wwPDB X-ray Structure Validation Summary Report (i)

Feb 25, 2024 – 05:26 AM EST

PDB ID	:	5CH7
Title	:	Crystal structure of the perchlorate reductase PcrAB - Phe164 gate switch intermediate - from Azospira suillum PS
Authors	:	Tsai, C.-L.; Tainer, J.A.
Deposited on	:	2015-07-10
Resolution	:	2.20 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 (i) 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 (i)) were used in the production of this report:

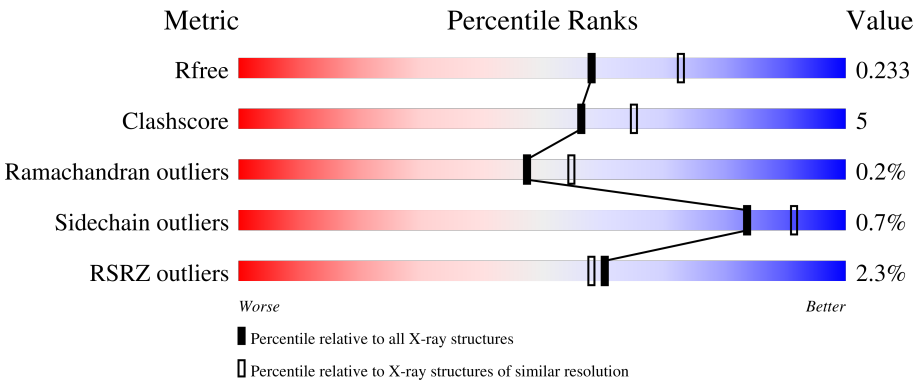
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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 2.20 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}	130704	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (2.20-2.20)

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 <=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	899	.% 90% 9% •
1	C	899	3% 85% 14% ••
1	E	899	2% 87% 11% •
2	B	333	.% 92% 7% •
2	D	333	8% 78% 19% ••

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Mol	Chain	Length	Quality of chain
2	F	333	87% 11% •

2 Entry composition (i)

There are 14 unique types of molecules in this entry. The entry contains 31660 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.

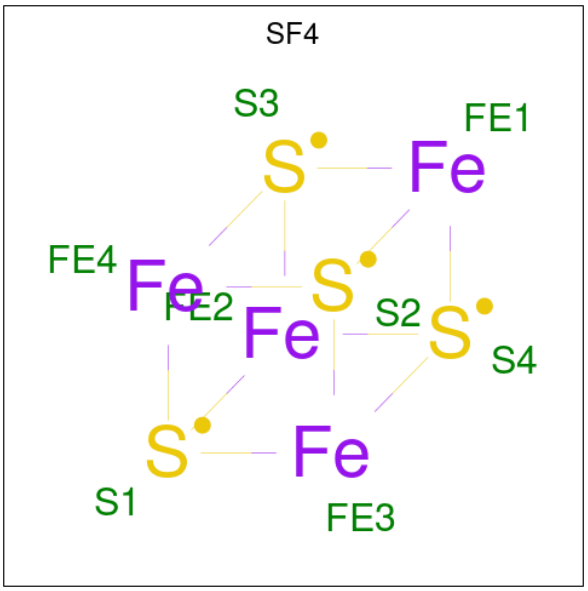
- Molecule 1 is a protein called DMSO reductase family type II enzyme, molybdopterin subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	894	7180	4586	1246	1310	38	0	3	0
1	C	891	7151	4568	1239	1306	38	0	1	0
1	E	892	7171	4583	1240	1310	38	0	3	0

- Molecule 2 is a protein called DMSO reductase family type II enzyme, iron-sulfur subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	329	2564	1627	447	465	25	0	0	0
2	D	327	2547	1616	444	463	24	0	0	0
2	F	328	2568	1631	448	465	24	0	2	0

- Molecule 3 is IRON/SULFUR CLUSTER (three-letter code: SF4) (formula: Fe_4S_4).

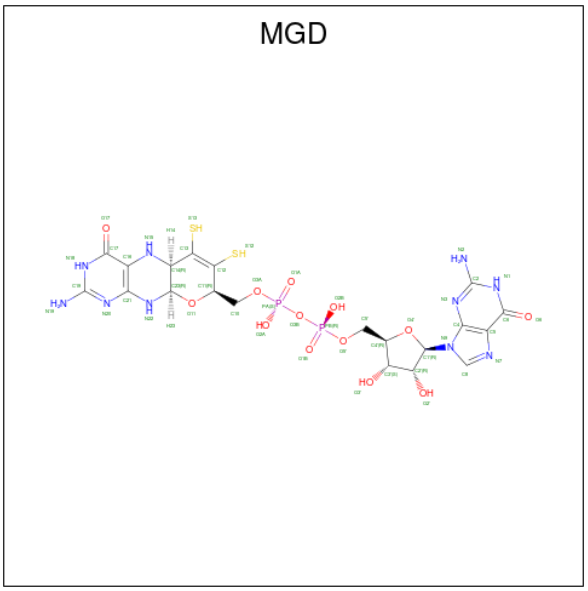


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	Fe	S		
3	A	1	8	4	4	0	0
3	B	1	8	4	4	0	0
3	B	1	8	4	4	0	0
3	B	1	8	4	4	0	0
3	C	1	8	4	4	0	0
3	D	1	8	4	4	0	0
3	D	1	8	4	4	0	0
3	D	1	8	4	4	0	0
3	E	1	8	4	4	0	0
3	F	1	8	4	4	0	0
3	F	1	8	4	4	0	0
3	F	1	8	4	4	0	0

- Molecule 4 is MOLYBDENUM ATOM (three-letter code: MO) (formula: Mo).

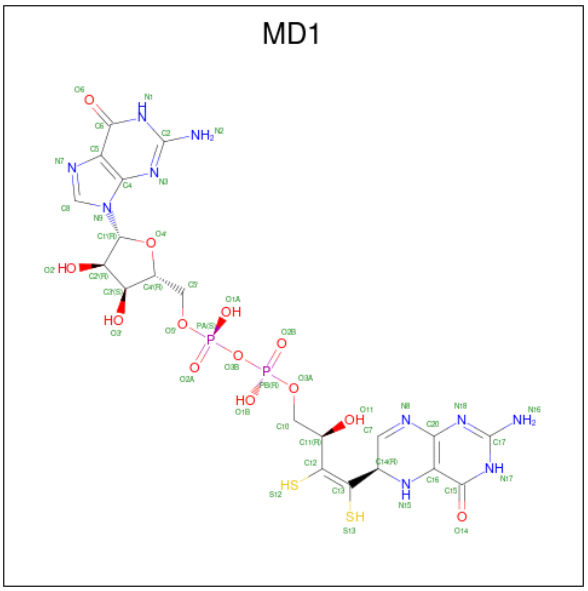
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Mo		
4	A	1	1	1	0	0
			Total	Mo		
4	C	1	1	1	0	0
			Total	Mo		
4	E	1	1	1	0	0

- Molecule 5 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 (three-letter code: MGD) (formula: $C_{20}H_{26}N_{10}O_{13}P_2S_2$).



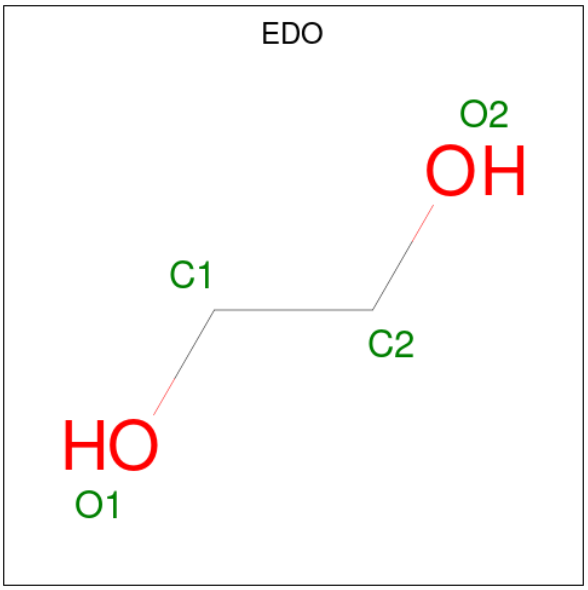
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
			Total	C	N	O	P	S		
5	A	1	47	20	10	13	2	2	0	0
			Total	C	N	O	P	S		
5	C	1	47	20	10	13	2	2	0	0
			Total	C	N	O	P	S		
5	E	1	47	20	10	13	2	2	0	0

- Molecule 6 is PHOSPHORIC ACID 4-(2-AMINO-4-OXO-3,4,5,6,-TETRAHYDRO-PTERIDIN-6-YL)-2-HYDROXY-3,4-DIMERCAPTO-BUT-3-EN-YL ESTER GUANYLATE ESTER (three-letter code: MD1) (formula: $C_{20}H_{26}N_{10}O_{13}P_2S_2$).



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

- Molecule 7 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).



