



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 28, 2026 – 09:21 PM UTC

PDB ID : 6VCG / pdb_00006vcg
Title : Crystal structure of Nitrosotalea devanaterrea carotenoid cleavage dioxygenase, cobalt form
Authors : Daruwalla, A.; Shi, W.; Kiser, P.D.
Deposited on : 2019-12-20
Resolution : 2.30 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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

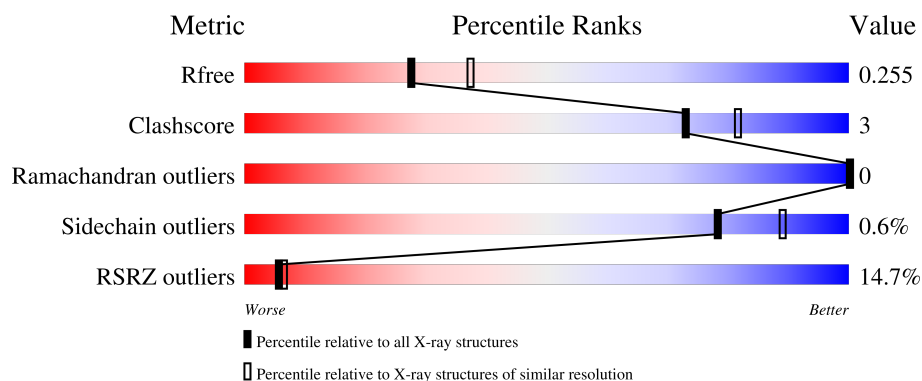
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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	6319 (2.30-2.30)
Clashscore	190562	6919 (2.30-2.30)
Ramachandran outliers	187476	6854 (2.30-2.30)
Sidechain outliers	187428	6854 (2.30-2.30)
RSRZ outliers	180081	6325 (2.30-2.30)

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	472	8% 88% 8% .
1	B	472	2% 88% 7% .
1	C	472	6% 89% 7% .
1	D	472	5% 88% 8% .
1	E	472	38% 79% 10% 10%

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Mol	Chain	Length	Quality of chain
1	F	472	24% 83% 7% 9%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 21658 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 carotenoid cleavage dioxygenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	453	Total	C	N	O	S	0	2	0
			3624	2335	589	693	7			
1	B	453	Total	C	N	O	S	0	2	0
			3643	2351	595	690	7			
1	C	453	Total	C	N	O	S	0	1	0
			3604	2326	588	683	7			
1	D	453	Total	C	N	O	S	0	0	0
			3597	2320	586	684	7			
1	E	423	Total	C	N	O	S	0	0	0
			3348	2161	541	639	7			
1	F	430	Total	C	N	O	S	0	0	0
			3372	2179	551	634	8			

- Molecule 2 is COBALT (II) ION (CCD ID: CO) (formula: Co) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Co	0	0
			1	1		
2	B	1	Total	Co	0	0
			1	1		
2	C	1	Total	Co	0	0
			1	1		
2	D	1	Total	Co	0	0
			1	1		
2	E	1	Total	Co	0	0
			1	1		
2	F	1	Total	Co	0	0
			1	1		

- Molecule 3 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total 1	Na 1	0	0
3	C	1	Total 1	Na 1	0	0

- Molecule 4 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

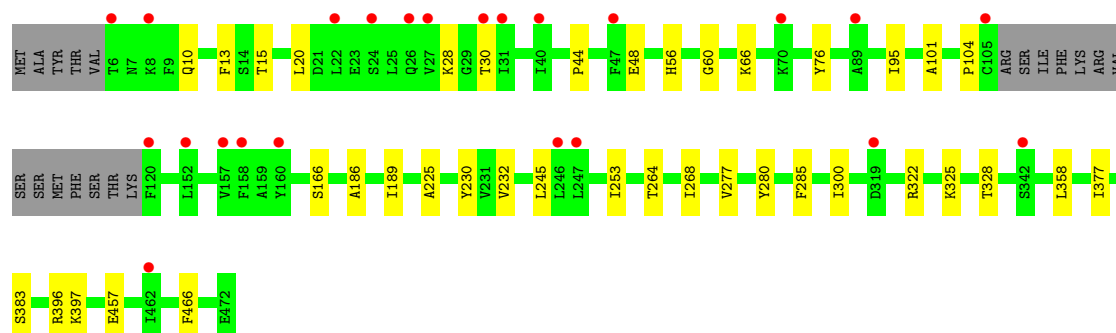
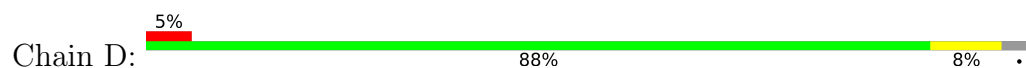
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	C	1	Total 1	Cl 1	0	0
4	E	1	Total 1	Cl 1	0	0

- Molecule 5 is water.

