



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 02:34 AM UTC

PDB ID : 6CYL / pdb_00006cyl
Title : Crystal Structure of Superoxide Dismutase double mutant (G74Q+Q149G) from *Trichoderma reesei*
Authors : Mendoza Rengifo, E.; Garratt, R.C.; Pereira, H.M.; Ferreira Jr., J.R.S.
Deposited on : 2018-04-06
Resolution : 1.80 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

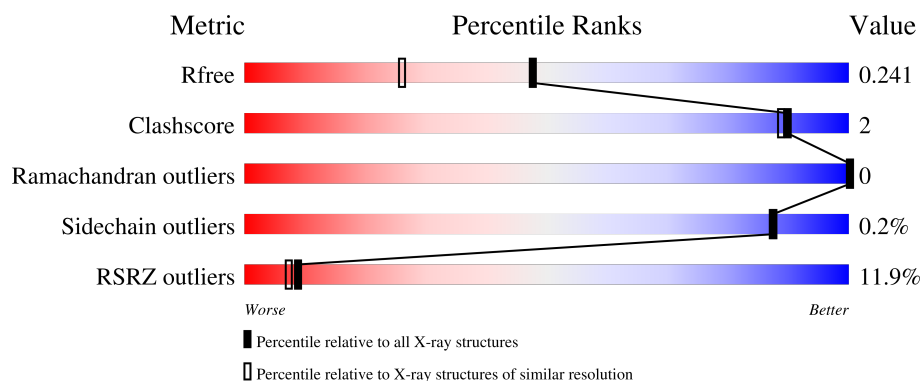
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.80 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	7662 (1.80-1.80)
Clashscore	190562	8479 (1.80-1.80)
Ramachandran outliers	187476	8391 (1.80-1.80)
Sidechain outliers	187428	8390 (1.80-1.80)
RSRZ outliers	180081	7663 (1.80-1.80)

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	211	5% 90% 7%
1	B	211	7% 89% 5% 7%
1	C	211	5% 88% 5% 7%
1	D	211	27% 87% 6% 7%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 6775 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 Superoxide dismutase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	196	Total	C	N	O	S	0	0	0
			1520	977	254	285	4			
1	B	197	Total	C	N	O	S	0	0	0
			1525	981	255	285	4			
1	C	197	Total	C	N	O	S	0	0	0
			1525	981	255	285	4			
1	D	197	Total	C	N	O	S	0	0	0
			1523	980	255	284	4			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	74	GLN	GLY	engineered mutation	UNP G0RQS7
A	149	GLY	GLN	engineered mutation	UNP G0RQS7
B	74	GLN	GLY	engineered mutation	UNP G0RQS7
B	149	GLY	GLN	engineered mutation	UNP G0RQS7
C	74	GLN	GLY	engineered mutation	UNP G0RQS7
C	149	GLY	GLN	engineered mutation	UNP G0RQS7
D	74	GLN	GLY	engineered mutation	UNP G0RQS7
D	149	GLY	GLN	engineered mutation	UNP G0RQS7

- Molecule 2 is MANGANESE (II) ION (CCD ID: MN) (formula: Mn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Mn	0	0
			1	1		
2	B	1	Total	Mn	0	0
			1	1		
2	C	1	Total	Mn	0	0
			1	1		
2	D	1	Total	Mn	0	0
			1	1		

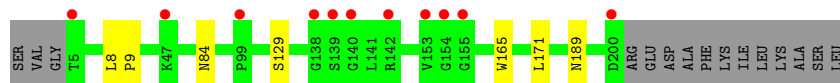
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	216	Total 216	O 216	0	0
3	B	175	Total 175	O 175	0	0
3	C	176	Total 176	O 176	0	0
3	D	111	Total 111	O 111	0	0

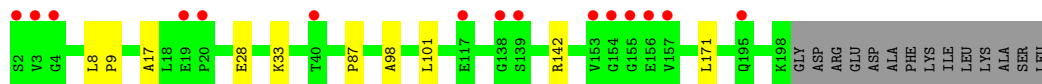
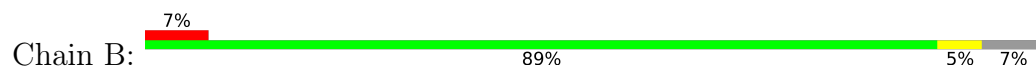
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