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

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
7	A	1	4	2	2	0	0
			Total	C	O		
7	A	1	4	2	2	0	0
			Total	C	O		
7	A	1	4	2	2	0	0
			Total	C	O		
7	B	1	4	2	2	0	0
			Total	C	O		
7	B	1	4	2	2	0	0
			Total	C	O		
7	B	1	4	2	2	0	0
			Total	C	O		
7	C	1	4	2	2	0	0
			Total	C	O		
7	C	1	4	2	2	0	0
			Total	C	O		
7	D	1	4	2	2	0	0
			Total	C	O		
7	D	1	4	2	2	0	0
			Total	C	O		
7	E	1	4	2	2	0	0
			Total	C	O		
7	E	1	4	2	2	0	0
			Total	C	O		
7	E	1	4	2	2	0	0
			Total	C	O		
7	F	1	4	2	2	0	0
			Total	C	O		
7	F	1	4	2	2	0	0

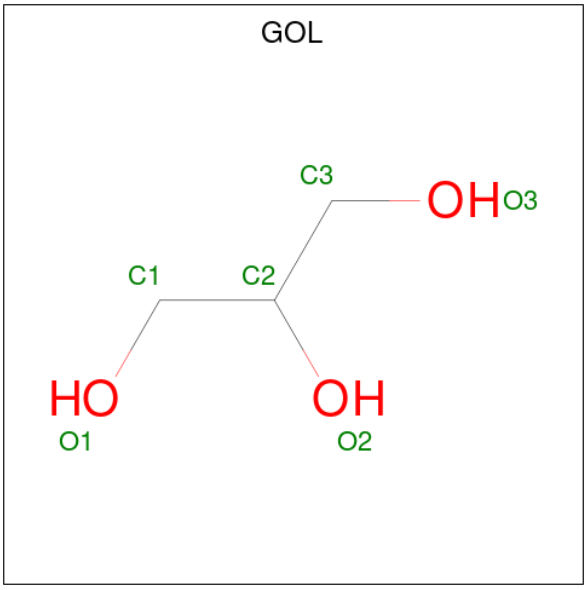
- Molecule 8 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Na		
8	A	1	1	1	0	0
			Total	Na		
8	C	1	1	1	0	0
			Total	Na		
8	E	1	1	1	0	0
			Total	Na		
8	F	1	1	1	0	0

- Molecule 9 is ZINC ION (three-letter code: ZN) (formula: Zn).

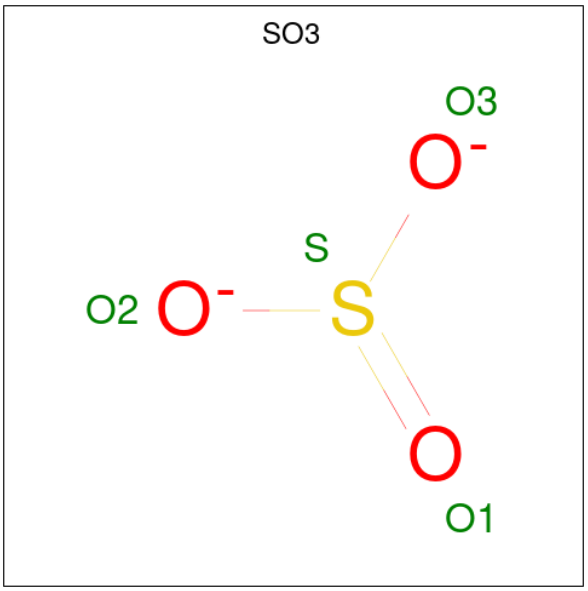
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Zn		
9	A	1	1	1	0	0
9	C	1	1	1	0	0
9	E	1	1	1	0	0

- Molecule 10 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



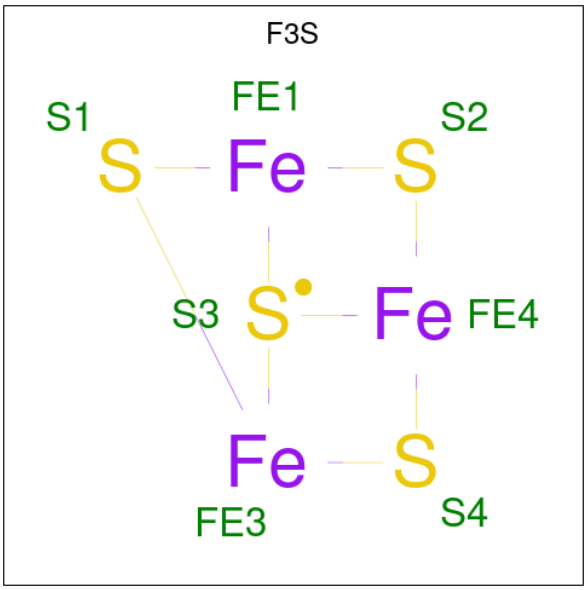
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
10	A	1	6	3	3	0	0

- Molecule 11 is SULFITE ION (three-letter code: SO3) (formula: O_3S).



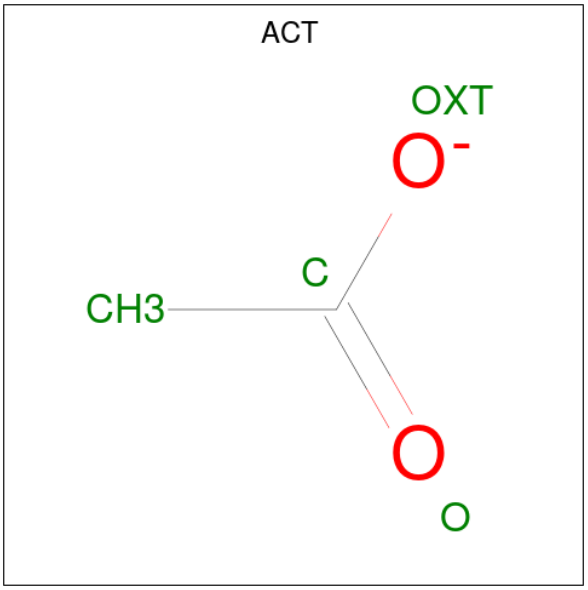
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
11	A	1	Total O S 4 3 1	0	0
11	A	1	Total O S 4 3 1	0	0
11	C	1	Total O S 4 3 1	0	0
11	C	1	Total O S 4 3 1	0	0
11	E	1	Total O S 4 3 1	0	0

- Molecule 12 is FE3-S4 CLUSTER (three-letter code: F3S) (formula: Fe_3S_4).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	Fe	S		
12	B	1	7	3	4	0	0
			Total	Fe	S		
12	D	1	7	3	4	0	0
			Total	Fe	S		
12	F	1	7	3	4	0	0

- Molecule 13 is ACETATE ION (three-letter code: ACT) (formula: $C_2H_3O_2$).



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

- Molecule 14 is water.

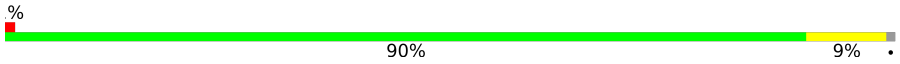
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
14	A	531	531	531	0	0
			Total	O		
14	B	273	273	273	0	0
			Total	O		
14	C	362	362	362	0	0
			Total	O		
14	D	92	92	92	0	0
			Total	O		
14	E	520	520	520	0	0
			Total	O		
14	F	198	198	198	0	0

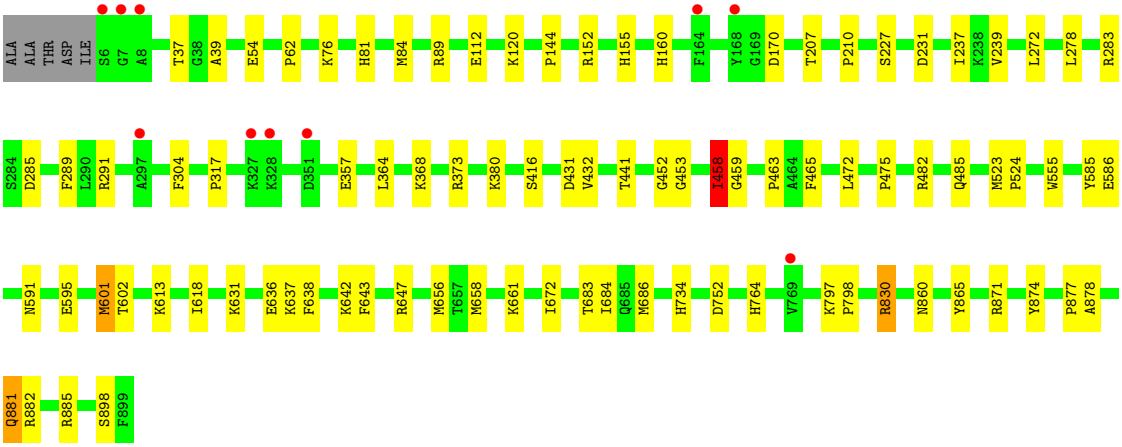
3 Residue-property plots (i)

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: DMSO reductase family type II enzyme, molybdopterin subunit

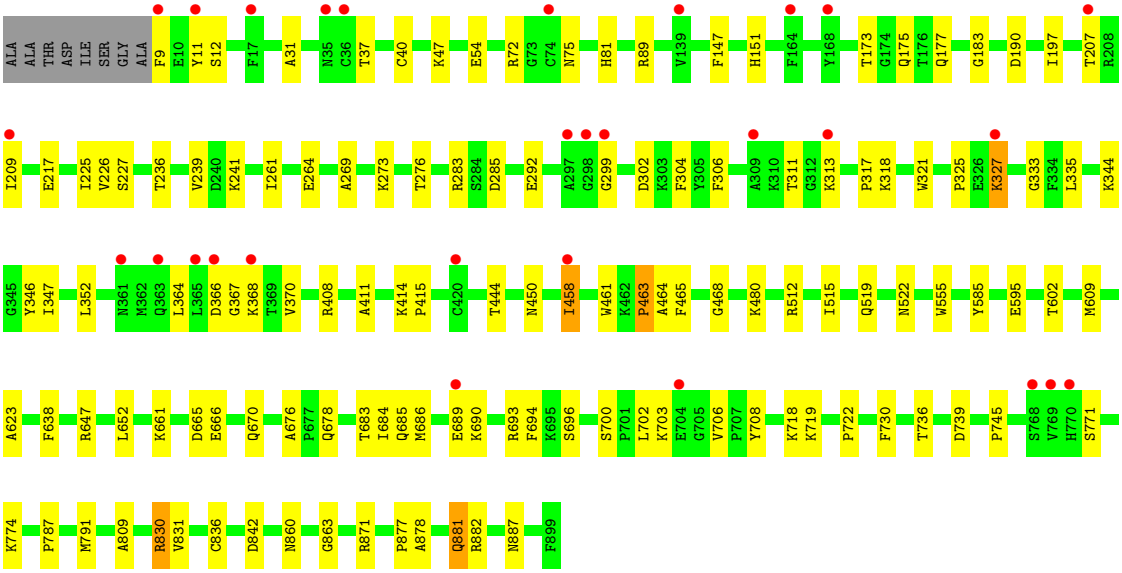
Chain A:





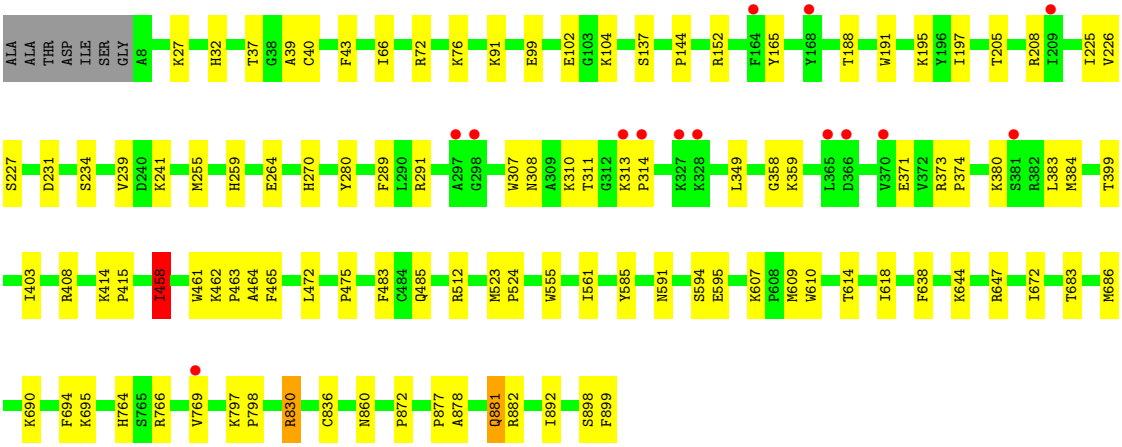
• Molecule 1: DMSO reductase family type II enzyme, molybdopterin subunit

Chain C:



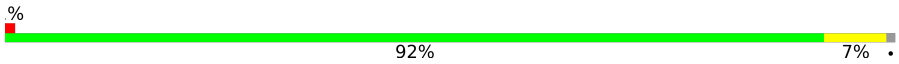
• Molecule 1: DMSO reductase family type II enzyme, molybdopterin subunit

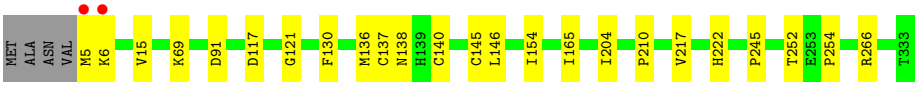
Chain E:



• Molecule 2: DMSO reductase family type II enzyme, iron-sulfur subunit

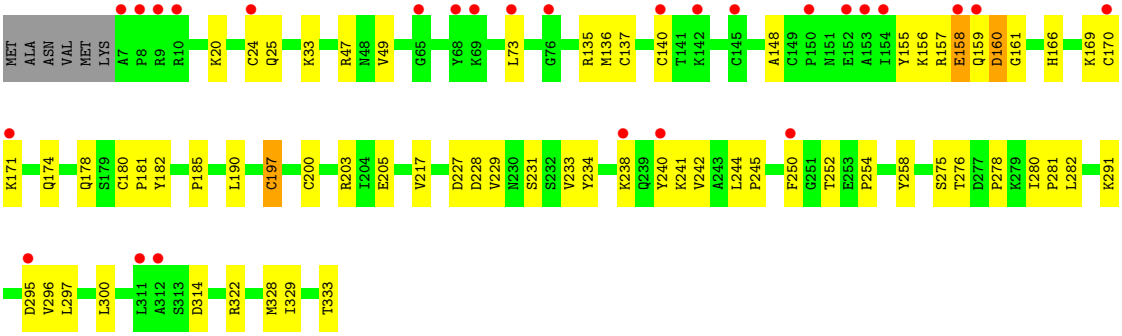
Chain B:





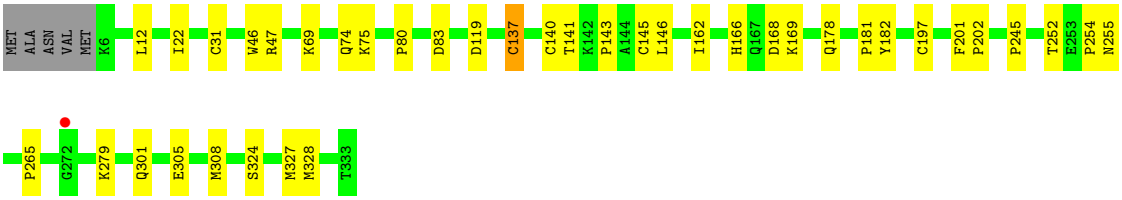
• Molecule 2: DMSO reductase family type II enzyme, iron-sulfur subunit

Chain D:



• Molecule 2: DMSO reductase family type II enzyme, iron-sulfur subunit

Chain F:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	132.88Å 175.67Å 193.28Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.38 – 2.20 48.38 – 2.20	Depositor EDS
% Data completeness (in resolution range)	99.9 (48.38-2.20) 99.9 (48.38-2.20)	Depositor EDS
R_{merge}	0.20	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.33 (at 2.20Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.178 , 0.233 0.179 , 0.233	Depositor DCC
R_{free} test set	11303 reflections (4.95%)	wwPDB-VP
Wilson B-factor (Å^2)	29.6	Xtriage
Anisotropy	0.187	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.32 , 42.1	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	31660	wwPDB-VP
Average B, all atoms (Å^2)	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.07% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ 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: SO3, MGD, MO, NA, F3S, SF4, GOL, EDO, MD1, ZN, ACT

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	0.56	0/7399	0.65	2/10039 (0.0%)
1	C	0.50	0/7364	0.61	1/9993 (0.0%)
1	E	0.56	0/7391	0.64	2/10030 (0.0%)
2	B	0.60	0/2632	0.67	1/3567 (0.0%)
2	D	0.43	0/2615	0.59	0/3546
2	F	0.55	0/2642	0.65	0/3580
All	All	0.54	0/30043	0.63	6/40755 (0.0%)

There are no bond length outliers.

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	830	ARG	NE-CZ-NH2	-7.18	116.71	120.30
1	E	830	ARG	NE-CZ-NH2	-6.67	116.97	120.30
1	A	830	ARG	NE-CZ-NH1	5.89	123.25	120.30
2	B	117	ASP	CB-CG-OD1	5.62	123.36	118.30
1	E	830	ARG	NE-CZ-NH1	5.22	122.91	120.30

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	7180	0	7003	61	0
1	C	7151	0	6964	80	0
1	E	7171	0	6984	73	0
2	B	2564	0	2534	14	0
2	D	2547	0	2513	45	0
2	F	2568	0	2546	27	0
3	A	8	0	0	0	0
3	B	24	0	0	0	0
3	C	8	0	0	0	0
3	D	24	0	0	1	0
3	E	8	0	0	0	0
3	F	24	0	0	1	0
4	A	1	0	0	0	0
4	C	1	0	0	0	0
4	E	1	0	0	0	0
5	A	47	0	21	2	0
5	C	47	0	20	2	0
5	E	47	0	20	0	0
6	A	47	0	22	1	0
6	C	47	0	22	1	0
6	E	47	0	22	1	0
7	A	16	0	24	1	0
7	B	12	0	18	1	0
7	C	8	0	12	0	0
7	D	8	0	12	0	0
7	E	12	0	18	2	0
7	F	8	0	12	0	0
8	A	1	0	0	0	0
8	C	1	0	0	0	0
8	E	1	0	0	0	0
8	F	1	0	0	0	0
9	A	1	0	0	0	0
9	C	1	0	0	0	0
9	E	1	0	0	0	0
10	A	6	0	8	1	0
11	A	8	0	0	0	0
11	C	8	0	0	0	0
11	E	4	0	0	0	0
12	B	7	0	0	0	0
12	D	7	0	0	0	0
12	F	7	0	0	0	0
13	C	4	0	3	0	0
14	A	531	0	0	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
14	B	273	0	0	1	0
14	C	362	0	0	7	0
14	D	92	0	0	1	0
14	E	520	0	0	12	0
14	F	198	0	0	2	0
All	All	31660	0	28778	291	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 5.