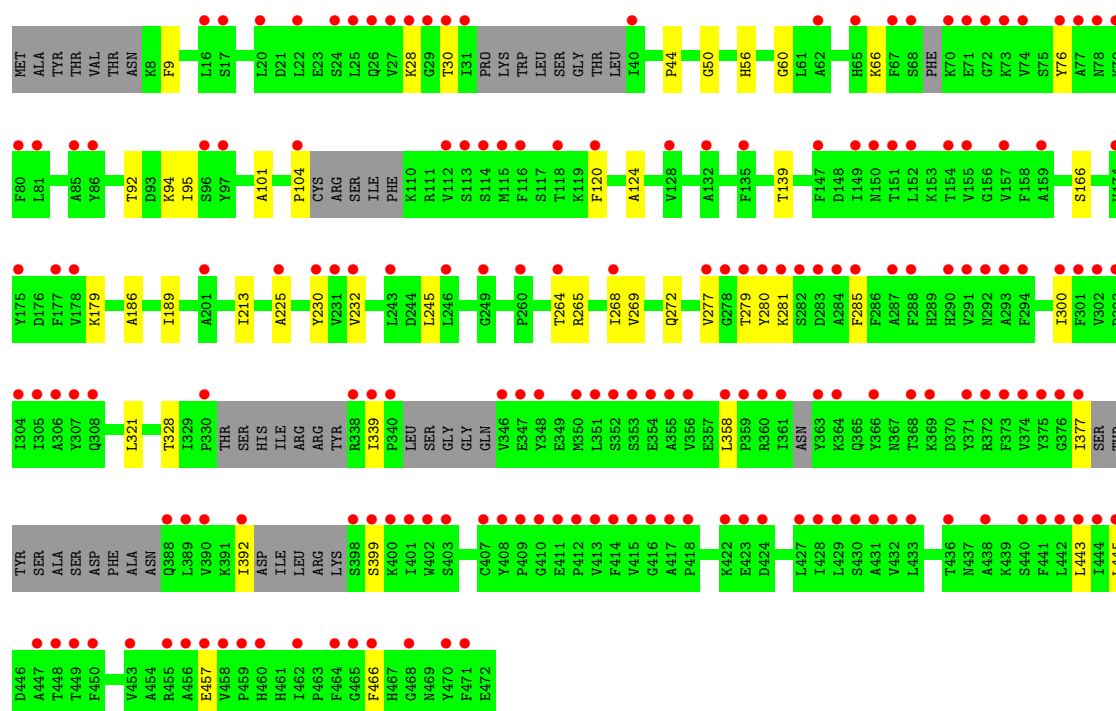
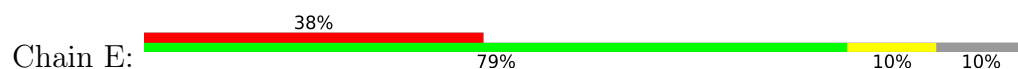
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	110	Total 110	O 110	0	0
5	B	135	Total 135	O 135	0	0
5	C	89	Total 89	O 89	0	0
5	D	84	Total 84	O 84	0	0
5	E	21	Total 21	O 21	0	0
5	F	21	Total 21	O 21	0	0



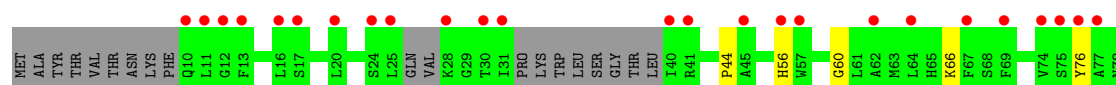
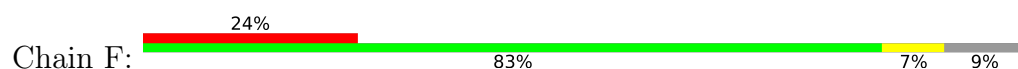
- Molecule 1: carotenoid cleavage dioxygenase

