



wwPDB X-ray Structure Validation Summary Report ⓘ

Sep 9, 2026 – 09:59 pm BST

PDB ID : 5ODC / pdb_00005odc
Title : Heterodisulfide reductase / [NiFe]-hydrogenase complex from Methanothermococcus thermolithotrophicus at 2.3 Å resolution
Authors : Wagner, T.; Koch, J.; Ermler, U.; Shima, S.
Deposited on : 2017-07-05
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
Mogul	:	1.8.4, CSD as541be (2020)
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	:	9.0.015 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.50

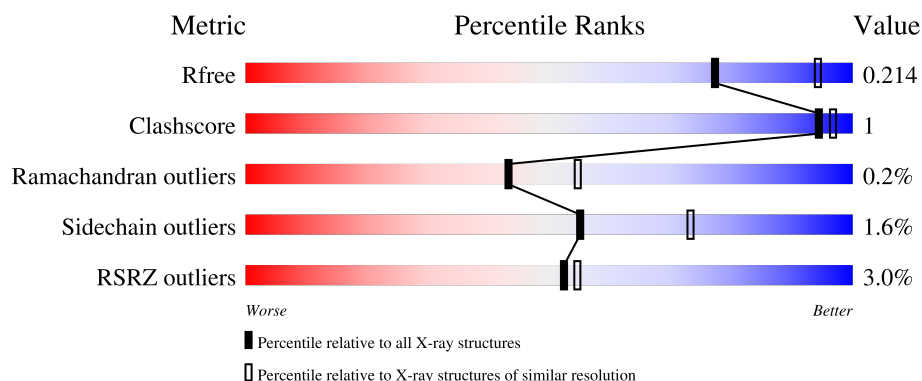
1 Overall quality at a glance

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	654	0% 96% •
1	G	654	0% 94% 5% •
2	B	291	0% 97% •
2	H	291	17% 96% •
3	C	184	2% 96% •

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Mol	Chain	Length	Quality of chain
3	I	184	17% 90% 6%
4	D	140	91% 7%
4	J	140	90% 9%
5	E	299	% 96%
5	K	299	% 94% 5%
6	F	473	% 86% 8% 5%
6	L	473	3% 87% 7% 5%

2 Entry composition

There are 20 unique types of molecules in this entry. The entry contains 32275 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 Heterodisulfide reductase, subunit A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	653	Total	C	N	O	S	0	0	0
			4984	3145	846	944	49			
1	G	653	Total	C	N	O	S	0	0	0
			4984	3145	846	944	49			

- Molecule 2 is a protein called Heterodisulfide reductase, subunit B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	291	Total	C	N	O	S	0	0	0
			2236	1420	379	413	24			
2	H	291	Total	C	N	O	S	0	0	0
			2236	1420	379	413	24			

- Molecule 3 is a protein called Heterodisulfide reductase, subunit C.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	184	Total	C	N	O	S	0	0	0
			1425	890	247	274	14			
3	I	173	Total	C	N	O	S	0	0	0
			1335	831	233	257	14			

- Molecule 4 is a protein called Methyl-viologen reducing hydrogenase subunit D.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	138	Total	C	N	O	S	0	0	0
			1106	703	188	203	12			
4	J	138	Total	C	N	O	S	0	0	0
			1106	703	188	203	12			

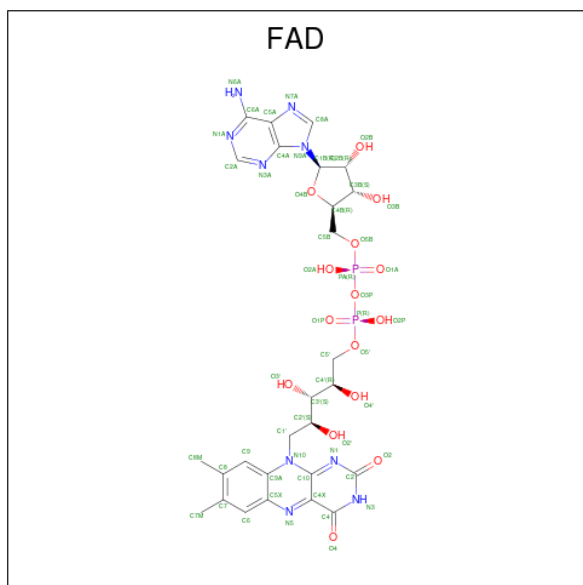
- Molecule 5 is a protein called Methyl-viologen reducing hydrogenase subunit G.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	E	298	Total	C	N	O	S	0	0	0
			2258	1425	369	445	19			
5	K	298	Total	C	N	O	S	0	0	0
			2258	1425	369	445	19			

- Molecule 6 is a protein called Methyl-viologen reducing hydrogenase subunit A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	F	447	Total	C	N	O	S	0	0	0
			3521	2230	600	672	19			
6	L	447	Total	C	N	O	S	0	0	0
			3521	2230	600	672	19			

- Molecule 7 is FLAVIN-ADENINE DINUCLEOTIDE (CCD ID: FAD) (formula: $C_{27}H_{33}N_9O_{15}P_2$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
7	A	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
7	G	1	Total	C	N	O	P	0	0
			53	27	9	15	2		

- Molecule 8 is SODIUM ION (CCD ID: NA) (formula: Na).

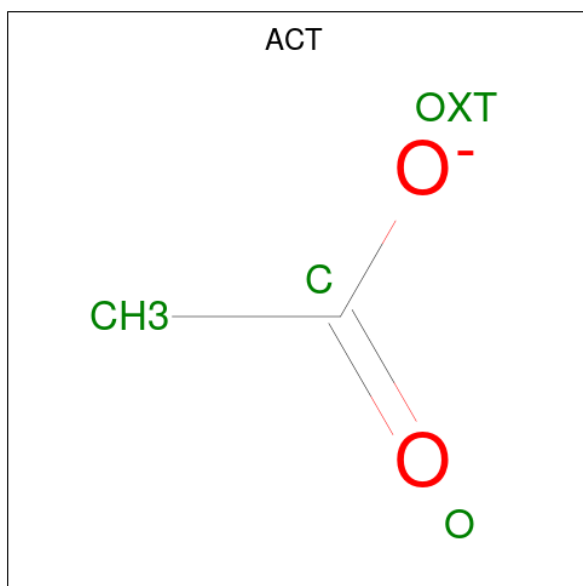
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	1	Total	Na	0	0
			1	1		

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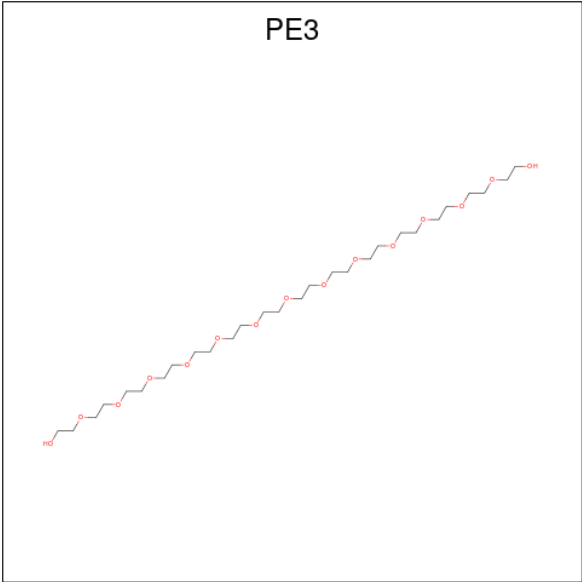
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	G	1	Total	Na	0	0
			1	1		

- Molecule 9 is ACETATE ION (CCD ID: ACT) (formula: $C_2H_3O_2$).



