



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 05:28 PM UTC

PDB ID : 8RC9 / pdb_00008rc9
Title : W-formate dehydrogenase from *Desulfovibrio vulgaris* - Co-crystallized with Formate and Exposed to air for 2 h
Authors : Vilela-Alves, G.; Manuel, R.R.; Pereira, I.C.; Romao, M.J.; Mota, C.
Deposited on : 2023-12-06
Resolution : 2.06 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
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
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

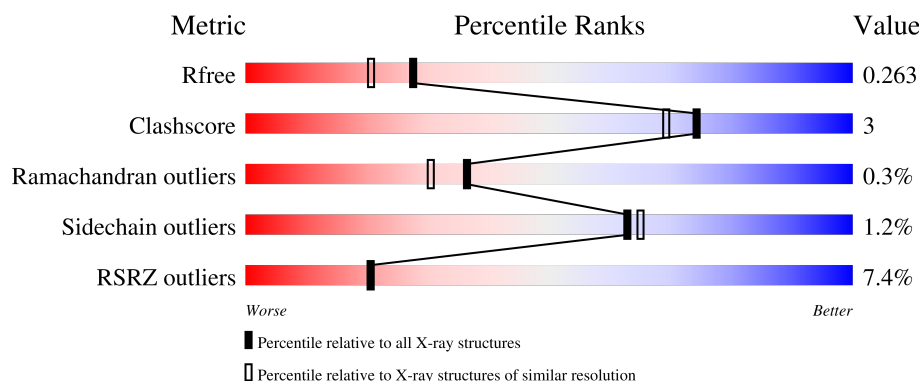
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

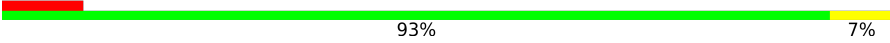
The reported resolution of this entry is 2.06 Å.

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	3774 (2.08-2.04)
Clashscore	190562	3883 (2.08-2.04)
Ramachandran outliers	187476	3860 (2.08-2.04)
Sidechain outliers	187428	3860 (2.08-2.04)
RSRZ outliers	180081	3775 (2.08-2.04)

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	1013	
2	B	214	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
9	OXY	A	1110	-	-	X	-

2 Entry composition

There are 10 unique types of molecules in this entry. The entry contains 9587 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 Formate dehydrogenase, alpha subunit, selenocysteine-containing.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	966	Total	C	N	O	S	Se	0	0	0
			7566	4823	1319	1382	41	1			

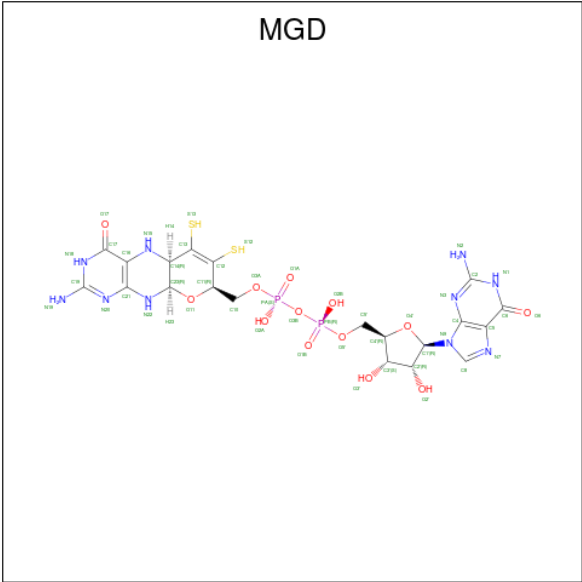
There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1006	TRP	-	expression tag	UNP Q72EJ1
A	1007	SER	-	expression tag	UNP Q72EJ1
A	1008	HIS	-	expression tag	UNP Q72EJ1
A	1009	PRO	-	expression tag	UNP Q72EJ1
A	1010	GLN	-	expression tag	UNP Q72EJ1
A	1011	PHE	-	expression tag	UNP Q72EJ1
A	1012	GLU	-	expression tag	UNP Q72EJ1
A	1013	LYS	-	expression tag	UNP Q72EJ1

- Molecule 2 is a protein called Formate dehydrogenase, beta subunit, putative.

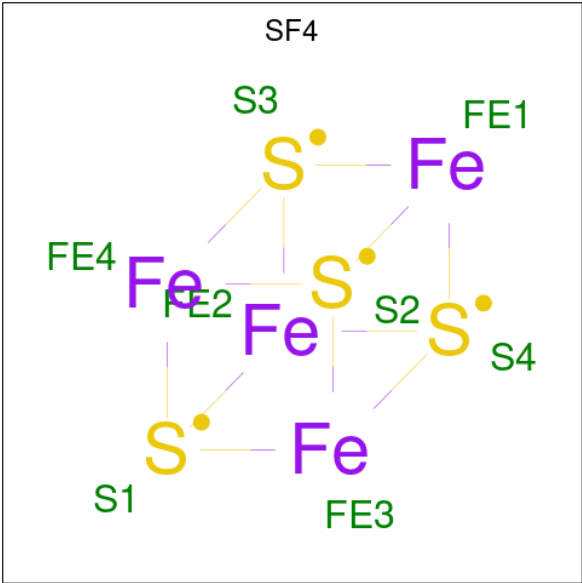
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	214	Total	C	N	O	S	0	0	0
			1664	1041	291	316	16			

