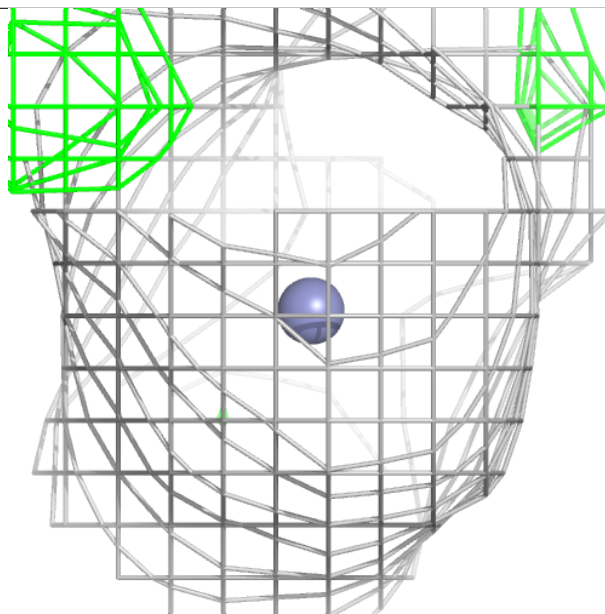
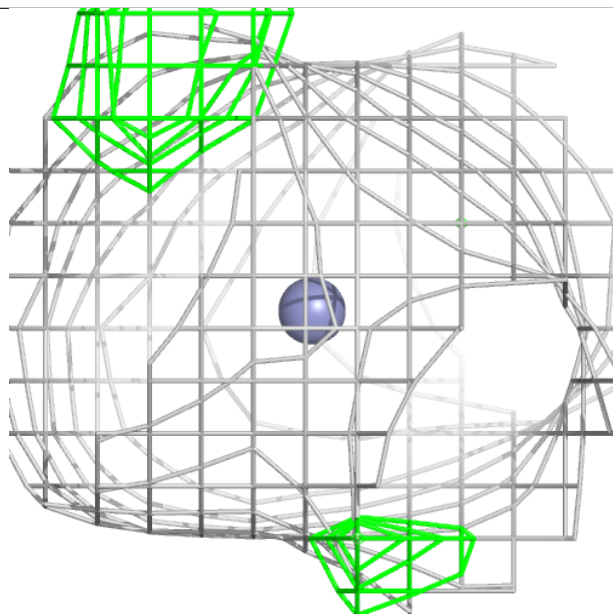
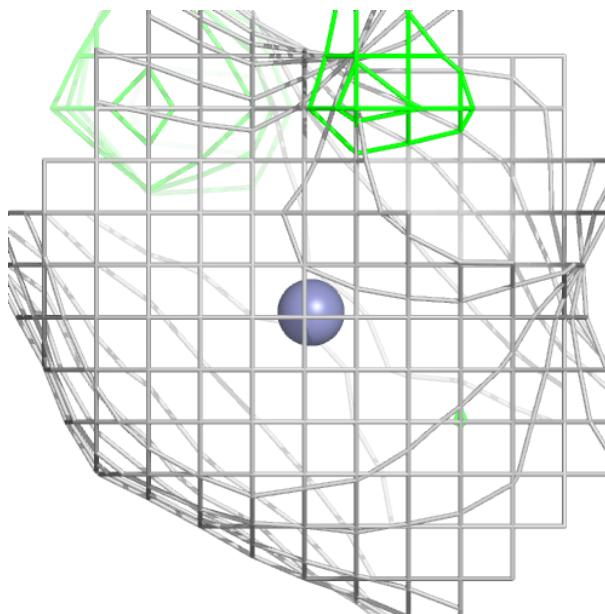
Electron density around ZN F 504:

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



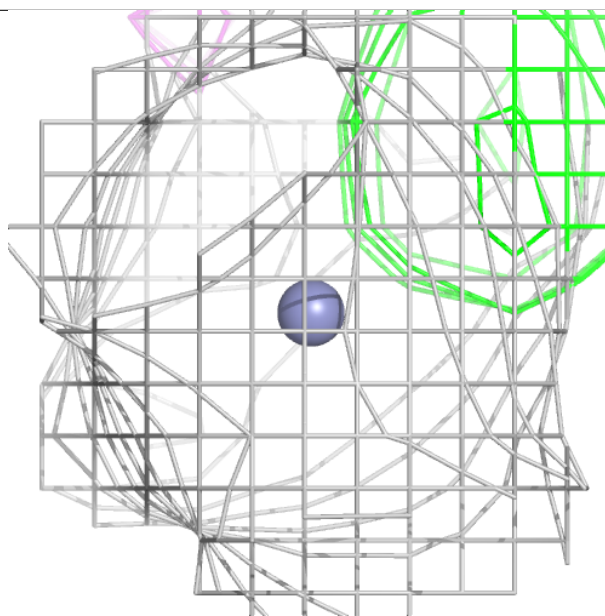
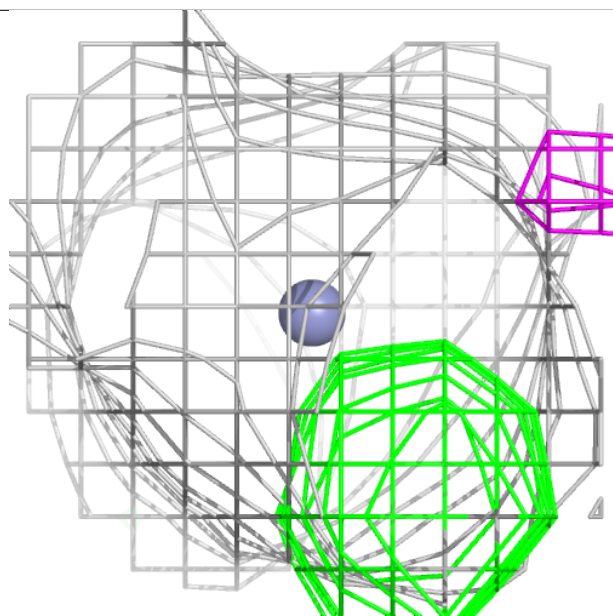
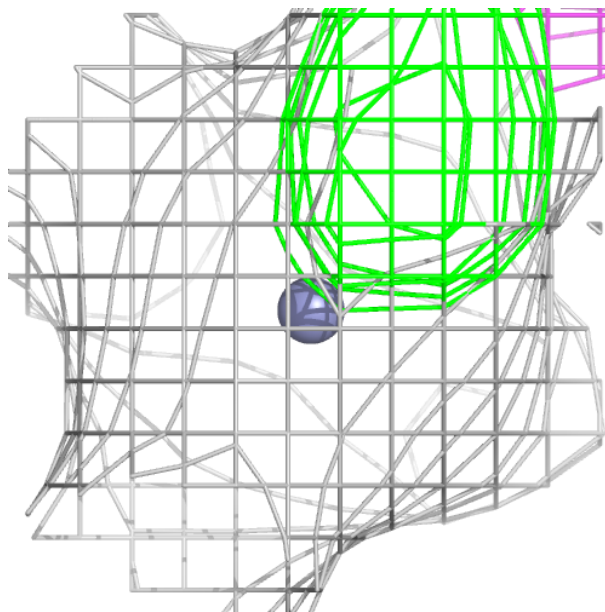
Electron density around ZN F 503:

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and green (positive)



