



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 03:10 AM UTC

PDB ID : 8QDR / pdb_00008qdr
Title : Vitis vinifera dimeric 13S-lipoxygenase LOXA in a detergent bound open conformation
Authors : Wild, K.; Sinning, I.
Deposited on : 2023-08-30
Resolution : 2.00 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

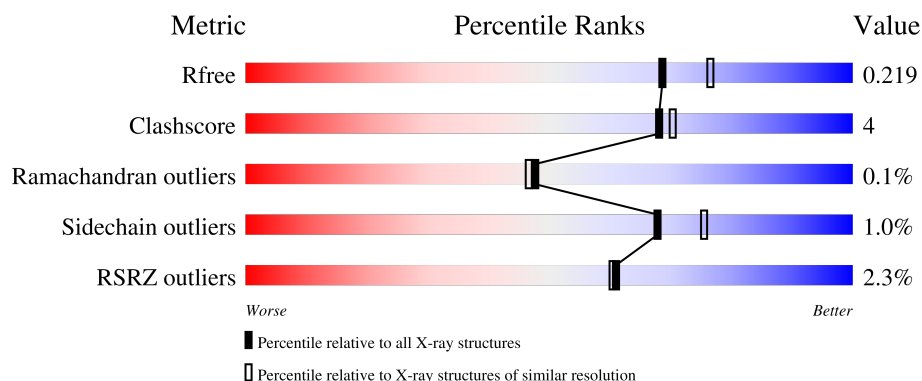
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

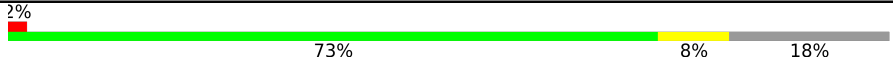
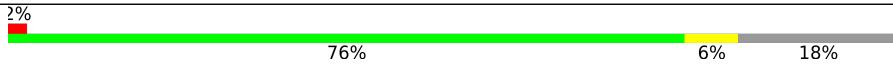
The reported resolution of this entry is 2.00 Å.

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	10052 (2.00-2.00)
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (2.00-2.00)

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	863	
1	B	863	

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 12100 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 Lipoxxygenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	706	Total	C	N	O	S	0	6	0
			5713	3672	962	1067	12			
1	B	705	Total	C	N	O	S	0	0	0
			5672	3643	955	1062	12			

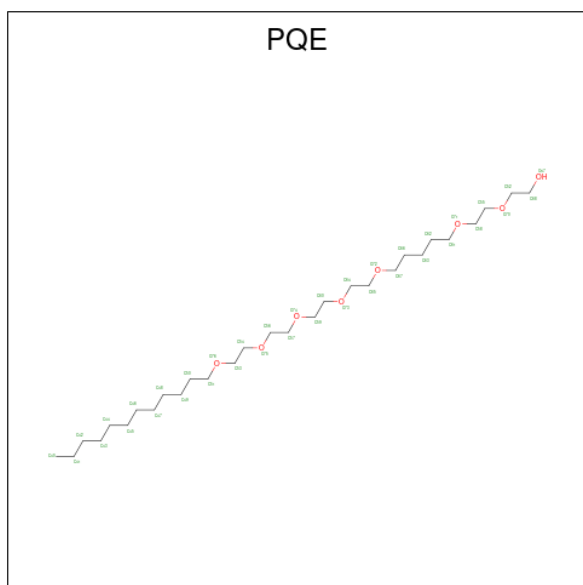
There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	39	MET	-	initiating methionine	UNP D7SLA9
A	40	HIS	-	expression tag	UNP D7SLA9
A	41	HIS	-	expression tag	UNP D7SLA9
A	42	HIS	-	expression tag	UNP D7SLA9
A	43	HIS	-	expression tag	UNP D7SLA9
A	44	HIS	-	expression tag	UNP D7SLA9
A	45	HIS	-	expression tag	UNP D7SLA9
A	46	GLY	-	expression tag	UNP D7SLA9
A	47	SER	-	expression tag	UNP D7SLA9
B	39	MET	-	initiating methionine	UNP D7SLA9
B	40	HIS	-	expression tag	UNP D7SLA9
B	41	HIS	-	expression tag	UNP D7SLA9
B	42	HIS	-	expression tag	UNP D7SLA9
B	43	HIS	-	expression tag	UNP D7SLA9
B	44	HIS	-	expression tag	UNP D7SLA9
B	45	HIS	-	expression tag	UNP D7SLA9
B	46	GLY	-	expression tag	UNP D7SLA9
B	47	SER	-	expression tag	UNP D7SLA9

- Molecule 2 is FE (III) ION (CCD ID: FE) (formula: Fe) (labeled as "Ligand of Interest" by depositor).