The worst 5 of 291 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:89:ARG:NH1	14:A:1101:HOH:O	1.94	1.01
1:E:226:VAL:HG22	1:E:241:LYS:HB3	1.56	0.87
1:E:308:ASN:HB3	1:E:311:THR:HG22	1.59	0.83
1:A:482:ARG:HB3	1:A:523:MET:HE3	1.65	0.79
1:E:860:ASN:HD22	1:E:878:ALA:H	1.32	0.77

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	895/899 (100%)	860 (96%)	33 (4%)	2 (0%)	47	55
1	C	890/899 (99%)	838 (94%)	49 (6%)	3 (0%)	41	46
1	E	893/899 (99%)	850 (95%)	41 (5%)	2 (0%)	47	55
2	B	327/333 (98%)	317 (97%)	9 (3%)	1 (0%)	41	46
2	D	325/333 (98%)	303 (93%)	21 (6%)	1 (0%)	41	46

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	F	328/333 (98%)	313 (95%)	15 (5%)	0	100	100
All	All	3658/3696 (99%)	3481 (95%)	168 (5%)	9 (0%)	47	55

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	458	ILE
1	C	458	ILE
2	D	205	GLU
1	E	458	ILE
2	B	6	LYS

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	768/768 (100%)	762 (99%)	6 (1%)	81	90
1	C	765/768 (100%)	758 (99%)	7 (1%)	78	88
1	E	767/768 (100%)	762 (99%)	5 (1%)	84	91
2	B	278/281 (99%)	278 (100%)	0	100	100
2	D	276/281 (98%)	273 (99%)	3 (1%)	73	85
2	F	279/281 (99%)	278 (100%)	1 (0%)	91	96
All	All	3133/3147 (100%)	3111 (99%)	22 (1%)	84	91

5 of 22 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	D	160	ASP
1	E	165	TYR
1	E	137	SER
1	E	458	ILE
1	C	11	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 6 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	881	GLN
1	E	860	ASN
1	E	881	GLN
1	A	881	GLN
1	A	860	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 monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 54 ligands modelled in this entry, 10 are monoatomic - leaving 44 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	$\#\|Z\| > 2$
7	EDO	A	1012	-	3,3,3	0.51	0	2,2,2	0.24	0
6	MD1	E	1004	4	39,51,51	3.73	11 (28%)	38,78,78	1.93	13 (34%)
7	EDO	C	1005	-	3,3,3	0.77	0	2,2,2	0.36	0
7	EDO	E	1006	-	3,3,3	0.89	0	2,2,2	0.43	0
12	F3S	F	401	2	0,9,9	-	-	-		
3	SF4	D	404	2	0,12,12	-	-	-		
7	EDO	E	1007	-	3,3,3	0.55	0	2,2,2	0.32	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
11	SO3	E	1008	9	1,3,3	1.21	0	0,3,3	-	-
7	EDO	F	405	-	3,3,3	0.62	0	2,2,2	0.36	0
6	MD1	C	1004	4	39,51,51	3.98	9 (23%)	38,78,78	1.88	11 (28%)
7	EDO	B	406	-	3,3,3	0.57	0	2,2,2	0.31	0
10	GOL	A	1010	-	5,5,5	0.27	0	5,5,5	0.62	0
3	SF4	B	402	2	0,12,12	-	-	-		
3	SF4	D	403	2	0,12,12	-	-	-		
7	EDO	C	1006	-	3,3,3	0.57	0	2,2,2	0.26	0
7	EDO	E	1005	-	3,3,3	0.74	0	2,2,2	0.47	0
12	F3S	D	402	2	0,9,9	-	-	-		
13	ACT	C	1008	-	3,3,3	0.76	0	3,3,3	1.06	0
5	MGD	A	1003	4	41,52,52	5.66	25 (60%)	40,81,81	3.00	14 (35%)
7	EDO	A	1007	-	3,3,3	0.57	0	2,2,2	0.22	0
3	SF4	C	1001	1	0,12,12	-	-	-		
3	SF4	B	404	2	0,12,12	-	-	-		
3	SF4	F	404	2	0,12,12	-	-	-		
3	SF4	D	405	2	0,12,12	-	-	-		
3	SF4	A	1001	1	0,12,12	-	-	-		
3	SF4	F	403	2	0,12,12	-	-	-		
5	MGD	E	1003	4	41,52,52	5.53	25 (60%)	40,81,81	2.51	9 (22%)
7	EDO	D	406	-	3,3,3	0.50	0	2,2,2	0.37	0
12	F3S	B	401	2	0,9,9	-	-	-		
7	EDO	A	1005	-	3,3,3	0.80	0	2,2,2	0.39	0
3	SF4	E	1001	1	0,12,12	-	-	-		
11	SO3	C	1009	-	1,3,3	0.77	0	0,3,3	-	-
7	EDO	B	405	-	3,3,3	0.30	0	2,2,2	0.67	0
7	EDO	D	401	-	3,3,3	0.71	0	2,2,2	0.12	0
11	SO3	A	1013	-	1,3,3	0.88	0	0,3,3	-	-
7	EDO	F	406	-	3,3,3	0.52	0	2,2,2	0.49	0
5	MGD	C	1003	4	41,52,52	5.60	27 (65%)	40,81,81	2.64	13 (32%)
7	EDO	B	407	-	3,3,3	0.76	0	2,2,2	0.23	0
6	MD1	A	1004	4	39,51,51	4.00	11 (28%)	38,78,78	2.03	12 (31%)
7	EDO	A	1006	-	3,3,3	0.54	0	2,2,2	0.31	0
3	SF4	F	402	2	0,12,12	-	-	-		
3	SF4	B	403	2	0,12,12	-	-	-		
11	SO3	A	1011	9	1,3,3	1.05	0	0,3,3	-	-
11	SO3	C	1010	9	1,3,3	0.81	0	0,3,3	-	-

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
7	EDO	A	1012	-	-	0/1/1/1	-
6	MD1	E	1004	4	-	2/18/59/59	0/5/5/5
7	EDO	C	1005	-	-	0/1/1/1	-
7	EDO	E	1006	-	-	0/1/1/1	-
12	F3S	F	401	2	-	-	0/3/3/3
3	SF4	D	404	2	-	-	0/6/5/5
7	EDO	E	1007	-	-	0/1/1/1	-
7	EDO	F	405	-	-	0/1/1/1	-
6	MD1	C	1004	4	-	4/18/59/59	0/5/5/5
7	EDO	B	406	-	-	0/1/1/1	-
10	GOL	A	1010	-	-	0/4/4/4	-
3	SF4	B	402	2	-	-	0/6/5/5
3	SF4	D	403	2	-	-	0/6/5/5
7	EDO	C	1006	-	-	0/1/1/1	-
7	EDO	E	1005	-	-	0/1/1/1	-
12	F3S	D	402	2	-	-	0/3/3/3
7	EDO	A	1007	-	-	1/1/1/1	-
5	MGD	A	1003	4	-	2/18/66/66	0/6/6/6
3	SF4	C	1001	1	-	-	0/6/5/5
3	SF4	B	404	2	-	-	0/6/5/5
3	SF4	F	404	2	-	-	0/6/5/5
3	SF4	D	405	2	-	-	0/6/5/5
3	SF4	A	1001	1	-	-	0/6/5/5
5	MGD	E	1003	4	-	2/18/66/66	0/6/6/6
7	EDO	D	406	-	-	0/1/1/1	-
3	SF4	F	403	2	-	-	0/6/5/5
12	F3S	B	401	2	-	-	0/3/3/3
7	EDO	A	1005	-	-	0/1/1/1	-
3	SF4	E	1001	1	-	-	0/6/5/5
7	EDO	D	401	-	-	0/1/1/1	-
7	EDO	B	405	-	-	0/1/1/1	-
7	EDO	F	406	-	-	0/1/1/1	-
7	EDO	B	407	-	-	0/1/1/1	-
5	MGD	C	1003	4	-	0/18/66/66	0/6/6/6
6	MD1	A	1004	4	-	4/18/59/59	0/5/5/5
7	EDO	A	1006	-	-	0/1/1/1	-
3	SF4	F	402	2	-	-	0/6/5/5
3	SF4	B	403	2	-	-	0/6/5/5

The worst 5 of 108 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	1003	MGD	C23-C14	-19.14	1.38	1.53
5	E	1003	MGD	C23-C14	-19.03	1.38	1.53
5	C	1003	MGD	C23-C14	-18.51	1.38	1.53
5	E	1003	MGD	C16-C21	14.97	1.64	1.38
5	A	1003	MGD	C16-C21	14.72	1.63	1.38

The worst 5 of 72 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	A	1003	MGD	O11-C23-N22	-15.12	93.03	108.57
5	C	1003	MGD	O11-C23-N22	-12.58	95.64	108.57
5	E	1003	MGD	O11-C23-N22	-12.27	95.95	108.57
6	C	1004	MD1	O11-C11-C12	-5.20	101.68	111.05
6	E	1004	MD1	N3-C2-N1	-4.96	120.61	127.22

There are no chirality outliers.

5 of 15 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	1003	MGD	C5'-O5'-PB-O1B
6	C	1004	MD1	C10-O3A-PB-O1B
5	A	1003	MGD	C5'-O5'-PB-O3B
6	C	1004	MD1	C10-O3A-PB-O3B
6	A	1004	MD1	C10-O3A-PB-O2B

There are no ring outliers.

