



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 03:49 AM UTC

PDB ID : 5ICK / pdb_00005ick
Title : A unique binding model of FXR LBD with feroline
Authors : Lu, Y.; Li, Y.
Deposited on : 2016-02-23
Resolution : 2.47 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

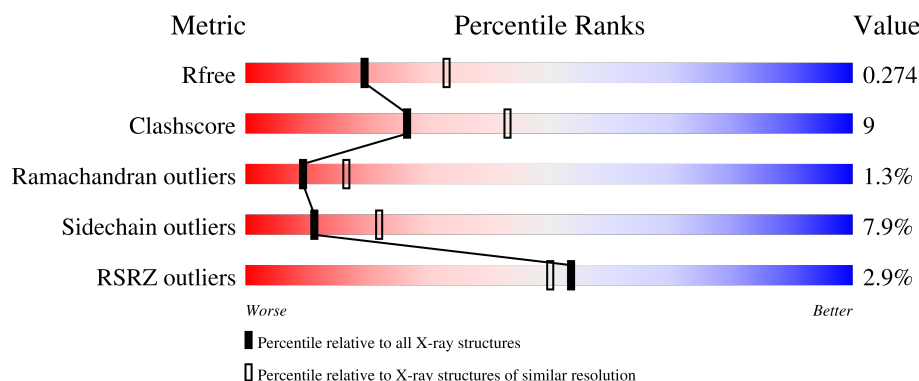
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.47 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	7589 (2.50-2.46)
Clashscore	190562	8295 (2.50-2.46)
Ramachandran outliers	187476	8164 (2.50-2.46)
Sidechain outliers	187428	8166 (2.50-2.46)
RSRZ outliers	180081	7593 (2.50-2.46)

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	229	3% 81% 17% .
1	B	229	3% 81% 14% ..
2	C	11	82% 18%
2	D	11	91% 9%

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
3	FEZ	A	501	-	-	X	-
3	FEZ	B	501	-	-	X	-
3	FEZ	B	502	-	-	X	-

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 4079 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.

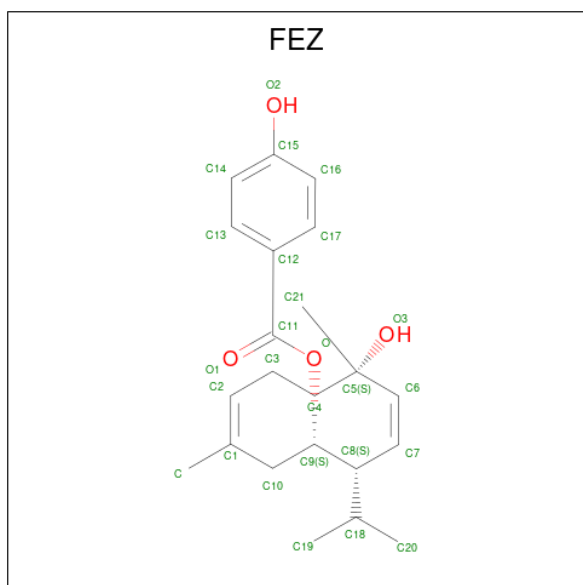
- Molecule 1 is a protein called Bile acid receptor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	229	Total	C	N	O	S	0	0	0
			1881	1202	316	352	11			
1	B	229	Total	C	N	O	S	0	0	0
			1881	1202	316	352	11			

- Molecule 2 is a protein called Nuclear receptor coactivator 2.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	11	Total	C	N	O	0	0	0
			93	60	16	17			
2	D	10	Total	C	N	O	0	0	0
			85	56	15	14			

- Molecule 3 is (1S,2S,3Z,5S,8Z)-5-hydroxy-5,9-dimethyl-2-(propan-2-yl)cyclodeca-3,8-dien-1-yl 4-hydroxybenzoate (CCD ID: FEZ) (formula: C₂₂H₃₀O₄).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			26	22	4		
3	B	1	Total	C	O	0	0
			26	22	4		
3	B	1	Total	C	O	0	0
			26	22	4		

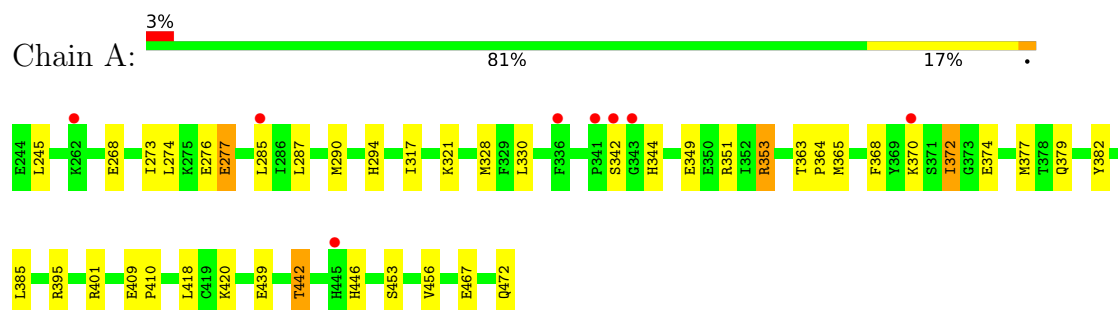
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	28	Total	O	0	0
			28	28		
4	B	28	Total	O	0	0
			28	28		
4	C	3	Total	O	0	0
			3	3		
4	D	2	Total	O	0	0
			2	2		

