wwPDB X-ray Structure Validation Summary Report (i)

Aug 24, 2026 – 11:12 pm BST

PDB ID	:	5G5H / pdb_00005g5h
Title	:	Escherichia coli Periplasmic Aldehyde Oxidase R440H mutant
Authors	:	Correia, M.A.S.; Otrelo-Cardoso, A.R.; Romao, M.J.; Santos-Silva, T.
Deposited on	:	2016-05-25
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 (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:

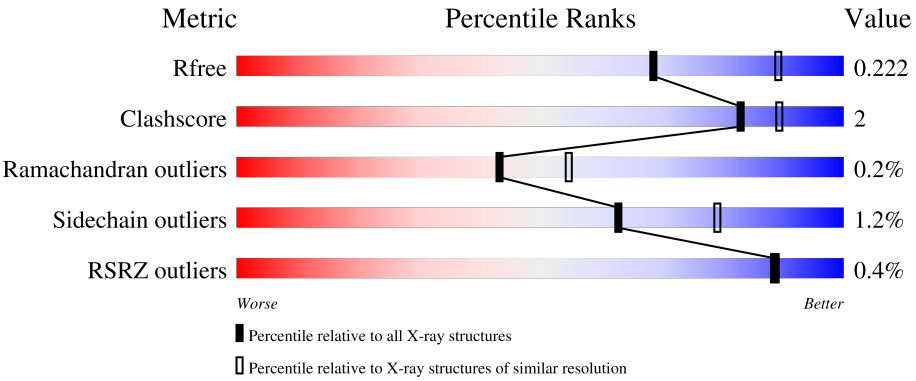
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.015 (Gargrove)
Density-Fitness	:	1.0.12
Ideal 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 (i)

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 <=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	229	% 75% . 24%
2	B	318	% 95% . .
3	C	732	95% .

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
11	F5K	C	1749	-	-	X	-

2 Entry composition (i)

There are 12 unique types of molecules in this entry. The entry contains 9954 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 Aldehyde oxidoreductase iron-sulfur-binding subunit PaoA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	173	Total	C	N	O	S	0	0	0
			1272	781	226	252	13			

- Molecule 2 is a protein called Aldehyde oxidoreductase FAD-binding subunit PaoB.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	316	Total	C	N	O	S	0	0	0
			2368	1490	432	438	8			

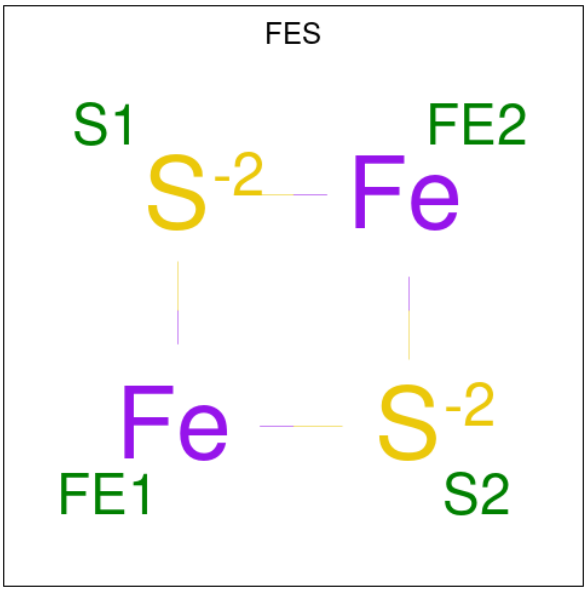
- Molecule 3 is a protein called Aldehyde oxidoreductase molybdenum-binding subunit PaoC.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	730	Total	C	N	O	S	0	3	0
			5488	3425	978	1059	26			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	88	VAL	ALA	conflict	UNP P77489
C	391	GLY	ASP	conflict	UNP P77489
C	440	HIS	ARG	engineered mutation	UNP P77489

- Molecule 4 is FE2/S2 (INORGANIC) CLUSTER (CCD ID: FES) (formula: Fe_2S_2).