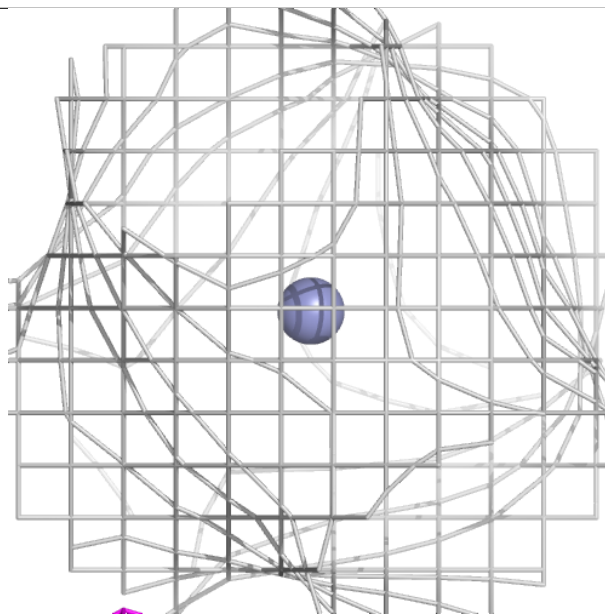
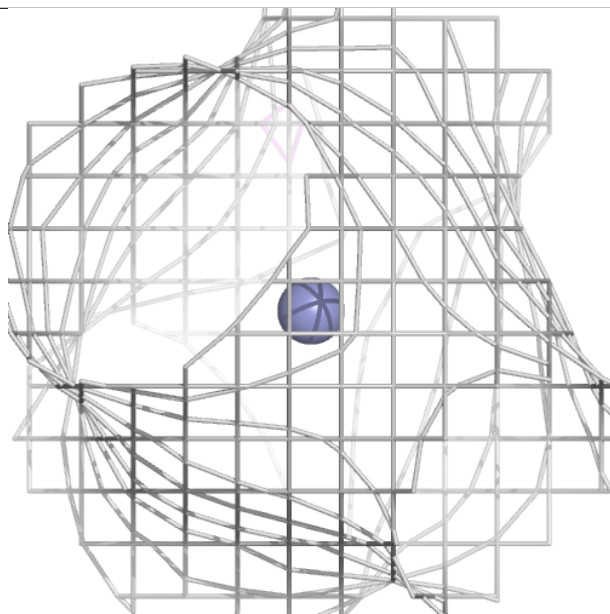
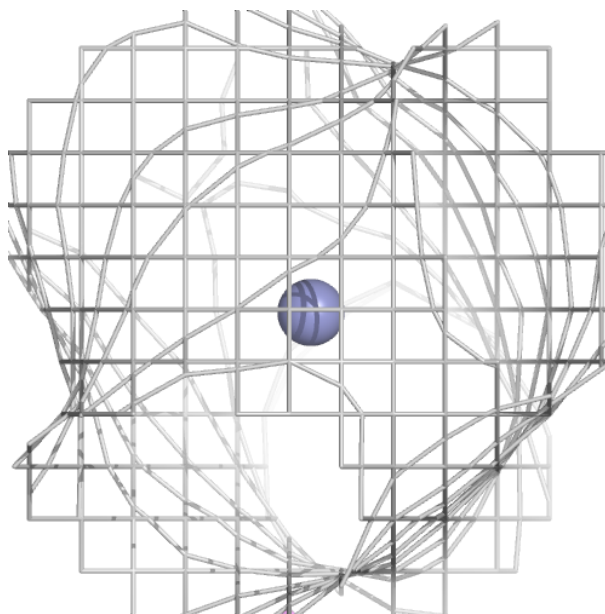
Electron density around ZN B 503:

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



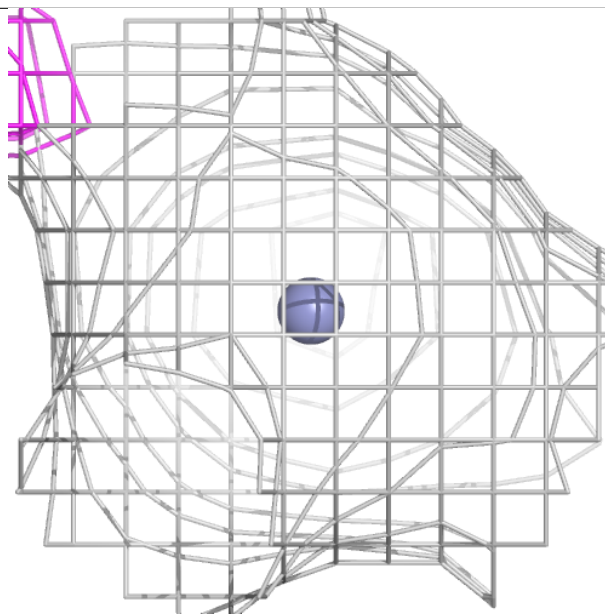
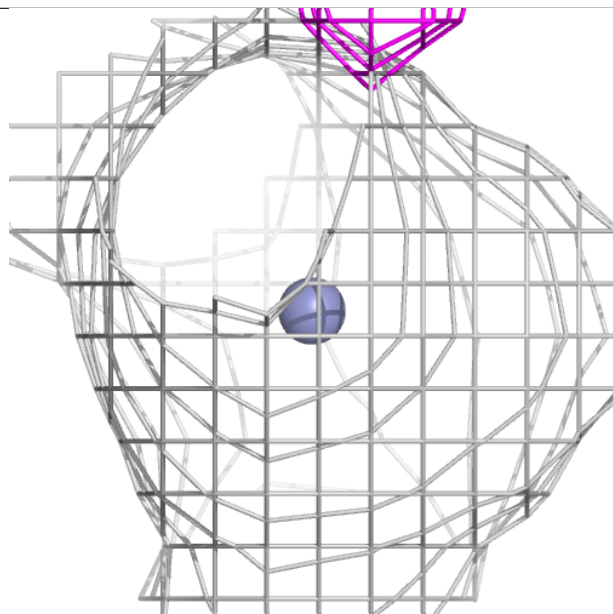
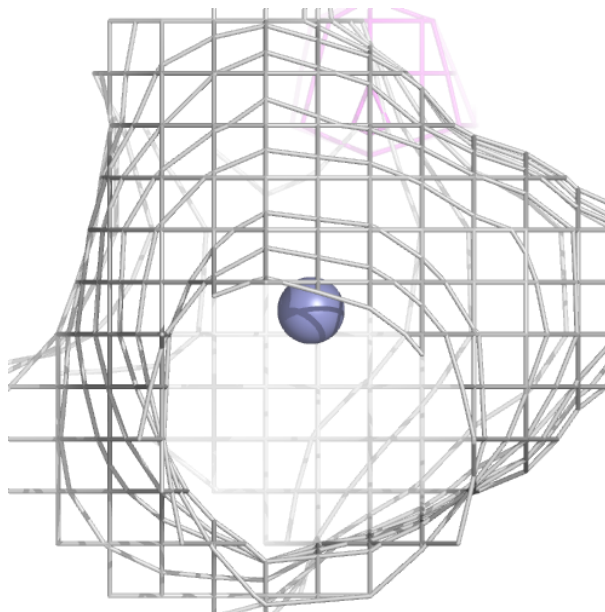
Electron density around ZN B 504:

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



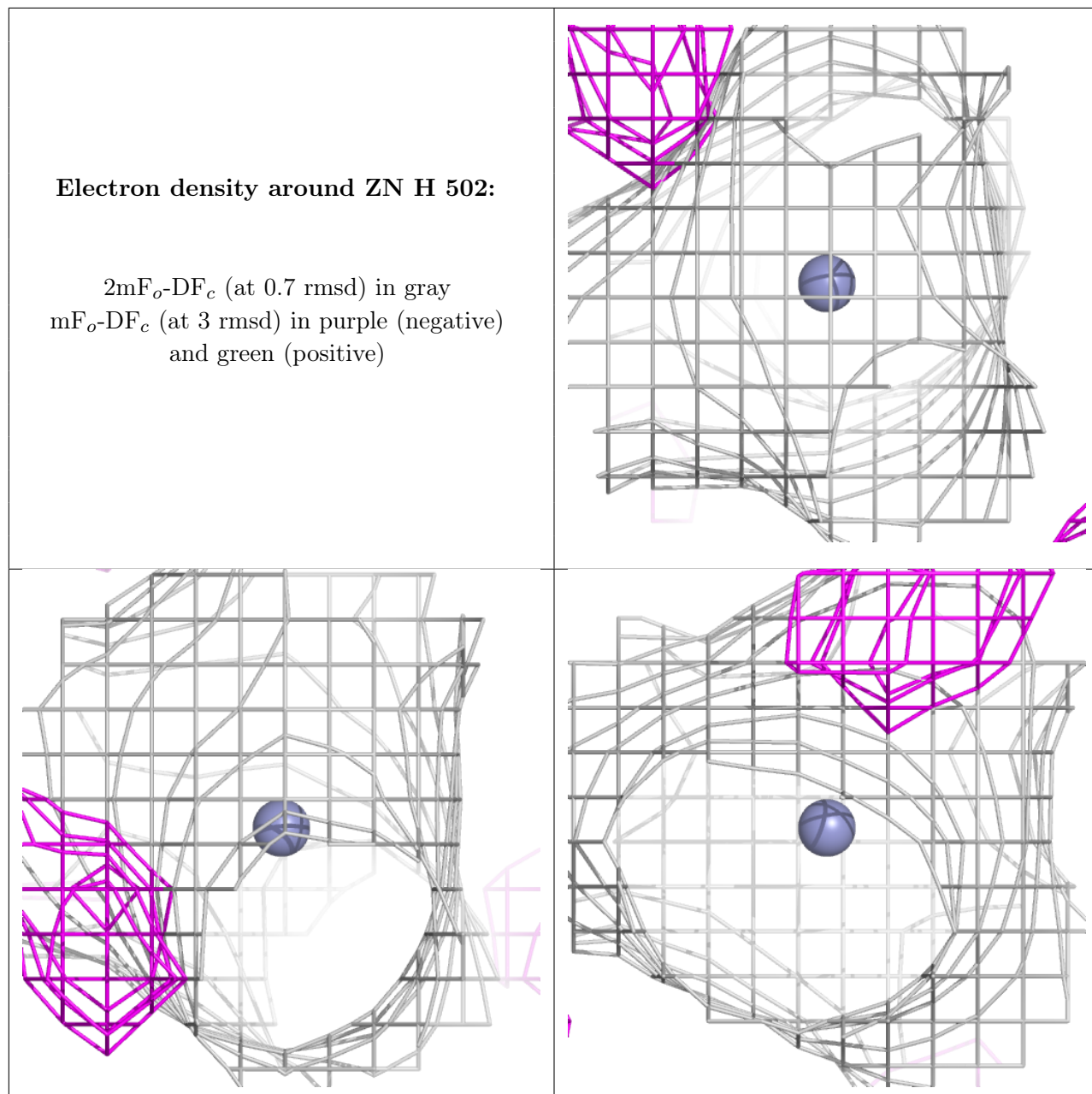
Electron density around ZN H 501:

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and green (positive)



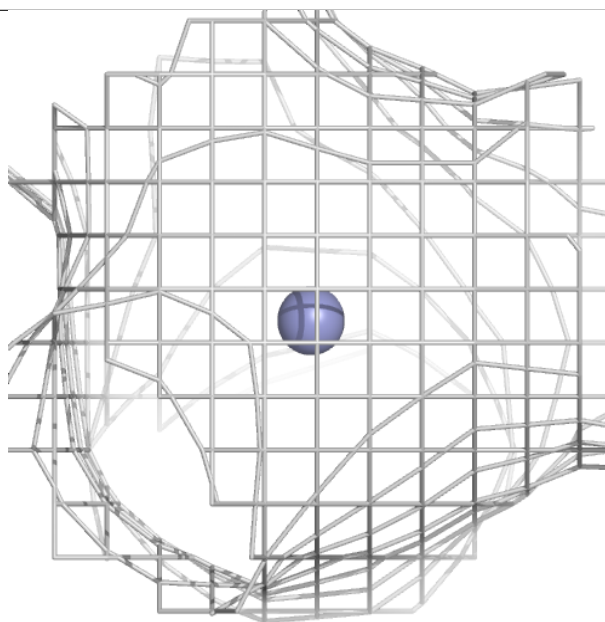
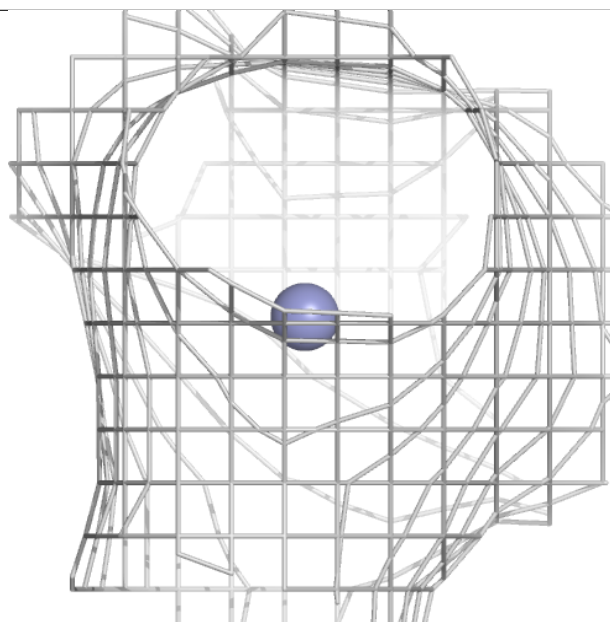
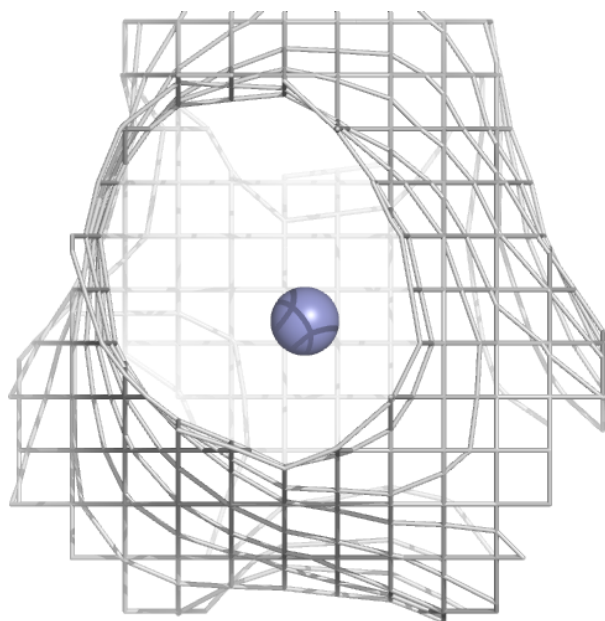
Electron density around ZN H 502:

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



Electron density around ZN D 502:

$2mF_o-DF_c$ (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.