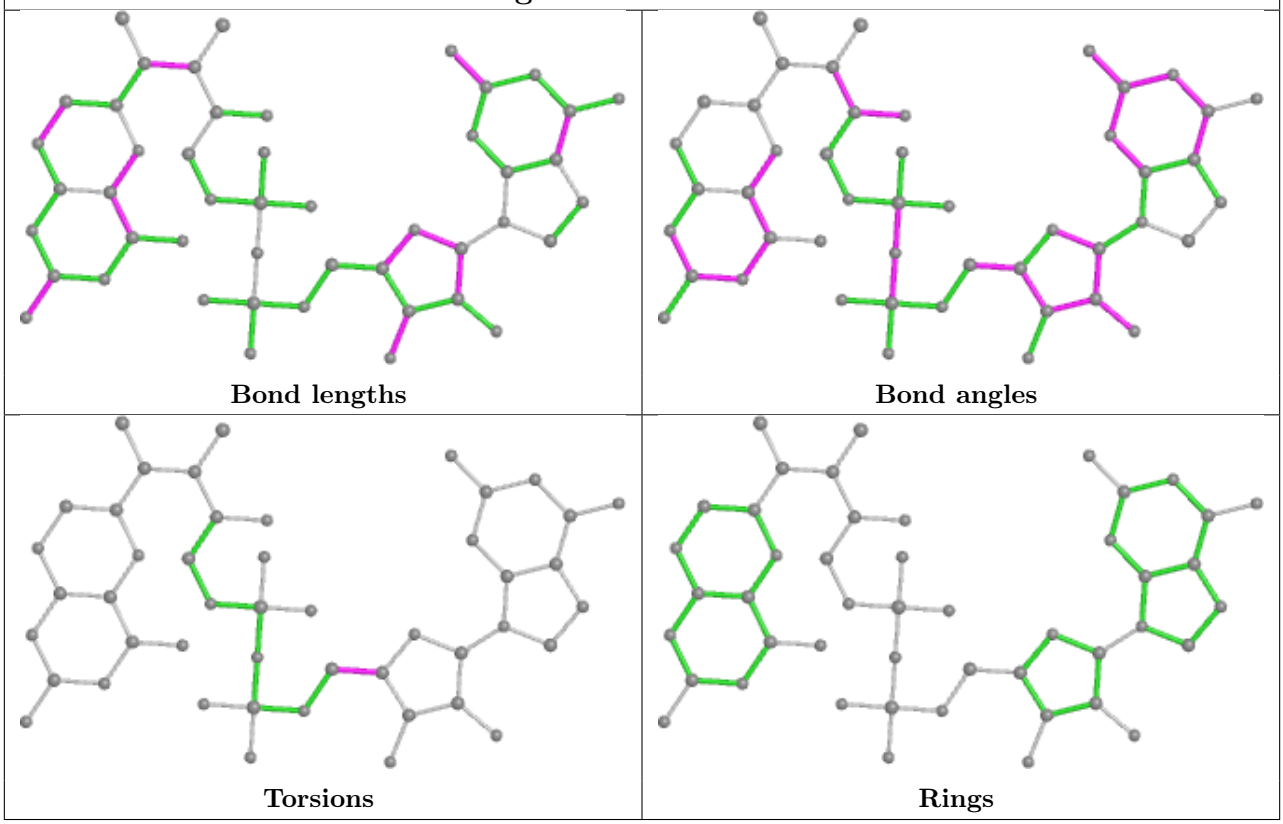
11 monomers are involved in 14 short contacts:

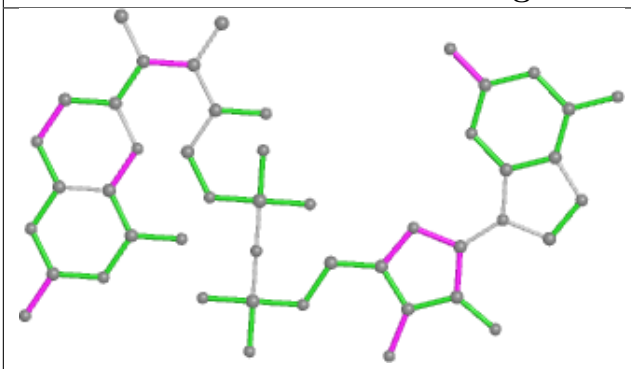
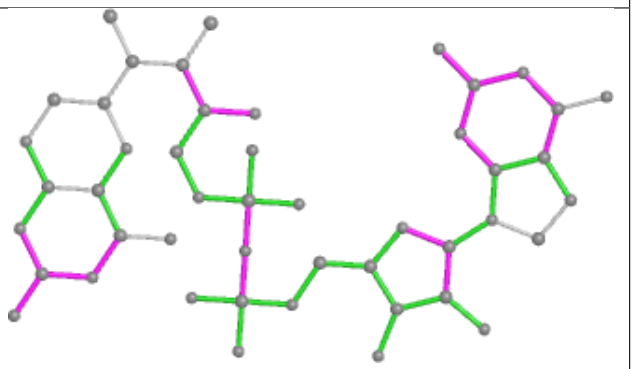
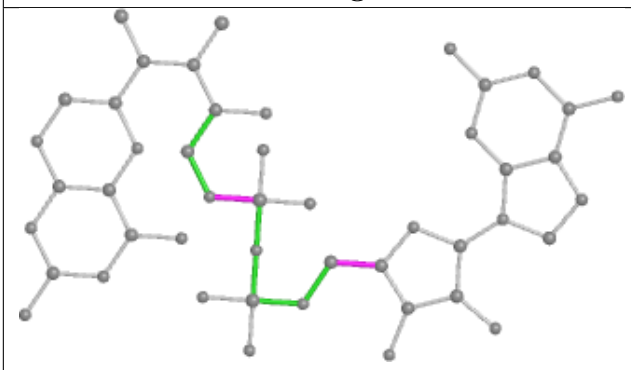
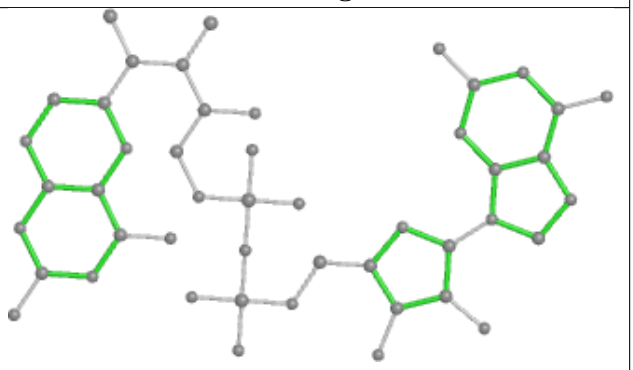
Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	A	1012	EDO	1	0
6	E	1004	MD1	1	0
7	E	1006	EDO	2	0
6	C	1004	MD1	1	0
10	A	1010	GOL	1	0
5	A	1003	MGD	2	0
3	F	404	SF4	1	0
3	D	405	SF4	1	0
5	C	1003	MGD	2	0
7	B	407	EDO	1	0
6	A	1004	MD1	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths,

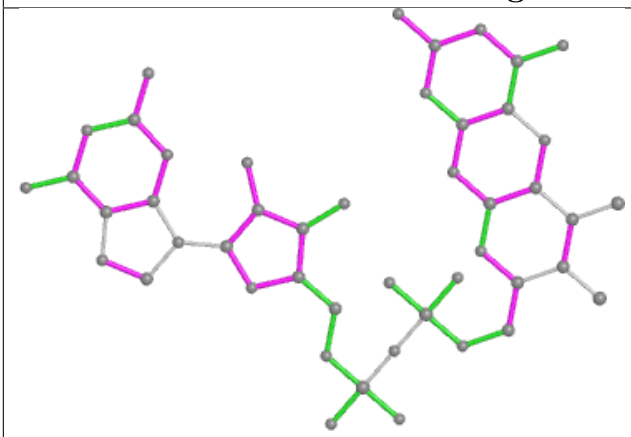
bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 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.