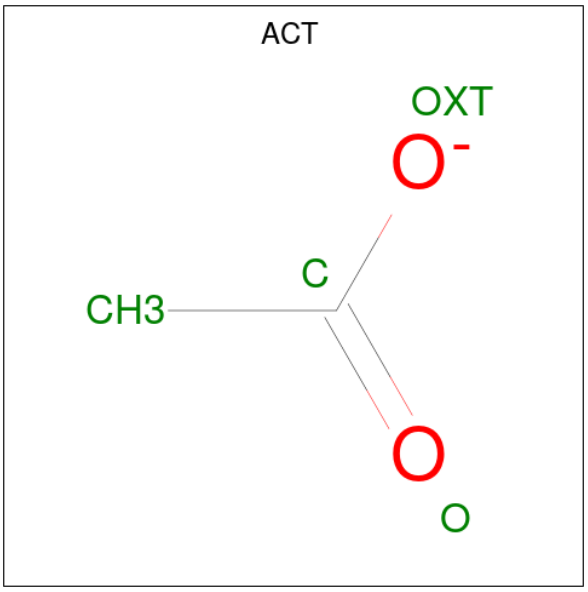


Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total Fe S 4 2 2	0	0
4	A	1	Total Fe S 4 2 2	0	0

- Molecule 5 is IODIDE ION (CCD ID: IOD) (formula: I).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total I 1 1	0	0
5	B	3	Total I 3 3	0	0
5	C	4	Total I 4 4	0	0

- Molecule 6 is ACETATE ION (CCD ID: ACT) (formula: $C_2H_3O_2$).

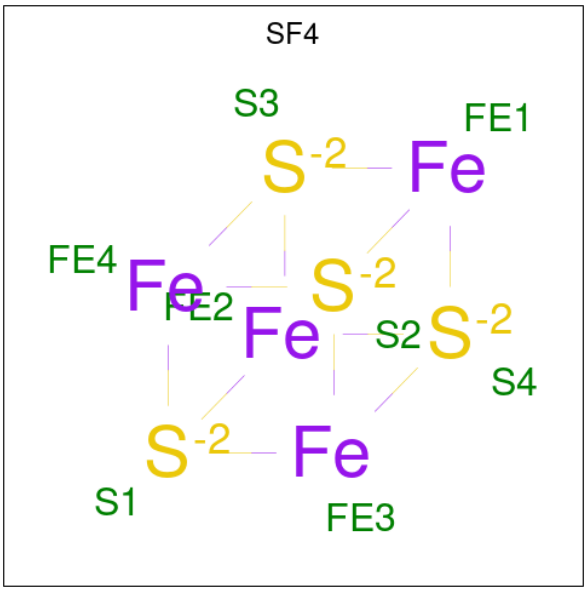


Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	1	Total C O 4 2 2	0	0
6	C	1	Total C O 4 2 2	0	0
6	C	1	Total C O 4 2 2	0	0

- Molecule 7 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

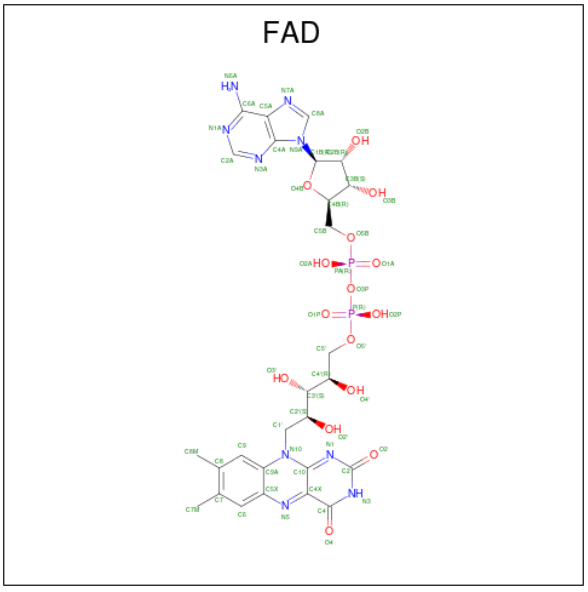
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	1	Total Cl 1 1	0	0
7	B	3	Total Cl 3 3	0	0
7	C	6	Total Cl 6 6	0	0

- Molecule 8 is IRON/SULFUR CLUSTER (CCD ID: SF4) (formula: Fe_4S_4).



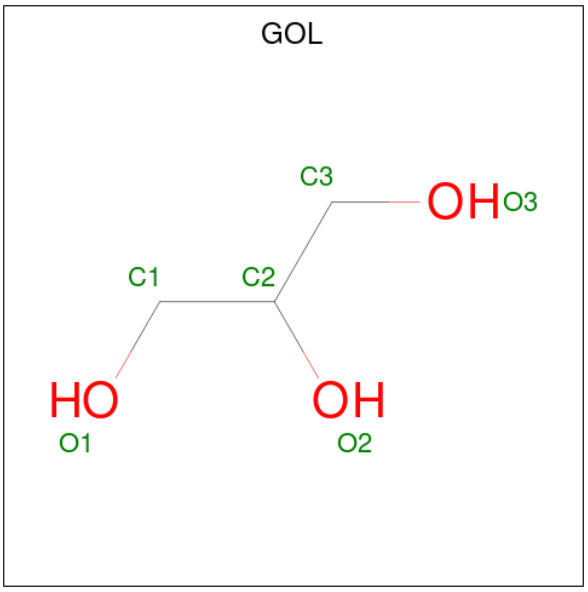
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	Fe	S		
8	B	1	8	4	4	0	0

- Molecule 9 is FLAVIN-ADENINE DINUCLEOTIDE (CCD ID: FAD) (formula: $C_{27}H_{33}N_9O_{15}P_2$).



