Full wwPDB X-ray Structure Validation Report (i)

Nov 16, 2023 – 10:39 AM JST

PDB ID	:	6LLF
Title	:	Biphenyl-2,2',3-triol-soaked resting complex of Oxy and Fd in carbazole 1,9a-dioxygenase
Authors	:	Wang, Y.X.; Suzuki-Minakuchi, C.; Nojiri, H.
Deposited on	:	2019-12-23
Resolution	:	1.93 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 (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:

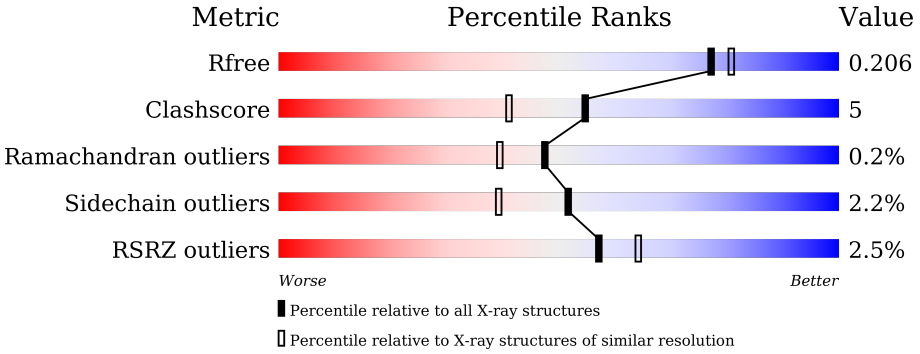
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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 1.93 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}	130704	4310 (1.96-1.92)
Clashscore	141614	1023 (1.94-1.94)
Ramachandran outliers	138981	1007 (1.94-1.94)
Sidechain outliers	138945	1007 (1.94-1.94)
RSRZ outliers	127900	4250 (1.96-1.92)

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	392	.% 86% 13% •
1	B	392	.% 89% 10% •
1	C	392	89% 10% ••
2	D	115	18% 83% 7% 10%
2	E	115	2% 80% 12% 8%
2	F	115	5% 81% 9% • 10%

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
6	EDO	C	406	-	-	X	-
7	GOL	C	408	-	-	X	-

2 Entry composition (i)

There are 10 unique types of molecules in this entry. The entry contains 13321 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 Terminal oxygenase component of carbazole.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	388	3147	2010	537	587	13	0	4	0
1	B	389	3168	2025	543	587	13	0	6	0
1	C	388	3174	2029	543	589	13	0	8	0

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	385	LEU	-	expression tag	UNP Q84II6
A	386	GLU	-	expression tag	UNP Q84II6
A	387	HIS	-	expression tag	UNP Q84II6
A	388	HIS	-	expression tag	UNP Q84II6
A	389	HIS	-	expression tag	UNP Q84II6
A	390	HIS	-	expression tag	UNP Q84II6
A	391	HIS	-	expression tag	UNP Q84II6
A	392	HIS	-	expression tag	UNP Q84II6
B	385	LEU	-	expression tag	UNP Q84II6
B	386	GLU	-	expression tag	UNP Q84II6
B	387	HIS	-	expression tag	UNP Q84II6
B	388	HIS	-	expression tag	UNP Q84II6
B	389	HIS	-	expression tag	UNP Q84II6
B	390	HIS	-	expression tag	UNP Q84II6
B	391	HIS	-	expression tag	UNP Q84II6
B	392	HIS	-	expression tag	UNP Q84II6
C	385	LEU	-	expression tag	UNP Q84II6
C	386	GLU	-	expression tag	UNP Q84II6
C	387	HIS	-	expression tag	UNP Q84II6
C	388	HIS	-	expression tag	UNP Q84II6
C	389	HIS	-	expression tag	UNP Q84II6
C	390	HIS	-	expression tag	UNP Q84II6
C	391	HIS	-	expression tag	UNP Q84II6

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Chain	Residue	Modelled	Actual	Comment	Reference
C	392	HIS	-	expression tag	UNP Q84II6