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

- Molecule 3 is 3,6,12,15,18,21,24-HEPTAOXAHEXATRIACONTAN-1-OL (CCD ID: PQE) (formula: $C_{29}H_{60}O_8$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C O 10 6 4	0	0
3	B	1	Total C O 10 6 4	0	0

- Molecule 4 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: $C_2H_6O_2$).



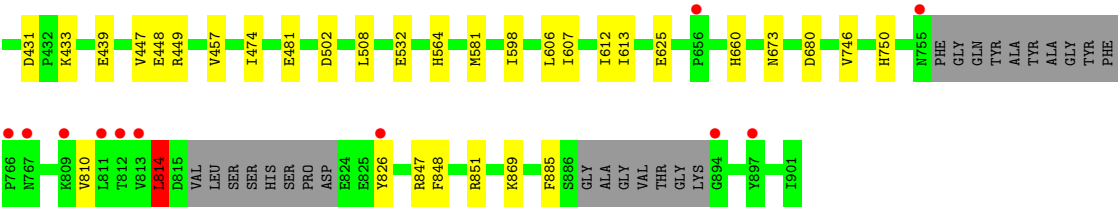
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			4	2	2		
4	A	1	Total	C	O	0	0
			4	2	2		
4	A	1	Total	C	O	0	0
			4	2	2		
4	B	1	Total	C	O	0	0
			4	2	2		
4	B	1	Total	C	O	0	0
			4	2	2		
4	B	1	Total	C	O	0	0
			4	2	2		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	347	Total	O	0	0
			347	347		
5	B	322	Total	O	0	0
			322	322		

- Molecule 1: Lipoxygenase





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	85.91Å 105.82Å 88.53Å 90.00° 92.84° 90.00°	Depositor
Resolution (Å)	40.80 – 2.00 40.80 – 2.00	Depositor EDS
% Data completeness (in resolution range)	99.8 (40.80-2.00) 99.7 (40.80-2.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.54 (at 2.00Å)	Xtriage
Refinement program	PHENIX (1.10.1_2155: ???)	Depositor
R, R_{free}	0.174 , 0.218 0.175 , 0.219	Depositor DCC
R_{free} test set	5302 reflections (4.97%)	wwPDB-VP
Wilson B-factor (Å ²)	28.1	Xtriage
Anisotropy	0.449	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 54.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.004 for l,k,-h 0.026 for h,-k,-l 0.018 for l,-k,h	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	12100	wwPDB-VP
Average B, all atoms (Å ²)	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.58% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: EDO, PQE, FE

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	0.33	0/5889	0.49	0/8005
1	B	0.32	0/5829	0.50	0/7926
All	All	0.32	0/11718	0.49	0/15931

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	5713	0	5617	46	0
1	B	5672	0	5567	35	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	10	0	12	3	0
3	B	10	0	12	3	0
4	A	12	0	18	3	0
4	B	12	0	18	2	0
5	A	347	0	0	7	2
5	B	322	0	0	8	2
All	All	12100	0	11244	82	2