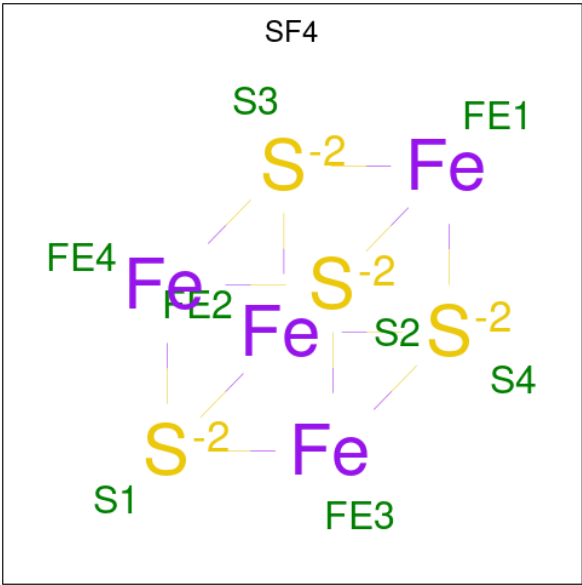
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
9	A	1	Total	C	O	0	0
			4	2	2		
9	B	1	Total	C	O	0	0
			4	2	2		
9	F	1	Total	C	O	0	0
			4	2	2		
9	G	1	Total	C	O	0	0
			4	2	2		
9	G	1	Total	C	O	0	0
			4	2	2		

- Molecule 10 is 3,6,9,12,15,18,21,24,27,30,33,36,39-TRIDECAOXAHENTETRACONTANE-1,41-DIOL (CCD ID: PE3) (formula: $C_{28}H_{58}O_{15}$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
10	A	1	Total	C	O	0	0
			11	7	4		

- Molecule 11 is IRON/SULFUR CLUSTER (CCD ID: SF4) (formula: Fe₄S₄).



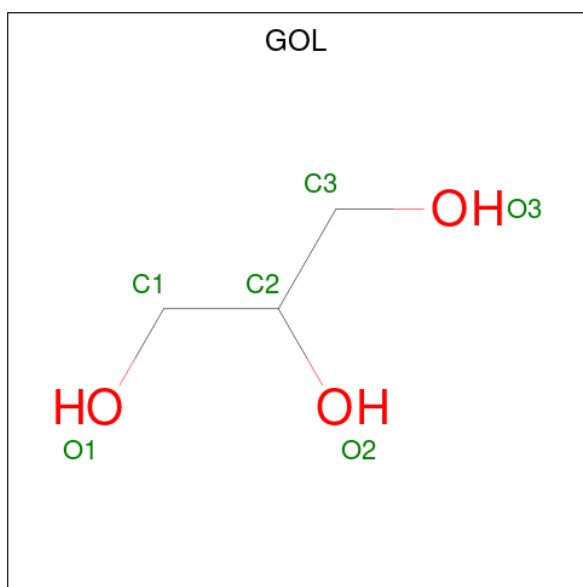
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
11	A	1	Total	Fe	S	0	0
			8	4	4		
11	A	1	Total	Fe	S	0	0
			8	4	4		
11	A	1	Total	Fe	S	0	0
			8	4	4		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
11	A	1	Total 8	Fe 4	S 4	0	0
11	A	1	Total 8	Fe 4	S 4	0	0
11	A	1	Total 8	Fe 4	S 4	0	0
11	C	1	Total 8	Fe 4	S 4	0	0
11	C	1	Total 8	Fe 4	S 4	0	0
11	E	1	Total 8	Fe 4	S 4	0	0
11	E	1	Total 8	Fe 4	S 4	0	0
11	E	1	Total 8	Fe 4	S 4	0	0
11	G	1	Total 8	Fe 4	S 4	0	0
11	G	1	Total 8	Fe 4	S 4	0	0
11	G	1	Total 8	Fe 4	S 4	0	0
11	G	1	Total 8	Fe 4	S 4	0	0
11	G	1	Total 8	Fe 4	S 4	0	0
11	G	1	Total 8	Fe 4	S 4	0	0
11	I	1	Total 8	Fe 4	S 4	0	0
11	I	1	Total 8	Fe 4	S 4	0	0
11	K	1	Total 8	Fe 4	S 4	0	0
11	K	1	Total 8	Fe 4	S 4	0	0
11	K	1	Total 8	Fe 4	S 4	0	0

- Molecule 12 is GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃).



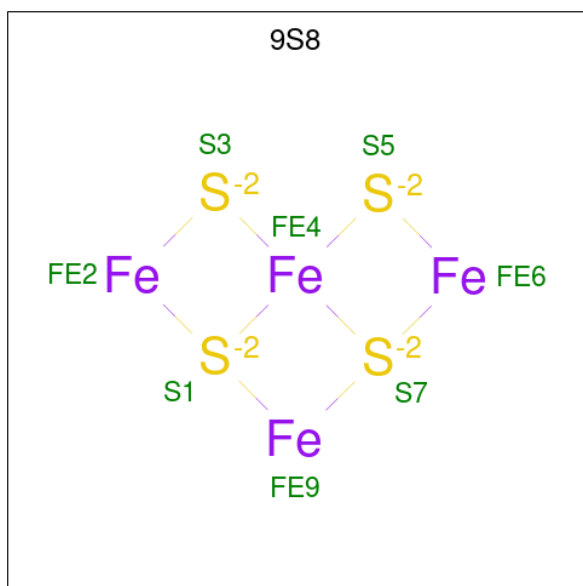
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
12	A	1	Total	C	O	0	0
			6	3	3		
12	A	1	Total	C	O	0	0
			6	3	3		
12	A	1	Total	C	O	0	0
			6	3	3		
12	A	1	Total	C	O	0	0
			6	3	3		
12	B	1	Total	C	O	0	0
			6	3	3		
12	C	1	Total	C	O	0	0
			6	3	3		
12	D	1	Total	C	O	0	0
			6	3	3		
12	E	1	Total	C	O	0	0
			6	3	3		
12	G	1	Total	C	O	0	0
			6	3	3		
12	G	1	Total	C	O	0	0
			6	3	3		
12	G	1	Total	C	O	0	0
			6	3	3		
12	K	1	Total	C	O	0	0
			6	3	3		
12	K	1	Total	C	O	0	0
			6	3	3		

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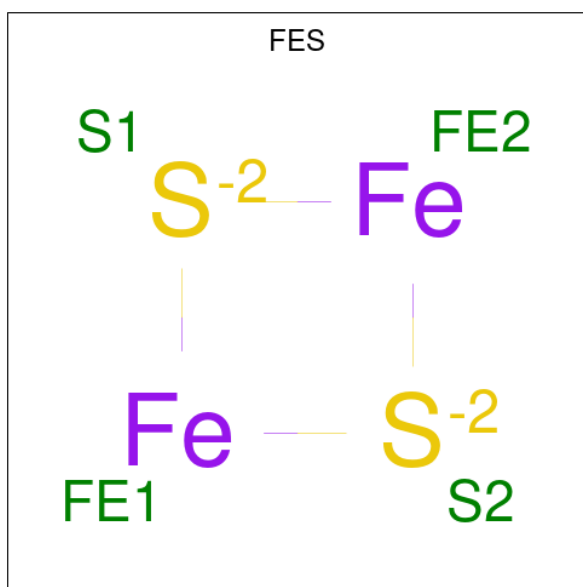
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
12	K	1	Total	C	O	0	0
			6	3	3		

- Molecule 13 is Non-cubane [4Fe-4S]-cluster (CCD ID: 9S8) (formula: Fe_4S_4).