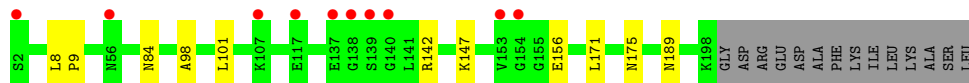
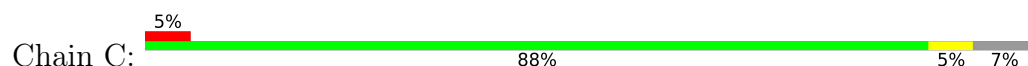
- Molecule 1: Superoxide dismutase



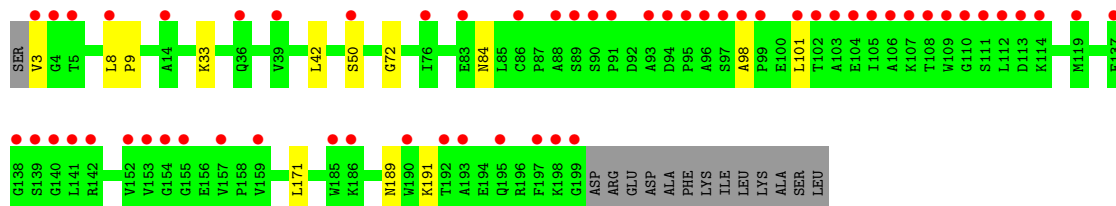
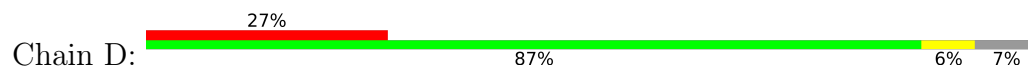
- Molecule 1: Superoxide dismutase



- Molecule 1: Superoxide dismutase



- Molecule 1: Superoxide dismutase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	62.57Å 78.43Å 158.28Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	79.14 – 1.80 79.14 – 1.80	Depositor EDS
% Data completeness (in resolution range)	99.9 (79.14-1.80) 99.9 (79.14-1.80)	Depositor EDS
R_{merge}	0.16	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.60 (at 1.80Å)	Xtriage
Refinement program	PHENIX 1.11.1 _2575	Depositor
R, R_{free}	0.242 , 0.261 0.242 , 0.241	Depositor DCC
R_{free} test set	3680 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	14.1	Xtriage
Anisotropy	0.451	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 41.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.41$, $\langle L^2 \rangle = 0.24$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.88	EDS
Total number of atoms	6775	wwPDB-VP
Average B, all atoms (Å ²)	18.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.62% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: MN

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	0.10	0/1564	0.29	0/2132
1	B	0.10	0/1569	0.28	0/2139
1	C	0.11	0/1569	0.27	0/2139
1	D	0.10	0/1567	0.28	0/2136
All	All	0.10	0/6269	0.28	0/8546

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1520	0	1472	4	0
1	B	1525	0	1482	6	0
1	C	1525	0	1482	8	0
1	D	1523	0	1480	7	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
3	A	216	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	175	0	0	0	0
3	C	176	0	0	1	0
3	D	111	0	0	0	0
All	All	6775	0	5916	21	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 2.

All (21) 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:C:142:ARG:NH1	1:C:156:GLU:OE2	2.32	0.62
1:A:171:LEU:HD23	1:B:171:LEU:HD23	1.83	0.60
1:B:28:GLU:OE2	1:B:33:LYS:NZ	2.38	0.57
1:D:98:ALA:HB1	1:D:101:LEU:HB3	1.87	0.56
1:B:142:ARG:HD2	1:C:142:ARG:HD2	1.88	0.55
1:C:171:LEU:HD23	1:D:171:LEU:HD23	1.90	0.53
1:A:8:LEU:HD12	1:A:9:PRO:HD2	1.93	0.50
1:C:147:LYS:NZ	3:C:405:HOH:O	2.37	0.49
1:D:3:VAL:HG11	1:D:50:SER:OG	2.13	0.48
1:D:84:ASN:HA	1:D:189:ASN:HB3	1.95	0.48
1:B:8:LEU:HD12	1:B:9:PRO:HD2	1.98	0.46
1:D:8:LEU:HD12	1:D:9:PRO:HD2	1.97	0.46
1:C:8:LEU:HD12	1:C:9:PRO:HD2	1.98	0.46
1:B:98:ALA:HB1	1:B:101:LEU:HB3	1.97	0.46
1:C:84:ASN:HA	1:C:189:ASN:HB3	1.98	0.46
1:D:42:LEU:HD22	1:D:72:GLY:HA2	1.99	0.44
1:A:84:ASN:HA	1:A:189:ASN:HB3	2.00	0.44
1:C:98:ALA:HB1	1:C:101:LEU:HB3	2.00	0.44
1:A:129:SER:HB3	1:A:165:TRP:CE2	2.54	0.43
1:B:17:ALA:HB1	1:B:87:PRO:HG3	2.02	0.41
1:C:175:ASN:ND2	1:D:33:LYS:HB3	2.36	0.41