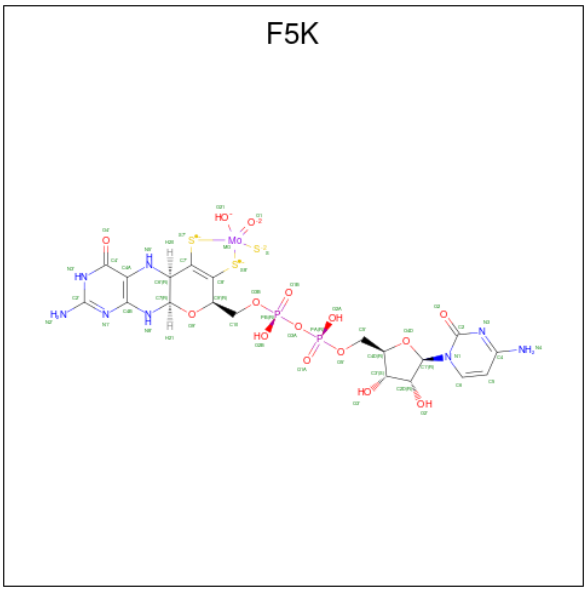
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
9	B	1	53	27	9	15	2	0	0

- Molecule 10 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



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

- Molecule 11 is Molybdopterin cytosine dinucleotide hydroxy-oxo-sulfido-molybdenum (CCD ID: F5K) (formula: $C_{19}H_{25}MoN_8O_{15}P_2S_3$).



Mol	Chain	Residues	Atoms							ZeroOcc	AltConf
11	C	1	Total	C	Mo	N	O	P	S	0	0
			48	19	1	8	15	2	3		

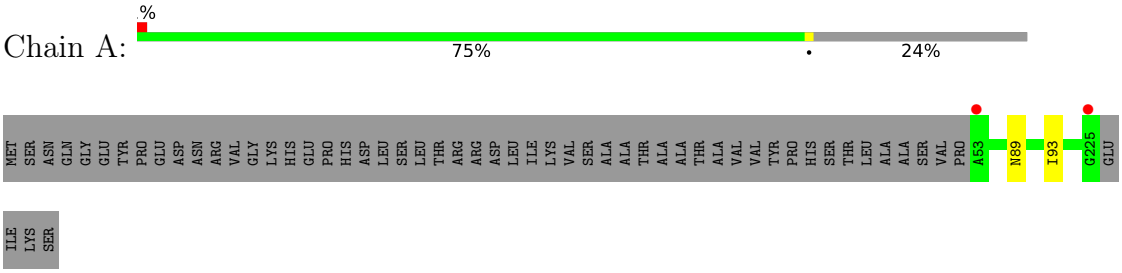
- Molecule 12 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
12	A	111	Total	O	0	0
			111	111		
12	B	155	Total	O	0	0
			155	155		
12	C	395	Total	O	0	0
			395	395		

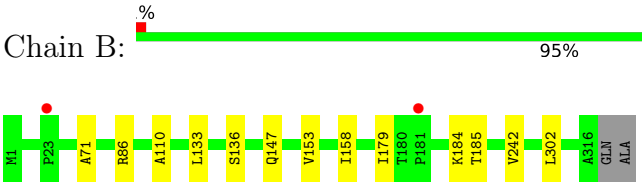
3 Residue-property plots (i)

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.

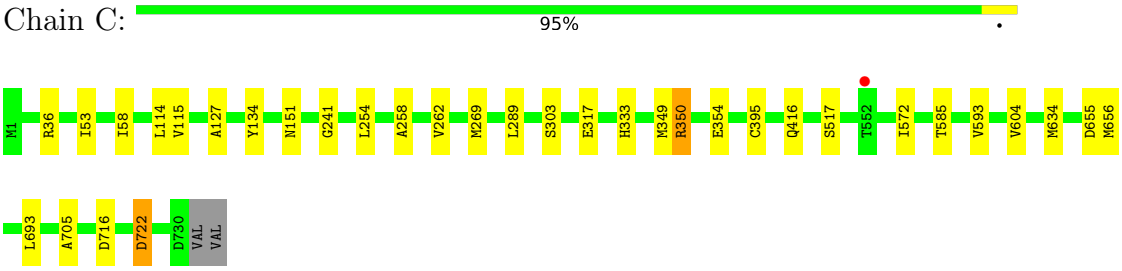
• Molecule 1: Aldehyde oxidoreductase iron-sulfur-binding subunit PaoA