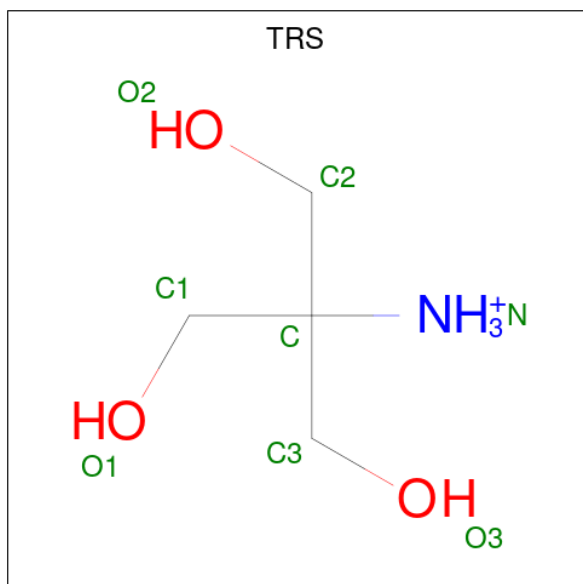
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
13	B	1	Total	Fe	S	0	0
			8	4	4		
13	B	1	Total	Fe	S	0	0
			8	4	4		
13	H	1	Total	Fe	S	0	0
			8	4	4		
13	H	1	Total	Fe	S	0	0
			8	4	4		

- Molecule 14 is FE2/S2 (INORGANIC) CLUSTER (CCD ID: FES) (formula: Fe_2S_2).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
14	D	1	Total	Fe	S	0	0
			4	2	2		
14	J	1	Total	Fe	S	0	0
			4	2	2		

- Molecule 15 is 2-AMINO-2-HYDROXYMETHYL-PROPANE-1,3-DIOL (CCD ID: TRS) (formula: C₄H₁₂NO₃).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
15	D	1	Total	C	N	O	0	0
			8	4	1	3		

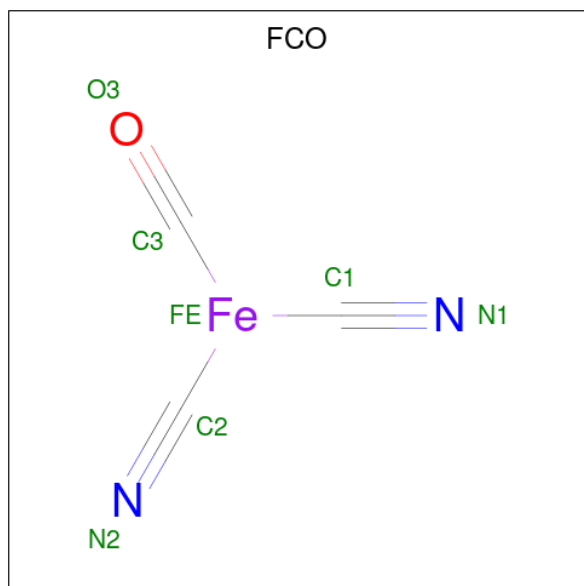
- Molecule 16 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
16	F	1	Total	Ca	0	0
			1	1		
16	L	1	Total	Ca	0	0
			1	1		

- Molecule 17 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
17	F	1	Total	Mg	0	0
			1	1		
17	I	1	Total	Mg	0	0
			1	1		

- Molecule 18 is CARBONMONOXIDE-(DICYANO) IRON (CCD ID: FCO) (formula: C₃FeN₂O).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
18	F	1	Total	C	Fe	N	O	0	0
			7	3	1	2	1		
18	L	1	Total	C	Fe	N	O	0	0
			7	3	1	2	1		

- Molecule 19 is NICKEL (II) ION (CCD ID: NI) (formula: Ni).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
19	F	1	Total 1	Ni 1	0	0
19	L	1	Total 1	Ni 1	0	0

- Molecule 20 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
20	A	180	Total 180	O 180	0	0
20	B	52	Total 52	O 52	0	0
20	C	29	Total 29	O 29	0	0
20	D	52	Total 52	O 52	0	0
20	E	71	Total 71	O 71	0	0
20	F	78	Total 78	O 78	0	0
20	G	182	Total 182	O 182	0	0
20	H	10	Total 10	O 10	0	0
20	I	23	Total 23	O 23	0	0
20	J	48	Total 48	O 48	0	0
20	K	65	Total 65	O 65	0	0
20	L	42	Total 42	O 42	0	0

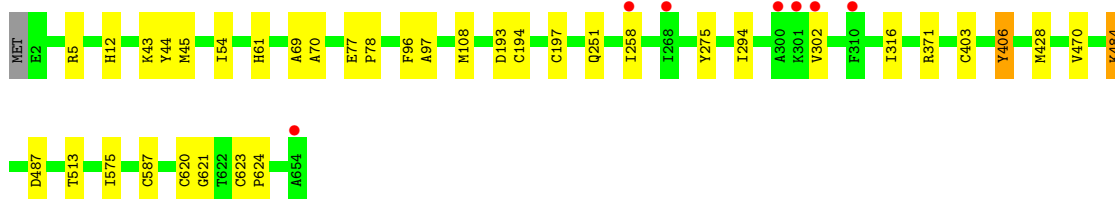
3 Residue-property plots [i](#)

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: Heterodisulfide reductase, subunit A



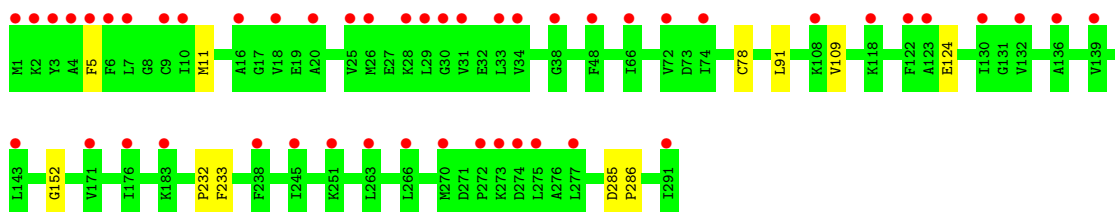
- Molecule 1: Heterodisulfide reductase, subunit A



- Molecule 2: Heterodisulfide reductase, subunit B



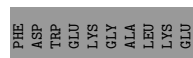
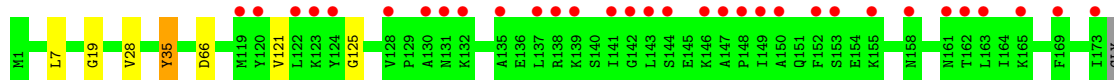
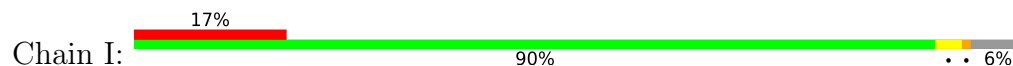
- Molecule 2: Heterodisulfide reductase, subunit B



- Molecule 3: Heterodisulfide reductase, subunit C



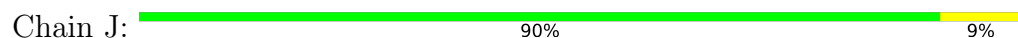
- Molecule 3: Heterodisulfide reductase, subunit C



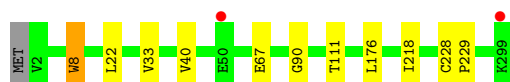
- Molecule 4: Methyl-viologen reducing hydrogenase subunit D



- Molecule 4: Methyl-viologen reducing hydrogenase subunit D



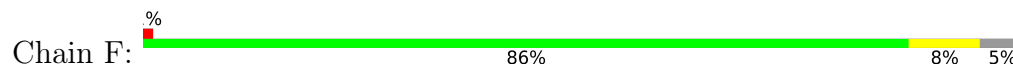
- Molecule 5: Methyl-viologen reducing hydrogenase subunit G