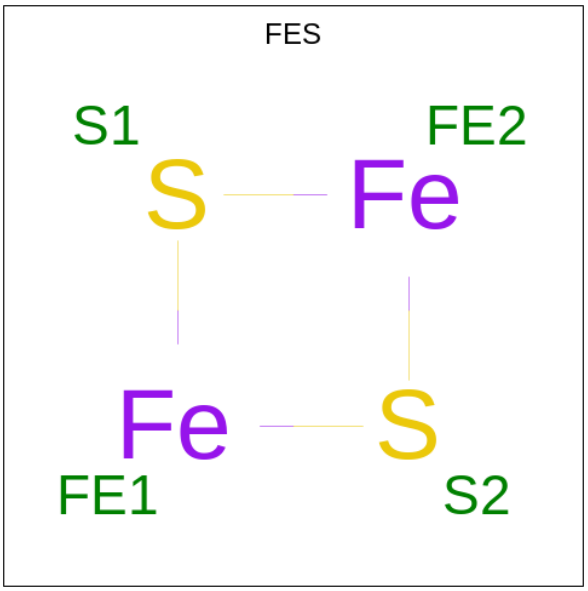
- Molecule 2 is a protein called Ferredoxin CarAc.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	D	104	771	485	129	150	7	0	1	0
			Total	C	N	O	S			
2	E	106	788	496	132	153	7	0	1	0
			Total	C	N	O	S			
2	F	104	780	490	130	153	7	0	2	0

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	108	LEU	-	expression tag	UNP Q8GI16
D	109	GLU	-	expression tag	UNP Q8GI16
D	110	HIS	-	expression tag	UNP Q8GI16
D	111	HIS	-	expression tag	UNP Q8GI16
D	112	HIS	-	expression tag	UNP Q8GI16
D	113	HIS	-	expression tag	UNP Q8GI16
D	114	HIS	-	expression tag	UNP Q8GI16
D	115	HIS	-	expression tag	UNP Q8GI16
E	108	LEU	-	expression tag	UNP Q8GI16
E	109	GLU	-	expression tag	UNP Q8GI16
E	110	HIS	-	expression tag	UNP Q8GI16
E	111	HIS	-	expression tag	UNP Q8GI16
E	112	HIS	-	expression tag	UNP Q8GI16
E	113	HIS	-	expression tag	UNP Q8GI16
E	114	HIS	-	expression tag	UNP Q8GI16
E	115	HIS	-	expression tag	UNP Q8GI16
F	108	LEU	-	expression tag	UNP Q8GI16
F	109	GLU	-	expression tag	UNP Q8GI16
F	110	HIS	-	expression tag	UNP Q8GI16
F	111	HIS	-	expression tag	UNP Q8GI16
F	112	HIS	-	expression tag	UNP Q8GI16
F	113	HIS	-	expression tag	UNP Q8GI16
F	114	HIS	-	expression tag	UNP Q8GI16
F	115	HIS	-	expression tag	UNP Q8GI16

- Molecule 3 is FE2/S2 (INORGANIC) CLUSTER (three-letter code: FES) (formula: Fe_2S_2).

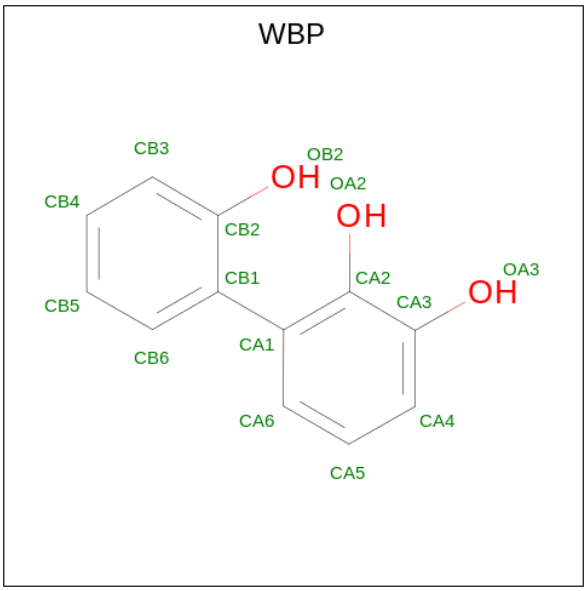


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	Fe	S		
3	A	1	4	2	2	0	0
3	B	1	4	2	2	0	0
3	C	1	4	2	2	0	0
3	D	1	4	2	2	0	0
3	E	1	4	2	2	0	0
3	F	1	4	2	2	0	0

- Molecule 4 is FE (II) ION (three-letter code: FE2) (formula: Fe).

