



Full wwPDB X-ray Structure Validation Report ⓘ

Sep 1, 2025 – 10:37 AM JST

PDB ID : 9JSQ / pdb_00009jsq
Title : The mutant structure of Dihydroxyacid dehydratase (DHAD)-I177F
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Deposited on : 2024-10-01
Resolution : 2.45 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0rc1
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 2.0rc1
EDS : 3.0
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4 : 9.0.006 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.45.1

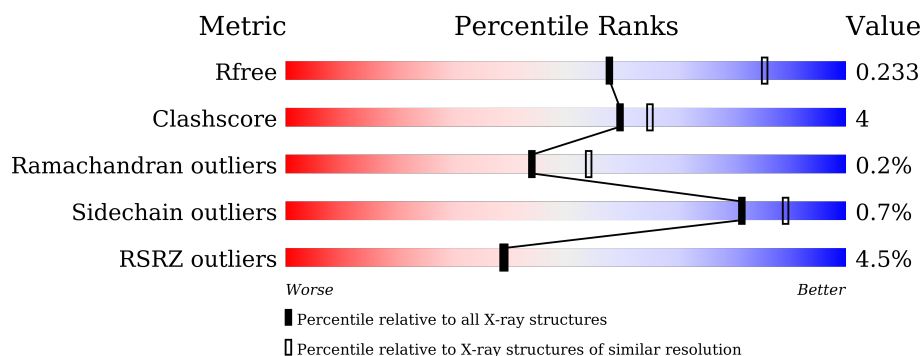
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.45 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}	164625	1096 (2.46-2.46)
Clashscore	180529	1178 (2.46-2.46)
Ramachandran outliers	177936	1170 (2.46-2.46)
Sidechain outliers	177891	1170 (2.46-2.46)
RSRZ outliers	164620	1096 (2.46-2.46)

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	580	<div> <div>4%</div> <div>85%</div> <div>10%</div> <div>5%</div> </div>

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 4163 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.

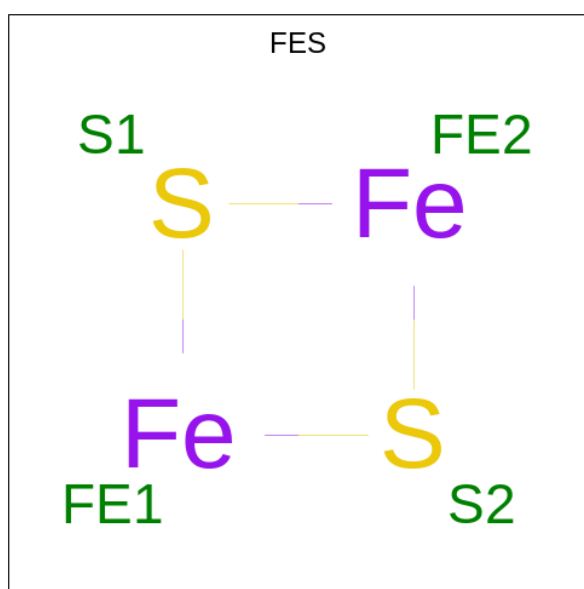
- Molecule 1 is a protein called Dihydroxy-acid dehydratase, chloroplastic.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	551	4141	2594	701	811	35	0	7	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-5	GLY	-	expression tag	UNP Q9LIR4
A	177	PHE	ILE	engineered mutation	UNP Q9LIR4
A	525	ALA	LYS	engineered mutation	UNP Q9LIR4
A	526	ALA	LYS	engineered mutation	UNP Q9LIR4

- Molecule 2 is FE2/S2 (INORGANIC) CLUSTER (CCD ID: FES) (formula: Fe_2S_2) (labeled as "Ligand of Interest" by depositor).



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

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	18	Total	O	0	0
			18	18		

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.