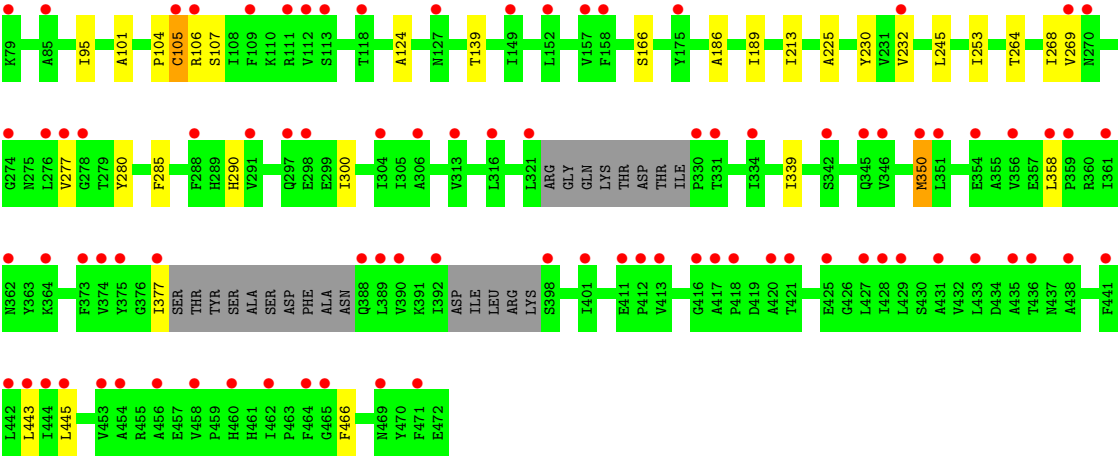


- Molecule 1: carotenoid cleavage dioxygenase



- Molecule 1: carotenoid cleavage dioxygenase





4 Data and refinement statistics

Property	Value	Source
Space group	P 61	Depositor
Cell constants a, b, c, α , β , γ	108.01Å 108.01Å 491.61Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	49.44 – 2.30 49.44 – 2.30	Depositor EDS
% Data completeness (in resolution range)	99.8 (49.44-2.30) 99.8 (49.44-2.30)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.97 (at 2.29Å)	Xtriage
Refinement program	REFMAC 5.8.0258	Depositor
R, R_{free}	0.238 , 0.254 0.241 , 0.255	Depositor DCC
R_{free} test set	7076 reflections (4.97%)	wwPDB-VP
Wilson B-factor (Å ²)	56.4	Xtriage
Anisotropy	0.229	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 57.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	0.036 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	21658	wwPDB-VP
Average B, all atoms (Å ²)	75.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.16% 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: NA, CO, CL

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	1.00	0/3717	1.28	4/5049 (0.1%)
1	B	1.01	1/3736 (0.0%)	1.28	3/5066 (0.1%)
1	C	1.01	1/3697 (0.0%)	1.27	2/5021 (0.0%)
1	D	1.02	0/3690	1.28	2/5015 (0.0%)
1	E	1.01	0/3426	1.28	1/4644 (0.0%)
1	F	1.02	0/3456	1.28	1/4691 (0.0%)
All	All	1.01	2/21722 (0.0%)	1.28	13/29486 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	329	ILE	N-CA	5.24	1.50	1.46
1	B	329	ILE	N-CA	5.16	1.50	1.46

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	105	CYS	CB-CA-C	-7.78	107.60	116.54
1	D	30	THR	CA-C-N	6.19	127.05	122.59
1	D	30	THR	C-N-CA	6.19	127.05	122.59
1	B	30	THR	CA-C-N	5.94	126.87	122.59
1	B	30	THR	C-N-CA	5.94	126.87	122.59

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	3624	0	3461	24	0
1	B	3643	0	3526	19	0
1	C	3604	0	3448	21	0
1	D	3597	0	3433	21	0
1	E	3348	0	3183	30	0
1	F	3372	0	3181	23	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
2	E	1	0	0	0	0
2	F	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
4	C	1	0	0	0	0
4	E	1	0	0	0	0
5	A	110	0	0	2	0
5	B	135	0	0	2	0
5	C	89	0	0	4	0
5	D	84	0	0	0	0
5	E	21	0	0	0	0
5	F	21	0	0	1	0
All	All	21658	0	20232	134	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.

The worst 5 of 134 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:358:LEU:HD12	1:D:377:ILE:HD12	1.69	0.75
1:A:358:LEU:HD12	1:A:377:ILE:HD12	1.73	0.71
1:E:358:LEU:HD12	1:E:377:ILE:HD12	1.72	0.70
1:B:166:SER:HB2	1:B:186:ALA:HB1	1.75	0.69
1:D:358:LEU:HD12	1:D:377:ILE:CD1	2.23	0.69

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	451/472 (96%)	432 (96%)	19 (4%)	0	100	100
1	B	451/472 (96%)	432 (96%)	19 (4%)	0	100	100
1	C	450/472 (95%)	431 (96%)	19 (4%)	0	100	100
1	D	449/472 (95%)	430 (96%)	19 (4%)	0	100	100
1	E	405/472 (86%)	392 (97%)	13 (3%)	0	100	100
1	F	418/472 (89%)	400 (96%)	18 (4%)	0	100	100
All	All	2624/2832 (93%)	2517 (96%)	107 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	387/417 (93%)	385 (100%)	2 (0%)	81	90
1	B	392/417 (94%)	387 (99%)	5 (1%)	61	77
1	C	382/417 (92%)	381 (100%)	1 (0%)	86	93
1	D	382/417 (92%)	379 (99%)	3 (1%)	73	86
1	E	355/417 (85%)	354 (100%)	1 (0%)	86	93
1	F	350/417 (84%)	348 (99%)	2 (1%)	78	89

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	2248/2502 (90%)	2234 (99%)	14 (1%)	78 89