• Molecule 2: Aldehyde oxidoreductase FAD-binding subunit PaoB



• Molecule 3: Aldehyde oxidoreductase molybdenum-binding subunit PaoC



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	109.84Å 78.26Å 151.73Å 90.00° 99.93° 90.00°	Depositor
Resolution (Å)	48.27 – 2.30 48.27 – 2.30	Depositor EDS
% Data completeness (in resolution range)	98.0 (48.27-2.30) 97.9 (48.27-2.30)	Depositor EDS
R_{merge}	0.21	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.81 (at 2.29Å)	Xtriage
Refinement program	REFMAC 5.8.0107	Depositor
R, R_{free}	0.164 , 0.220 0.173 , 0.222	Depositor DCC
R_{free} test set	2811 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å^2)	22.6	Xtriage
Anisotropy	0.546	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.37 , 40.7	EDS
L-test for twinning[2]	$< \|L\| > = 0.47$, $< L^2 > = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	9954	wwPDB-VP
Average B, all atoms (Å^2)	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.15% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: CSD, FAD, ACT, IOD, GOL, FES, SF4, CL, F5K

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	0.68	0/1288	0.85	0/1748
2	B	0.64	0/2412	0.83	0/3281
3	C	0.66	0/5597	0.86	0/7602
All	All	0.65	0/9297	0.85	0/12631

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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	1272	0	1263	1	0
2	B	2368	0	2413	5	0
3	C	5488	0	5435	18	0
4	A	8	0	0	0	0
5	A	1	0	0	0	0
5	B	3	0	0	0	0
5	C	4	0	0	1	0
6	A	4	0	3	0	0
6	C	8	0	6	1	0
7	A	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	B	3	0	0	0	0
7	C	6	0	0	0	0
8	B	8	0	0	0	0
9	B	53	0	31	0	0
10	C	18	0	24	1	0
11	C	48	0	0	23	0
12	A	111	0	0	0	0
12	B	155	0	0	0	0
12	C	395	0	0	0	0
All	All	9954	0	9175	45	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 2.

The worst 5 of 45 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)
11:C:1749:F5K:C2D	11:C:1749:F5K:C1'	1.79	1.60
11:C:1749:F5K:C4D	11:C:1749:F5K:C3'	1.76	1.59
11:C:1749:F5K:C4B	11:C:1749:F5K:C4A	1.78	1.58
11:C:1749:F5K:N3	11:C:1749:F5K:C2	1.70	1.50
11:C:1749:F5K:N5'	11:C:1749:F5K:C6'	1.86	1.38

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	171/229 (75%)	165 (96%)	6 (4%)	0	100	100
2	B	314/318 (99%)	308 (98%)	6 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
3	C	730/732 (100%)	707 (97%)	21 (3%)	2 (0%)	36 46
All	All	1215/1279 (95%)	1180 (97%)	33 (3%)	2 (0%)	43 55

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	C	241	GLY
3	C	350	ARG

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	139/186 (75%)	138 (99%)	1 (1%)	76 87
2	B	243/244 (100%)	240 (99%)	3 (1%)	63 79
3	C	566/565 (100%)	559 (99%)	7 (1%)	63 79
All	All	948/995 (95%)	937 (99%)	11 (1%)	63 79

5 of 11 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	C	416	GLN
3	C	656	MET
3	C	722	ASP
3	C	716	ASP
3	C	151	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 14 such sidechains are listed below:

Mol	Chain	Res	Type
3	C	122	GLN
3	C	161	ASN
3	C	442	ASN

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Mol	Chain	Res	Type
3	C	386	GLN
3	C	416	GLN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

1 non-standard protein/DNA/RNA residue is modelled in this entry.