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 (82) 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:B:95:ASP:N	5:B:1103:HOH:O	2.06	0.88
1:A:532:GLU:OE1	5:A:1101:HOH:O	1.97	0.81
1:A:404[A]:GLU:OE1	1:A:407[A]:ARG:NH2	2.17	0.77
1:A:792:LYS:NZ	5:A:1102:HOH:O	2.16	0.76
1:B:532:GLU:OE1	5:B:1102:HOH:O	2.06	0.71
1:B:221:ARG:HH11	1:B:581:MET:HE2	1.57	0.69
1:A:881:LEU:HD23	1:A:893:LYS:HG3	1.75	0.67
1:B:481:GLU:HG3	5:B:1174:HOH:O	1.98	0.63
1:B:229:ARG:NH2	5:B:1101:HOH:O	2.01	0.60
1:A:138:GLU:OE2	1:A:170:ARG:NH1	2.32	0.60
1:A:404[A]:GLU:OE2	1:A:408:GLN:NE2	2.35	0.59
1:B:673:ASN:HA	4:B:1003:EDO:H22	1.83	0.59
1:B:255:ASP:HA	1:B:286:ILE:HD12	1.85	0.59
1:A:160:GLN:HB2	1:A:199:LYS:HG2	1.85	0.58
1:A:635:TRP:HB2	4:A:1003:EDO:H21	1.83	0.58
1:A:163:HIS:CE1	1:A:167:MET:HE1	2.39	0.57
1:B:131:ARG:NH1	5:B:1109:HOH:O	2.38	0.56
1:A:841:ILE:HG13	5:A:1416:HOH:O	2.05	0.56
1:A:401:ARG:NH1	1:A:403:GLU:OE1	2.39	0.55
1:B:145:PHE:CE2	1:B:147:ILE:HD11	2.41	0.55
1:A:464:LYS:NZ	5:A:1106:HOH:O	2.34	0.54
1:A:255:ASP:HA	1:A:286:ILE:HD12	1.89	0.54
1:B:213:THR:HG23	1:B:581:MET:HE1	1.90	0.53
1:B:448:GLU:HG3	1:B:457:VAL:HG23	1.91	0.53
1:B:221:ARG:NH1	1:B:581:MET:HE2	2.23	0.53
1:B:660:HIS:CD2	4:B:1003:EDO:H11	2.44	0.52
1:A:74:VAL:HG22	1:A:172:ILE:HG12	1.92	0.52
1:B:431:ASP:OD1	1:B:433:LYS:HG2	2.09	0.52
1:A:634:GLN:HB2	4:A:1003:EDO:H11	1.93	0.51
1:A:746:VAL:HA	1:A:750:HIS:HB3	1.92	0.51
1:B:502:ASP:HB3	1:B:869:LYS:HD2	1.92	0.51
1:A:787:ARG:HG3	1:A:791[B]:HIS:CE1	2.46	0.50
1:A:161:ASN:O	1:A:193:LYS:HB3	2.12	0.50
1:A:184:PHE:CE2	1:A:204:THR:HG22	2.47	0.49
1:B:848:PHE:CE2	3:B:1002:PQE:H651	2.47	0.49
1:A:498:PHE:HB2	1:A:508:LEU:HD11	1.95	0.49
1:B:625:GLU:HG3	5:B:1170:HOH:O	2.13	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:403:GLU:OE2	1:A:407[A]:ARG:NH1	2.46	0.47
1:A:465:LYS:NZ	5:A:1123:HOH:O	2.46	0.47
1:B:660:HIS:ND1	1:B:680:ASP:OD2	2.31	0.47
1:B:160:GLN:HG2	1:B:162:GLU:OE2	2.15	0.47
1:A:163:HIS:ND1	1:A:167:MET:HE1	2.29	0.47
3:B:1002:PQE:H641	3:B:1002:PQE:H591	1.59	0.47
1:A:73:THR:HG23	1:A:140:THR:HG23	1.97	0.47
1:B:106:LEU:HB3	1:B:160:GLN:HB3	1.96	0.46
1:B:74:VAL:HG22	1:B:172:ILE:HG12	1.97	0.46
1:B:121:GLU:OE2	1:B:219:GLU:HB2	2.16	0.45
1:B:851:ARG:NH1	5:B:1112:HOH:O	2.42	0.45
1:A:203:PHE:CE1	1:A:581:MET:HE2	2.51	0.45
1:B:564:HIS:HE1	1:B:598:ILE:HG21	1.82	0.45
1:A:571:ILE:HG12	1:A:592:PHE:CG	2.52	0.45
1:A:851:ARG:NH2	5:A:1117:HOH:O	2.43	0.45
1:A:123:LYS:HB2	1:A:123:LYS:HE3	1.73	0.44
1:A:832:GLU:HB2	1:A:835:TRP:CD2	2.52	0.44
1:A:680:ASP:O	1:A:684:GLU:HG2	2.17	0.44
1:B:826:TYR:CD2	1:B:885:PHE:HA	2.53	0.44
1:A:848:PHE:HE2	3:A:1002:PQE:H651	1.82	0.44
1:B:848:PHE:HE2	3:B:1002:PQE:H651	1.83	0.44
1:A:564:HIS:CE1	4:A:1005:EDO:H12	2.53	0.43
1:A:203:PHE:CD1	1:A:581:MET:HE2	2.54	0.43
1:A:277:CYS:HB2	1:A:596:MET:HE3	2.01	0.42
1:B:847:ARG:O	1:B:851:ARG:HG3	2.18	0.42
1:A:257[B]:SER:OG	1:A:259:GLU:HG2	2.18	0.42
1:A:830:HIS:ND1	3:A:1002:PQE:O75	2.47	0.42
1:A:100:TRP:CZ3	1:A:167:MET:HE2	2.54	0.42
1:A:167:MET:HE3	1:A:167:MET:HB2	1.61	0.42
1:A:150:ASP:OD2	5:A:1103:HOH:O	2.21	0.42
1:A:284:SER:HB3	1:A:287:ASP:O	2.20	0.42
1:B:606:LEU:HD23	1:B:612:ILE:HD12	2.01	0.42
1:B:607:ILE:HG22	1:B:613:ILE:HD12	2.02	0.41
1:B:826:TYR:HB3	5:B:1346:HOH:O	2.19	0.41
1:A:848:PHE:CE2	3:A:1002:PQE:H651	2.54	0.41
1:B:439:GLU:H	1:B:439:GLU:CD	2.28	0.41
1:A:828:GLY:HA3	1:A:852:LEU:HD12	2.03	0.41
1:B:95:ASP:HB3	1:B:164:HIS:CD2	2.56	0.41
1:A:403:GLU:OE2	1:A:407[A]:ARG:NH2	2.53	0.41
1:A:520:LYS:HA	1:A:520:LYS:HD3	1.86	0.41
1:A:631:TYR:CZ	1:A:721:LYS:HD2	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:746:VAL:HA	1:B:750:HIS:HB3	2.03	0.41
1:B:810:VAL:O	1:B:814:LEU:HD22	2.20	0.41
1:A:745:TRP:CZ3	1:A:749:GLY:HA3	2.56	0.40
1:B:447:VAL:HG13	1:B:508:LEU:HD13	2.03	0.40