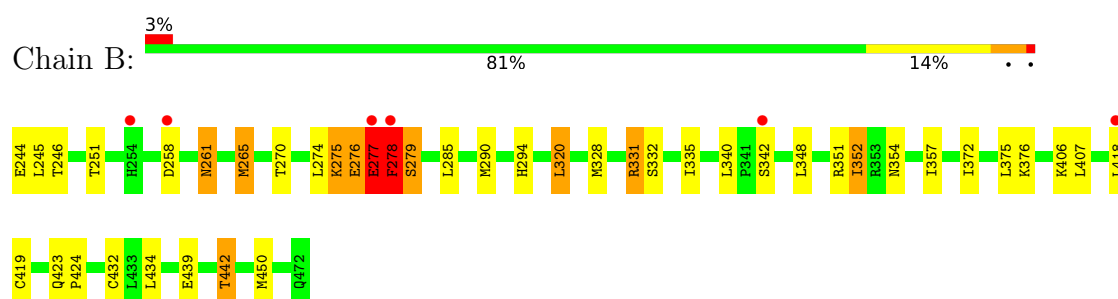
3 Residue-property plots

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.

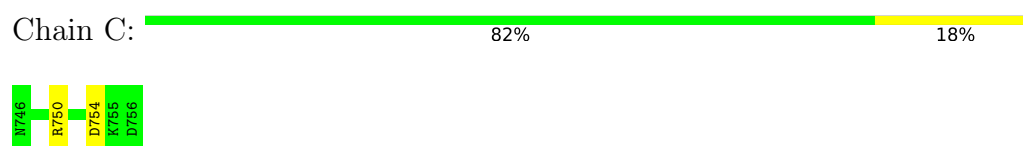
• Molecule 1: Bile acid receptor



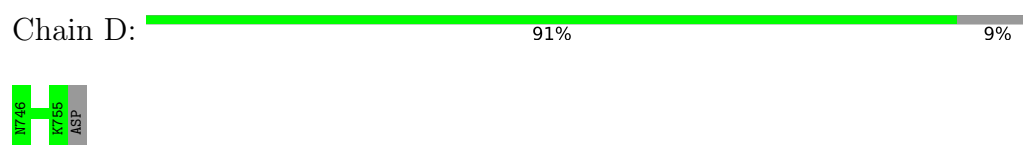
• Molecule 1: Bile acid receptor



• Molecule 2: Nuclear receptor coactivator 2



• Molecule 2: Nuclear receptor coactivator 2



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	56.16Å 34.91Å 134.91Å 90.00° 90.51° 90.00°	Depositor
Resolution (Å)	50.01 – 2.47 50.01 – 2.47	Depositor EDS
% Data completeness (in resolution range)	98.5 (50.01-2.47) 98.5 (50.01-2.47)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	10.94 (at 2.48Å)	Xtriage
Refinement program	REFMAC 5.8.0135	Depositor
R, R_{free}	0.212 , 0.277 (Not available) , 0.274	Depositor DCC
R_{free} test set	938 reflections (4.85%)	wwPDB-VP
Wilson B-factor (Å ²)	34.3	Xtriage
Anisotropy	0.157	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 27.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.032 for h,-k,-l	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	4079	wwPDB-VP
Average B, all atoms (Å ²)	41.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.80% 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: FEZ

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	0.98	0/1921	1.10	0/2595
1	B	0.94	0/1921	1.16	8/2595 (0.3%)
2	C	1.08	0/93	1.33	0/124
2	D	0.93	0/85	1.05	0/113
All	All	0.96	0/4020	1.13	8/5427 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	B	0	4

There are no bond length outliers.

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	342	SER	N-CA-C	7.71	120.66	111.33
1	B	352	ILE	CB-CA-C	-6.53	103.20	112.22
1	B	276	GLU	N-CA-C	6.38	124.40	110.80
1	B	261	ASN	N-CA-C	5.81	118.08	111.11
1	B	246	THR	CA-C-N	5.12	124.30	118.97
1	B	246	THR	C-N-CA	5.12	124.30	118.97
1	B	450	MET	CG-SD-CE	-5.01	89.87	100.90
1	B	331	ARG	CG-CD-NE	5.01	123.02	112.00

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	244	GLU	Peptide
1	B	275	LYS	Peptide
1	B	277	GLU	Peptide
1	B	278	PHE	Peptide

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	1881	0	1876	26	0
1	B	1881	0	1876	24	0
2	C	93	0	97	1	0
2	D	85	0	93	0	0
3	A	26	0	0	13	0
3	B	52	0	0	28	0
4	A	28	0	0	0	0
4	B	28	0	0	0	0
4	C	3	0	0	0	0
4	D	2	0	0	0	0
All	All	4079	0	3942	74	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 9.