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	$\#\|Z\| > 2$
3	CSD	C	395	3	3,7,8	0.92	0	1,8,10	2.55	1 (100%)

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
3	CSD	C	395	3	-	1/2/6/8	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	C	395	CSD	OD1-SG-CB	-2.55	100.68	105.54

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	C	395	CSD	CA-CB-SG-OD1

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 29 ligands modelled in this entry, 18 are monoatomic - 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	$\#\|Z\| > 2$
6	ACT	C	1742	-	3,3,3	0.77	0	3,3,3	0.66	0
4	FES	A	1227	1	0,4,4	-	-	-		
10	GOL	C	1746	-	5,5,5	0.66	0	5,5,5	0.99	0
4	FES	A	1226	1	0,4,4	-	-	-		
9	FAD	B	1318	-	56,58,58	2.07	18 (32%)	81,89,89	2.26	30 (37%)
11	F5K	C	1749	3	43,53,53	9.73	32 (74%)	48,86,86	6.78	33 (68%)
10	GOL	C	1744	-	5,5,5	0.36	0	5,5,5	0.41	0
6	ACT	C	1743	-	3,3,3	0.77	0	3,3,3	1.20	0
10	GOL	C	1745	-	5,5,5	0.34	0	5,5,5	0.53	0
8	SF4	B	1317	2	0,12,12	-	-	-		
6	ACT	A	1229	-	3,3,3	0.79	0	3,3,3	0.61	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
10	GOL	C	1746	-	-	3/4/4/4	-
4	FES	A	1227	1	-	-	0/1/1/1
4	FES	A	1226	1	-	-	0/1/1/1
9	FAD	B	1318	-	-	0/34/50/50	0/6/6/6
11	F5K	C	1749	3	-	3/22/78/78	0/6/6/6
10	GOL	C	1745	-	-	0/4/4/4	-
10	GOL	C	1744	-	-	2/4/4/4	-
8	SF4	B	1317	2	-	-	0/6/5/5

The worst 5 of 50 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
11	C	1749	F5K	C6'-N5'	34.28	1.86	1.46
11	C	1749	F5K	C4A-C4B	23.38	1.78	1.38
11	C	1749	F5K	C10-C9'	-22.09	1.22	1.52
11	C	1749	F5K	C7-C6'	18.65	1.68	1.53
11	C	1749	F5K	C2-N3	16.94	1.70	1.36

The worst 5 of 63 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
11	C	1749	F5K	C7'-C8'-S8'	28.88	136.54	120.15
11	C	1749	F5K	O9'-C7-C6'	-13.64	99.86	108.96
11	C	1749	F5K	C5-C4-N3	-12.67	99.77	121.33
11	C	1749	F5K	N1-C2-N3	-12.12	96.74	118.81
11	C	1749	F5K	O4'-C4'-C4A	-9.35	105.81	127.24

There are no chirality outliers.

5 of 8 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
10	C	1744	GOL	O1-C1-C2-C3
10	C	1746	GOL	C1-C2-C3-O3
11	C	1749	F5K	C3'-C4D-C5'-O5'
11	C	1749	F5K	O4D-C4D-C5'-O5'
10	C	1744	GOL	O1-C1-C2-O2

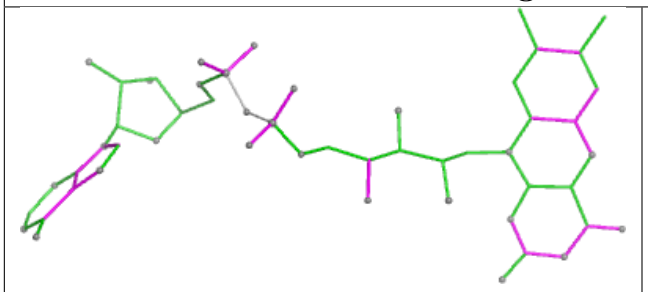
There are no ring outliers.

3 monomers are involved in 25 short contacts:

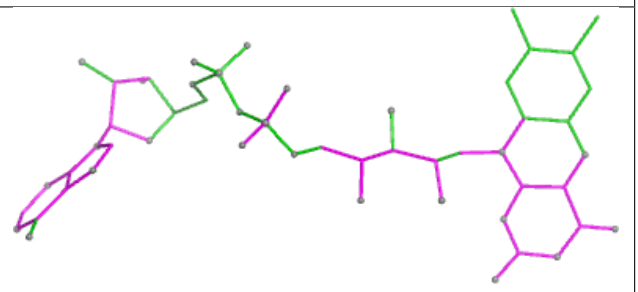
Mol	Chain	Res	Type	Clashes	Symm-Clashes
11	C	1749	F5K	23	0
6	C	1743	ACT	1	0
10	C	1745	GOL	1	0

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 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.