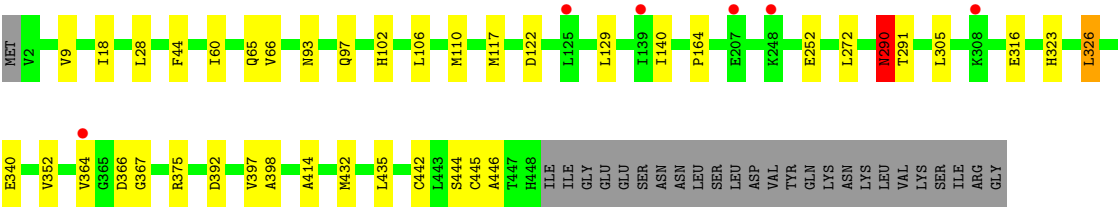


- Molecule 5: Methyl-viologen reducing hydrogenase subunit G

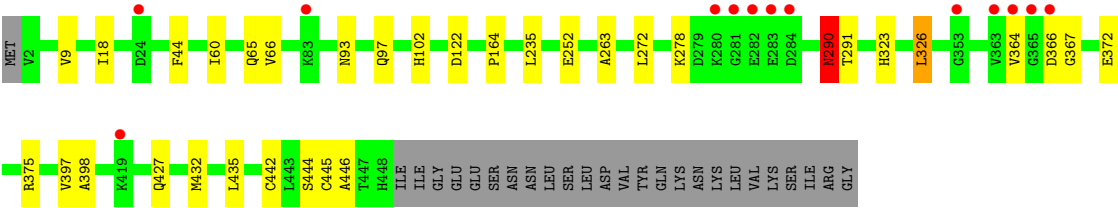
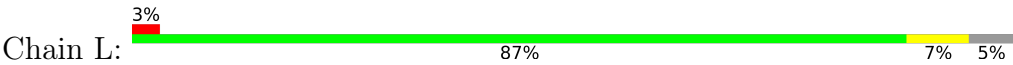


- Molecule 6: Methyl-viologen reducing hydrogenase subunit A





● Molecule 6: Methyl-viologen reducing hydrogenase subunit A



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	378.05Å 98.45Å 137.88Å 90.00° 110.70° 90.00°	Depositor
Resolution (Å)	49.22 – 2.30 49.22 – 2.30	Depositor EDS
% Data completeness (in resolution range)	97.3 (49.22-2.30) 97.3 (49.22-2.30)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.14 (at 2.29Å)	Xtriage
Refinement program	BUSTER 2.10.1	Depositor
R, R_{free}	0.178 , 0.200 0.193 , 0.214	Depositor DCC
R_{free} test set	10353 reflections (4.93%)	wwPDB-VP
Wilson B-factor (Å ²)	33.6	Xtriage
Anisotropy	0.575	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 47.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	0.023 for -h-2*k,l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	32275	wwPDB-VP
Average B, all atoms (Å ²)	49.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.18% 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: SF4, MG, ACT, FCO, CA, NA, FES, NI, TRS, GOL, FAD, PE3, 9S8

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	0.53	0/5076	0.94	1/6860 (0.0%)
1	G	0.53	1/5076 (0.0%)	0.94	3/6860 (0.0%)
2	B	0.52	0/2277	0.95	2/3070 (0.1%)
2	H	0.52	0/2277	0.94	1/3070 (0.0%)
3	C	0.55	0/1446	0.97	2/1946 (0.1%)
3	I	0.52	0/1353	0.98	0/1822
4	D	0.51	0/1132	0.98	1/1520 (0.1%)
4	J	0.50	0/1132	0.98	1/1520 (0.1%)
5	E	0.53	0/2297	0.97	4/3113 (0.1%)
5	K	0.53	0/2297	0.96	5/3113 (0.2%)
6	F	0.53	0/3590	1.00	7/4853 (0.1%)
6	L	0.53	0/3590	1.00	7/4853 (0.1%)
All	All	0.53	1/31543 (0.0%)	0.97	34/42600 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	G	316	ILE	CG1-CD1	-5.10	1.31	1.51

The worst 5 of 34 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	E	22	LEU	N-CA-C	-7.88	103.12	112.89
5	K	22	LEU	N-CA-C	-7.85	103.16	112.89
6	L	290	ASN	CA-CB-CG	7.61	120.21	112.60
6	L	44	PHE	CA-CB-CG	6.49	120.29	113.80
6	F	44	PHE	CA-CB-CG	6.42	120.22	113.80

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	4984	0	4979	11	0
1	G	4984	0	4979	19	0
2	B	2236	0	2243	2	0
2	H	2236	0	2243	3	0
3	C	1425	0	1441	3	0
3	I	1335	0	1358	5	0
4	D	1106	0	1074	5	0
4	J	1106	0	1074	6	0
5	E	2258	0	2265	3	0
5	K	2258	0	2265	3	0
6	F	3521	0	3503	16	0
6	L	3521	0	3503	15	0
7	A	53	0	31	0	0
7	G	53	0	31	0	0
8	A	1	0	0	0	0
8	G	1	0	0	0	0
9	A	4	0	3	0	0
9	B	4	0	3	0	0
9	F	4	0	3	0	0
9	G	8	0	6	0	0
10	A	11	0	12	0	0
11	A	48	0	0	0	0
11	C	16	0	0	0	0
11	E	24	0	0	0	0
11	G	48	0	0	0	0
11	I	16	0	0	0	0
11	K	24	0	0	0	0
12	A	24	0	32	0	0
12	B	6	0	8	0	0
12	C	6	0	8	0	0
12	D	6	0	8	0	0
12	E	6	0	8	0	0
12	G	24	0	32	1	0
12	K	18	0	24	0	0
13	B	16	0	0	0	0
13	H	16	0	0	0	0
14	D	4	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
14	J	4	0	0	0	0
15	D	8	0	12	0	0
16	F	1	0	0	0	0
16	L	1	0	0	0	0
17	F	1	0	0	0	0
17	I	1	0	0	0	0
18	F	7	0	0	0	0
18	L	7	0	0	0	0
19	F	1	0	0	0	0
19	L	1	0	0	0	0
20	A	180	0	0	0	0
20	B	52	0	0	0	0
20	C	29	0	0	0	0
20	D	52	0	0	0	0
20	E	71	0	0	0	0
20	F	78	0	0	0	0
20	G	182	0	0	0	0
20	H	10	0	0	0	0
20	I	23	0	0	0	0
20	J	48	0	0	0	0
20	K	65	0	0	0	0
20	L	42	0	0	0	0
All	All	32275	0	31148	80	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 1.