5 of 14 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	20	LEU
1	D	10	GLN
1	F	350	MET
1	E	281	LYS
1	F	107	SER

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	194	ASN
1	C	180	ASN
1	E	461	HIS
1	F	333	HIS

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 10 ligands modelled in this entry, 10 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

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

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

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

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	453/472 (95%)	0.81	40 (8%) 15 17	29, 67, 99, 126	2 (0%)
1	B	453/472 (95%)	0.22	9 (1%) 65 66	21, 56, 85, 105	2 (0%)
1	C	453/472 (95%)	0.69	27 (5%) 27 29	24, 73, 110, 133	1 (0%)
1	D	453/472 (95%)	0.57	23 (5%) 33 35	43, 69, 103, 132	0
1	E	423/472 (89%)	2.04	180 (42%) 0 0	44, 88, 165, 198	0
1	F	430/472 (91%)	1.42	113 (26%) 1 2	51, 87, 136, 148	0
All	All	2665/2832 (94%)	0.94	392 (14%) 6 6	21, 72, 128, 198	5 (0%)

The worst 5 of 392 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	374	VAL	7.0
1	E	31	ILE	6.9
1	E	373	PHE	6.7
1	E	355	ALA	6.2
1	E	375	TYR	6.1

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

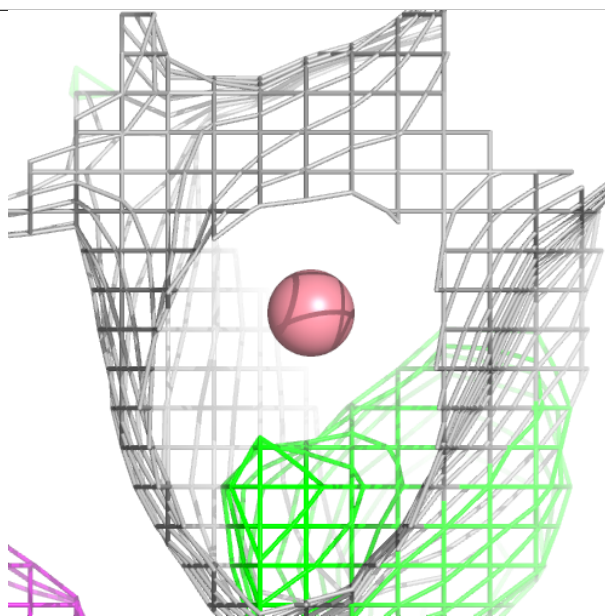
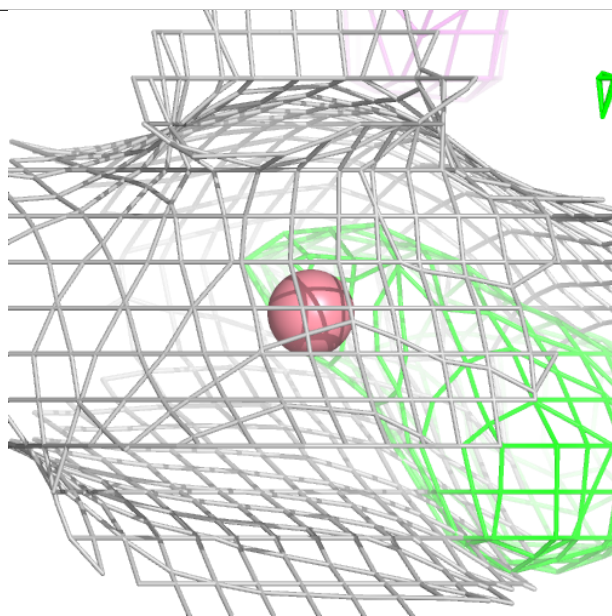
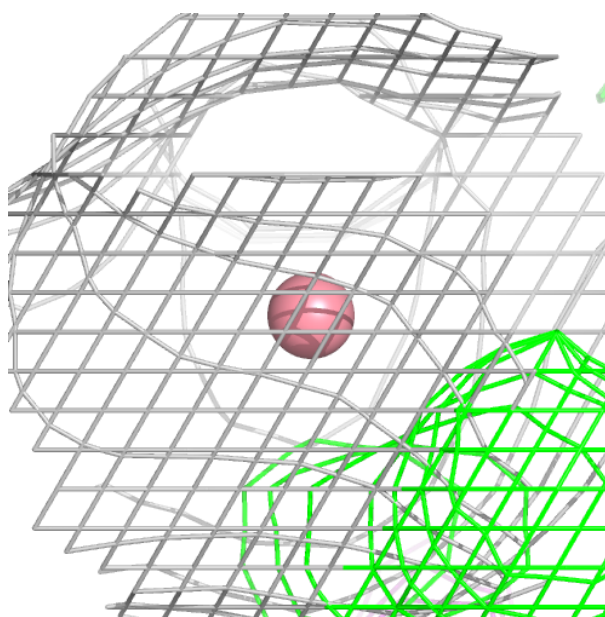
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	CL	C	503	1/1	0.92	0.12	79,79,79,79	0
4	CL	E	502	1/1	0.95	0.18	60,60,60,60	0
2	CO	F	1000	1/1	0.97	0.05	71,71,71,71	0
3	NA	B	502	1/1	0.97	0.07	70,70,70,70	0
3	NA	C	502	1/1	0.98	0.09	67,67,67,67	0
2	CO	E	501	1/1	0.99	0.04	61,61,61,61	0
2	CO	C	501	1/1	1.00	0.02	54,54,54,54	0
2	CO	D	1000	1/1	1.00	0.02	53,53,53,53	0
2	CO	A	1000	1/1	1.00	0.02	42,42,42,42	0
2	CO	B	501	1/1	1.00	0.01	38,38,38,38	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.