Ligand MD1 E 1004

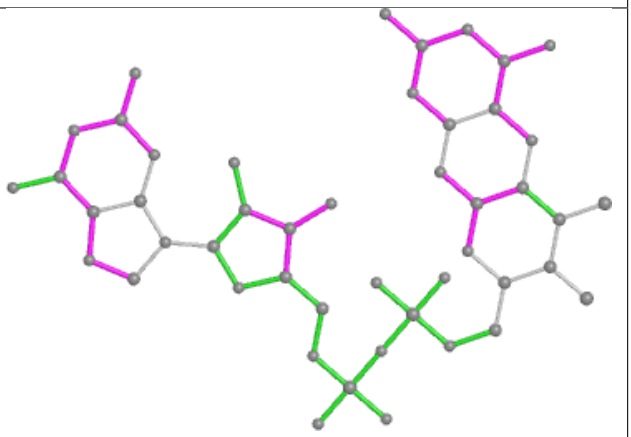


Ligand MD1 C 1004	
 Bond lengths	 Bond angles
 Torsions	 Rings

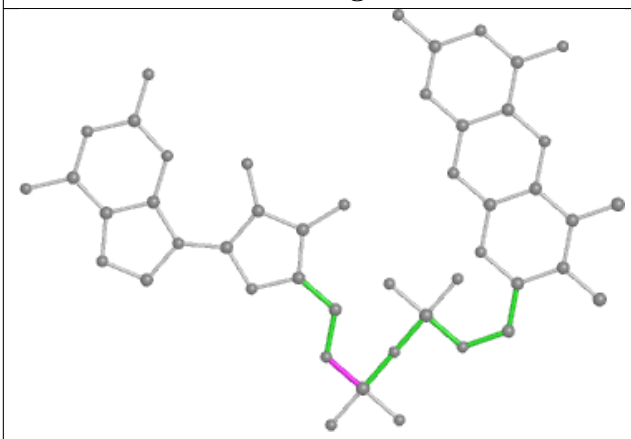
Ligand MGD A 1003



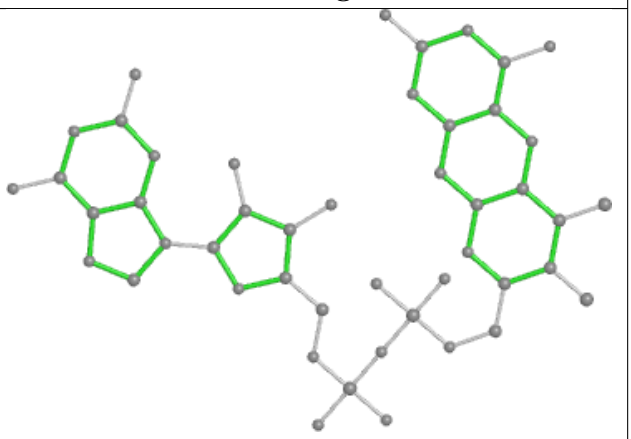
Bond lengths



Bond angles

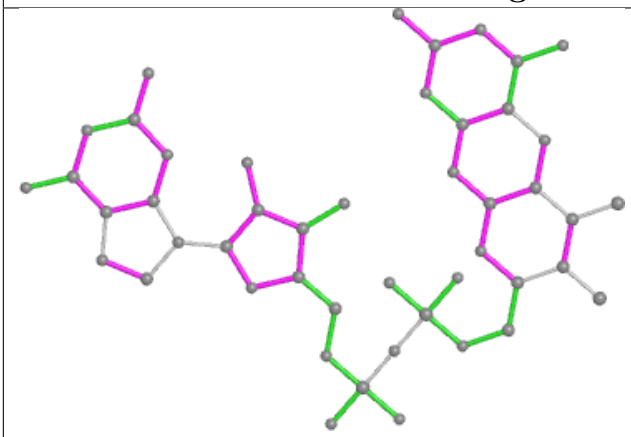


Torsions



Rings

Ligand MGD E 1003



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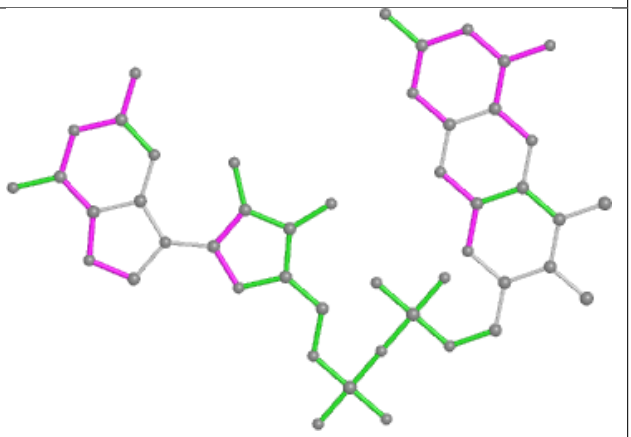
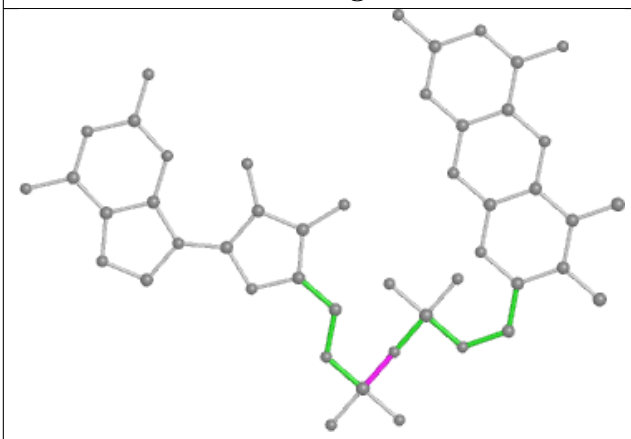
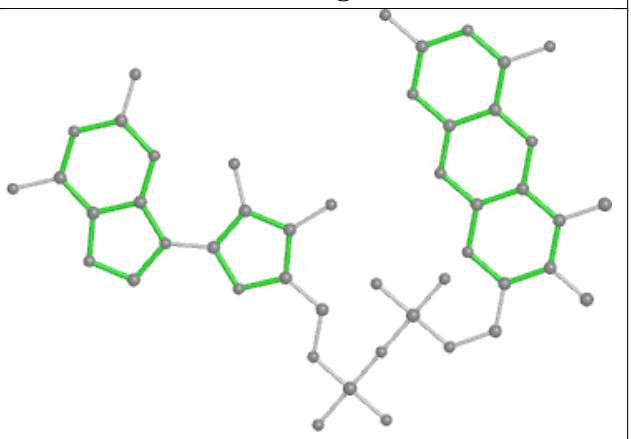