The worst 5 of 80 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)
6:L:323:HIS:HB2	6:L:326:LEU:HD23	1.64	0.78
1:A:194:CYS:HB2	1:A:197:CYS:SG	2.30	0.70
1:A:236:LYS:HD2	1:A:317:ILE:HD12	1.76	0.67
4:D:17:THR:HG21	4:D:65:GLY:HA3	1.79	0.65
2:H:5:PHE:CZ	2:H:11:MET:HE1	2.35	0.61

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	651/654 (100%)	629 (97%)	21 (3%)	1 (0%)	43	55
1	G	651/654 (100%)	627 (96%)	22 (3%)	2 (0%)	36	46
2	B	289/291 (99%)	277 (96%)	12 (4%)	0	100	100
2	H	289/291 (99%)	275 (95%)	14 (5%)	0	100	100
3	C	182/184 (99%)	181 (100%)	1 (0%)	0	100	100
3	I	171/184 (93%)	170 (99%)	1 (1%)	0	100	100
4	D	136/140 (97%)	131 (96%)	5 (4%)	0	100	100
4	J	136/140 (97%)	133 (98%)	3 (2%)	0	100	100
5	E	296/299 (99%)	287 (97%)	9 (3%)	0	100	100
5	K	296/299 (99%)	287 (97%)	9 (3%)	0	100	100
6	F	445/473 (94%)	436 (98%)	7 (2%)	2 (0%)	30	38
6	L	445/473 (94%)	433 (97%)	10 (2%)	2 (0%)	30	38
All	All	3987/4082 (98%)	3866 (97%)	114 (3%)	7 (0%)	43	55

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	F	291	THR
6	F	398	ALA
6	L	291	THR
6	L	398	ALA
1	A	70	ALA

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	540/541 (100%)	534 (99%)	6 (1%)	65	81
1	G	540/541 (100%)	534 (99%)	6 (1%)	65	81
2	B	242/242 (100%)	238 (98%)	4 (2%)	53	72
2	H	242/242 (100%)	238 (98%)	4 (2%)	53	72
3	C	157/157 (100%)	156 (99%)	1 (1%)	78	89
3	I	149/157 (95%)	147 (99%)	2 (1%)	61	77
4	D	117/119 (98%)	116 (99%)	1 (1%)	70	84
4	J	117/119 (98%)	115 (98%)	2 (2%)	53	72
5	E	255/256 (100%)	251 (98%)	4 (2%)	55	73
5	K	255/256 (100%)	247 (97%)	8 (3%)	35	52
6	F	386/410 (94%)	377 (98%)	9 (2%)	44	63
6	L	386/410 (94%)	380 (98%)	6 (2%)	55	73
All	All	3386/3450 (98%)	3333 (98%)	53 (2%)	55	73

5 of 53 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	G	470	VAL
3	I	35	TYR
6	L	252	GLU
1	G	484	LYS
2	H	109	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 25 such sidechains are listed below:

Mol	Chain	Res	Type
6	F	136	HIS
1	G	593	GLN
6	L	401	GLN
1	G	385	GLN
1	G	636	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 62 ligands modelled in this entry, 8 are monoatomic - leaving 54 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	$\# Z > 2$
12	GOL	C	203	-	5,5,5	0.27	0	5,5,5	0.32	0
11	SF4	I	202	3	0,12,12	-	-	-		
12	GOL	B	304	-	5,5,5	0.32	0	5,5,5	0.40	0
9	ACT	A	703	-	3,3,3	0.96	0	3,3,3	1.08	0
11	SF4	G	708	1	0,12,12	-	-	-		
12	GOL	K	305	-	5,5,5	0.26	0	5,5,5	0.13	0
11	SF4	A	705	1	0,12,12	-	-	-		
13	9S8	B	301	2	2,10,10	0.99	0	-		
18	FCO	L	502	6	1,6,6	3.90	1 (100%)	-		
9	ACT	G	704	-	3,3,3	1.03	0	3,3,3	1.02	0
12	GOL	G	711	-	5,5,5	0.21	0	5,5,5	0.26	0
13	9S8	B	302	2	2,10,10	1.38	0	-		
12	GOL	A	714	-	5,5,5	0.27	0	5,5,5	0.21	0
12	GOL	K	304	-	5,5,5	0.30	0	5,5,5	0.62	0
11	SF4	E	301	5	0,12,12	-	-	-		
11	SF4	E	303	5	0,12,12	-	-	-		
12	GOL	G	712	-	5,5,5	0.28	0	5,5,5	0.09	0
14	FES	J	201	4	0,4,4	-	-	-		
12	GOL	G	714	-	5,5,5	0.32	0	5,5,5	0.21	0
11	SF4	A	709	1	0,12,12	-	-	-		
15	TRS	D	202	-	7,7,7	0.30	0	9,9,9	0.40	0
12	GOL	A	713	-	5,5,5	0.30	0	5,5,5	0.44	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
7	FAD	G	701	-	56,58,58	1.47	8 (14%)	81,89,89	1.72	18 (22%)
9	ACT	G	703	-	3,3,3	1.14	0	3,3,3	0.89	0
9	ACT	B	303	-	3,3,3	1.03	0	3,3,3	0.97	0
11	SF4	C	201	3	0,12,12	-	-	-	-	-
11	SF4	A	708	1	0,12,12	-	-	-	-	-
11	SF4	C	202	3	0,12,12	-	-	-	-	-
11	SF4	A	707	1	0,12,12	-	-	-	-	-
11	SF4	K	301	5	0,12,12	-	-	-	-	-
11	SF4	K	302	5	0,12,12	-	-	-	-	-
11	SF4	K	303	5	0,12,12	-	-	-	-	-
18	FCO	F	504	6	1,6,6	4.13	1 (100%)	-	-	-
9	ACT	F	503	-	3,3,3	1.02	0	3,3,3	1.00	0
12	GOL	G	713	-	5,5,5	0.32	0	5,5,5	0.25	0
11	SF4	G	706	1	0,12,12	-	-	-	-	-
11	SF4	G	709	1	0,12,12	-	-	-	-	-
12	GOL	E	304	-	5,5,5	0.28	0	5,5,5	0.17	0
12	GOL	A	711	-	5,5,5	0.26	0	5,5,5	0.39	0
11	SF4	G	707	1	0,12,12	-	-	-	-	-
11	SF4	G	710	1	0,12,12	-	-	-	-	-
11	SF4	G	705	1	0,12,12	-	-	-	-	-
12	GOL	K	306	-	5,5,5	0.26	0	5,5,5	0.14	0
13	9S8	H	301	2	2,10,10	0.99	0	-	-	-
11	SF4	A	710	1	0,12,12	-	-	-	-	-
13	9S8	H	302	2	2,10,10	1.06	0	-	-	-
7	FAD	A	701	-	56,58,58	1.41	9 (16%)	81,89,89	1.77	21 (25%)
11	SF4	A	706	1	0,12,12	-	-	-	-	-
12	GOL	D	203	-	5,5,5	0.26	0	5,5,5	0.29	0
11	SF4	I	203	3	0,12,12	-	-	-	-	-
14	FES	D	201	4	0,4,4	-	-	-	-	-
11	SF4	E	302	5	0,12,12	-	-	-	-	-
12	GOL	A	712	-	5,5,5	0.28	0	5,5,5	0.11	0
10	PE3	A	704	-	10,10,42	0.52	0	9,9,41	0.14	0