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:A:1418:HOH:O	5:B:1280:HOH:O[1_654]	1.94	0.26
5:A:1296:HOH:O	5:B:1139:HOH:O[2_748]	1.98	0.22

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	700/863 (81%)	683 (98%)	17 (2%)	0	100	100
1	B	693/863 (80%)	674 (97%)	18 (3%)	1 (0%)	48	46
All	All	1393/1726 (81%)	1357 (97%)	35 (2%)	1 (0%)	48	46

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	814	LEU

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	621/750 (83%)	612 (99%)	9 (1%)	59	66
1	B	615/750 (82%)	612 (100%)	3 (0%)	81	87
All	All	1236/1500 (82%)	1224 (99%)	12 (1%)	68	75

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

Mol	Chain	Res	Type
1	A	212	GLU
1	A	597	GLU
1	A	610	ASP
1	A	612	ILE
1	A	618	THR
1	A	729	ASP
1	A	768	ARG
1	A	798	LEU
1	A	816	VAL
1	B	449	ARG
1	B	474	ILE
1	B	814	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	463	GLN
1	B	589	HIS
1	B	634	GLN
1	B	755	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 10 ligands modelled in this entry, 2 are monoatomic - leaving 8 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
4	EDO	B	1004	-	3,3,3	0.45	0	2,2,2	0.42	0
3	PQE	A	1002	-	9,9,36	0.52	0	8,8,35	0.36	0
3	PQE	B	1002	-	9,9,36	0.52	0	8,8,35	0.51	0
4	EDO	A	1005	2	3,3,3	0.38	0	2,2,2	0.27	0
4	EDO	A	1004	-	3,3,3	0.46	0	2,2,2	0.53	0
4	EDO	A	1003	-	3,3,3	0.38	0	2,2,2	0.64	0
4	EDO	B	1005	2	3,3,3	0.42	0	2,2,2	0.34	0
4	EDO	B	1003	-	3,3,3	0.44	0	2,2,2	0.19	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
4	EDO	B	1004	-	-	0/1/1/1	-
3	PQE	A	1002	-	-	5/7/7/34	-
3	PQE	B	1002	-	-	5/7/7/34	-
4	EDO	A	1005	2	-	0/1/1/1	-
4	EDO	A	1004	-	-	1/1/1/1	-
4	EDO	A	1003	-	-	1/1/1/1	-
4	EDO	B	1005	2	-	1/1/1/1	-
4	EDO	B	1003	-	-	1/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (14) torsion outliers are listed below:

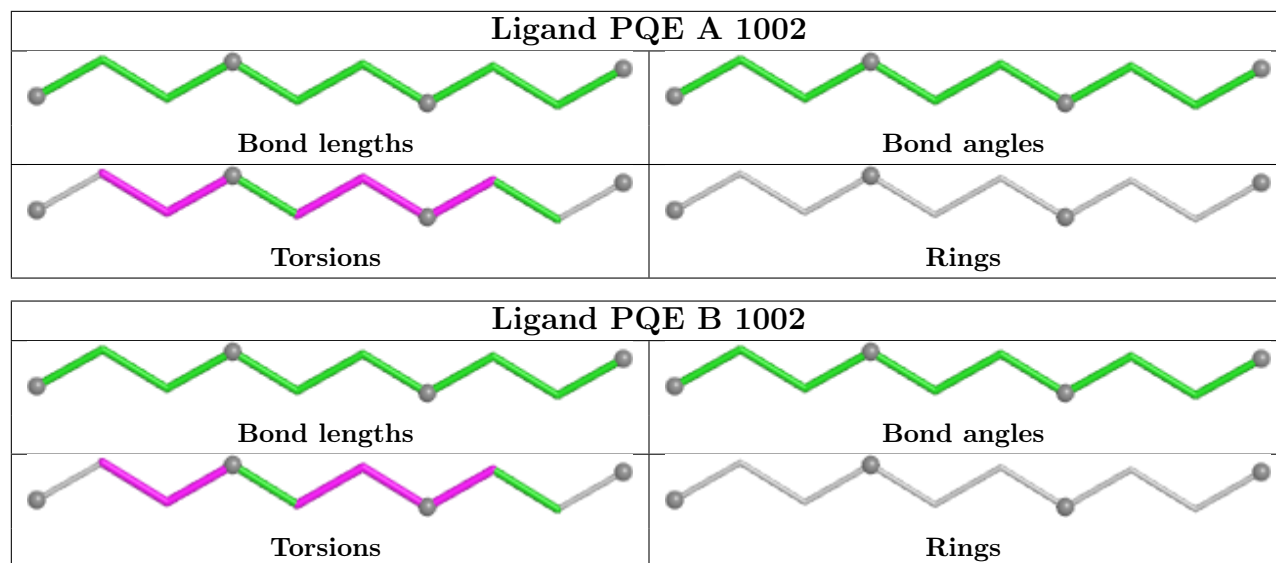
Mol	Chain	Res	Type	Atoms
3	B	1002	PQE	C59-C60-O73-C64
3	A	1002	PQE	C59-C60-O73-C64
3	A	1002	PQE	O75-C56-C57-O74
3	B	1002	PQE	O75-C56-C57-O74
4	B	1003	EDO	O1-C1-C2-O2
3	B	1002	PQE	C65-C64-O73-C60
3	A	1002	PQE	C65-C64-O73-C60
3	B	1002	PQE	C56-C57-O74-C59
3	A	1002	PQE	C56-C57-O74-C59
4	B	1005	EDO	O1-C1-C2-O2
3	B	1002	PQE	O74-C59-C60-O73
4	A	1004	EDO	O1-C1-C2-O2
4	A	1003	EDO	O1-C1-C2-O2
3	A	1002	PQE	O74-C59-C60-O73

There are no ring outliers.

5 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1002	PQE	3	0
3	B	1002	PQE	3	0
4	A	1005	EDO	1	0
4	A	1003	EDO	2	0
4	B	1003	EDO	2	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	706/863 (81%)	-0.24	14 (1%) 65 64	15, 32, 66, 111	6 (0%)
1	B	705/863 (81%)	-0.17	18 (2%) 57 56	19, 34, 73, 107	0
All	All	1411/1726 (81%)	-0.20	32 (2%) 61 60	15, 33, 70, 111	6 (0%)

All (32) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	756	PHE	5.6
1	A	78	LEU	4.7
1	A	816	VAL	4.5
1	B	80	VAL	4.1
1	B	813	VAL	3.9
1	A	897	TYR	3.8
1	A	894	GLY	3.7
1	A	305	PHE	3.4
1	B	826	TYR	3.2
1	B	812	THR	3.1
1	A	286	ILE	3.0
1	B	811	LEU	2.8
1	B	766	PRO	2.8
1	B	656	PRO	2.6
1	B	897	TYR	2.6
1	B	305	PHE	2.5
1	B	767	ASN	2.5
1	A	886	SER	2.5
1	B	809	LYS	2.5
1	B	286	ILE	2.5
1	B	894	GLY	2.5
1	A	400	PHE	2.4
1	A	811	LEU	2.3
1	B	178	PRO	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	824	GLU	2.3
1	B	70	VAL	2.3
1	A	729	ASP	2.2
1	A	826	TYR	2.2
1	B	755	ASN	2.1
1	B	116	PRO	2.0
1	B	182	ILE	2.0
1	A	791[A]	HIS	2.0