- Molecule 3 is 2-AMINO-5,6-DIMERCAPTO-7-METHYL-3,7,8A,9-TETRAHYDRO-8-OXA-1,3,9,10-TETRAAZA-ANTHRACEN-4-ONE GUANOSINE DINUCLEOTIDE (CCD ID: MGD) (formula: C₂₀H₂₆N₁₀O₁₃P₂S₂).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	
3	A	1	Total	C	N	O	P	S	0	0
			47	20	10	13	2	2		
3	A	1	Total	C	N	O	P	S	0	0
			47	20	10	13	2	2		

- Molecule 4 is IRON/SULFUR CLUSTER (CCD ID: SF4) (formula: Fe₄S₄).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Fe S	0	0
			8	4 4		
4	B	1	Total	Fe S	0	0
			8	4 4		

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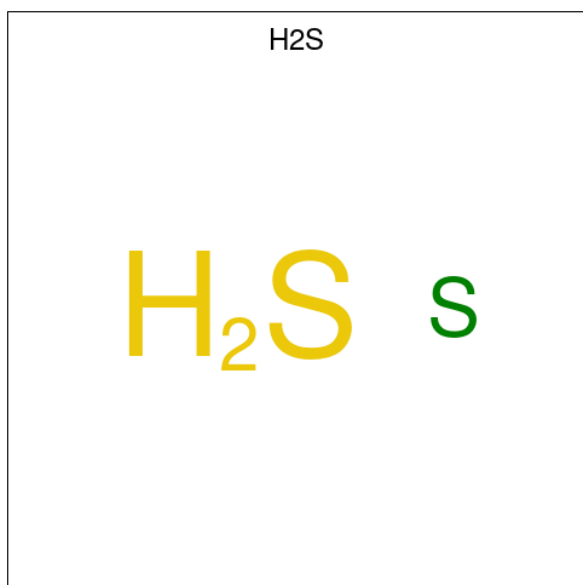
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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	B	1	Total	Fe	S	0	0
			8	4	4		
4	B	1	Total	Fe	S	0	0
			8	4	4		

- Molecule 5 is TUNGSTEN ION (CCD ID: W) (formula: W).

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

- Molecule 6 is HYDROSULFURIC ACID (CCD ID: H2S) (formula: H₂S).



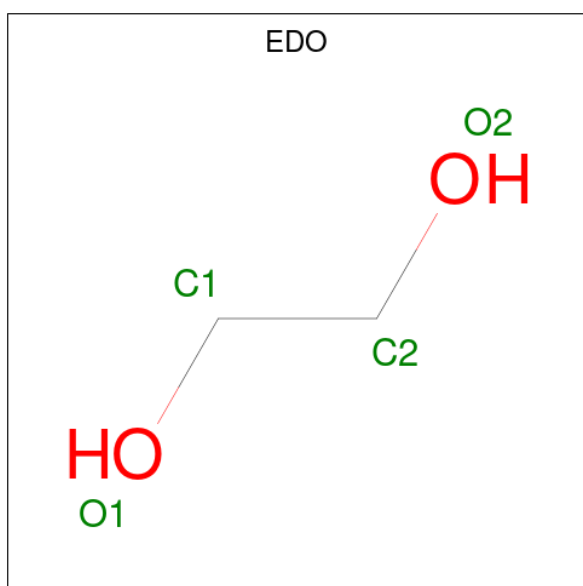
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	1	Total	S	0	0
			1	1		

- Molecule 7 is GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃).



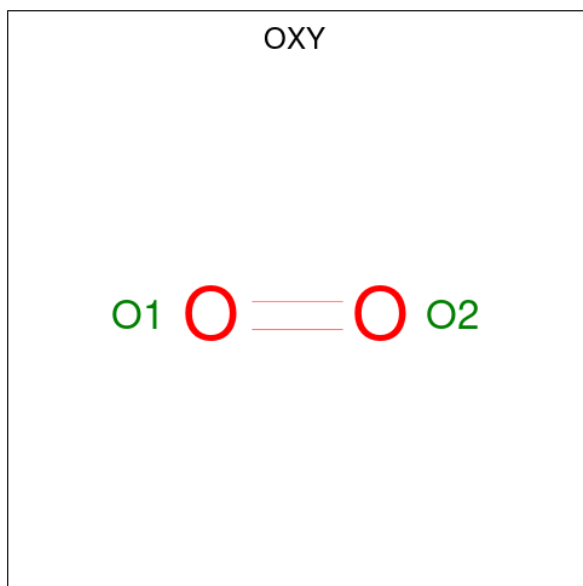
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	1	Total	C	O	0	0
			6	3	3		
7	A	1	Total	C	O	0	0
			6	3	3		

- Molecule 8 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: $C_2H_6O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	A	1	Total	C	O	0	0
			4	2	2		
8	A	1	Total	C	O	0	0
			4	2	2		

- Molecule 9 is OXYGEN MOLECULE (CCD ID: OXY) (formula: O₂).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	1	Total	O	0	0
			2	2		