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	A	194/211 (92%)	190 (98%)	4 (2%)	0	100	100
1	B	195/211 (92%)	191 (98%)	4 (2%)	0	100	100
1	C	195/211 (92%)	191 (98%)	4 (2%)	0	100	100
1	D	195/211 (92%)	189 (97%)	6 (3%)	0	100	100
All	All	779/844 (92%)	761 (98%)	18 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	157/169 (93%)	157 (100%)	0	100	100
1	B	158/169 (94%)	158 (100%)	0	100	100
1	C	158/169 (94%)	158 (100%)	0	100	100
1	D	157/169 (93%)	156 (99%)	1 (1%)	78	77
All	All	630/676 (93%)	629 (100%)	1 (0%)	87	87

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	191	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such

sidechains are listed below:

Mol	Chain	Res	Type
1	A	36	GLN
1	A	183	ASN
1	C	183	ASN
1	D	56	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	196/211 (92%)	0.41	11 (5%) 30 29	6, 12, 28, 45	0
1	B	197/211 (93%)	0.69	15 (7%) 20 18	6, 15, 31, 42	0
1	C	197/211 (93%)	0.60	10 (5%) 33 32	7, 16, 29, 40	0
1	D	197/211 (93%)	1.45	58 (29%) 1 1	9, 23, 43, 55	0
All	All	787/844 (93%)	0.79	94 (11%) 9 7	6, 16, 37, 55	0

All (94) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	103	ALA	5.5
1	D	110	GLY	5.1
1	D	101	LEU	4.7
1	D	107	LYS	4.6
1	D	138	GLY	4.6
1	D	153	VAL	4.6
1	C	153	VAL	4.5
1	D	96	ALA	4.4
1	D	98	ALA	4.3
1	D	102	THR	4.1
1	B	155	GLY	4.1
1	C	139	SER	4.0
1	D	199	GLY	4.0
1	D	91	PRO	4.0
1	C	107	LYS	3.8
1	D	99	PRO	3.8
1	A	139	SER	3.8
1	D	95	PRO	3.7
1	B	154	GLY	3.6
1	C	117	GLU	3.6
1	D	111	SER	3.5

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Mol	Chain	Res	Type	RSRZ
1	A	138	GLY	3.5
1	D	139	SER	3.5
1	D	197	PHE	3.5
1	D	36	GLN	3.4
1	D	140	GLY	3.3
1	C	138	GLY	3.3
1	B	138	GLY	3.3
1	D	106	ALA	3.2
1	D	108	THR	3.2
1	C	154	GLY	3.1
1	B	2	SER	3.1
1	D	190	TRP	3.0
1	B	156	GLU	3.0
1	D	97	SER	2.9
1	D	195	GLN	2.9
1	D	109	TRP	2.9
1	B	3	VAL	2.9
1	D	154	GLY	2.9
1	A	140	GLY	2.9
1	D	88	ALA	2.9
1	D	142	ARG	2.8
1	D	3	VAL	2.8
1	D	89	SER	2.8
1	B	4	GLY	2.7
1	D	105	ILE	2.7
1	D	119	MET	2.7
1	D	8	LEU	2.7
1	D	155	GLY	2.7
1	B	195	GLN	2.7
1	D	112	LEU	2.7
1	D	137	GLU	2.7
1	C	140	GLY	2.6
1	A	200	ASP	2.6
1	A	155	GLY	2.6
1	D	159	VAL	2.5
1	A	5	THR	2.5
1	B	40	THR	2.5
1	B	153	VAL	2.5
1	D	113	ASP	2.5
1	D	5	THR	2.5
1	A	47	LYS	2.5
1	D	186	LYS	2.5