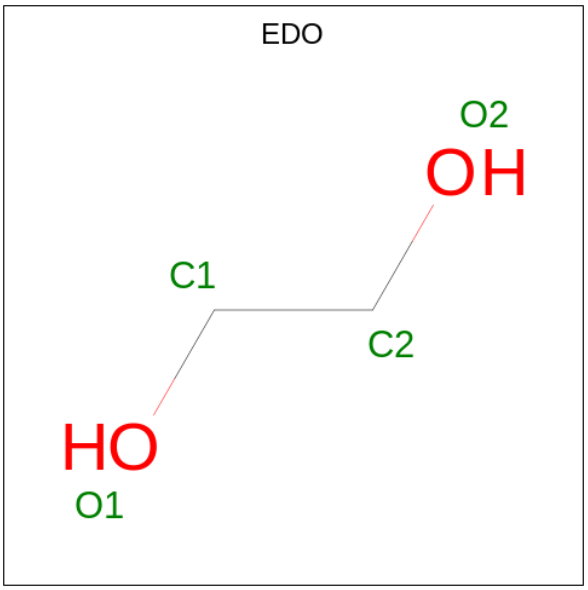
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Fe		
4	A	1	1	1	0	0
4	B	1	1	1	0	0
4	C	1	1	1	0	0

- Molecule 5 is 3-(2-hydroxyphenyl)benzene-1,2-diol (three-letter code: WBP) (formula: $C_{12}H_{10}O_3$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
5	A	1	30	24	6	0	1
			Total	C	O		
5	B	1	15	12	3	0	0
			Total	C	O		
5	C	1	15	12	3	0	0

- Molecule 6 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).



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

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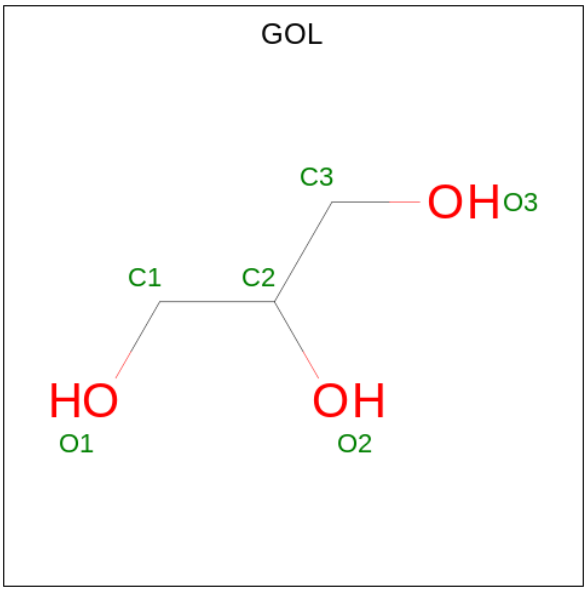
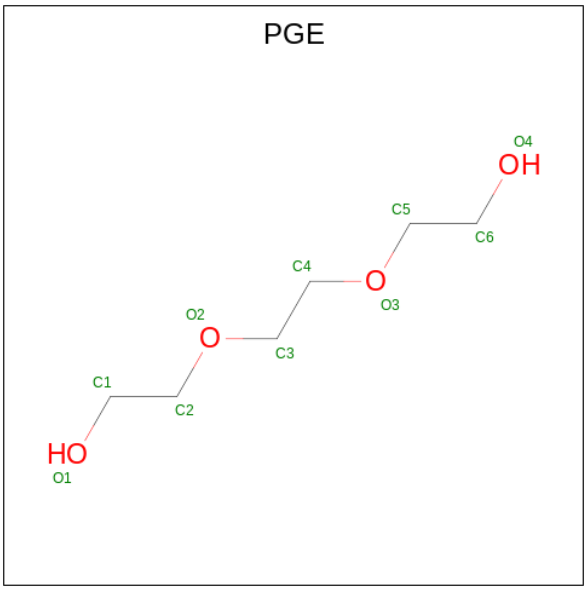
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
6	A	1	4	2	2	0	0
			Total	C	O		
6	A	1	4	2	2	0	0
			Total	C	O		
6	A	1	4	2	2	0	0
			Total	C	O		
6	A	1	4	2	2	0	0
			Total	C	O		
6	A	1	4	2	2	0	0
			Total	C	O		
6	B	1	4	2	2	0	0
			Total	C	O		
6	B	1	4	2	2	0	0
			Total	C	O		
6	B	1	4	2	2	0	0
			Total	C	O		
6	B	1	4	2	2	0	0
			Total	C	O		
6	C	1	4	2	2	0	0
			Total	C	O		
6	C	1	4	2	2	0	0
			Total	C	O		
6	C	1	4	2	2	0	0
			Total	C	O		
6	C	1	4	2	2	0	0
			Total	C	O		
6	D	1	4	2	2	0	0
			Total	C	O		
6	E	1	4	2	2	0	0
			Total	C	O		
6	F	1	4	2	2	0	0