- Chain A:
-
- 4% 85% 10% 5%
- GLY SER ILE CYS SER ALA Q3 P12 ILE THR ASP T16 M17 K21 S24 R25 P29 K30 S57 L71 F91 M107 R114 I117 K140 K141 N142 M143 P156 G163 T164 G168 H18 PHE GLN ASP LYS THR TYR ASP F177 V178 S179 A180 F181 Q182 I183 F187 V188 S191 I192 S193 D194 R197 K198 L201 H201 H202 SER CYS PRO GLY ALA GLY ALA CYS G212 G213 W214 Y215 N218 A239 A257 L258 L259 K260 W261 T270 S273 V279 R299 V317 P318 F319 L320 K321 D322 L323 K324 P325 S326 K328 Y329 K336 R345 Y346 L350 M353 L365 L369 S374 E377 P388 I389 K390 G393 H394 L402 T412 E463 L462 F468 S469 G490 G491 S492 H493 G494 I519 E574

4 Data and refinement statistics

Property	Value	Source
Space group	P 42 21 2	Depositor
Cell constants a, b, c, α , β , γ	135.49Å 135.49Å 66.86Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	38.94 – 2.45 38.94 – 2.45	Depositor EDS
% Data completeness (in resolution range)	95.9 (38.94-2.45) 95.9 (38.94-2.45)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.91 (at 2.45Å)	Xtriage
Refinement program	PHENIX 1.19.2_4158	Depositor
R, R_{free}	0.198 , 0.233 0.198 , 0.233	Depositor DCC
R_{free} test set	1125 reflections (4.80%)	wwPDB-VP
Wilson B-factor (Å ²)	46.3	Xtriage
Anisotropy	0.056	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 45.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	4163	wwPDB-VP
Average B, all atoms (Å ²)	54.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.52% 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: FES

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	0.09	0/4211	0.27	0/5685

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 [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	4141	0	4162	35	0
2	A	4	0	0	0	0
3	A	18	0	0	0	0
All	All	4163	0	4162	35	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 4.

All (35) 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:107:MET:HE2	1:A:463:GLU:H	1.61	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:213:GLY:O	1:A:218:ASN:ND2	2.33	0.59
1:A:114:ARG:HB2	1:A:141[A]:LYS:HB3	1.87	0.56
1:A:194:ASP:O	1:A:198:LYS:HG2	2.07	0.54
1:A:321:ALA:HB1	1:A:323:LEU:HD23	1.91	0.53
1:A:12:PRO:HG3	1:A:25:ARG:HB2	1.91	0.52
1:A:117:ILE:HD13	1:A:142[B]:ASN:HB3	1.92	0.50
1:A:183:SER:HB2	1:A:197:ARG:HG3	1.92	0.50
1:A:377:GLU:H	1:A:377:GLU:CD	2.20	0.49
1:A:164:THR:OG1	1:A:218:ASN:OD1	2.26	0.48
1:A:57:SER:HB3	1:A:91:PHE:CZ	2.49	0.47
1:A:319:PHE:HE2	1:A:321:ALA:HB3	1.80	0.47
1:A:323:LEU:O	1:A:327:GLY:N	2.44	0.47
1:A:345:ARG:HD2	1:A:369:LEU:O	2.15	0.47
1:A:213:GLY:H	1:A:215:TYR:HE2	1.64	0.45
1:A:71:LEU:HD23	1:A:71:LEU:HA	1.83	0.45
1:A:482:LEU:HG	1:A:488:PHE:CZ	2.51	0.45
1:A:463:GLU:OE2	1:A:489:SER:OG	2.29	0.45
1:A:24:SER:O	1:A:29:PRO:HD3	2.16	0.45
1:A:257:GLU:O	1:A:261:MET:HG3	2.17	0.44
1:A:346:TYR:CZ	1:A:350:LEU:HD11	2.52	0.44
1:A:320:LEU:HD23	1:A:388:PRO:HB3	1.99	0.44
1:A:390:LYS:NZ	1:A:393:GLY:O	2.49	0.44
1:A:197:ARG:O	1:A:201:LEU:HG	2.18	0.43
1:A:324:LYS:HB3	1:A:324:LYS:HE3	1.70	0.43
1:A:163:GLY:HA3	1:A:239:ALA:HA	2.00	0.43
1:A:156:PRO:HG2	1:A:259:LEU:HD23	2.00	0.43
1:A:402:LEU:HD11	1:A:519:ILE:HG12	2.01	0.43
1:A:323:LEU:HD13	1:A:329:TYR:HB2	2.01	0.43
1:A:394:HIS:CE1	1:A:412:THR:HG22	2.54	0.42
1:A:299:ARG:HD2	1:A:299:ARG:HA	1.78	0.42
1:A:270:THR:H	1:A:273:SER:HG	1.66	0.42
1:A:353:MET:HE2	1:A:365:LEU:HD21	2.01	0.42
1:A:279:VAL:HG22	1:A:317:VAL:HG21	2.03	0.40
1:A:12:PRO:HD2	1:A:21:LYS:O	2.21	0.40