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Mol	Chain	Res	Type	RSRZ
1	D	4	GLY	2.4
1	B	139	SER	2.4
1	D	193	ALA	2.4
1	D	152	VAL	2.4
1	C	2	SER	2.4
1	B	157	VAL	2.3
1	D	157	VAL	2.3
1	D	86	CYS	2.3
1	D	114	LYS	2.3
1	A	153	VAL	2.3
1	D	83	GLU	2.3
1	D	50	SER	2.2
1	C	56	ASN	2.2
1	B	19	GLU	2.2
1	D	94	ASP	2.2
1	D	14	ALA	2.2
1	D	185	TRP	2.2
1	D	192	THR	2.2
1	B	20	PRO	2.2
1	D	39	VAL	2.1
1	D	90	SER	2.1
1	A	154	GLY	2.1
1	D	141	LEU	2.1
1	B	117	GLU	2.1
1	D	198	LYS	2.1
1	D	93	ALA	2.1
1	D	76	ILE	2.1
1	A	142	ARG	2.1
1	C	137	GLU	2.1
1	D	104	GLU	2.1
1	A	99	PRO	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

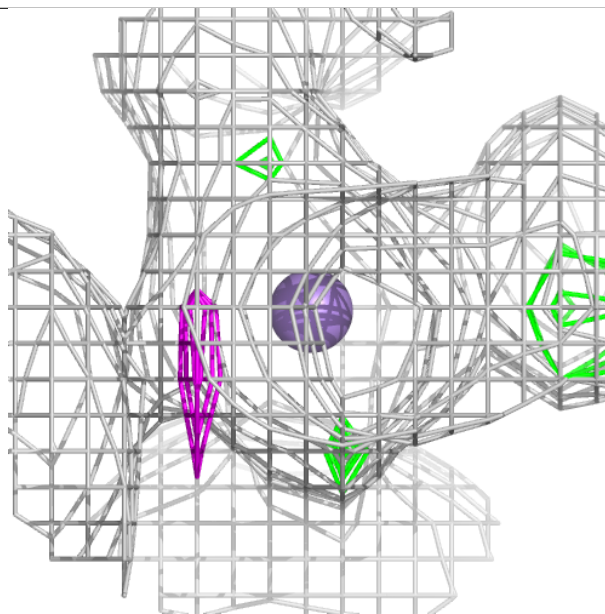
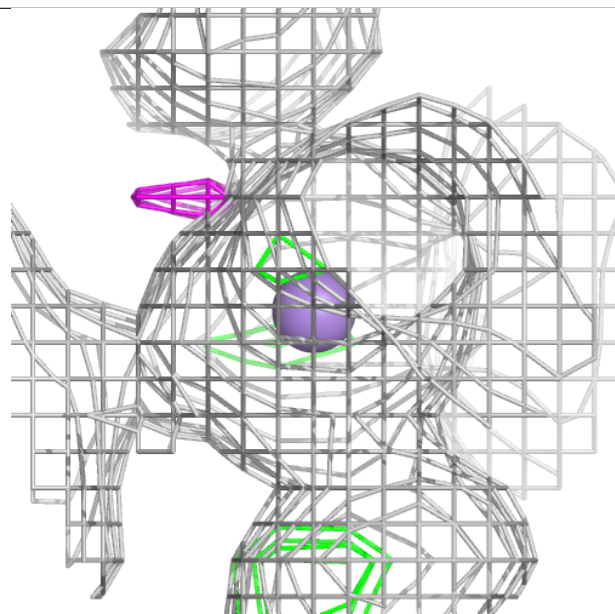
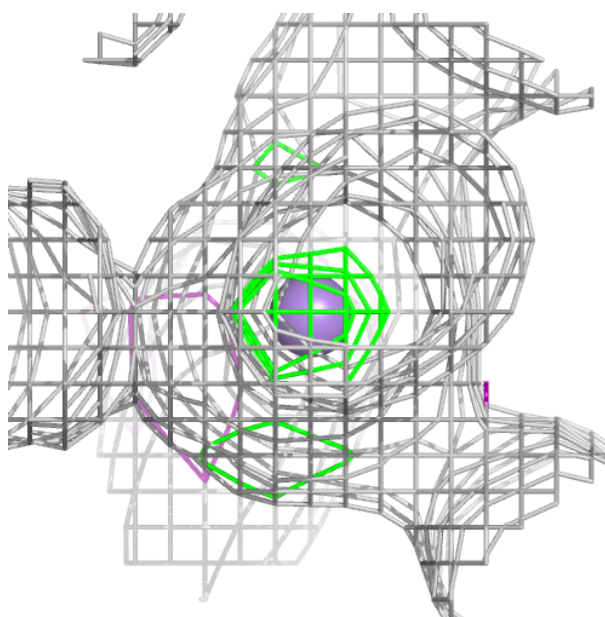
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	MN	D	301	1/1	0.98	0.03	11,11,11,11	0
2	MN	B	301	1/1	0.99	0.04	8,8,8,8	0
2	MN	C	301	1/1	0.99	0.02	8,8,8,8	0
2	MN	A	301	1/1	0.99	0.03	8,8,8,8	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.