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
12	GOL	C	203	-	-	4/4/4/4	-
11	SF4	I	202	3	-	-	0/6/5/5
12	GOL	B	304	-	-	4/4/4/4	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
11	SF4	G	708	1	-	-	0/6/5/5
12	GOL	K	305	-	-	2/4/4/4	-
11	SF4	A	705	1	-	-	0/6/5/5
13	9S8	B	301	2	-	-	0/3/3/3
13	9S8	B	302	2	-	-	0/3/3/3
12	GOL	A	714	-	-	0/4/4/4	-
12	GOL	K	304	-	-	2/4/4/4	-
11	SF4	E	301	5	-	-	0/6/5/5
11	SF4	E	303	5	-	-	0/6/5/5
12	GOL	G	712	-	-	4/4/4/4	-
14	FES	J	201	4	-	-	0/1/1/1
12	GOL	G	714	-	-	0/4/4/4	-
11	SF4	A	709	1	-	-	0/6/5/5
15	TRS	D	202	-	-	5/9/9/9	-
12	GOL	A	713	-	-	4/4/4/4	-
7	FAD	G	701	-	-	1/34/50/50	0/6/6/6
11	SF4	E	302	5	-	-	0/6/5/5
11	SF4	A	708	1	-	-	0/6/5/5
11	SF4	C	201	3	-	-	0/6/5/5
11	SF4	A	707	1	-	-	0/6/5/5
11	SF4	C	202	3	-	-	0/6/5/5
11	SF4	K	301	5	-	-	0/6/5/5
11	SF4	K	302	5	-	-	0/6/5/5
11	SF4	K	303	5	-	-	0/6/5/5
12	GOL	G	713	-	-	2/4/4/4	-
11	SF4	G	706	1	-	-	0/6/5/5
11	SF4	G	709	1	-	-	0/6/5/5
12	GOL	E	304	-	-	1/4/4/4	-
12	GOL	A	711	-	-	3/4/4/4	-
11	SF4	G	707	1	-	-	0/6/5/5
11	SF4	G	710	1	-	-	0/6/5/5
11	SF4	G	705	1	-	-	0/6/5/5
12	GOL	K	306	-	-	2/4/4/4	-
13	9S8	H	301	2	-	-	0/3/3/3
11	SF4	A	710	1	-	-	0/6/5/5
13	9S8	H	302	2	-	-	0/3/3/3
7	FAD	A	701	-	-	1/34/50/50	0/6/6/6
12	GOL	D	203	-	-	0/4/4/4	-
11	SF4	A	706	1	-	-	0/6/5/5
11	SF4	I	203	3	-	-	0/6/5/5

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
14	FES	D	201	4	-	-	0/1/1/1
12	GOL	G	711	-	-	2/4/4/4	-
12	GOL	A	712	-	-	4/4/4/4	-
10	PE3	A	704	-	-	4/8/8/40	-

The worst 5 of 19 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	G	701	FAD	C9A-C5X	5.39	1.50	1.41
7	A	701	FAD	C9A-C5X	5.33	1.50	1.41
7	G	701	FAD	C5A-C4A	4.57	1.47	1.39
7	A	701	FAD	C5A-C4A	4.25	1.46	1.39
18	F	504	FCO	O3-C3	4.13	1.21	1.16

The worst 5 of 39 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	G	701	FAD	C5A-C4A-N3A	-6.11	118.78	126.75
7	A	701	FAD	C5A-C4A-N3A	-5.72	119.29	126.75
7	G	701	FAD	N3A-C4A-N9A	4.84	135.05	127.08
7	A	701	FAD	N3A-C4A-N9A	4.75	134.91	127.08
7	G	701	FAD	C2A-N3A-C4A	4.12	121.47	111.75

There are no chirality outliers.

5 of 45 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
12	A	711	GOL	C1-C2-C3-O3
12	A	712	GOL	O1-C1-C2-C3
12	A	712	GOL	C1-C2-C3-O3
12	A	713	GOL	C1-C2-C3-O3
12	B	304	GOL	O1-C1-C2-C3

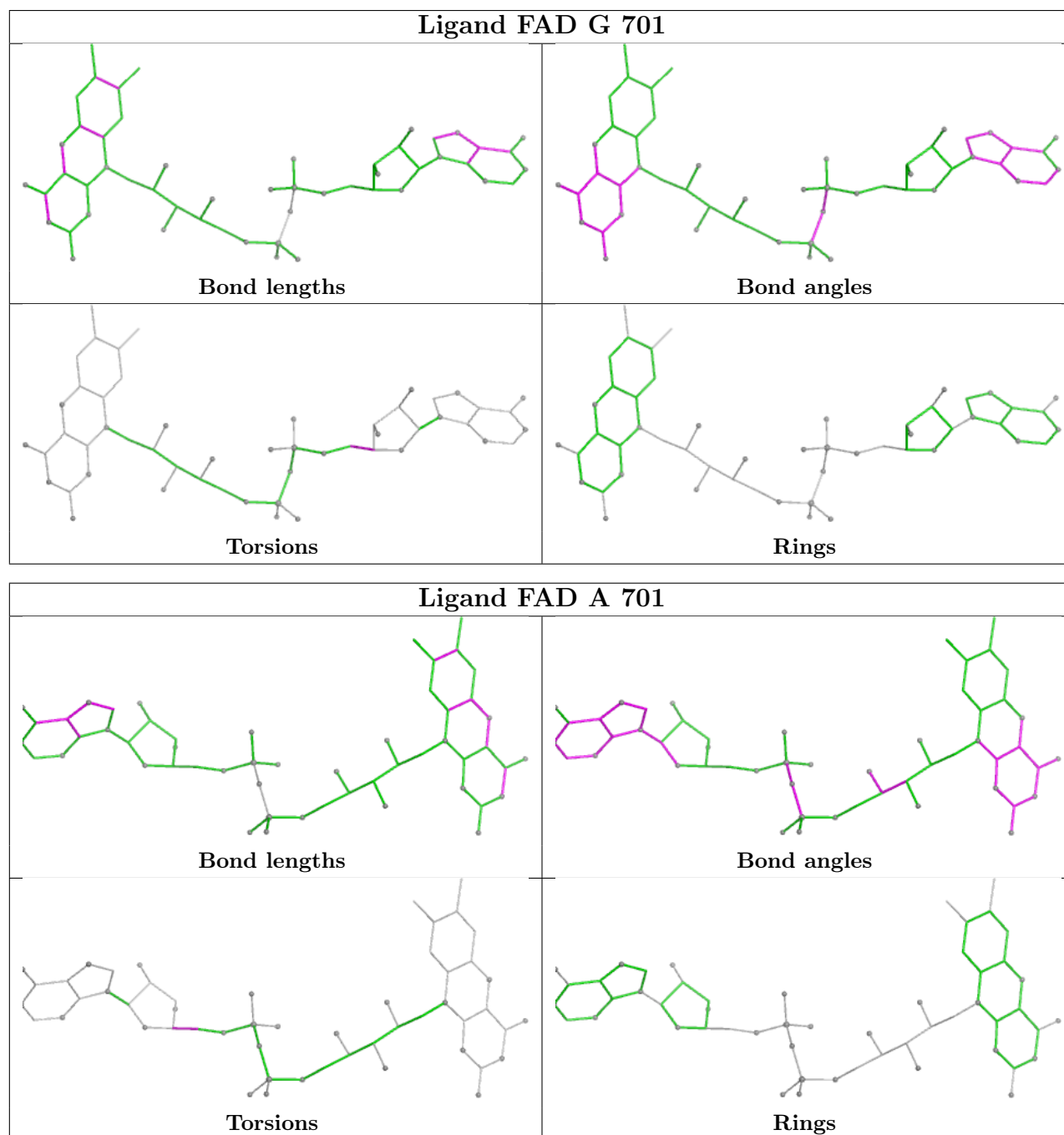
There are no ring outliers.