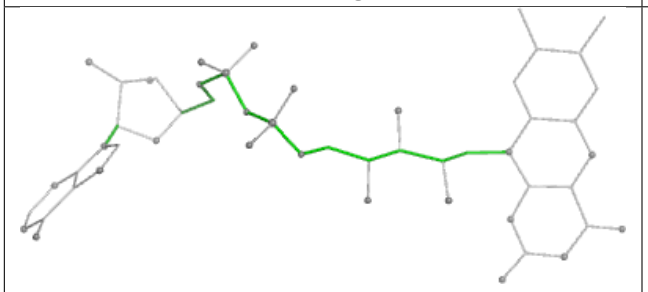
Ligand FAD B 1318



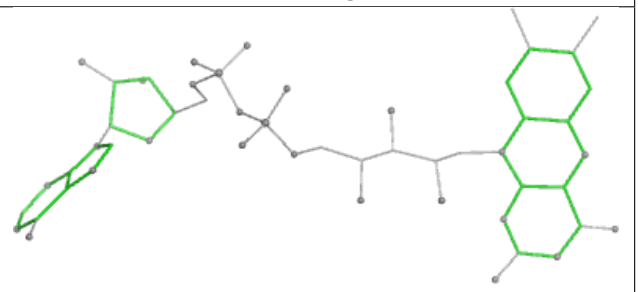
Bond lengths



Bond angles

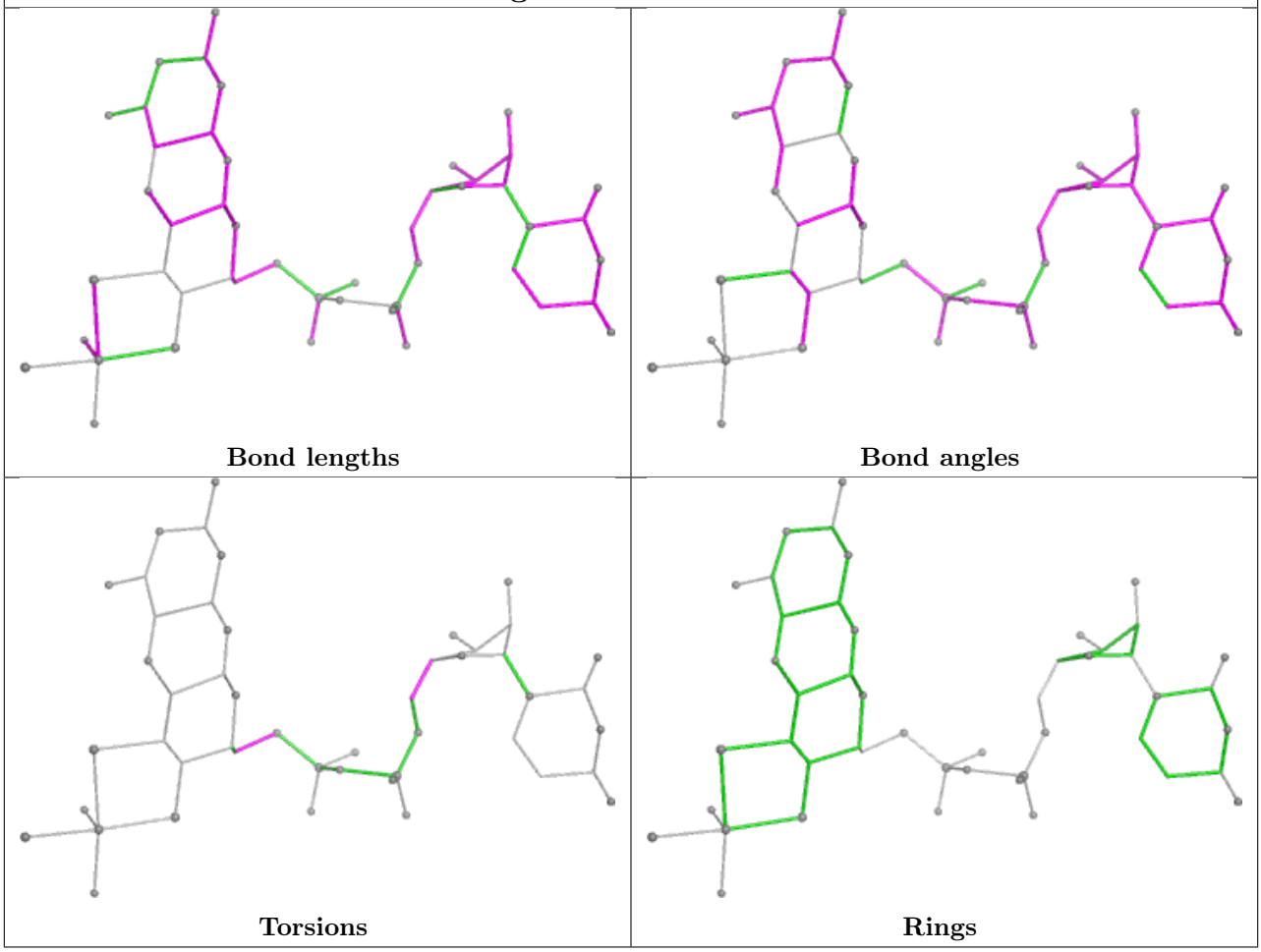


Torsions



Rings

Ligand F5K C 1749



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	173/229 (75%)	-0.29	2 (1%)	76	77	16, 25, 40, 54	0
2	B	316/318 (99%)	-0.17	2 (0%)	85	86	18, 29, 45, 68	0
3	C	729/732 (99%)	-0.31	1 (0%)	92	91	12, 23, 42, 71	3 (0%)
All	All	1218/1279 (95%)	-0.27	5 (0%)	88	89	12, 25, 43, 71	3 (0%)