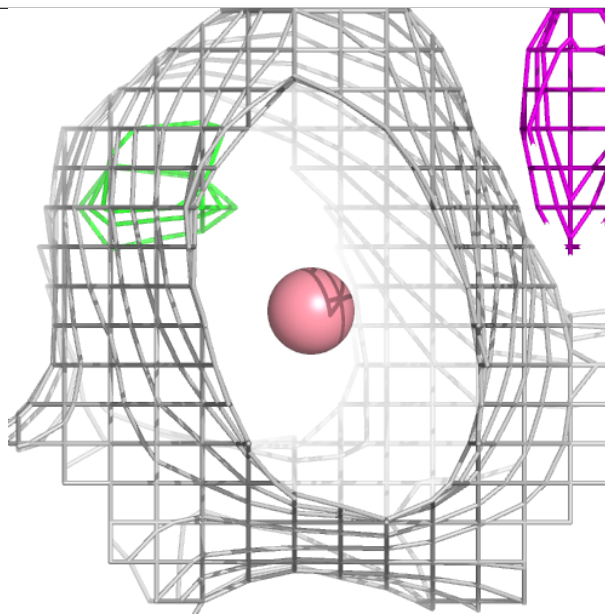
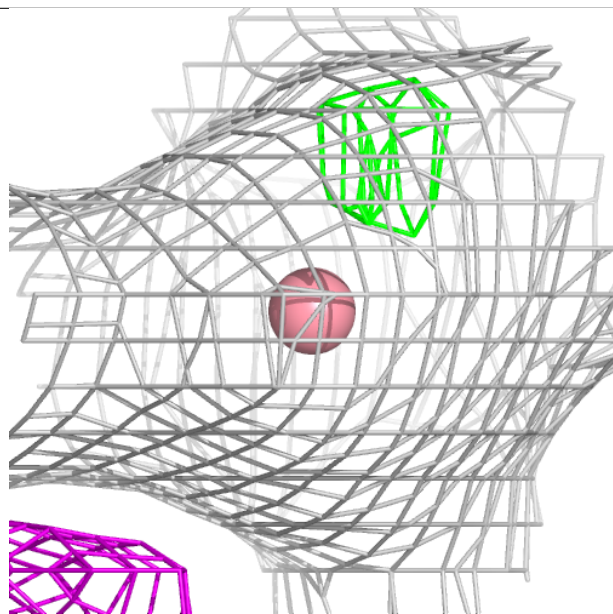
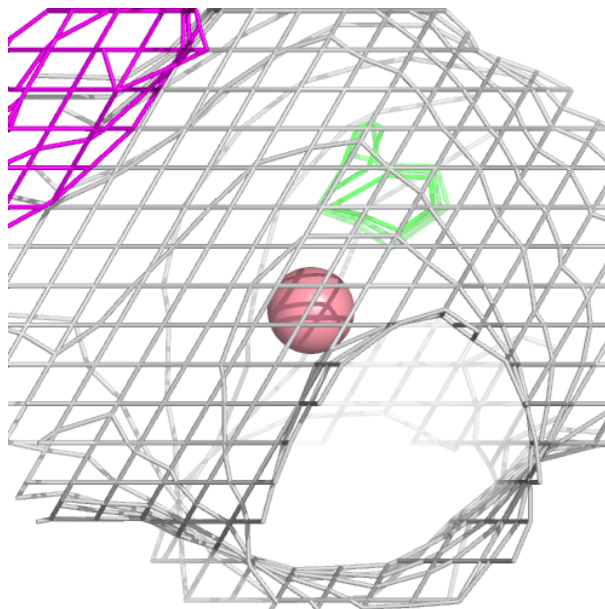
Electron density around CO F 1000:

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



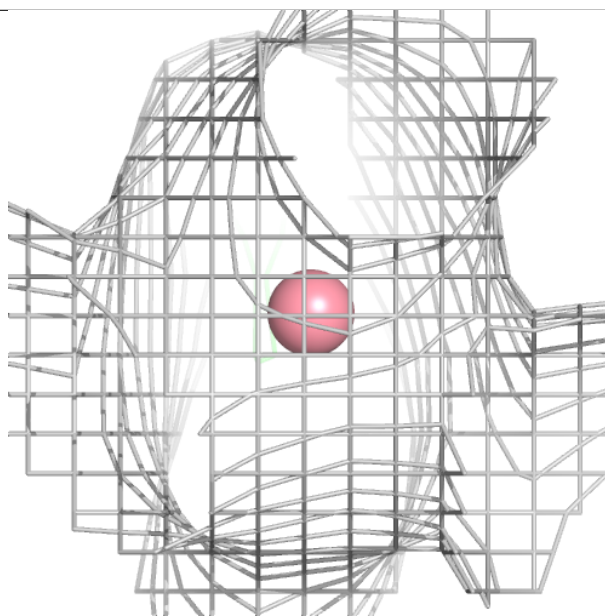
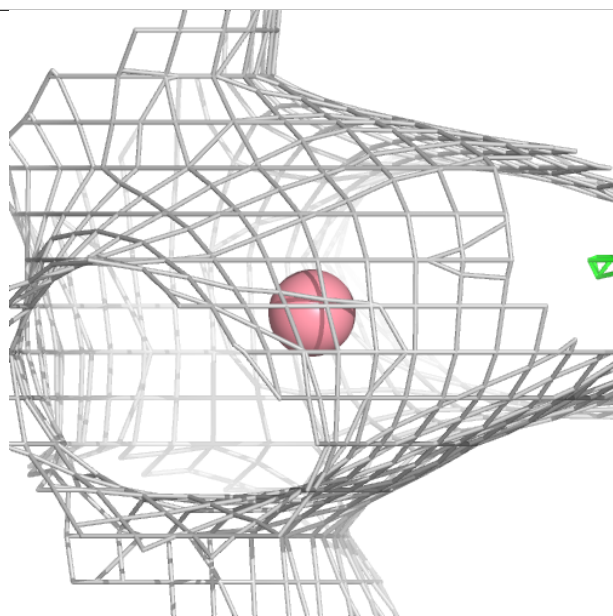
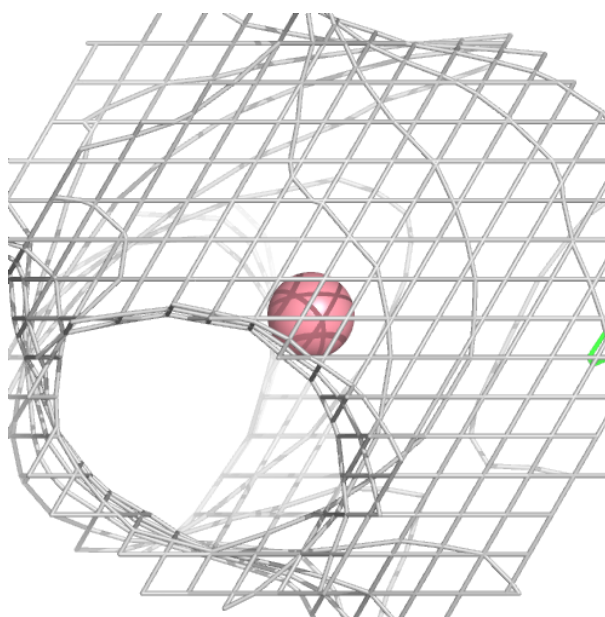
Electron density around CO E 501:

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



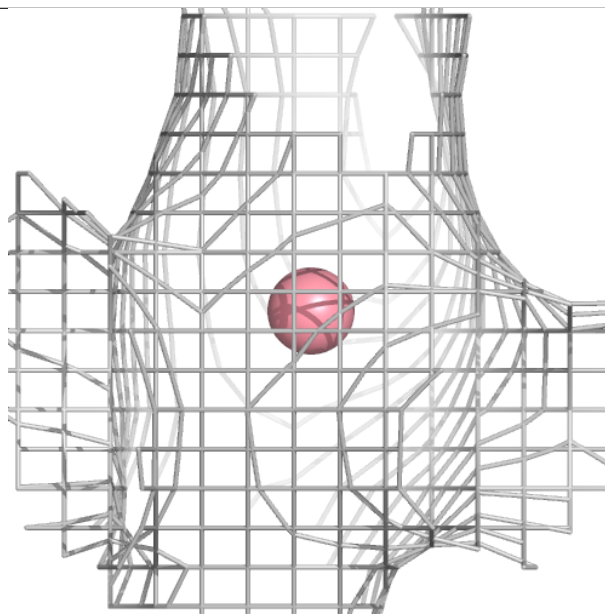
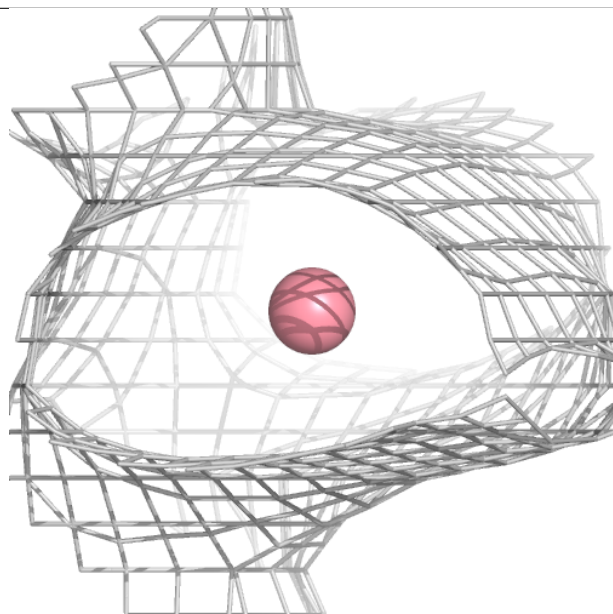
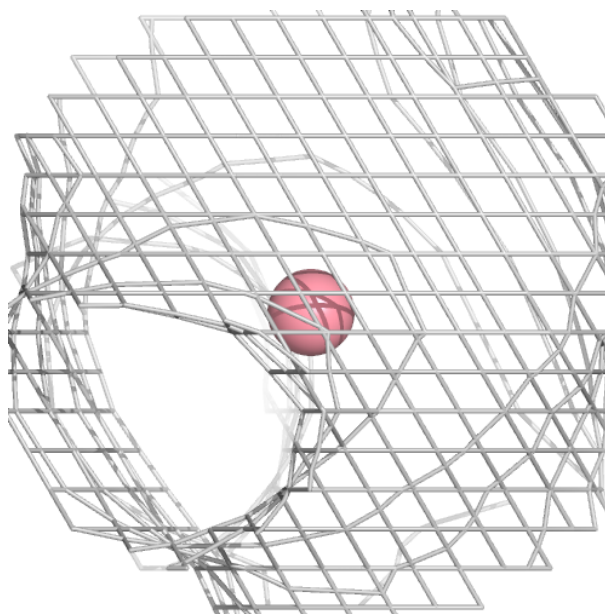
Electron density around CO C 501:

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



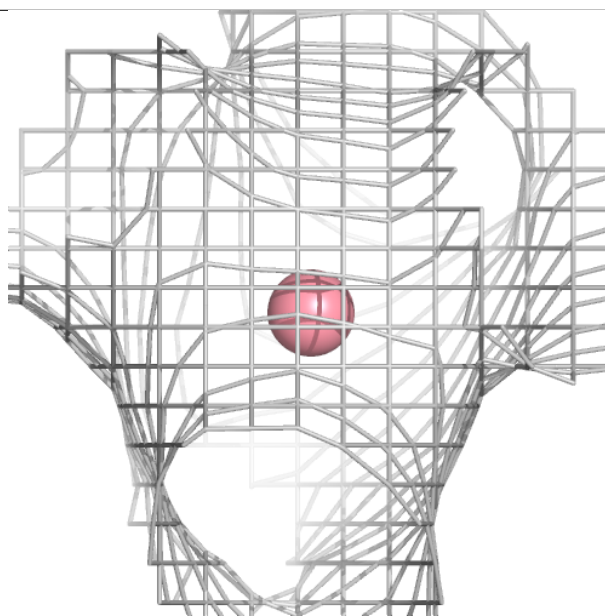
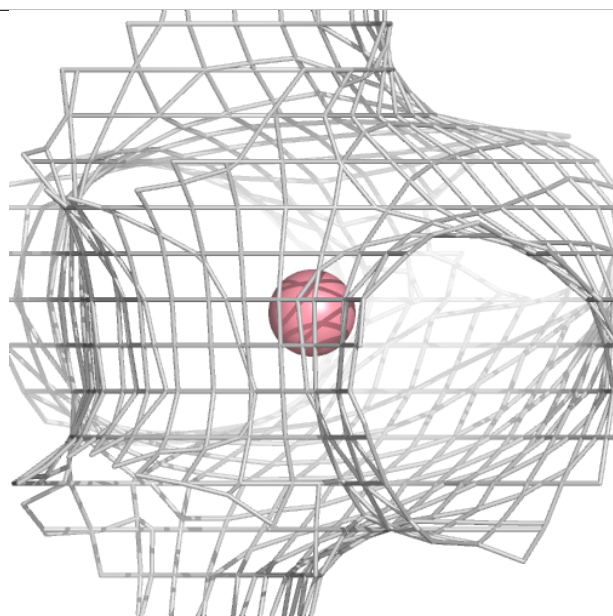
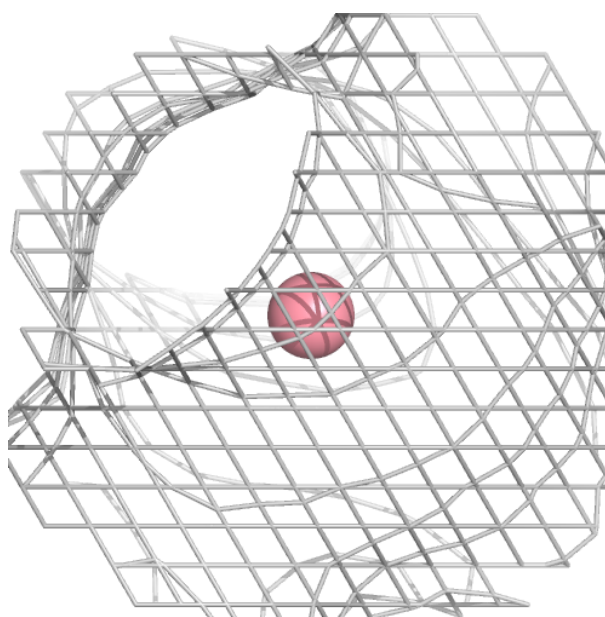
Electron density around CO D 1000:

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



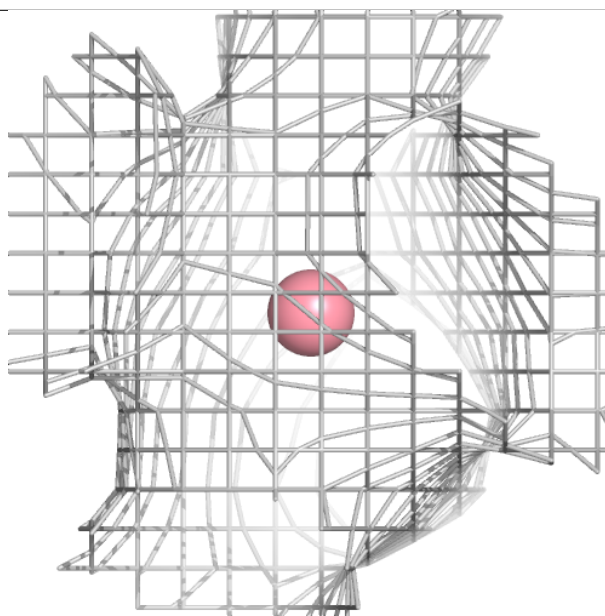
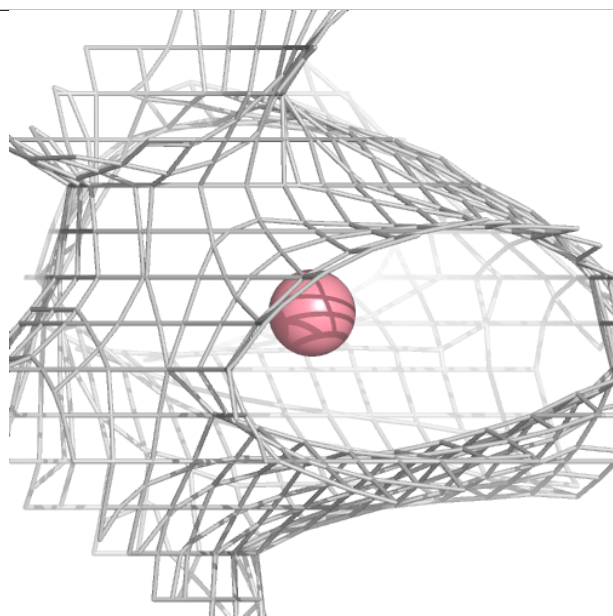
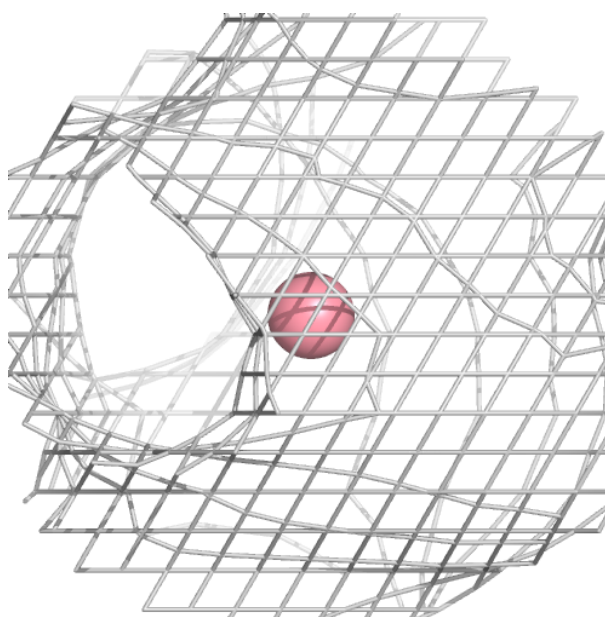
Electron density around CO A 1000:

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



Electron density around CO B 501:

$2mF_o-DF_c$ (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.