All (74) 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:365:MET:SD	3:A:501:FEZ:C21	2.47	1.02
1:A:294:HIS:CD2	3:A:501:FEZ:C19	2.45	1.00
1:B:294:HIS:CD2	3:B:502:FEZ:C19	2.48	0.96
1:B:352:ILE:HD11	3:B:501:FEZ:C21	2.04	0.87
1:B:294:HIS:HD2	3:B:502:FEZ:C19	1.92	0.81
3:A:501:FEZ:C2	3:A:501:FEZ:C18	2.60	0.79
3:B:502:FEZ:C18	3:B:502:FEZ:C2	2.60	0.79
3:B:501:FEZ:C18	3:B:501:FEZ:C2	2.60	0.79
1:B:277:GLU:O	1:B:279:SER:N	2.19	0.75
1:A:274:LEU:HD11	1:A:344:HIS:CE1	2.26	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:273:ILE:HD11	1:A:290:MET:HE1	1.72	0.70
1:A:294:HIS:HD2	3:A:501:FEZ:C19	2.00	0.70
1:B:332:SER:O	3:B:501:FEZ:C19	2.41	0.69
3:B:501:FEZ:C1	3:B:501:FEZ:C7	2.75	0.65
1:B:439:GLU:O	1:B:442:THR:HB	1.97	0.65
3:B:501:FEZ:C6	3:B:502:FEZ:C3	2.74	0.65
3:B:502:FEZ:C1	3:B:502:FEZ:C7	2.75	0.64
3:A:501:FEZ:C1	3:A:501:FEZ:C7	2.75	0.64
1:B:270:THR:HG21	1:B:340:LEU:HD21	1.81	0.62
1:A:276:GLU:O	1:A:351:ARG:NH2	2.34	0.60
1:A:377:MET:HE2	1:A:382:TYR:CE1	2.38	0.58
1:B:328:MET:SD	3:B:502:FEZ:C19	2.91	0.58
3:B:502:FEZ:C2	3:B:502:FEZ:C20	2.82	0.58
2:C:750:ARG:HD2	2:C:754:ASP:OD2	2.04	0.57
3:A:501:FEZ:C2	3:A:501:FEZ:C20	2.82	0.57
1:A:368:PHE:CZ	1:A:372:ILE:CD1	2.87	0.57
3:B:501:FEZ:C2	3:B:501:FEZ:C20	2.82	0.57
1:A:277:GLU:N	1:A:277:GLU:OE2	2.38	0.56
1:A:395:ARG:O	1:A:401:ARG:NH2	2.36	0.55
1:A:273:ILE:HD11	1:A:290:MET:CE	2.35	0.55
1:B:352:ILE:HG23	1:B:357:ILE:HD12	1.90	0.53
1:B:265:MET:HG2	1:B:335:ILE:HD11	1.89	0.52
1:B:352:ILE:CG2	1:B:357:ILE:HD12	2.39	0.52
1:A:377:MET:CE	1:A:382:TYR:CD1	2.94	0.51
1:A:439:GLU:O	1:A:442:THR:HB	2.10	0.51
1:A:368:PHE:CZ	1:A:372:ILE:HD11	2.47	0.50
1:B:290:MET:HB3	3:B:502:FEZ:C20	2.42	0.49
1:A:349:GLU:OE2	1:A:353:ARG:NH1	2.46	0.49
1:B:332:SER:C	3:B:501:FEZ:C19	2.86	0.49
1:A:328:MET:HE1	3:A:501:FEZ:O1	2.13	0.48
3:A:501:FEZ:C21	3:A:501:FEZ:C	2.92	0.48
1:A:287:LEU:HB3	3:A:501:FEZ:C10	2.44	0.48
3:B:501:FEZ:C21	3:B:501:FEZ:C	2.92	0.47
3:B:502:FEZ:C21	3:B:502:FEZ:C	2.92	0.47
1:B:352:ILE:CD1	3:B:501:FEZ:C21	2.87	0.47
3:B:501:FEZ:C1	3:B:501:FEZ:C6	2.92	0.47
1:B:348:LEU:HD13	3:B:501:FEZ:C3	2.45	0.47
3:B:502:FEZ:C1	3:B:502:FEZ:C6	2.92	0.47
1:A:317:ILE:O	1:A:321:LYS:HG3	2.15	0.46
3:A:501:FEZ:C1	3:A:501:FEZ:C6	2.92	0.46
1:B:375:LEU:O	1:B:376:LYS:C	2.58	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:502:FEZ:C2	3:B:502:FEZ:C8	2.94	0.46
3:A:501:FEZ:C2	3:A:501:FEZ:C8	2.94	0.46
3:B:501:FEZ:C2	3:B:501:FEZ:C8	2.94	0.46
1:B:277:GLU:HG3	1:B:351:ARG:HE	1.80	0.45
1:A:377:MET:HE2	1:A:382:TYR:CZ	2.52	0.45
3:B:501:FEZ:C7	3:B:502:FEZ:C3	2.95	0.45
1:A:409:GLU:HB2	1:A:410:PRO:HD3	1.98	0.45
1:A:273:ILE:HA	1:A:351:ARG:NH1	2.32	0.44
1:B:278:PHE:O	1:B:279:SER:CB	2.66	0.44
1:B:320:LEU:HD13	1:B:320:LEU:HA	1.91	0.44
1:A:290:MET:HB2	3:A:501:FEZ:C20	2.48	0.43
1:A:363:THR:HB	1:A:364:PRO:HD3	2.00	0.43
1:B:335:ILE:HG22	3:B:501:FEZ:C20	2.50	0.42
1:B:294:HIS:NE2	3:B:501:FEZ:O1	2.46	0.42
3:B:501:FEZ:C6	3:B:501:FEZ:C	2.98	0.42
3:B:502:FEZ:C	3:B:502:FEZ:C6	2.98	0.42
1:B:290:MET:CB	3:B:502:FEZ:C20	2.97	0.42
1:A:442:THR:HG23	1:A:446:HIS:CE1	2.55	0.42
3:A:501:FEZ:C	3:A:501:FEZ:C6	2.98	0.42
1:B:419:CYS:O	1:B:423:GLN:HB2	2.20	0.41
1:A:377:MET:HE2	1:A:382:TYR:CD1	2.55	0.41
1:A:268:GLU:OE1	1:A:268:GLU:N	2.52	0.41
1:B:423:GLN:N	1:B:424:PRO:CD	2.84	0.41