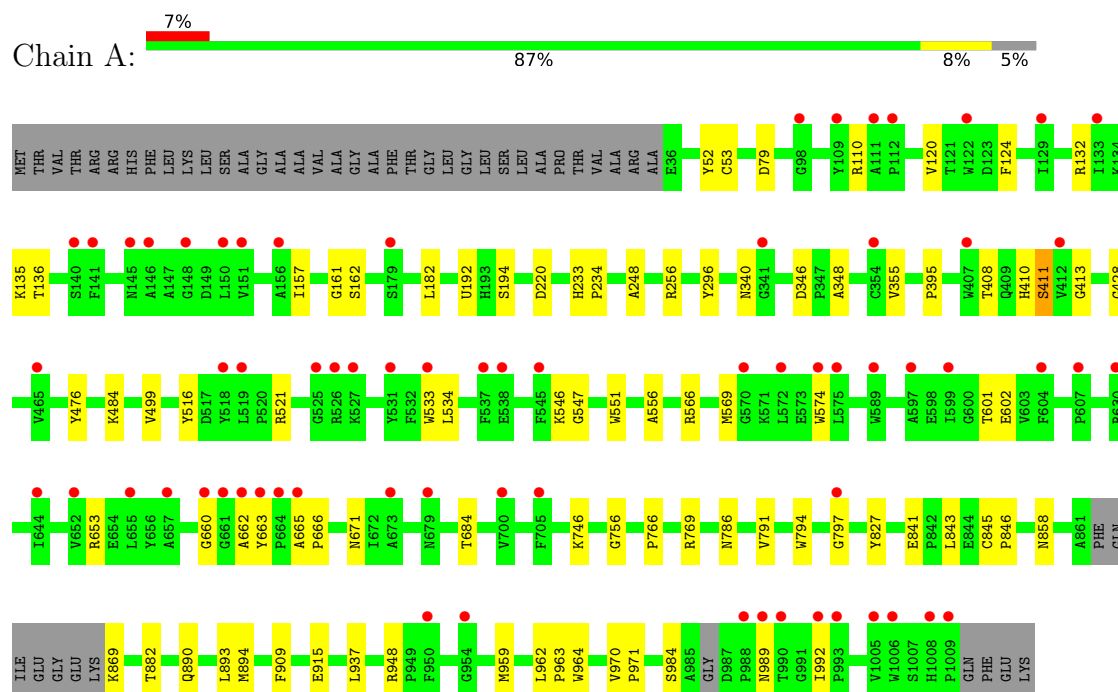
- Molecule 10 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	A	172	Total	O	0	0
			172	172		
10	B	35	Total	O	0	0
			35	35		

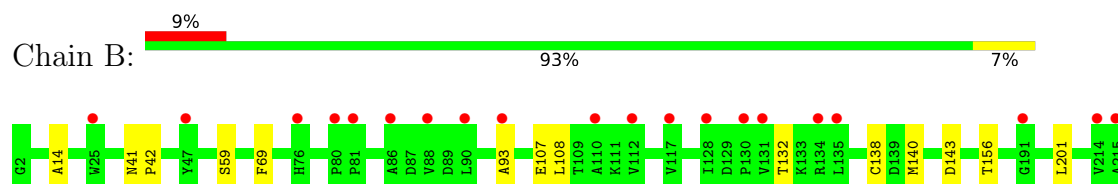
3 Residue-property plots

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

- Molecule 1: Formate dehydrogenase, alpha subunit, selenocysteine-containing



- Molecule 2: Formate dehydrogenase, beta subunit, putative



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	65.18Å 127.93Å 149.47Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	97.19 – 2.06 97.19 – 2.06	Depositor EDS
% Data completeness (in resolution range)	82.9 (97.19-2.06) 79.4 (97.19-2.06)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.58 (at 2.05Å)	Xtriage
Refinement program	REFMAC 5.8.0267	Depositor
R, R_{free}	0.206 , 0.255 0.216 , 0.263	Depositor DCC
R_{free} test set	3244 reflections (4.13%)	wwPDB-VP
Wilson B-factor (Å ²)	35.6	Xtriage
Anisotropy	0.060	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 32.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	9587	wwPDB-VP
Average B, all atoms (Å ²)	43.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.70% 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: OXY, EDO, MGD, GOL, SEC, SF4, H2S, W

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	1.01	1/7769 (0.0%)	1.37	3/10540 (0.0%)
2	B	1.04	0/1699	1.38	0/2302
All	All	1.02	1/9468 (0.0%)	1.37	3/12842 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	52	TYR	CA-C	5.20	1.55	1.52

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	410	HIS	CA-C-N	5.50	127.91	120.38
1	A	410	HIS	C-N-CA	5.50	127.91	120.38
1	A	791	VAL	N-CA-C	-5.19	106.74	111.67