- Molecule 7 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



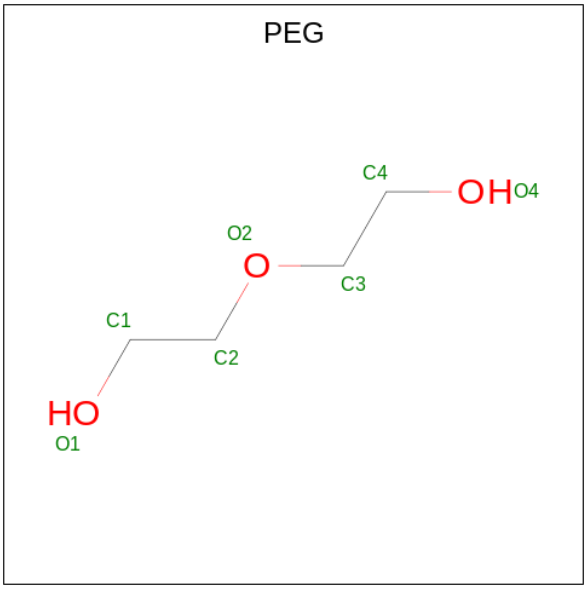
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
7	A	1	6	3	3	0	0
			Total	C	O		
7	A	1	6	3	3	0	0
			Total	C	O		
7	B	1	6	3	3	0	0
			Total	C	O		
7	C	1	6	3	3	0	0

- Molecule 8 is TRIETHYLENE GLYCOL (three-letter code: PGE) (formula: $C_6H_{14}O_4$).



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

- Molecule 9 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: $C_4H_{10}O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
9	B	1	7	4	3	0	0

- Molecule 10 is water.

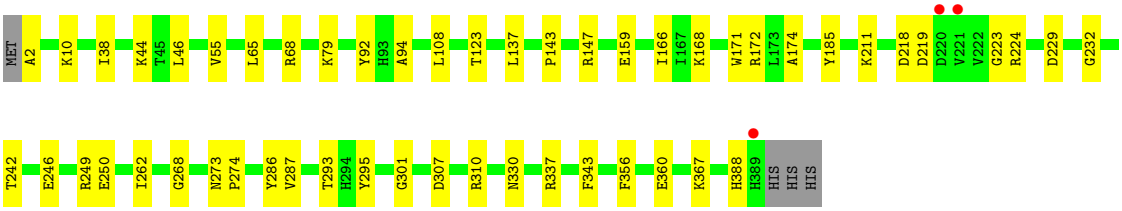
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
10	A	371	371	371	0	0
10	B	378	378	378	0	0
10	C	376	376	376	0	0
10	D	32	32	32	0	0
10	E	68	68	68	0	0
10	F	72	72	72	0	0