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	227/229 (99%)	221 (97%)	5 (2%)	1 (0%)	30	46
1	B	227/229 (99%)	215 (95%)	7 (3%)	5 (2%)	5	8

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	C	9/11 (82%)	9 (100%)	0	0	100	100
2	D	8/11 (73%)	8 (100%)	0	0	100	100
All	All	471/480 (98%)	453 (96%)	12 (2%)	6 (1%)	9	16

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	276	GLU
1	B	279	SER
1	B	278	PHE
1	A	245	LEU
1	B	274	LEU
1	B	277	GLU

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	212/212 (100%)	195 (92%)	17 (8%)	11	21
1	B	212/212 (100%)	194 (92%)	18 (8%)	10	19
2	C	10/10 (100%)	10 (100%)	0	100	100
2	D	9/10 (90%)	9 (100%)	0	100	100
All	All	443/444 (100%)	408 (92%)	35 (8%)	11	22

All (35) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	277	GLU
1	A	285	LEU
1	A	330	LEU
1	A	342	SER
1	A	353	ARG
1	A	370	LYS

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Mol	Chain	Res	Type
1	A	372	ILE
1	A	374	GLU
1	A	379	GLN
1	A	385	LEU
1	A	418	LEU
1	A	420	LYS
1	A	442	THR
1	A	453	SER
1	A	456	VAL
1	A	467	GLU
1	A	472	GLN
1	B	245	LEU
1	B	251	THR
1	B	258	ASP
1	B	261	ASN
1	B	265	MET
1	B	275	LYS
1	B	278	PHE
1	B	285	LEU
1	B	320	LEU
1	B	331	ARG
1	B	354	ASN
1	B	372	ILE
1	B	406	LYS
1	B	407	LEU
1	B	418	LEU
1	B	432	CYS
1	B	434	LEU
1	B	442	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	250	GLN
1	A	261	ASN
1	A	263	GLN
1	A	294	HIS
1	A	313	HIS
1	A	337	ASN
1	A	344	HIS
1	A	354	ASN
1	A	379	GLN

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Mol	Chain	Res	Type
1	A	416	GLN
1	A	446	HIS
1	A	472	GLN
1	B	267	GLN
1	B	283	ASN
1	B	337	ASN
1	B	396	GLN
1	B	416	GLN
1	B	446	HIS

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](#)

3 ligands are 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	FEZ	A	501	-	27,27,27	1.54	3 (11%)	34,38,38	3.39	15 (44%)
3	FEZ	B	502	-	27,27,27	1.54	3 (11%)	34,38,38	3.39	15 (44%)
3	FEZ	B	501	-	27,27,27	1.54	3 (11%)	34,38,38	3.39	15 (44%)

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	FEZ	A	501	-	-	12/33/33/33	0/1/2/2
3	FEZ	B	502	-	-	12/33/33/33	0/1/2/2
3	FEZ	B	501	-	-	12/33/33/33	0/1/2/2

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	502	FEZ	O-C9	-4.33	1.38	1.46
3	A	501	FEZ	O-C9	-4.29	1.38	1.46
3	B	501	FEZ	O-C9	-4.29	1.38	1.46
3	B	502	FEZ	O-C11	4.18	1.43	1.34
3	B	501	FEZ	O-C11	4.17	1.43	1.34
3	A	501	FEZ	O-C11	4.17	1.43	1.34
3	A	501	FEZ	C8-C18	-2.88	1.51	1.55
3	B	501	FEZ	C8-C18	-2.84	1.51	1.55
3	B	502	FEZ	C8-C18	-2.81	1.51	1.55