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	7566	0	7392	49	0
2	B	1664	0	1633	7	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	94	0	44	2	0
4	A	8	0	0	0	0
4	B	24	0	0	0	0
5	A	1	0	0	0	0
6	A	1	0	0	0	0
7	A	12	0	16	1	0
8	A	8	0	12	0	0
9	A	2	0	0	3	0
10	A	172	0	0	0	0
10	B	35	0	0	1	0
All	All	9587	0	9097	57	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 (57) 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:192:SEC:SE	9:A:1110:OXY:O1	2.46	0.83
1:A:120:VAL:HG21	1:A:124:PHE:CD2	2.15	0.82
1:A:192:SEC:SE	9:A:1110:OXY:O2	2.57	0.73
1:A:355:VAL:HG13	1:A:827:TYR:HB2	1.85	0.58
1:A:79:ASP:O	1:A:746:LYS:HE3	2.04	0.58
1:A:566:ARG:HA	1:A:569:MET:HE3	1.87	0.56
1:A:408:THR:O	1:A:413:GLY:HA3	2.07	0.54
2:B:41:ASN:HA	2:B:42:PRO:C	2.32	0.53
1:A:516:TYR:CE2	1:A:521:ARG:NH2	2.76	0.53
1:A:915:GLU:OE2	1:A:948:ARG:NH1	2.41	0.53
1:A:411:SER:CB	1:A:858:ASN:HD22	2.23	0.52
1:A:547:GLY:HA3	1:A:574:TRP:CZ2	2.45	0.51
1:A:346:ASP:OD1	1:A:348:ALA:HB3	2.10	0.51
1:A:970:VAL:CG2	1:A:971:PRO:HA	2.41	0.51
1:A:120:VAL:CG2	1:A:124:PHE:CD2	2.90	0.51
2:B:107:GLU:OE1	2:B:107:GLU:N	2.44	0.50
1:A:296:TYR:CE1	1:A:428:GLY:HA2	2.47	0.49
1:A:841:GLU:HG3	1:A:843:LEU:O	2.13	0.48
1:A:894:MET:SD	3:A:1102:MGD:H2'	2.53	0.48
1:A:136:THR:HG23	1:A:546:LYS:HD2	1.96	0.48
1:A:766:PRO:HG2	1:A:769:ARG:HD2	1.96	0.48
2:B:140:MET:O	2:B:140:MET:HG2	2.13	0.48
1:A:534:LEU:HD11	1:A:984:SER:O	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:110:ARG:NH1	1:A:601:THR:O	2.45	0.47
1:A:157:ILE:HG22	1:A:182:LEU:HD21	1.96	0.47
1:A:756:GLY:HA3	7:A:1107:GOL:H2	1.95	0.47
2:B:143:ASP:HB2	10:B:429:HOH:O	2.14	0.46
2:B:201:LEU:C	2:B:201:LEU:HD23	2.40	0.46
1:A:194:SER:HB2	1:A:992:ILE:HD11	1.97	0.46
1:A:890:GLN:HA	1:A:964:TRP:CH2	2.51	0.46
1:A:136:THR:HG23	1:A:546:LYS:CD	2.47	0.45
1:A:395:PRO:O	1:A:786:ASN:HB2	2.16	0.45
3:A:1102:MGD:S13	9:A:1110:OXY:O1	2.75	0.45
1:A:162:SER:HB2	1:A:551:TRP:O	2.17	0.45
1:A:411:SER:HB2	1:A:858:ASN:HD22	1.82	0.44
1:A:476:TYR:HE1	1:A:499:VAL:HG21	1.83	0.44
1:A:845:CYS:HB2	1:A:846:PRO:HD3	1.99	0.44
1:A:516:TYR:CD2	1:A:521:ARG:NH2	2.85	0.44
1:A:794:TRP:CZ2	1:A:797:GLY:HA2	2.53	0.43
1:A:161:GLY:HA3	1:A:551:TRP:O	2.19	0.43
1:A:893:LEU:C	1:A:893:LEU:HD23	2.44	0.43
1:A:132:ARG:NH2	1:A:602:GLU:OE2	2.51	0.43
1:A:665:ALA:HB3	1:A:666:PRO:HD3	2.00	0.43
2:B:93:ALA:HA	2:B:108:LEU:HB2	1.99	0.43
1:A:556:ALA:HB2	1:A:569:MET:HE1	1.99	0.43
1:A:937:LEU:C	1:A:937:LEU:HD12	2.43	0.42
1:A:909:PHE:CE2	1:A:963:PRO:HG3	2.55	0.42
1:A:340:ASN:O	1:A:484:LYS:HG3	2.20	0.41
1:A:411:SER:HB3	1:A:858:ASN:HD22	1.83	0.41
1:A:882:THR:HA	1:A:962:LEU:O	2.20	0.41
2:B:14:ALA:HB2	2:B:69:PHE:CG	2.56	0.41
1:A:220:ASP:O	1:A:248:ALA:HA	2.20	0.41
1:A:256:ARG:HG2	1:A:959:MET:HE1	2.03	0.41
1:A:574:TRP:HA	1:A:602:GLU:O	2.21	0.41
1:A:970:VAL:HG23	1:A:971:PRO:HA	2.03	0.40
1:A:161:GLY:HA2	1:A:162:SER:HA	1.91	0.40
1:A:233:HIS:N	1:A:234:PRO:HD3	2.37	0.40

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	959/1013 (95%)	917 (96%)	38 (4%)	4 (0%)	30	23
2	B	212/214 (99%)	201 (95%)	11 (5%)	0	100	100
All	All	1171/1227 (95%)	1118 (96%)	49 (4%)	4 (0%)	36	30

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	662	ALA
1	A	660	GLY
1	A	533	TRP
1	A	663	TYR

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	786/819 (96%)	778 (99%)	8 (1%)	68	71
2	B	185/185 (100%)	181 (98%)	4 (2%)	45	43
All	All	971/1004 (97%)	959 (99%)	12 (1%)	63	65