All (5) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	225	GLY	2.5
3	C	552	THR	2.2
2	B	23	PRO	2.1
2	B	181	PRO	2.1
1	A	53	ALA	2.0

6.2 Non-standard residues in protein, DNA, RNA chains

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
3	CSD	C	395	8/9	0.92	0.11	24,28,39,39	0

6.3 Carbohydrates

There are no oligosaccharides in this entry.

6.4 Ligands (i)

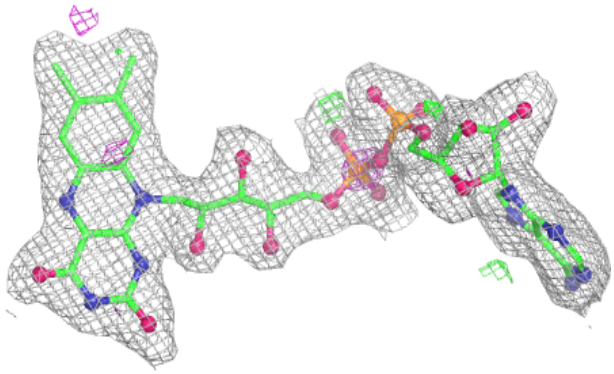
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

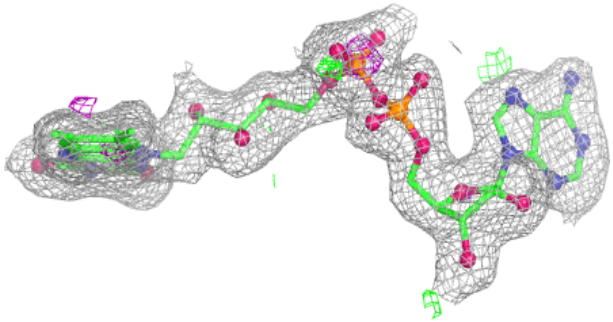
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
6	ACT	A	1229	4/4	0.71	0.18	46,47,48,49	0
6	ACT	C	1742	4/4	0.82	0.15	51,54,55,56	0
10	GOL	C	1745	6/6	0.83	0.18	47,50,53,55	0
10	GOL	C	1746	6/6	0.84	0.14	43,45,47,47	0
7	CL	C	1738	1/1	0.88	0.12	43,43,43,43	0
10	GOL	C	1744	6/6	0.89	0.11	41,44,46,46	0
7	CL	B	1322	1/1	0.90	0.09	50,50,50,50	0
6	ACT	C	1743	4/4	0.92	0.11	16,18,18,22	0
7	CL	C	1748	1/1	0.94	0.07	26,26,26,26	0
4	FES	A	1226	4/4	0.94	0.07	15,17,18,21	0
9	FAD	B	1318	53/53	0.95	0.07	15,18,24,25	0
11	F5K	C	1749	48/48	0.95	0.07	10,13,16,17	1
7	CL	C	1740	1/1	0.96	0.07	37,37,37,37	0
7	CL	C	1747	1/1	0.96	0.06	48,48,48,48	0
8	SF4	B	1317	8/8	0.97	0.04	25,27,30,30	0
7	CL	B	1324	1/1	0.97	0.05	37,37,37,37	0
5	IOD	C	1737	1/1	0.98	0.03	35,35,35,35	1
5	IOD	B	1320	1/1	0.98	0.07	54,54,54,54	1
5	IOD	B	1323	1/1	0.98	0.03	37,37,37,37	1
5	IOD	C	1735	1/1	0.98	0.05	29,29,29,29	1
7	CL	A	1230	1/1	0.98	0.12	10,10,10,10	0
7	CL	B	1321	1/1	0.98	0.04	21,21,21,21	0
5	IOD	A	1228	1/1	0.99	0.04	25,25,25,25	1
5	IOD	C	1734	1/1	0.99	0.03	33,33,33,33	1
5	IOD	B	1319	1/1	0.99	0.02	36,36,36,36	1
7	CL	C	1739	1/1	0.99	0.03	33,33,33,33	0
5	IOD	C	1736	1/1	0.99	0.02	37,37,37,37	1
7	CL	C	1741	1/1	0.99	0.08	22,22,22,22	0
4	FES	A	1227	4/4	0.99	0.03	13,14,15,17	0