All (45) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	502	FEZ	C5-C6-C7	10.15	142.32	127.11
3	B	501	FEZ	C5-C6-C7	10.14	142.31	127.11
3	A	501	FEZ	C5-C6-C7	10.13	142.29	127.11
3	B	502	FEZ	O-C11-C12	6.67	122.61	111.90
3	B	501	FEZ	O-C11-C12	6.67	122.61	111.90
3	A	501	FEZ	O-C11-C12	6.66	122.60	111.90
3	B	502	FEZ	O-C11-O1	-6.42	113.11	123.55
3	B	501	FEZ	O-C11-O1	-6.42	113.12	123.55
3	A	501	FEZ	O-C11-O1	-6.40	113.14	123.55
3	B	501	FEZ	C4-C5-C6	5.90	122.83	110.35
3	A	501	FEZ	C4-C5-C6	5.89	122.82	110.35
3	B	502	FEZ	C4-C5-C6	5.89	122.81	110.35
3	A	501	FEZ	O3-C5-C6	-4.56	99.45	109.21
3	B	502	FEZ	O3-C5-C6	-4.55	99.48	109.21
3	B	501	FEZ	O3-C5-C6	-4.55	99.48	109.21
3	B	501	FEZ	C20-C18-C8	4.44	119.80	111.76
3	A	501	FEZ	C20-C18-C8	4.44	119.79	111.76
3	B	502	FEZ	C20-C18-C8	4.42	119.75	111.76

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	501	FEZ	C8-C7-C6	4.21	138.19	125.09
3	B	501	FEZ	C8-C7-C6	4.21	138.16	125.09
3	B	502	FEZ	C8-C7-C6	4.20	138.13	125.09
3	B	502	FEZ	C10-C1-C2	-4.10	110.84	120.49
3	A	501	FEZ	C10-C1-C2	-4.09	110.89	120.49
3	B	501	FEZ	C10-C1-C2	-4.09	110.89	120.49
3	B	501	FEZ	C19-C18-C8	-3.92	104.67	111.76
3	B	502	FEZ	C19-C18-C8	-3.91	104.69	111.76
3	A	501	FEZ	C19-C18-C8	-3.91	104.69	111.76
3	B	501	FEZ	C3-C2-C1	3.86	136.46	127.62
3	A	501	FEZ	C3-C2-C1	3.85	136.43	127.62
3	B	502	FEZ	C3-C2-C1	3.84	136.41	127.62
3	B	502	FEZ	C-C1-C2	3.62	132.93	123.63
3	A	501	FEZ	C-C1-C2	3.62	132.91	123.63
3	B	501	FEZ	C-C1-C2	3.61	132.91	123.63
3	B	501	FEZ	C19-C18-C20	-2.87	102.69	110.58
3	A	501	FEZ	C19-C18-C20	-2.87	102.69	110.58
3	B	502	FEZ	C19-C18-C20	-2.86	102.72	110.58
3	B	501	FEZ	C17-C16-C15	-2.73	116.99	119.88
3	B	502	FEZ	C17-C16-C15	-2.73	116.99	119.88
3	A	501	FEZ	C17-C16-C15	-2.69	117.03	119.88
3	A	501	FEZ	O-C9-C10	-2.41	100.98	107.01
3	B	501	FEZ	O-C9-C10	-2.40	100.99	107.01
3	B	502	FEZ	O-C9-C10	-2.39	101.02	107.01
3	B	502	FEZ	C21-C5-C6	-2.31	106.12	111.21
3	B	501	FEZ	C21-C5-C6	-2.30	106.14	111.21
3	A	501	FEZ	C21-C5-C6	-2.29	106.17	111.21

There are no chirality outliers.

All (36) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	501	FEZ	C4-C5-C6-C7
3	A	501	FEZ	C5-C6-C7-C8
3	A	501	FEZ	C1-C10-C9-C8
3	A	501	FEZ	C6-C7-C8-C18
3	A	501	FEZ	C7-C8-C9-O
3	A	501	FEZ	C20-C18-C8-C7
3	A	501	FEZ	C19-C18-C8-C7
3	A	501	FEZ	C20-C18-C8-C9
3	A	501	FEZ	C19-C18-C8-C9
3	A	501	FEZ	O1-C11-O-C9