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	550/580 (95%)	533 (97%)	16 (3%)	1 (0%)	44	54

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	143	MET

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	454/471 (96%)	450 (99%)	4 (1%)	75	86

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	57	SER
1	A	141[A]	LYS
1	A	141[B]	LYS
1	A	336	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	493	HIS

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Mol	Chain	Res	Type
1	A	531	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](#)

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](#)

1 ligand 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	$\# Z > 2$
2	FES	A	601	1	0,4,4	-	-	-		

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
2	FES	A	601	1	-	-	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

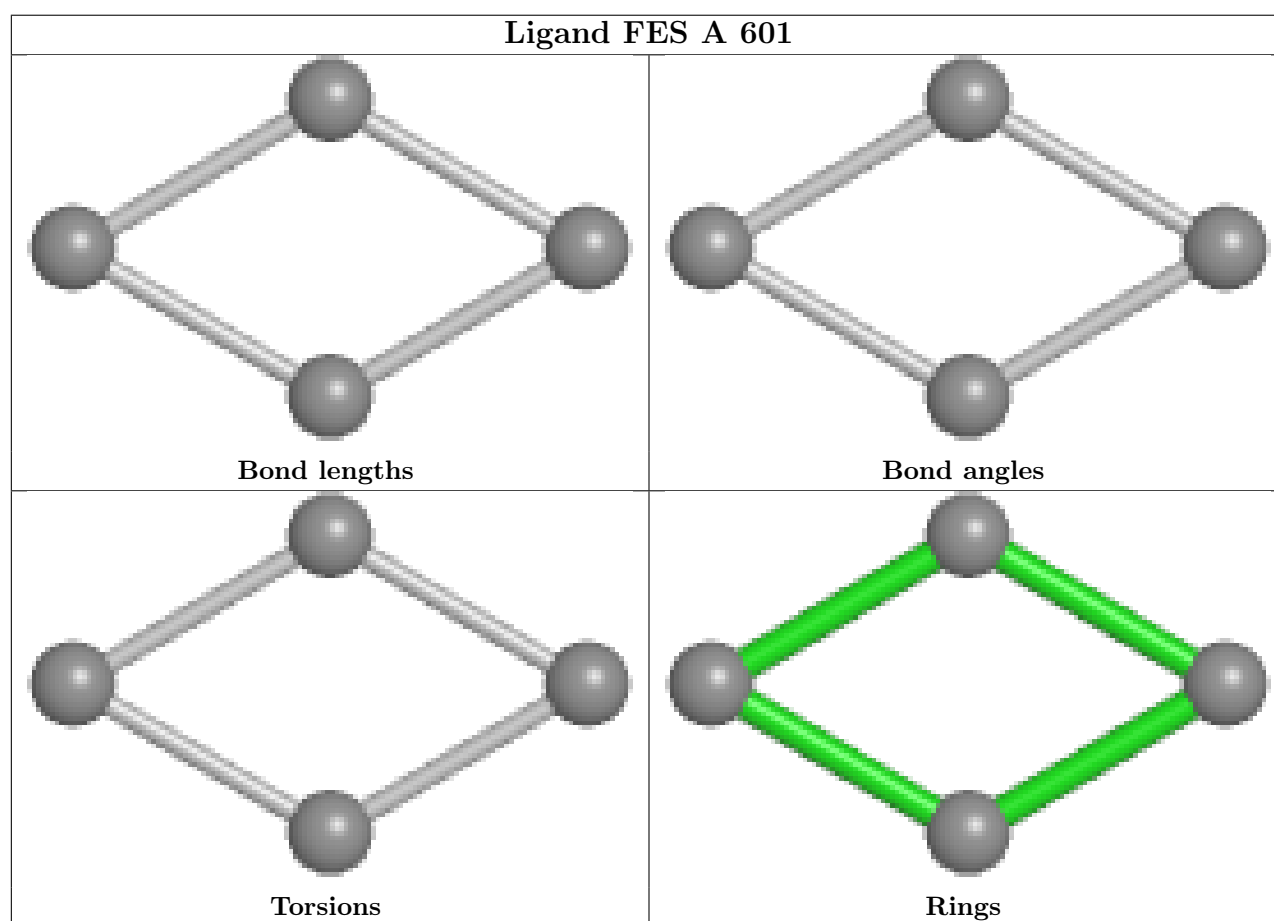
There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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 ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