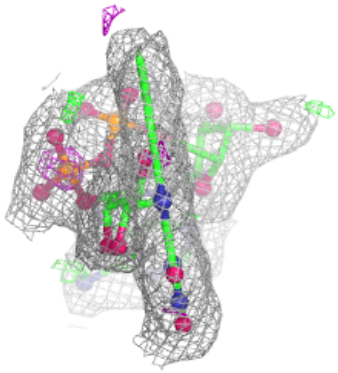
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around FAD B 1318:

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

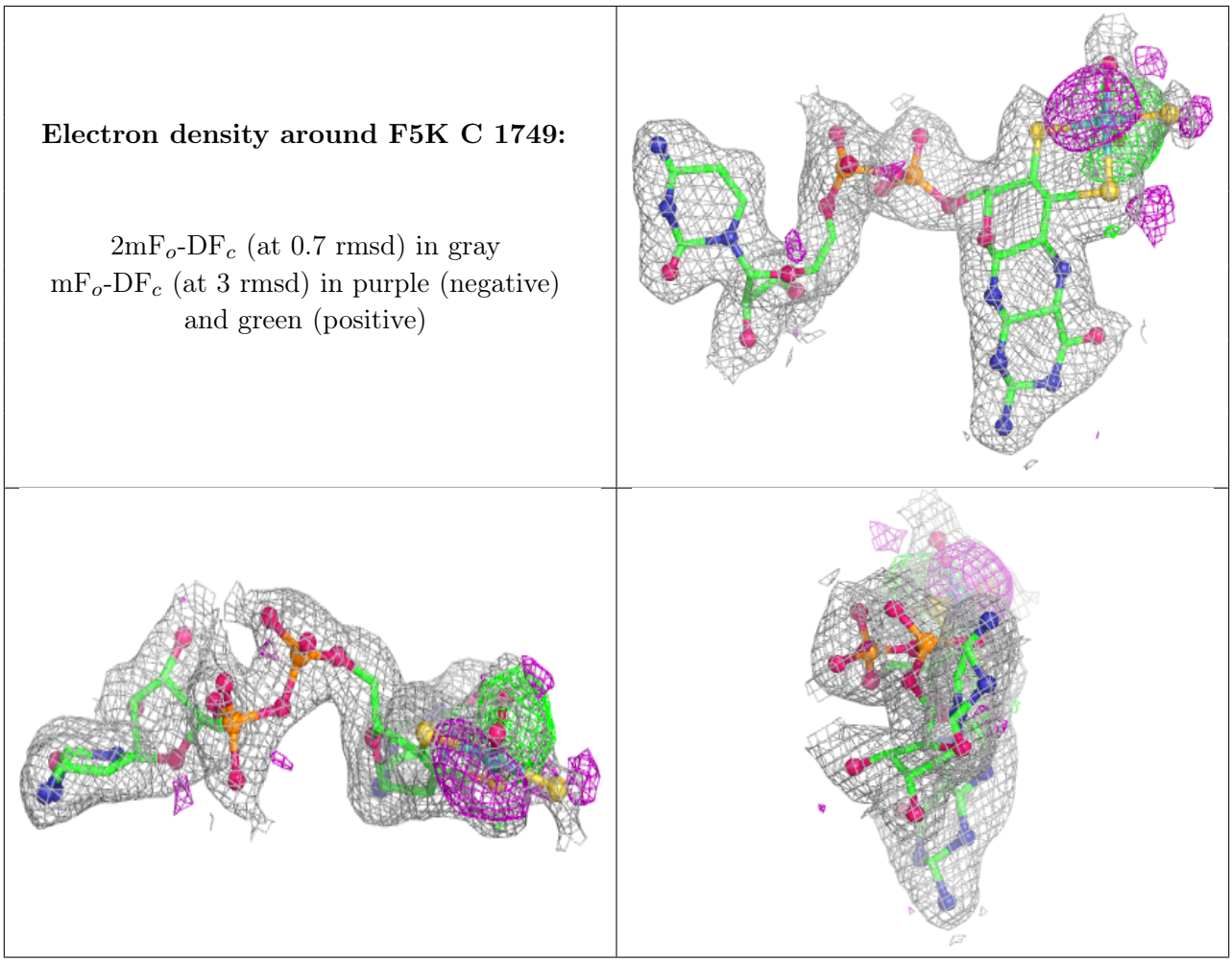






Electron density around F5K C 1749:

$2mF_o$-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.