Bond angles

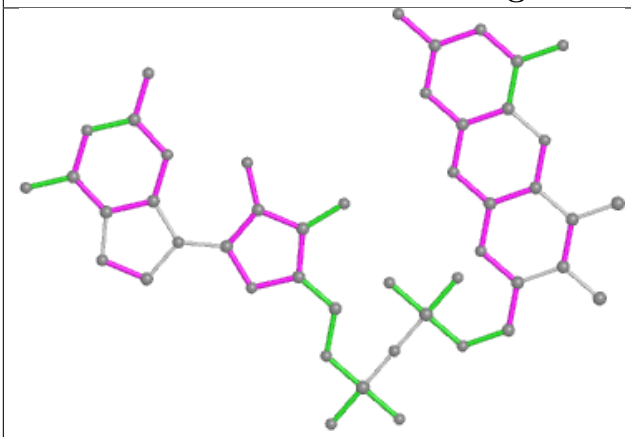


Torsions

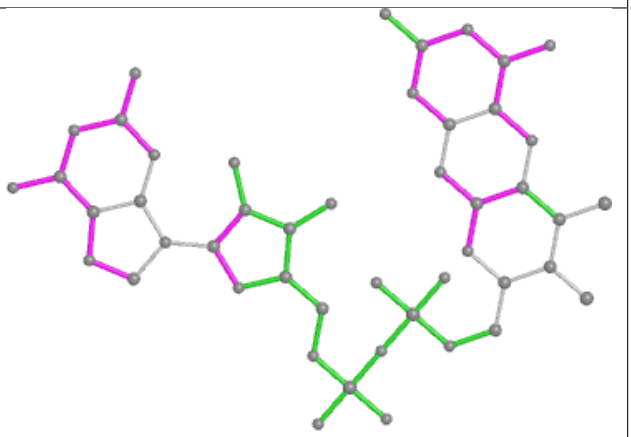


Rings

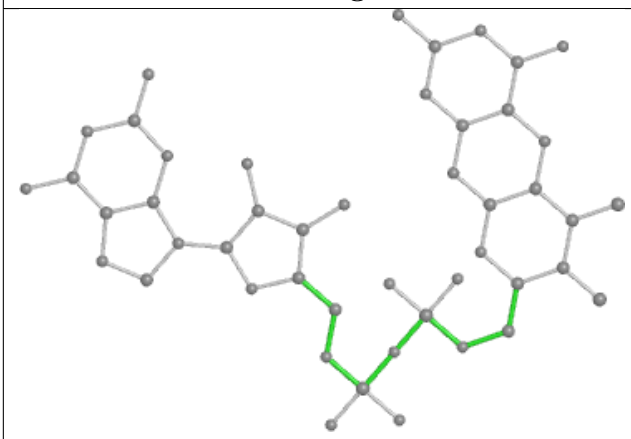
Ligand MGD C 1003



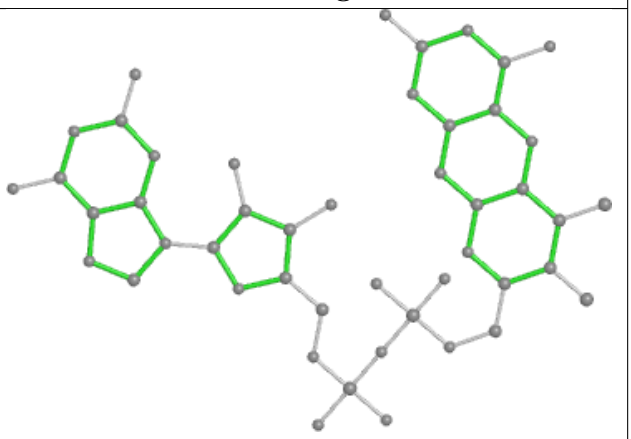
Bond lengths



Bond angles

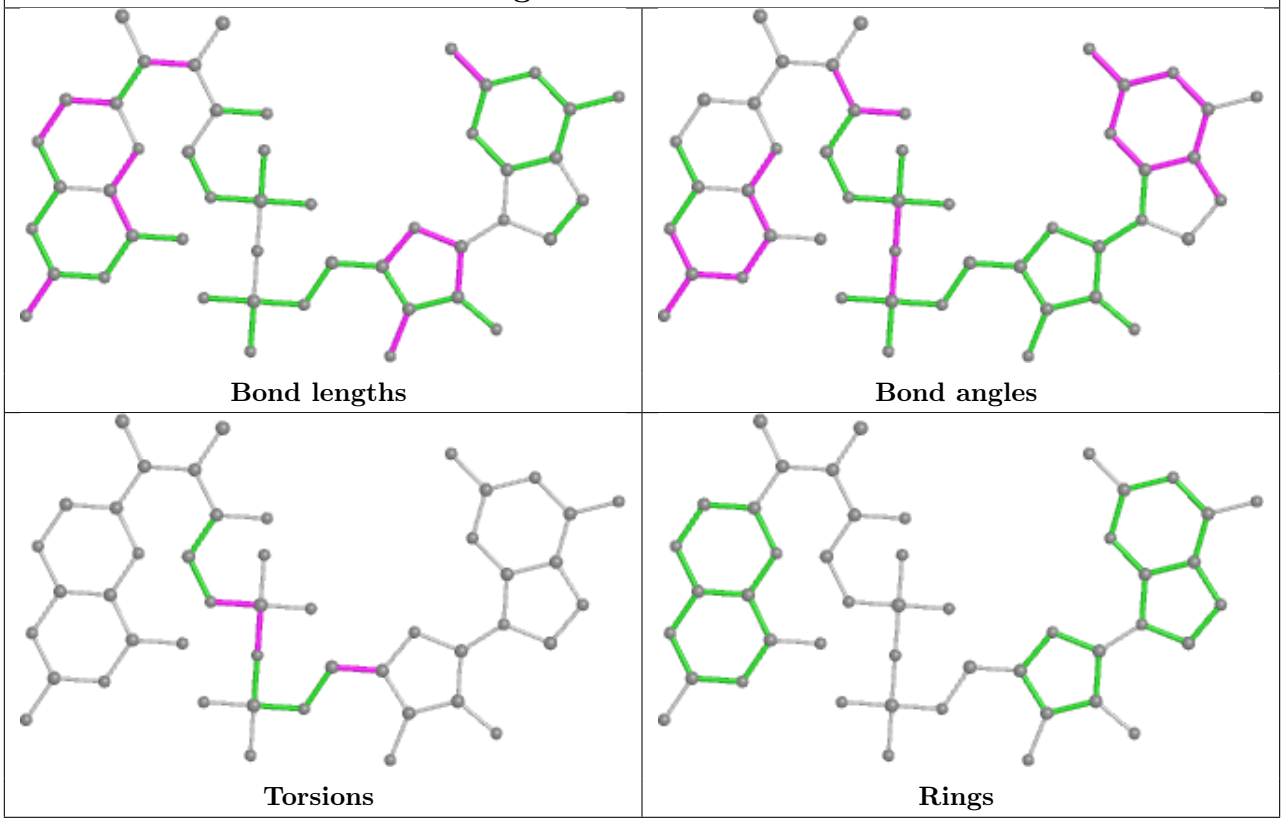


Torsions



Rings

Ligand MD1 A 1004



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	894/899 (99%)	-0.36	10 (1%)	80	79	16, 30, 49, 68	0
1	C	891/899 (99%)	-0.04	29 (3%)	46	44	19, 39, 62, 97	0
1	E	892/899 (99%)	-0.34	14 (1%)	72	70	17, 30, 51, 70	0
2	B	329/333 (98%)	-0.62	2 (0%)	89	88	17, 24, 38, 64	0
2	D	327/333 (98%)	0.43	27 (8%)	11	10	25, 54, 71, 89	0
2	F	328/333 (98%)	-0.36	1 (0%)	94	93	18, 32, 50, 66	0
All	All	3661/3696 (99%)	-0.23	83 (2%)	60	58	16, 32, 59, 97	0

The worst 5 of 83 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	11	TYR	5.5
1	A	8	ALA	5.2
1	C	9	PHE	4.7
1	C	164[A]	PHE	4.6
1	E	164[A]	PHE	4.2

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 monosaccharides 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(Å^2)	Q<0.9
11	SO3	E	1008	4/4	0.44	0.25	34,38,48,71	0
7	EDO	E	1006	4/4	0.71	0.23	34,35,38,41	0
7	EDO	C	1005	4/4	0.80	0.27	33,36,45,45	0
11	SO3	C	1010	4/4	0.83	0.17	61,62,70,83	0
11	SO3	A	1011	4/4	0.83	0.14	38,39,51,70	0
10	GOL	A	1010	6/6	0.84	0.21	35,42,48,48	0
7	EDO	B	407	4/4	0.85	0.23	34,36,37,42	0
7	EDO	F	406	4/4	0.88	0.23	39,42,43,44	0
7	EDO	E	1007	4/4	0.89	0.16	28,40,44,49	0
13	ACT	C	1008	4/4	0.89	0.14	31,36,40,44	0
3	SF4	D	403	8/8	0.90	0.06	39,45,57,57	0
7	EDO	A	1005	4/4	0.90	0.20	25,26,31,39	0
11	SO3	C	1009	4/4	0.91	0.29	43,48,50,68	0
7	EDO	B	406	4/4	0.91	0.14	32,34,40,41	0
7	EDO	A	1006	4/4	0.92	0.15	32,34,35,37	0
11	SO3	A	1013	4/4	0.93	0.35	38,42,42,57	0
3	SF4	D	405	8/8	0.94	0.10	34,48,53,54	0
7	EDO	E	1005	4/4	0.94	0.11	16,20,23,23	0
7	EDO	A	1012	4/4	0.94	0.18	21,22,27,29	0
8	NA	C	1007	1/1	0.95	0.21	26,26,26,26	0
12	F3S	D	402	7/7	0.95	0.05	53,58,64,74	0
7	EDO	A	1007	4/4	0.95	0.11	26,28,29,32	0
7	EDO	C	1006	4/4	0.96	0.08	20,24,25,27	0
7	EDO	D	406	4/4	0.96	0.15	30,36,37,38	0
3	SF4	F	404	8/8	0.96	0.10	26,28,29,29	0
5	MGD	C	1003	47/47	0.96	0.21	21,28,32,33	0
3	SF4	F	402	8/8	0.96	0.07	29,31,35,40	0
9	ZN	E	1010	1/1	0.97	0.07	33,33,33,33	0
6	MD1	A	1004	47/47	0.97	0.15	19,23,28,30	0
6	MD1	C	1004	47/47	0.97	0.16	20,29,32,35	0
5	MGD	A	1003	47/47	0.97	0.17	13,20,25,28	0
3	SF4	C	1001	8/8	0.97	0.14	34,36,40,42	0
5	MGD	E	1003	47/47	0.97	0.18	16,24,30,31	0
8	NA	A	1008	1/1	0.97	0.17	18,18,18,18	0
7	EDO	D	401	4/4	0.97	0.12	24,24,28,31	0
8	NA	F	407	1/1	0.97	0.09	41,41,41,41	0
7	EDO	F	405	4/4	0.98	0.12	23,23,23,25	0

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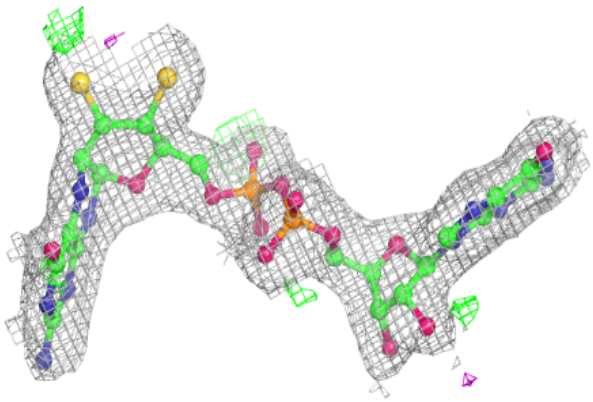
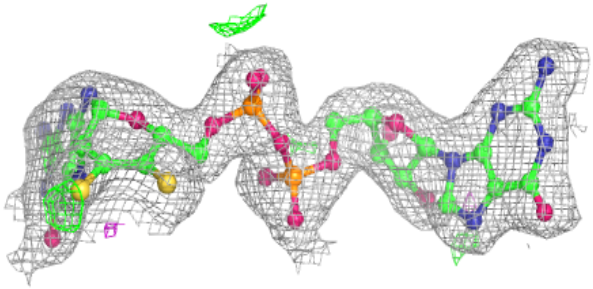
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	SF4	E	1001	8/8	0.98	0.12	19,22,25,26	0
6	MD1	E	1004	47/47	0.98	0.14	15,22,28,29	0
3	SF4	D	404	8/8	0.98	0.13	45,49,56,57	0
8	NA	E	1009	1/1	0.98	0.17	14,14,14,14	0
3	SF4	F	403	8/8	0.98	0.13	27,31,37,38	0
9	ZN	C	1011	1/1	0.98	0.07	58,58,58,58	0
12	F3S	F	401	7/7	0.98	0.04	28,31,33,36	0
3	SF4	B	402	8/8	0.98	0.08	22,24,24,30	0
3	SF4	B	403	8/8	0.99	0.10	19,22,24,28	0
4	MO	A	1002	1/1	0.99	0.08	33,33,33,33	0
7	EDO	B	405	4/4	0.99	0.09	22,22,23,23	0
4	MO	C	1002	1/1	0.99	0.10	38,38,38,38	0
9	ZN	A	1009	1/1	0.99	0.08	34,34,34,34	0
12	F3S	B	401	7/7	0.99	0.04	26,27,28,31	0
4	MO	E	1002	1/1	0.99	0.11	32,32,32,32	0
3	SF4	B	404	8/8	0.99	0.09	19,21,22,23	0
3	SF4	A	1001	8/8	0.99	0.13	20,22,26,26	0

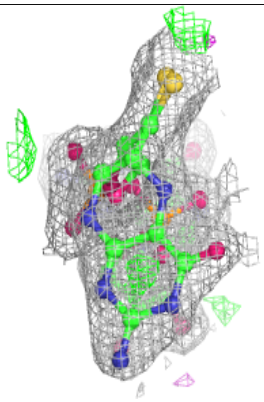
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around MGD C 1003:

2mF$_o$-DF$_c$ (at 0.7 rmsd) in gray
mF$_o$-DF$_c$ (at 3 rmsd) in purple (negative)
and green (positive)