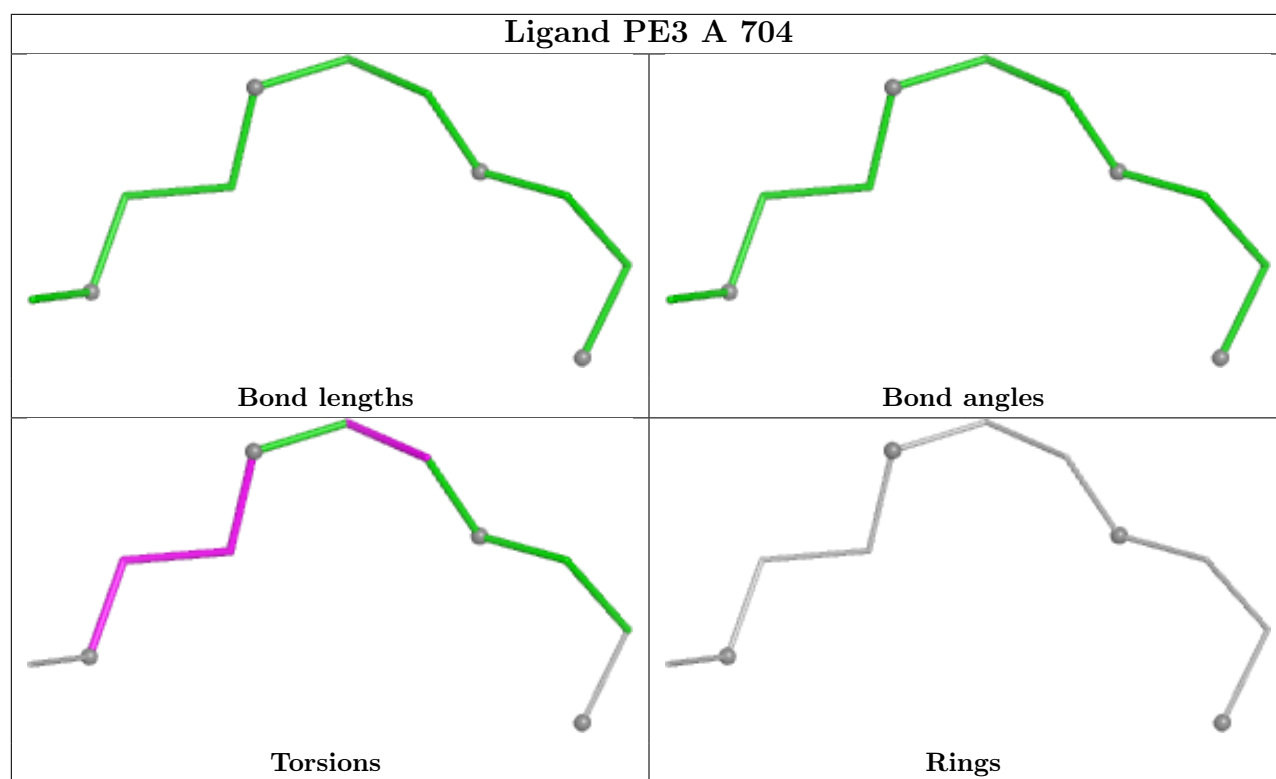
1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
12	G	711	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 [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	653/654 (99%)	-0.23	4 (0%) 85 86	24, 38, 65, 86	0
1	G	653/654 (99%)	-0.16	7 (1%) 78 79	25, 40, 78, 106	0
2	B	291/291 (100%)	0.25	2 (0%) 84 85	36, 50, 74, 90	0
2	H	291/291 (100%)	1.15	49 (16%) 4 5	42, 74, 109, 125	0
3	C	184/184 (100%)	0.14	3 (1%) 70 72	29, 49, 87, 126	0
3	I	173/184 (94%)	0.74	32 (18%) 3 4	27, 55, 113, 132	0
4	D	138/140 (98%)	-0.41	0 100 100	23, 34, 53, 80	0
4	J	138/140 (98%)	-0.31	0 100 100	29, 36, 62, 89	0
5	E	298/299 (99%)	-0.21	2 (0%) 84 85	23, 38, 66, 84	0
5	K	298/299 (99%)	0.09	3 (1%) 79 80	28, 45, 78, 98	0
6	F	447/473 (94%)	-0.01	6 (1%) 75 76	26, 45, 73, 91	0
6	L	447/473 (94%)	0.33	13 (2%) 53 56	32, 52, 85, 110	0
All	All	4011/4082 (98%)	0.08	121 (3%) 52 54	23, 44, 85, 132	0

The worst 5 of 121 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	G	654	ALA	5.1
1	A	654	ALA	5.1
3	I	122	LEU	4.4
2	H	291	ILE	4.4
6	L	282	GLU	4.3

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

6.3 Carbohydrates ⓘ

There are no 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
12	GOL	G	714	6/6	0.65	0.22	74,74,76,77	0
12	GOL	G	713	6/6	0.67	0.28	64,71,72,73	0
12	GOL	K	305	6/6	0.73	0.30	85,86,87,89	0
12	GOL	K	304	6/6	0.76	0.27	78,82,83,84	0
12	GOL	D	203	6/6	0.76	0.30	127,131,132,134	0
12	GOL	B	304	6/6	0.78	0.39	121,123,126,126	0
9	ACT	F	503	4/4	0.78	0.17	66,68,69,69	0
9	ACT	G	703	4/4	0.80	0.17	50,52,52,52	0
12	GOL	A	714	6/6	0.81	0.17	76,78,84,84	0
12	GOL	E	304	6/6	0.81	0.27	83,84,84,89	0
12	GOL	K	306	6/6	0.81	0.28	110,113,116,117	0
9	ACT	B	303	4/4	0.83	0.15	62,65,66,66	0
12	GOL	G	712	6/6	0.84	0.20	69,72,73,76	0
10	PE3	A	704	11/43	0.84	0.14	50,54,58,59	0
12	GOL	A	713	6/6	0.84	0.15	67,71,74,77	0
12	GOL	A	712	6/6	0.85	0.28	95,98,99,102	0
9	ACT	G	704	4/4	0.85	0.24	69,71,71,72	0
15	TRS	D	202	8/8	0.86	0.17	69,72,74,75	0
13	9S8	B	302	8/8	0.87	0.12	53,59,67,68	0
12	GOL	A	711	6/6	0.87	0.14	44,46,47,48	0
13	9S8	H	301	8/8	0.89	0.12	88,89,91,91	0
13	9S8	H	302	8/8	0.90	0.10	72,77,80,81	0
9	ACT	A	703	4/4	0.91	0.15	51,54,55,56	0
12	GOL	G	711	6/6	0.91	0.21	62,65,67,67	0
12	GOL	C	203	6/6	0.91	0.19	87,88,94,95	0
8	NA	A	702	1/1	0.91	0.26	49,49,49,49	0
13	9S8	B	301	8/8	0.93	0.07	51,57,59,60	0
11	SF4	G	707	8/8	0.94	0.07	98,100,100,103	0
11	SF4	G	709	8/8	0.95	0.07	88,90,91,92	0
17	MG	I	201	1/1	0.96	0.07	44,44,44,44	0
11	SF4	A	707	8/8	0.97	0.05	59,62,65,66	0
7	FAD	G	701	53/53	0.97	0.06	21,28,34,39	0