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Mol	Chain	Res	Type	Atoms
3	A	501	FEZ	C12-C11-O-C9
3	B	501	FEZ	C4-C5-C6-C7
3	B	501	FEZ	C5-C6-C7-C8
3	B	501	FEZ	C1-C10-C9-C8
3	B	501	FEZ	C6-C7-C8-C18
3	B	501	FEZ	C7-C8-C9-O
3	B	501	FEZ	C20-C18-C8-C7
3	B	501	FEZ	C19-C18-C8-C7
3	B	501	FEZ	C20-C18-C8-C9
3	B	501	FEZ	C19-C18-C8-C9
3	B	501	FEZ	O1-C11-O-C9
3	B	501	FEZ	C12-C11-O-C9
3	B	502	FEZ	C4-C5-C6-C7
3	B	502	FEZ	C5-C6-C7-C8
3	B	502	FEZ	C1-C10-C9-C8
3	B	502	FEZ	C6-C7-C8-C18
3	B	502	FEZ	C7-C8-C9-O
3	B	502	FEZ	C20-C18-C8-C7
3	B	502	FEZ	C19-C18-C8-C7
3	B	502	FEZ	C20-C18-C8-C9
3	B	502	FEZ	C19-C18-C8-C9
3	B	502	FEZ	O1-C11-O-C9
3	B	502	FEZ	C12-C11-O-C9
3	A	501	FEZ	C1-C10-C9-O
3	B	501	FEZ	C1-C10-C9-O
3	B	502	FEZ	C1-C10-C9-O

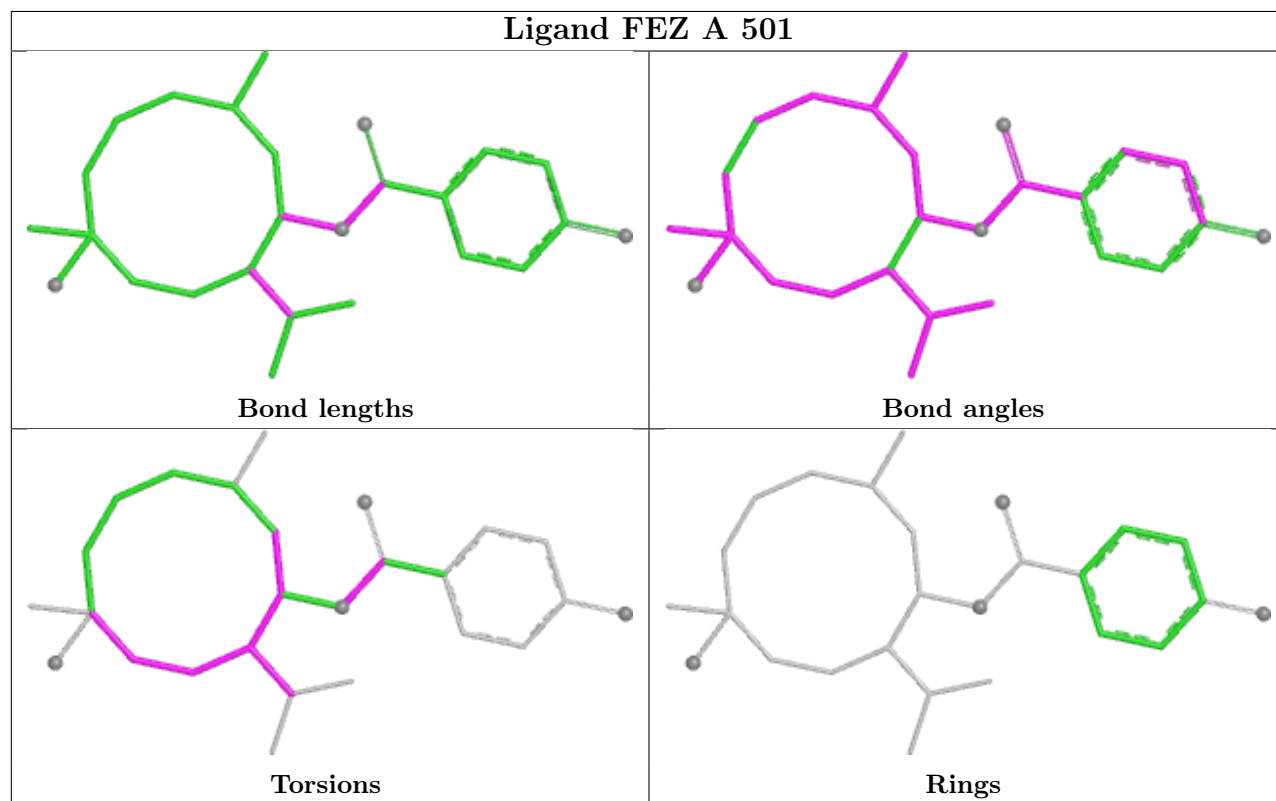
There are no ring outliers.