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

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

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ > 2		OWAB(Å ²)	Q < 0.9
1	A	551/580 (95%)	0.05	25 (4%)	39 39	25, 47, 95, 155	8 (1%)

All (25) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	178	VAL	6.1
1	A	141[A]	LYS	4.8
1	A	30	LYS	3.7
1	A	215	TYR	3.7
1	A	212	GLY	3.4
1	A	191	SER	3.3
1	A	16	THR	3.2
1	A	180	ALA	3.1
1	A	187	PHE	3.0
1	A	182	GLN	2.8
1	A	492	SER	2.6
1	A	493	HIS	2.5
1	A	17	ASN	2.4
1	A	320	LEU	2.4
1	A	140[A]	ASP	2.3
1	A	494	GLY	2.3
1	A	188	VAL	2.3
1	A	142[A]	ASN	2.2
1	A	177	PHE	2.2
1	A	490	GLY	2.1
1	A	491	GLY	2.1
1	A	181	PHE	2.1
1	A	374	SER	2.1
1	A	326	SER	2.1
1	A	192	ILE	2.1

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

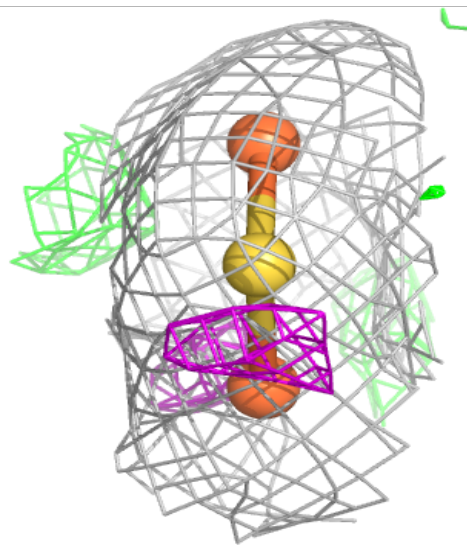
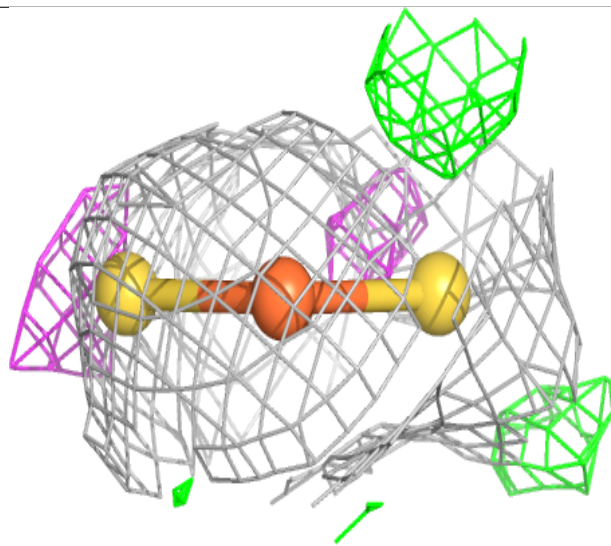
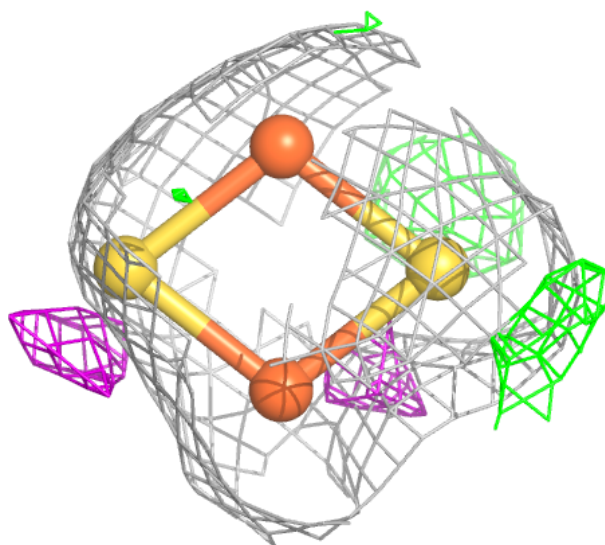
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	FES	A	601	4/4	0.78	0.14	56,90,91,95	4

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 FES A 601:

$2mF_o - DF_c$ (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.