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	53	CYS
1	A	135	LYS

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Mol	Chain	Res	Type
1	A	411	SER
1	A	653	ARG
1	A	671	ASN
1	A	684	THR
1	A	869	LYS
1	A	989	ASN
2	B	59	SER
2	B	132	THR
2	B	138	CYS
2	B	156	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	384	GLN
1	A	973	ASN
1	A	989	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 13 ligands modelled in this entry, 1 is monoatomic and 1 is modelled with single atom - leaving 11 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
4	SF4	B	302	2	0,12,12	-	-	-		
8	EDO	A	1108	-	3,3,3	0.18	0	2,2,2	0.46	0
9	OXY	A	1110	5	1,1,1	0.04	0	-		
8	EDO	A	1109	-	3,3,3	0.10	0	2,2,2	0.08	0
3	MGD	A	1102	5	47,52,52	0.67	1 (2%)	58,81,81	1.05	4 (6%)
3	MGD	A	1101	5	47,52,52	0.90	2 (4%)	58,81,81	1.12	4 (6%)
4	SF4	B	301	2	0,12,12	-	-	-		
4	SF4	A	1103	1	0,12,12	-	-	-		
7	GOL	A	1107	-	5,5,5	0.15	0	5,5,5	0.46	0
7	GOL	A	1106	-	5,5,5	0.10	0	5,5,5	0.37	0
4	SF4	B	303	2	0,12,12	-	-	-		

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
4	SF4	B	302	2	-	-	0/6/5/5
8	EDO	A	1108	-	-	1/1/1/1	-
8	EDO	A	1109	-	-	1/1/1/1	-
3	MGD	A	1102	5	-	6/22/66/66	0/6/6/6
3	MGD	A	1101	5	-	1/22/66/66	0/6/6/6
4	SF4	B	301	2	-	-	0/6/5/5
7	GOL	A	1107	-	-	1/4/4/4	-
4	SF4	A	1103	1	-	-	0/6/5/5
7	GOL	A	1106	-	-	2/4/4/4	-
4	SF4	B	303	2	-	-	0/6/5/5

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1101	MGD	C23-C14	4.11	1.56	1.53
3	A	1101	MGD	PA-O3B	2.74	1.62	1.59
3	A	1102	MGD	PA-O3B	2.26	1.61	1.59

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1101	MGD	O11-C23-C14	3.80	111.50	108.96
3	A	1101	MGD	C19-N20-C21	3.16	118.94	113.36
3	A	1102	MGD	O11-C23-N22	3.10	111.42	108.61
3	A	1101	MGD	C23-C14-N15	3.01	110.82	107.87
3	A	1102	MGD	C19-N20-C21	2.98	118.61	113.36
3	A	1102	MGD	C23-C14-N15	2.77	110.58	107.87
3	A	1101	MGD	C17-C16-N15	2.08	121.95	116.27
3	A	1102	MGD	O4'-C1'-C2'	-2.07	102.19	106.62

There are no chirality outliers.

All (12) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	1102	MGD	C5'-O5'-PB-O2B
3	A	1102	MGD	C4'-C5'-O5'-PB
7	A	1106	GOL	C1-C2-C3-O3
7	A	1107	GOL	O1-C1-C2-C3
3	A	1102	MGD	O4'-C4'-C5'-O5'
7	A	1106	GOL	O2-C2-C3-O3
3	A	1101	MGD	PA-O3B-PB-O5'
3	A	1102	MGD	C5'-O5'-PB-O3B
3	A	1102	MGD	C3'-C4'-C5'-O5'
8	A	1108	EDO	O1-C1-C2-O2
8	A	1109	EDO	O1-C1-C2-O2
3	A	1102	MGD	PA-O3B-PB-O2B