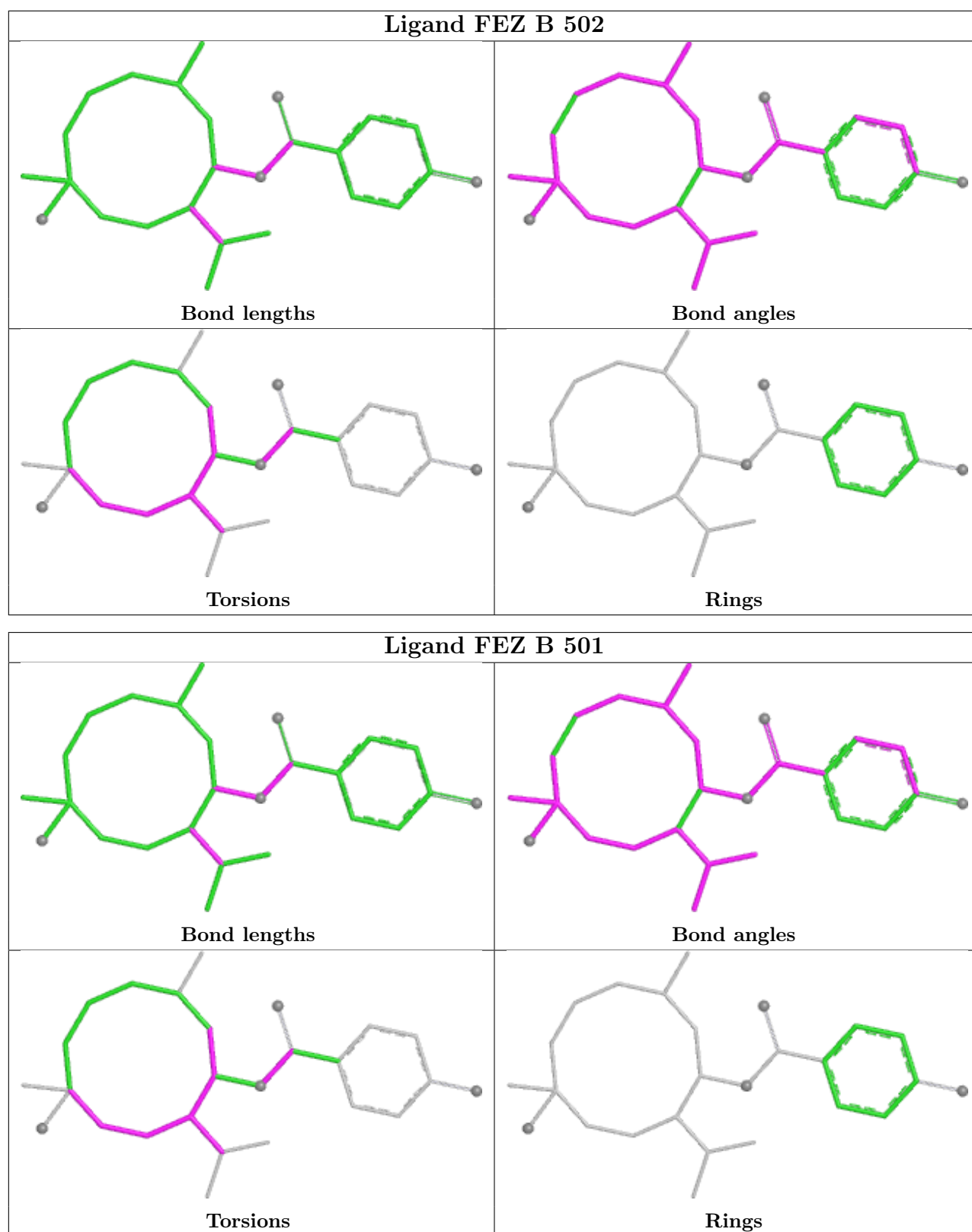
3 monomers are involved in 41 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	501	FEZ	13	0
3	B	502	FEZ	14	0
3	B	501	FEZ	16	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 ⓘ

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	229/229 (100%)	0.11	8 (3%) 47 43	18, 36, 64, 80	0
1	B	229/229 (100%)	0.25	6 (2%) 57 53	20, 40, 72, 102	0
2	C	11/11 (100%)	-0.06	0 100 100	25, 33, 46, 50	0
2	D	10/11 (90%)	0.03	0 100 100	28, 33, 43, 50	0
All	All	479/480 (99%)	0.17	14 (2%) 53 50	18, 38, 69, 102	0

All (14) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	278	PHE	3.1
1	A	343	GLY	2.7
1	A	285	LEU	2.7
1	A	262	LYS	2.5
1	A	370	LYS	2.5
1	B	277	GLU	2.5
1	A	336	PHE	2.4
1	B	418	LEU	2.3
1	A	342	SER	2.2
1	B	254	HIS	2.2
1	A	341	PRO	2.2
1	A	445	HIS	2.1
1	B	258	ASP	2.1
1	B	342	SER	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](#)