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

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 ⓘ

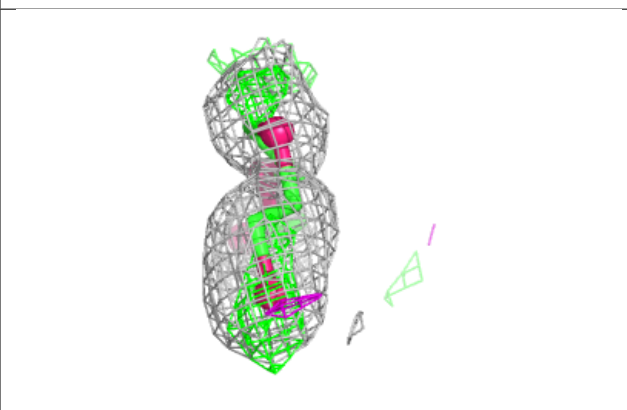
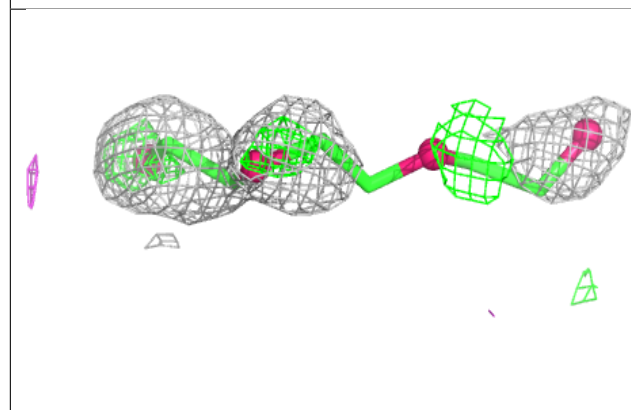
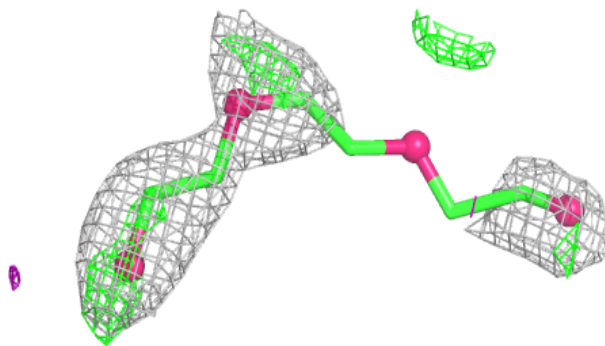
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	PQE	A	1002	10/37	0.80	0.25	54,84,107,108	0
4	EDO	A	1003	4/4	0.85	0.17	33,39,47,48	0
3	PQE	B	1002	10/37	0.86	0.18	54,62,77,79	0
4	EDO	A	1005	4/4	0.88	0.13	51,54,59,61	0
4	EDO	B	1005	4/4	0.90	0.12	45,49,50,56	0
4	EDO	B	1004	4/4	0.91	0.11	47,48,53,56	0
4	EDO	A	1004	4/4	0.93	0.10	45,47,49,56	0
4	EDO	B	1003	4/4	0.96	0.11	27,33,37,40	0
2	FE	A	1001	1/1	0.99	0.05	44,44,44,44	0
2	FE	B	1001	1/1	0.99	0.05	40,40,40,40	0