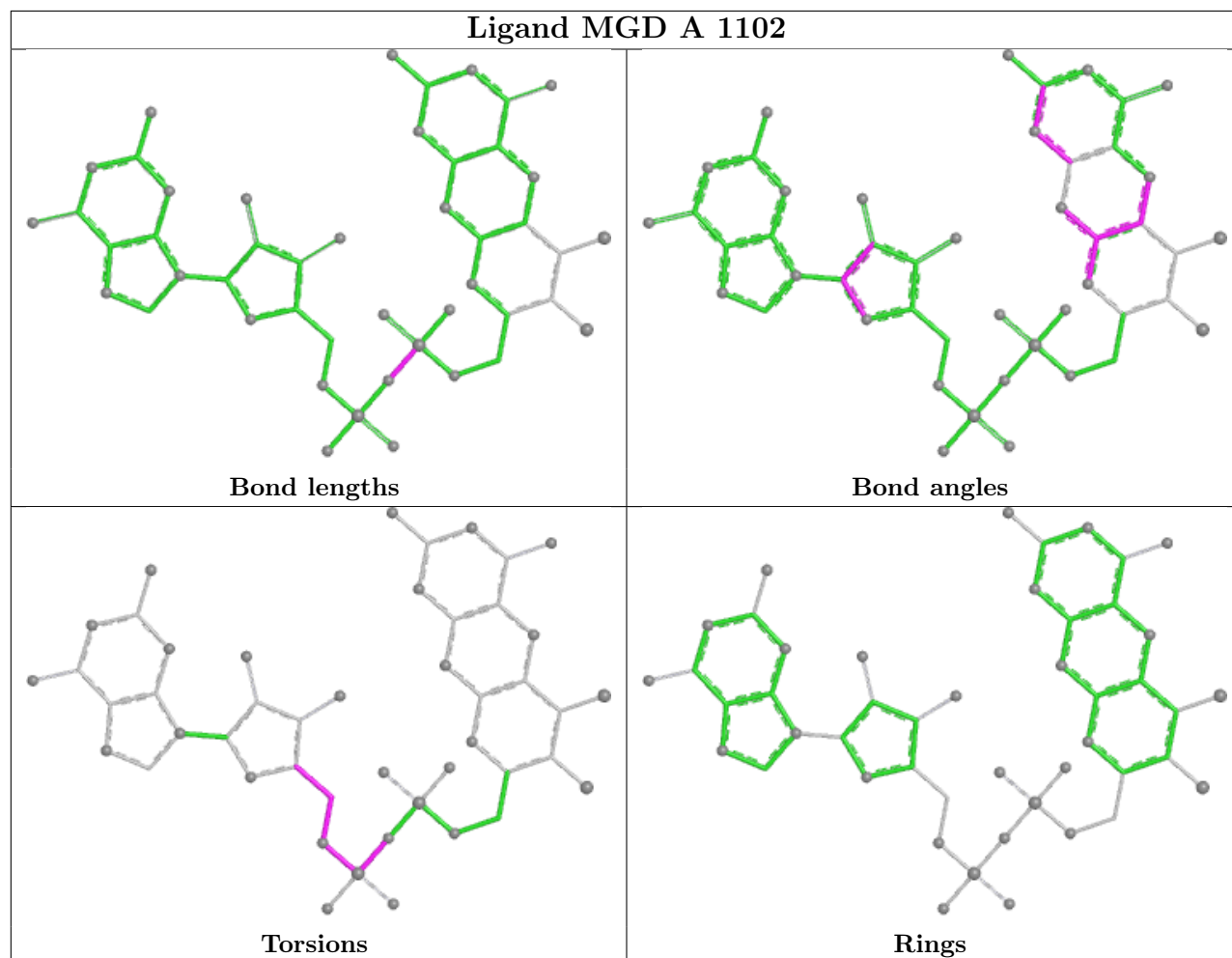
There are no ring outliers.

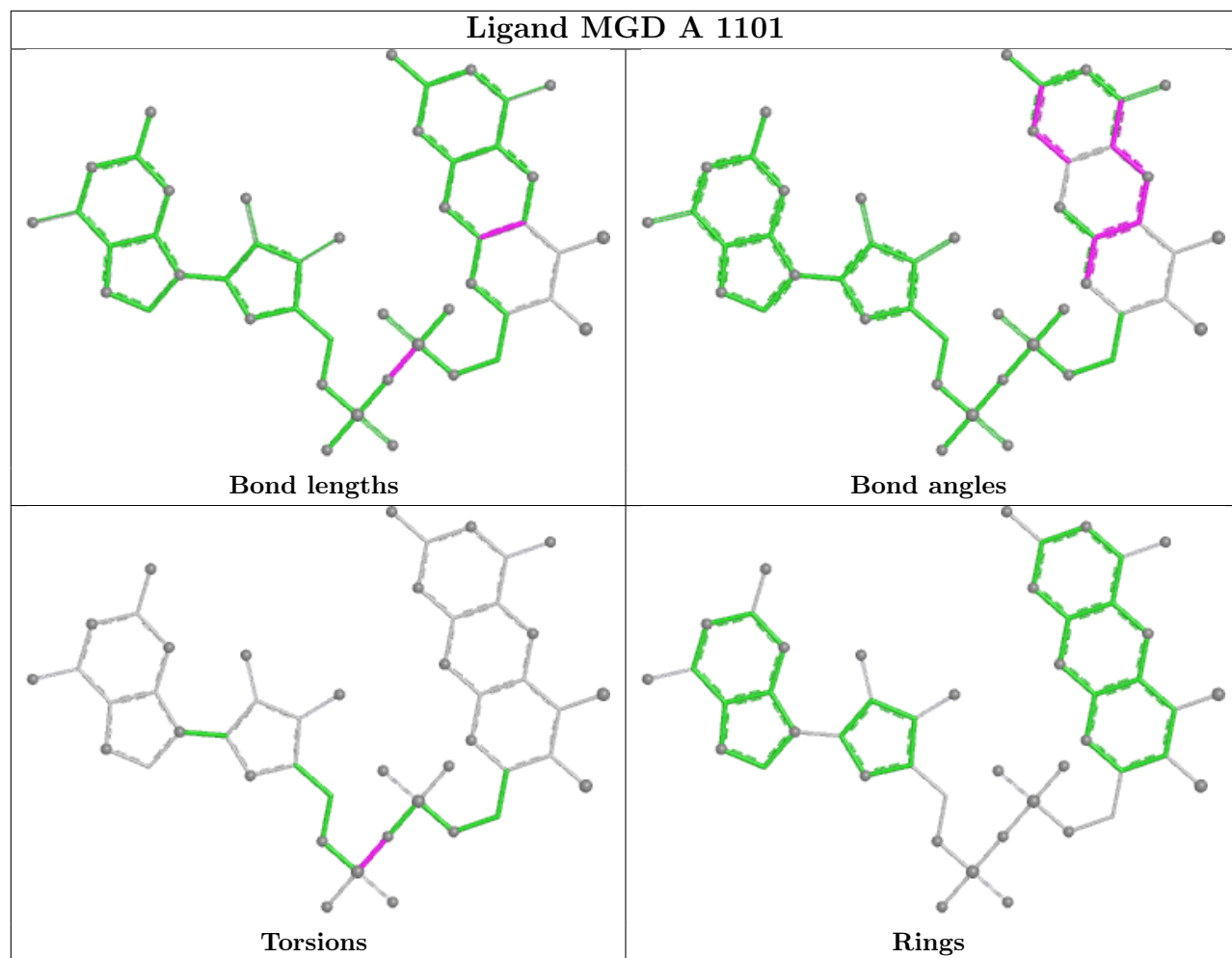
3 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
9	A	1110	OXY	3	0
3	A	1102	MGD	2	0
7	A	1107	GOL	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and