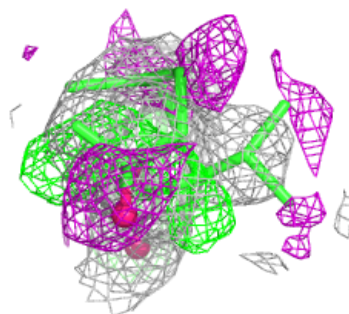
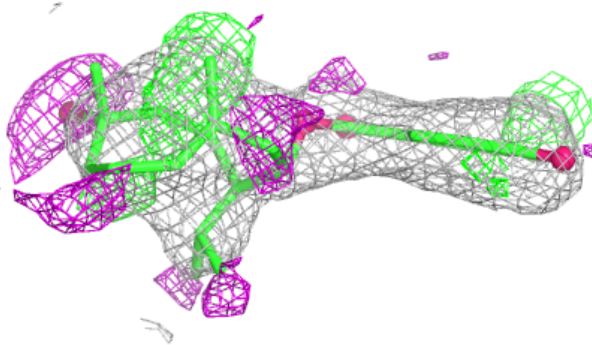
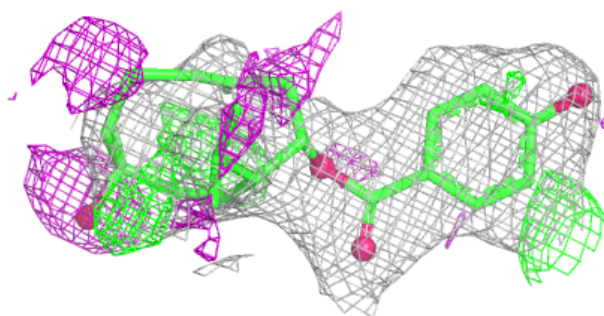
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	FEZ	B	502	26/26	0.77	0.21	28,38,47,48	0
3	FEZ	A	501	26/26	0.78	0.16	28,38,47,48	0
3	FEZ	B	501	26/26	0.83	0.17	28,38,47,48	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.

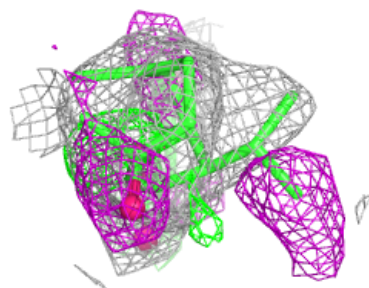
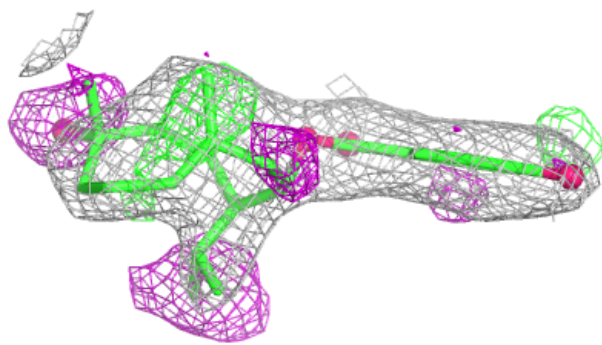
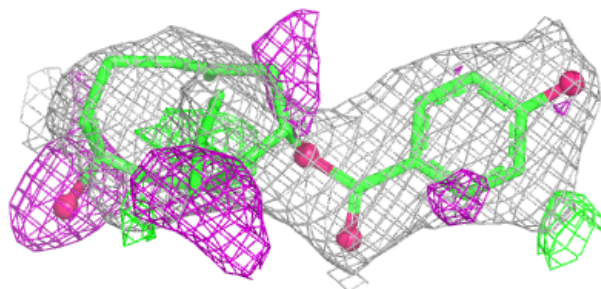
Electron density around FEZ B 502:

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

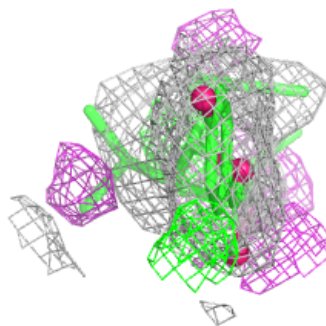
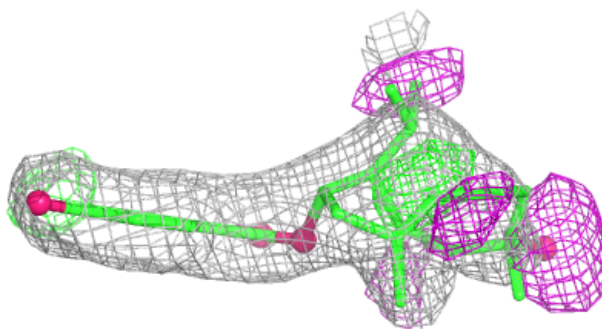
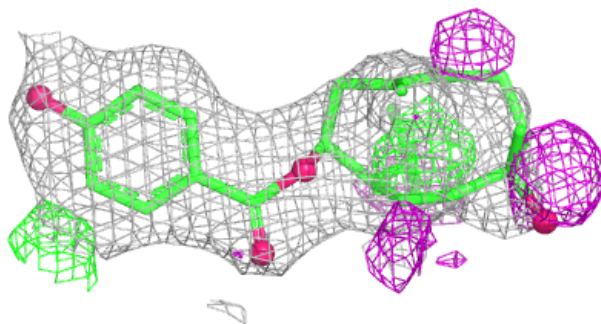


Electron density around FEZ A 501:

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

**Electron density around FEZ B 501:**

$2mF_o-DF_c$ (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.