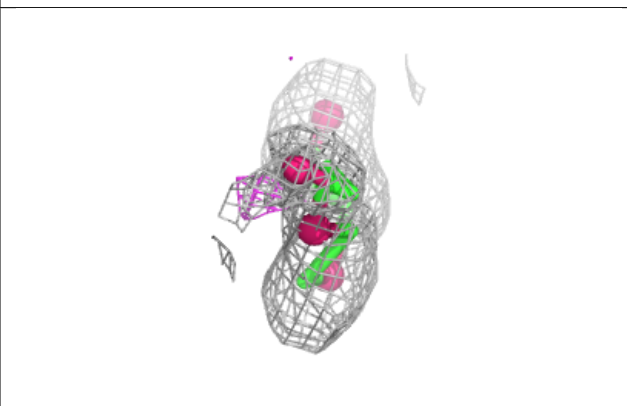
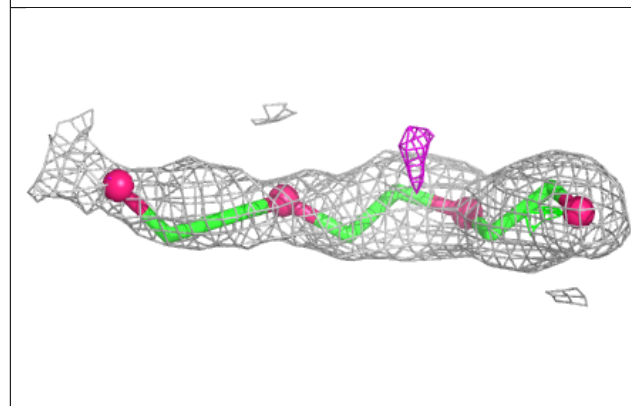
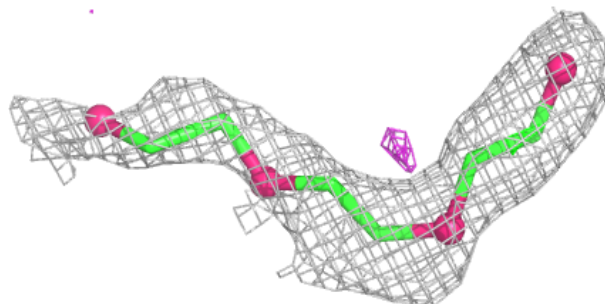
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around PQE A 1002:

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

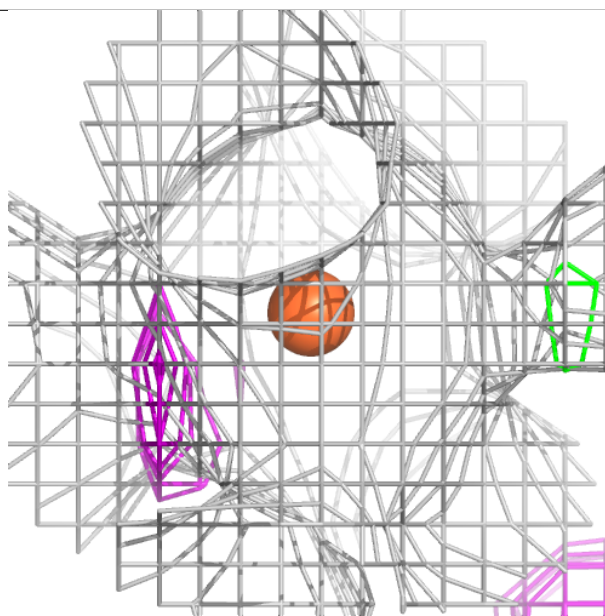
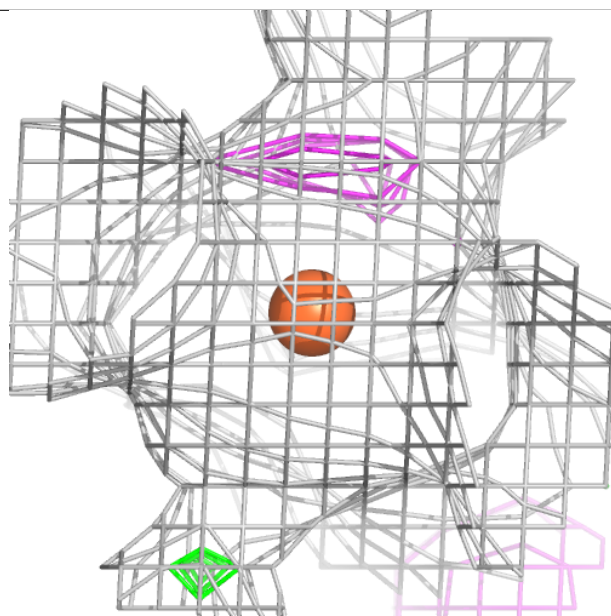
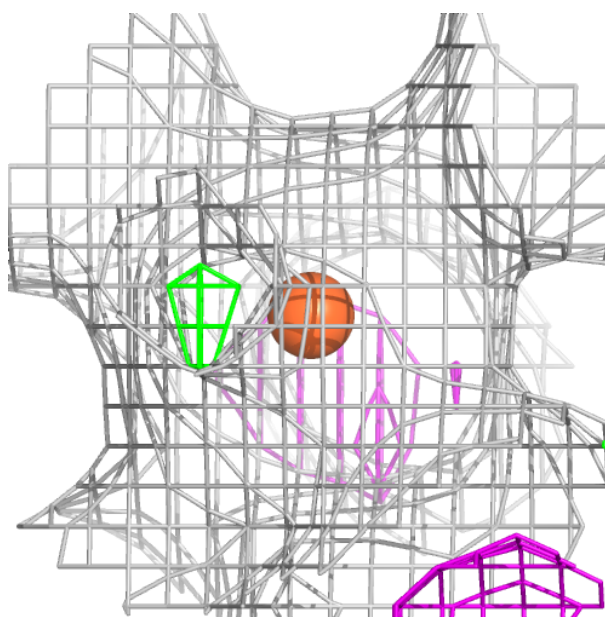
**Electron density around PQE B 1002:**