any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





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	965/1013 (95%)	0.70	67 (6%) 23 22	21, 41, 66, 132	0
2	B	214/214 (100%)	0.77	20 (9%) 14 14	27, 45, 70, 86	0
All	All	1179/1227 (96%)	0.71	87 (7%) 20 20	21, 42, 67, 132	0

All (87) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	989	ASN	4.6
1	A	988	PRO	4.5
1	A	992	ILE	4.3
1	A	597	ALA	4.0
1	A	657	ALA	4.0
1	A	990	THR	4.0
1	A	1009	PRO	3.8
1	A	644	ILE	3.7
1	A	407	TRP	3.5
1	A	662	ALA	3.5
1	A	575	LEU	3.5
1	A	1006	TRP	3.4
1	A	700	VAL	3.4
1	A	661	GLY	3.4
1	A	129	ILE	3.4
1	A	954	GLY	3.2
1	A	660	GLY	3.2
1	A	604	PHE	3.1
2	B	215	ALA	3.1
1	A	673	ALA	3.0
1	A	122	TRP	3.0
2	B	128	ILE	3.0
1	A	574	TRP	3.0
2	B	117	VAL	2.9

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Mol	Chain	Res	Type	RSRZ
2	B	131	VAL	2.9
1	A	527	LYS	2.8
1	A	109	TYR	2.8
1	A	655	LEU	2.8
1	A	133	ILE	2.8
1	A	663	TYR	2.8
1	A	111	ALA	2.8
2	B	112	VAL	2.8
2	B	135	LEU	2.8
1	A	1008	HIS	2.7
1	A	112	PRO	2.7
2	B	93	ALA	2.6
1	A	150	LEU	2.6
1	A	950	PHE	2.6
1	A	599	ILE	2.6
1	A	525	GLY	2.6
1	A	664	PRO	2.6
2	B	90	LEU	2.6
1	A	630	ARG	2.6
2	B	88	VAL	2.5
1	A	156	ALA	2.5
1	A	179	SER	2.5
1	A	705	PHE	2.5
1	A	570	GLY	2.5
2	B	25	TRP	2.5
2	B	134	ARG	2.4
1	A	589	TRP	2.4
2	B	191	GLY	2.4
1	A	545	PHE	2.4
1	A	533	TRP	2.4
1	A	518	TYR	2.3
2	B	47	TYR	2.3
1	A	665	ALA	2.3
1	A	148	GLY	2.3
1	A	652	VAL	2.3
1	A	146	ALA	2.3
2	B	110	ALA	2.3
1	A	797	GLY	2.3
2	B	80	PRO	2.2
1	A	145	ASN	2.2
2	B	81	PRO	2.2
1	A	341	GLY	2.2

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Mol	Chain	Res	Type	RSRZ
2	B	86	ALA	2.2
1	A	140	SER	2.2
1	A	526	ARG	2.2
1	A	679	ASN	2.2
2	B	130	PRO	2.2
1	A	465	VAL	2.2
1	A	354	CYS	2.2
1	A	993	PRO	2.1
1	A	572	LEU	2.1
1	A	537	PHE	2.1
1	A	412	VAL	2.1
2	B	76	HIS	2.1
1	A	538	GLU	2.1
1	A	531	TYR	2.1
1	A	1005	VAL	2.1
2	B	214	VAL	2.1
1	A	98	GLY	2.0
1	A	141	PHE	2.0
1	A	151	VAL	2.0
1	A	519	LEU	2.0
1	A	607	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 [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
9	OXY	A	1110	2/2	0.89	0.16	32,32,32,44	0
7	GOL	A	1106	6/6	0.92	0.12	42,44,47,49	0