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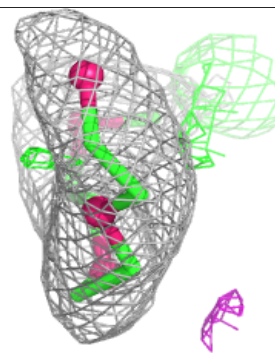
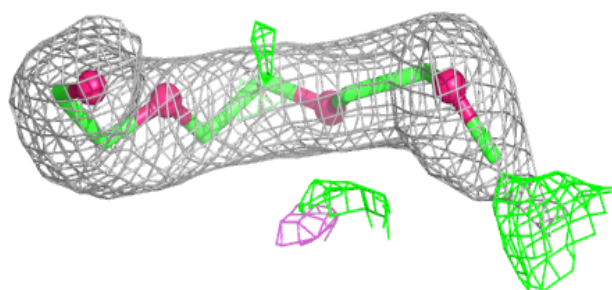
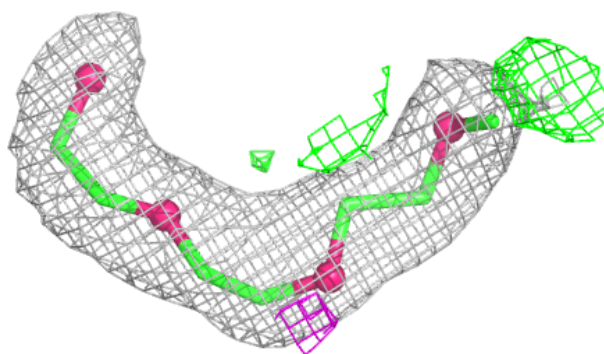
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
8	NA	G	702	1/1	0.97	0.18	43,43,43,43	0
11	SF4	A	706	8/8	0.97	0.04	52,56,58,62	0
11	SF4	I	202	8/8	0.98	0.04	44,46,52,53	0
11	SF4	I	203	8/8	0.98	0.05	41,44,47,48	0
11	SF4	K	301	8/8	0.98	0.07	43,44,50,51	0
11	SF4	K	302	8/8	0.98	0.05	40,49,54,55	0
11	SF4	K	303	8/8	0.98	0.04	50,54,57,59	0
11	SF4	A	709	8/8	0.98	0.05	31,40,42,45	0
11	SF4	C	202	8/8	0.98	0.05	44,48,52,53	0
11	SF4	E	302	8/8	0.98	0.06	39,45,49,49	0
11	SF4	G	705	8/8	0.98	0.05	42,49,50,52	0
11	SF4	G	706	8/8	0.98	0.04	36,43,45,47	0
7	FAD	A	701	53/53	0.98	0.05	15,26,32,32	0
14	FES	D	201	4/4	0.98	0.05	32,34,36,39	0
14	FES	J	201	4/4	0.98	0.04	28,29,36,38	0
11	SF4	A	705	8/8	0.98	0.04	39,42,45,46	0
17	MG	F	502	1/1	0.98	0.08	39,39,39,39	0
11	SF4	G	710	8/8	0.98	0.05	42,45,49,51	0
18	FCO	F	504	7/7	0.98	0.08	30,34,40,42	0
18	FCO	L	502	7/7	0.98	0.09	32,41,43,44	0
11	SF4	A	708	8/8	0.99	0.04	26,32,35,36	0
11	SF4	E	301	8/8	0.99	0.05	32,36,40,45	0
16	CA	L	501	1/1	0.99	0.05	38,38,38,38	0
11	SF4	G	708	8/8	0.99	0.04	32,38,39,42	0
11	SF4	A	710	8/8	0.99	0.04	34,37,43,44	0
11	SF4	E	303	8/8	0.99	0.04	36,40,47,47	0
11	SF4	C	201	8/8	0.99	0.04	34,39,44,46	0
19	NI	F	505	1/1	0.99	0.06	36,36,36,36	0
19	NI	L	503	1/1	0.99	0.04	36,36,36,36	0
16	CA	F	501	1/1	1.00	0.02	31,31,31,31	0

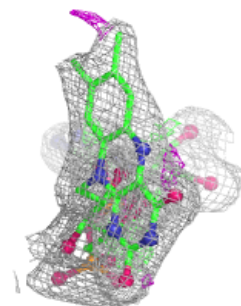
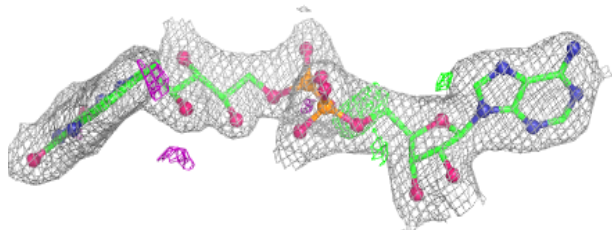
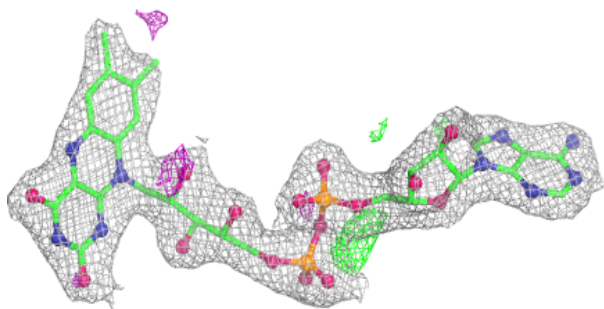
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

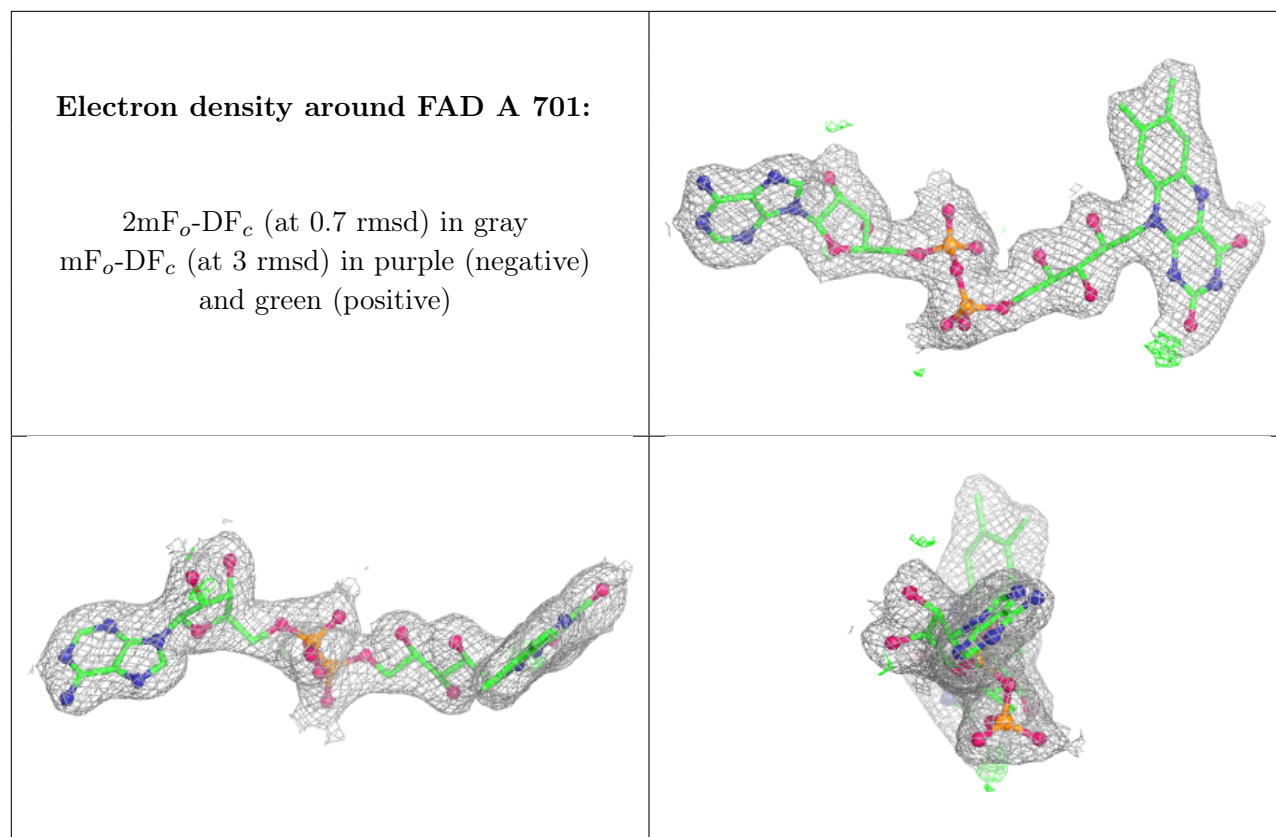
Electron density around PE3 A 704:

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

**Electron density around FAD G 701:**

$2mF_o-DF_c$ (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.