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



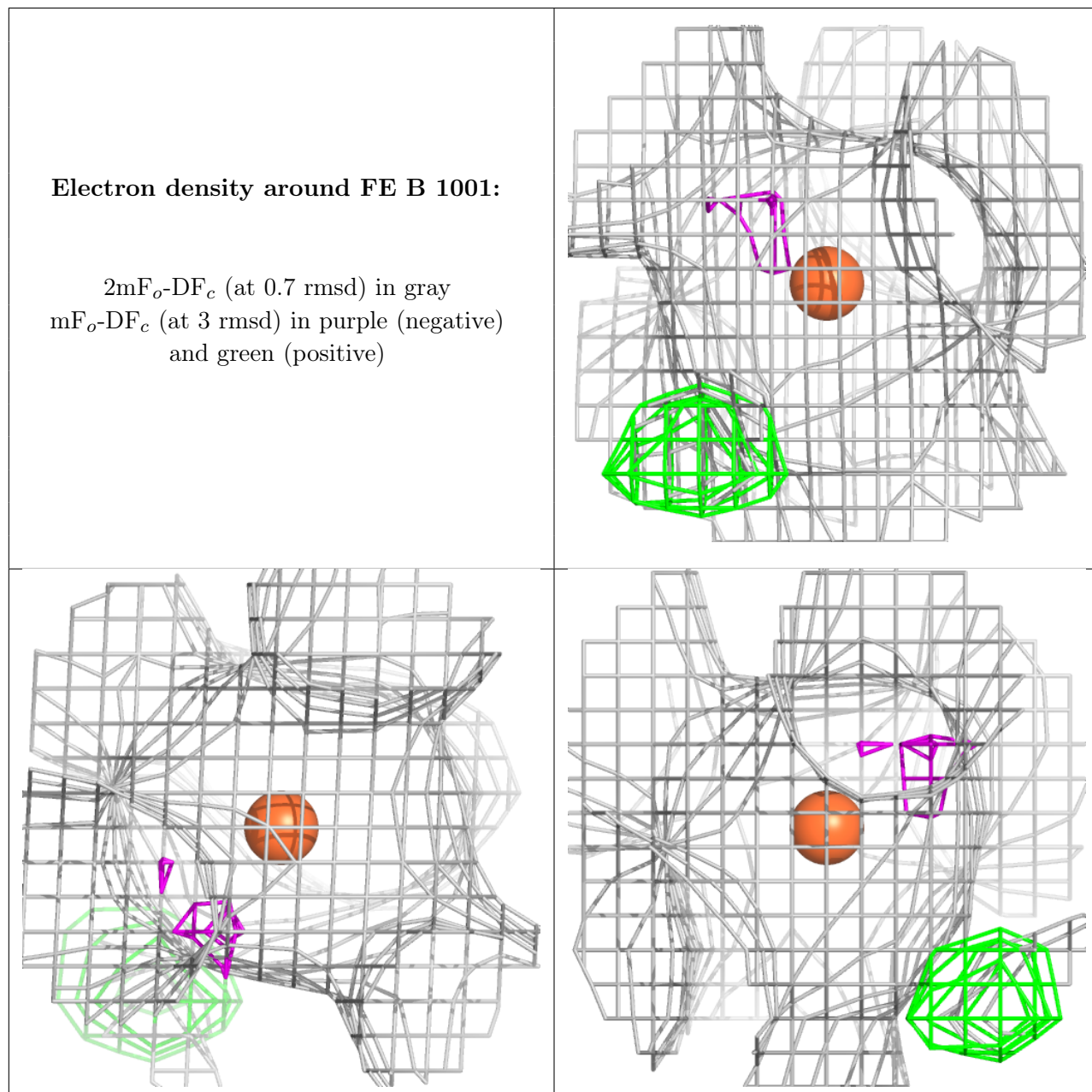
Electron density around FE A 1001:

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



Electron density around FE B 1001:

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



6.5 Other polymers ⓘ

There are no such residues in this entry.