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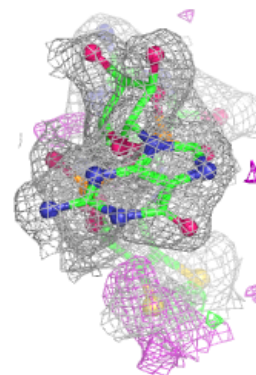
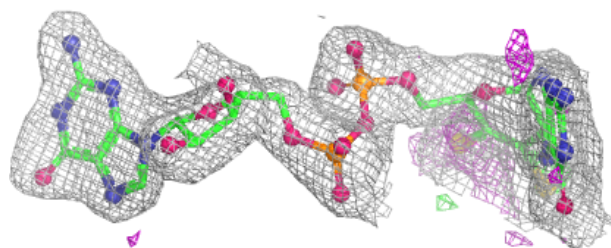
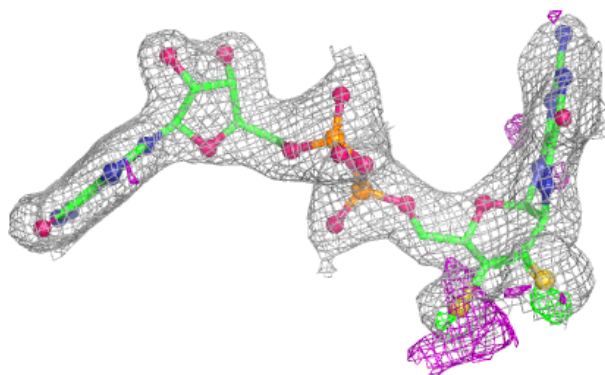
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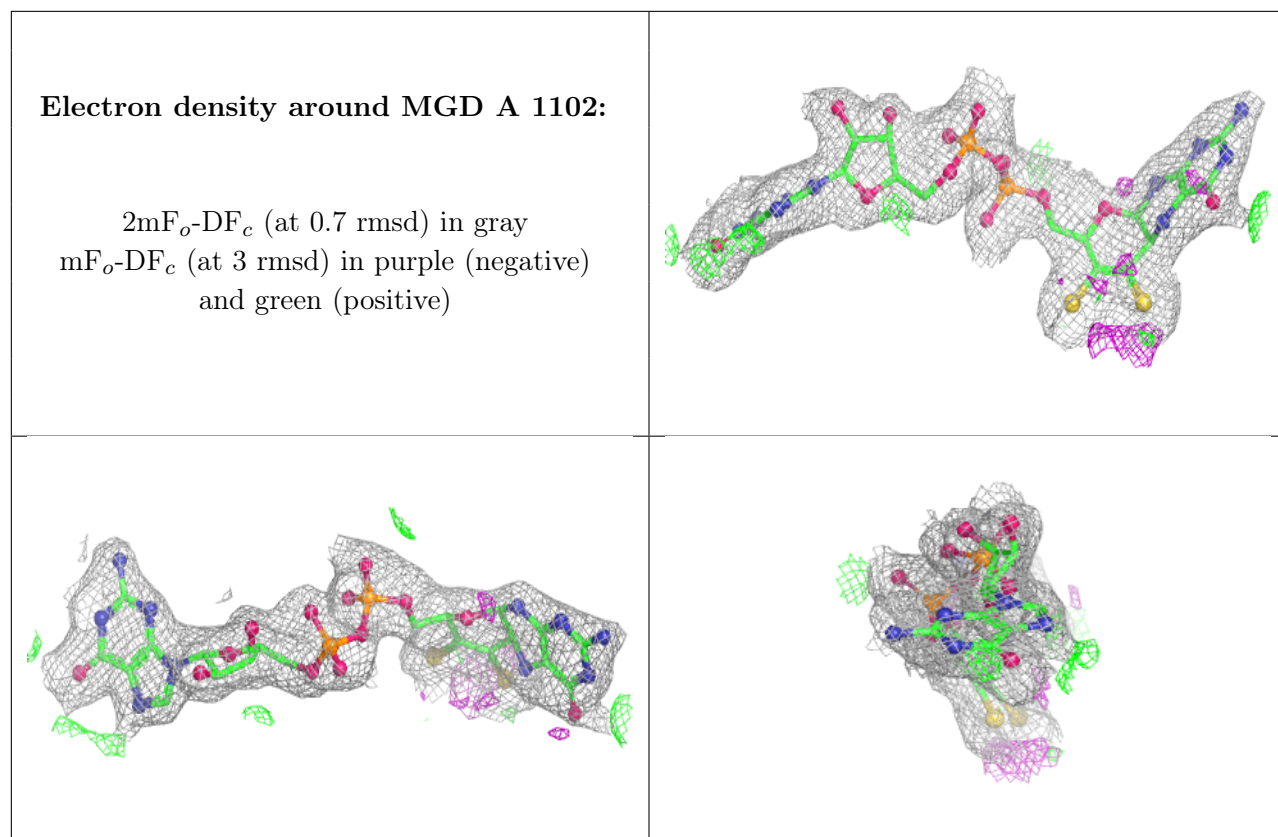
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
7	GOL	A	1107	6/6	0.92	0.16	36,44,45,48	0
8	EDO	A	1109	4/4	0.92	0.14	42,49,51,54	0
6	H2S	A	1105	1/1	0.92	0.19	58,58,58,58	0
8	EDO	A	1108	4/4	0.95	0.16	30,32,35,38	0
3	MGD	A	1101	47/47	0.96	0.07	22,27,32,36	0
3	MGD	A	1102	47/47	0.96	0.07	26,33,38,42	0
4	SF4	B	302	8/8	0.97	0.06	43,46,53,56	0
4	SF4	B	303	8/8	0.98	0.05	37,38,40,43	0
4	SF4	A	1103	8/8	0.99	0.04	24,27,27,27	0
4	SF4	B	301	8/8	0.99	0.05	28,29,30,31	0
5	W	A	1104	1/1	0.99	0.04	35,35,35,35	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 MGD A 1101:

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.