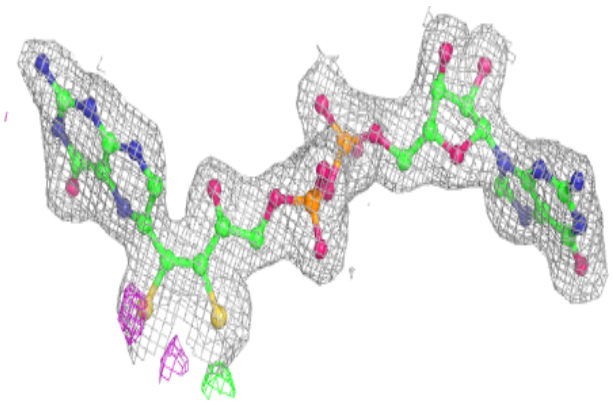


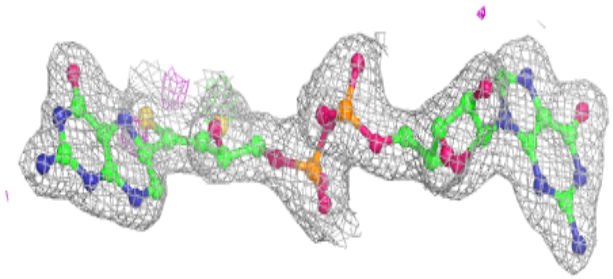


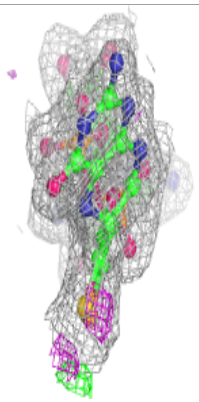


Electron density around MD1 A 1004:

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

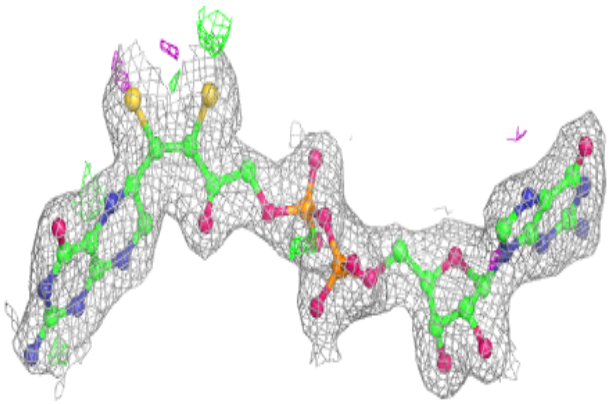


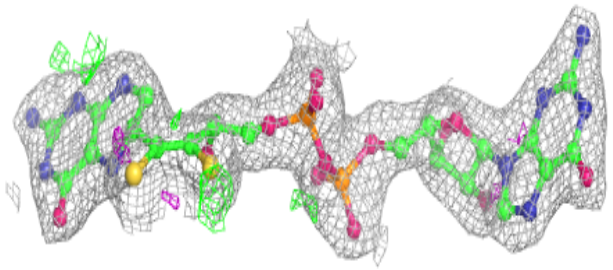


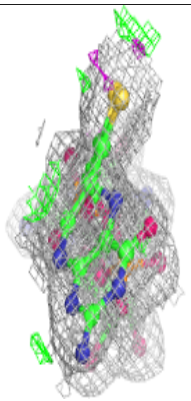


Electron density around MD1 C 1004:

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

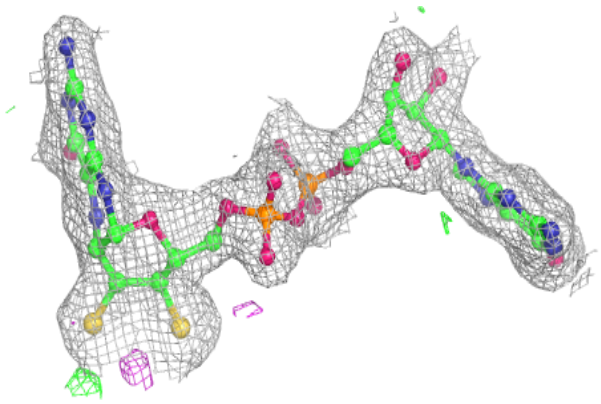


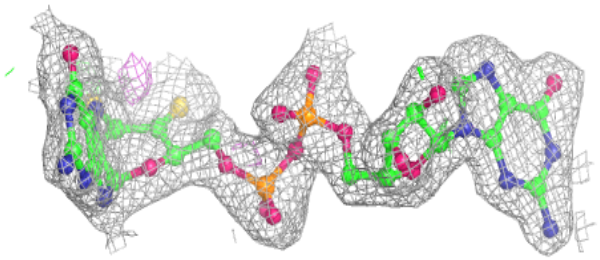


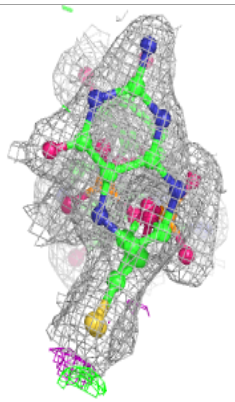


Electron density around MGD A 1003:

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

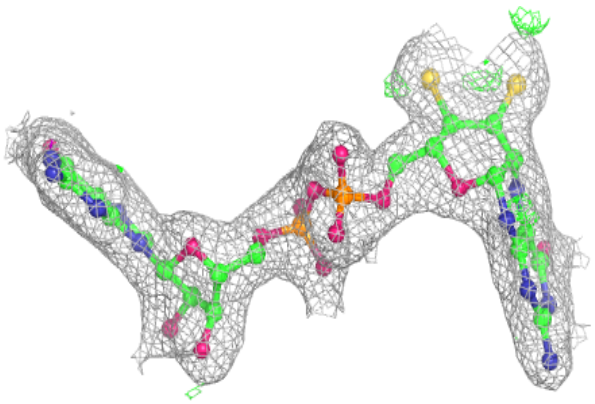


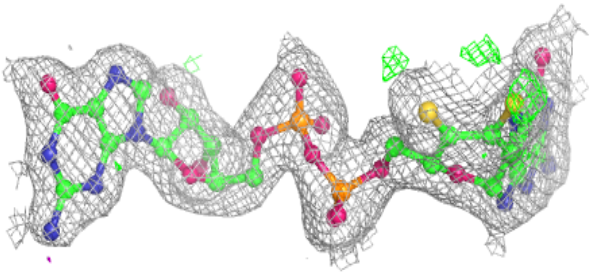


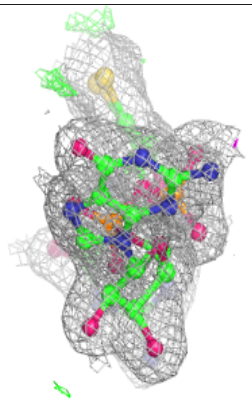


Electron density around MGD E 1003:

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

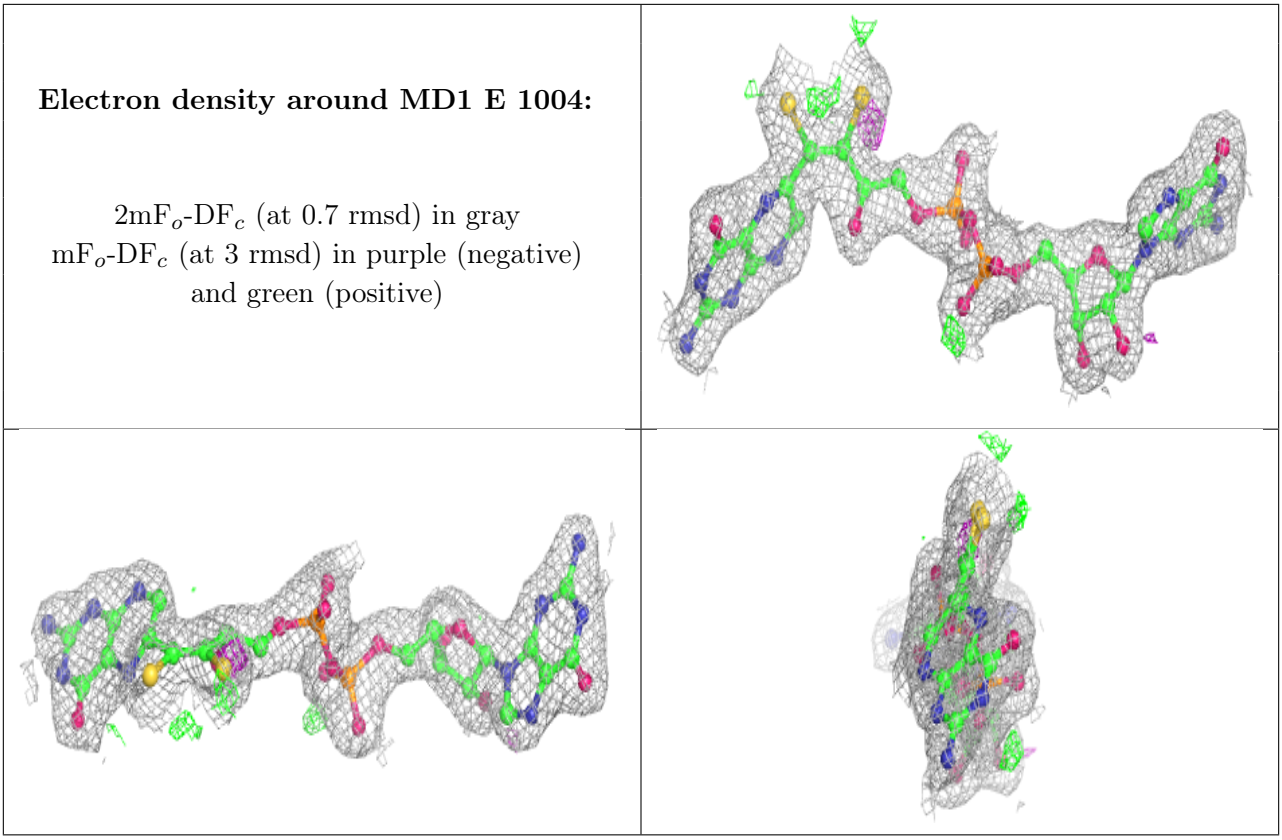






Electron density around MD1 E 1004:

$2mF_o$-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.