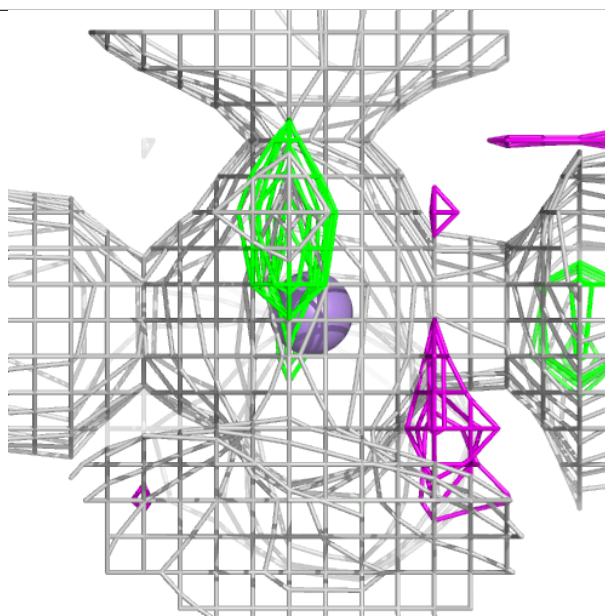
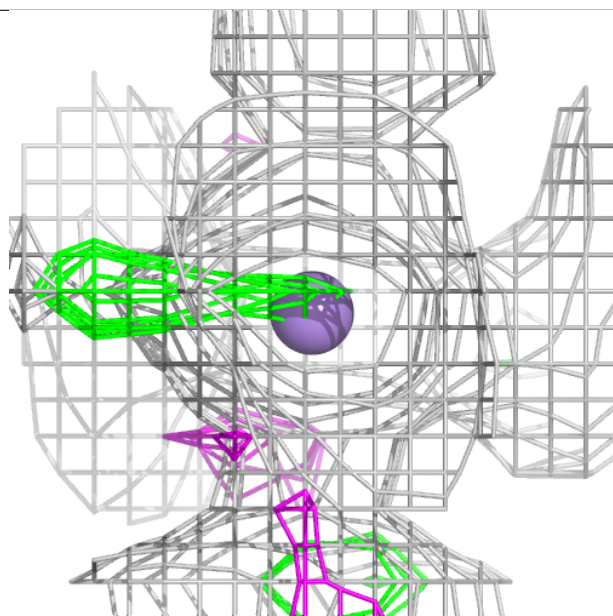
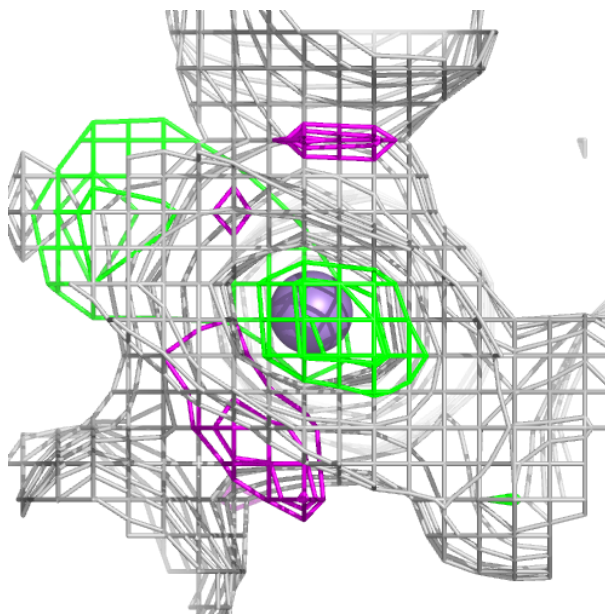
Electron density around MN D 301:

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



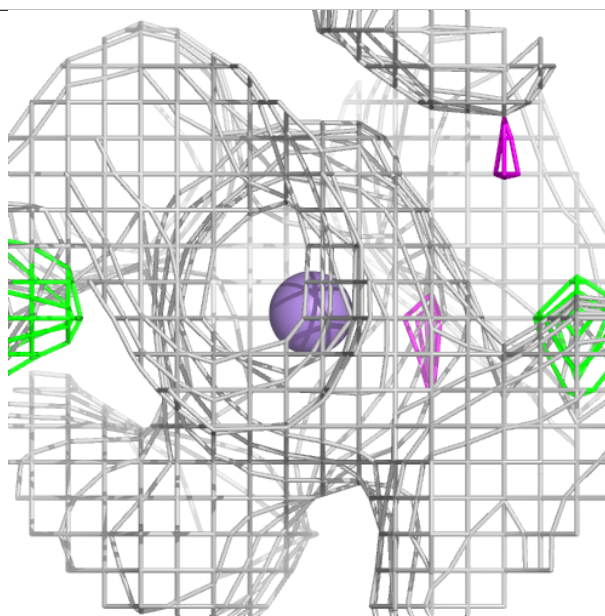
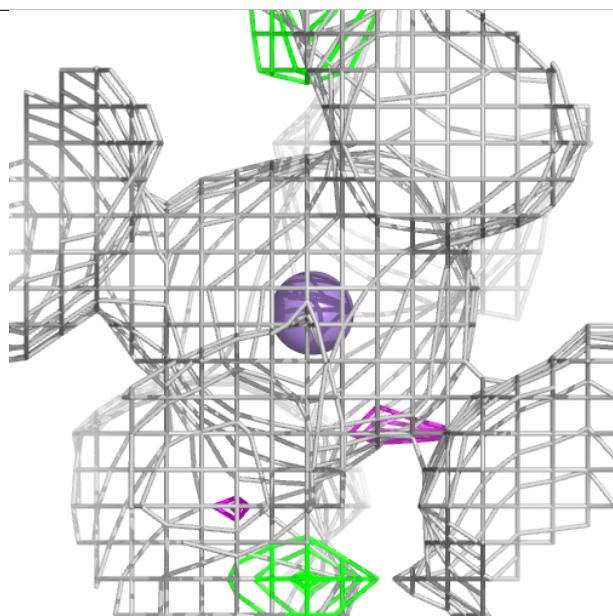
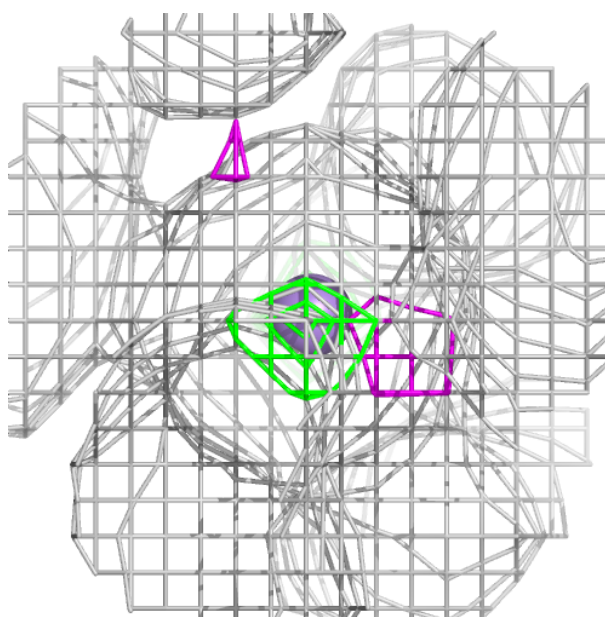
Electron density around MN B 301:

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



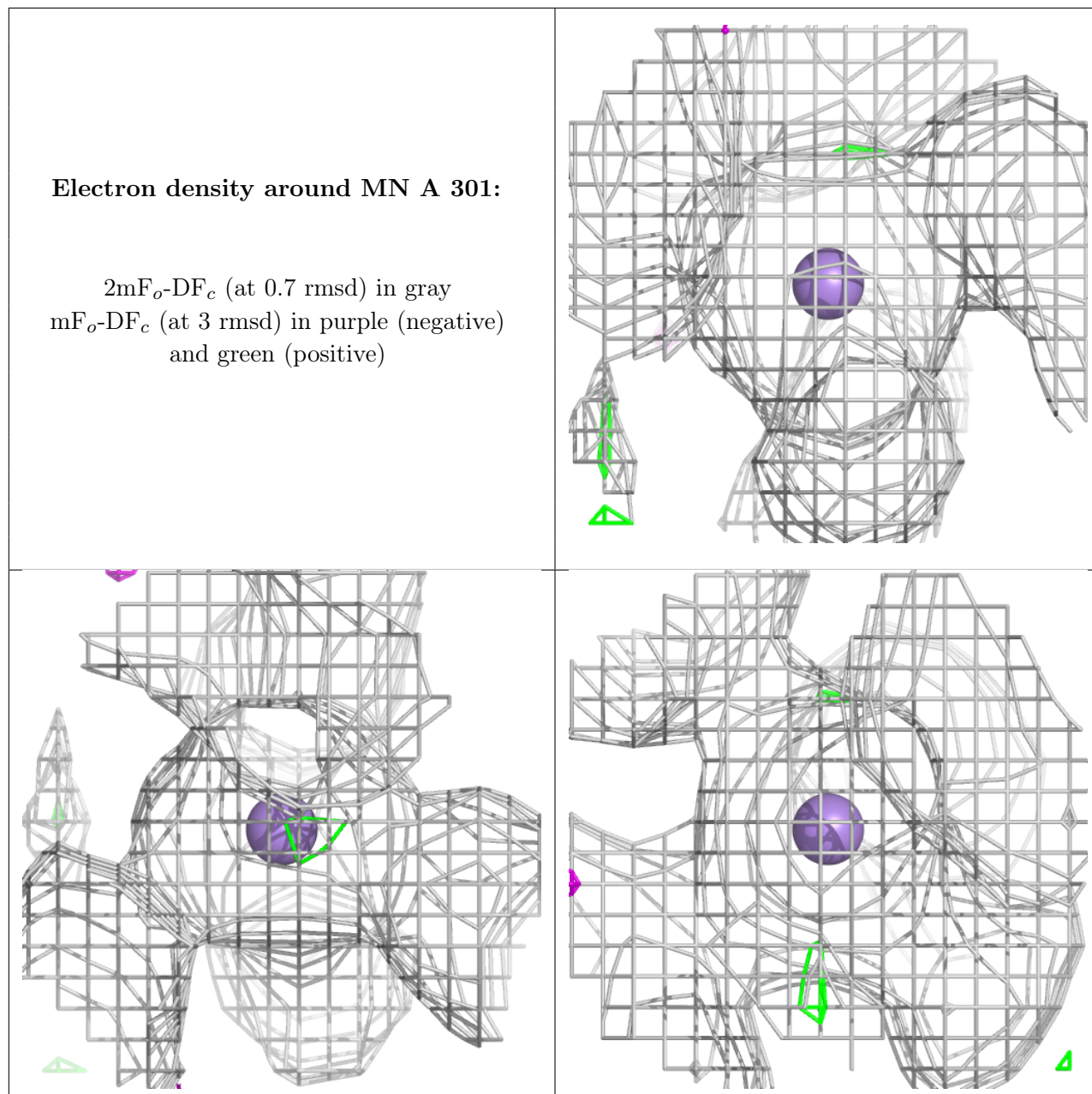
Electron density around MN C 301:

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



Electron density around MN A 301:

$2mF_o-DF_c$ (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.