3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

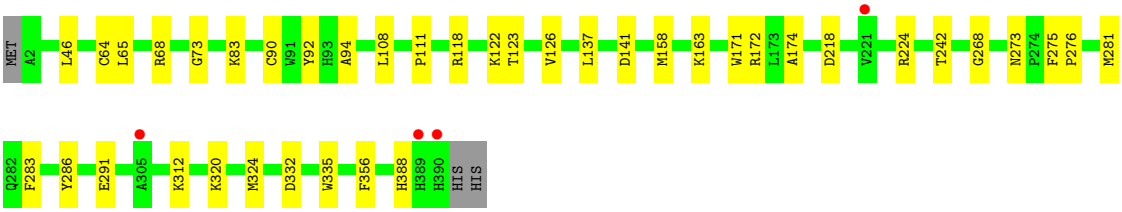
• Molecule 1: Terminal oxygenase component of carbazole

Chain A:



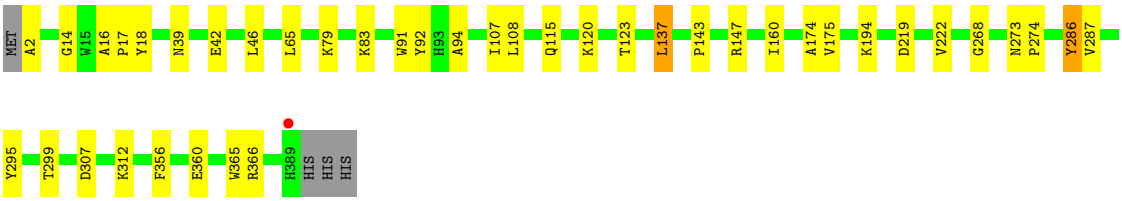
• Molecule 1: Terminal oxygenase component of carbazole

Chain B:



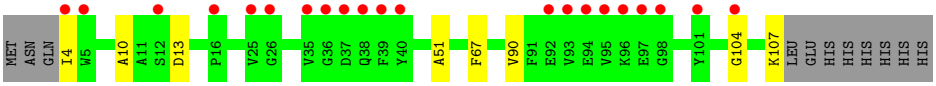
• Molecule 1: Terminal oxygenase component of carbazole

Chain C:



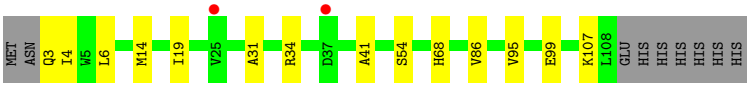
• Molecule 2: Ferredoxin CarAc

Chain D:



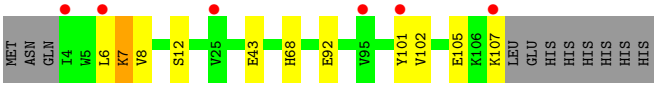
• Molecule 2: Ferredoxin CarAc

Chain E:



• Molecule 2: Ferredoxin CarAc

Chain F:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	98.29Å 89.68Å 105.02Å 90.00° 104.08° 90.00°	Depositor
Resolution (Å)	44.88 – 1.93 44.84 – 1.93	Depositor EDS
% Data completeness (in resolution range)	96.3 (44.88-1.93) 96.4 (44.84-1.93)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.68 (at 1.94Å)	Xtriage
Refinement program	REFMAC 5.8.0238	Depositor
R, R_{free}	0.158 , 0.200 0.167 , 0.206	Depositor DCC
R_{free} test set	6252 reflections (4.91%)	wwPDB-VP
Wilson B-factor (Å^2)	18.7	Xtriage
Anisotropy	0.069	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 45.2	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	13321	wwPDB-VP
Average B, all atoms (Å^2)	26.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.51% 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 (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: FE2, PEG, GOL, WBP, PGE, FES, EDO

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	0.74	1/3246 (0.0%)	0.86	1/4406 (0.0%)
1	B	0.72	0/3276	0.84	0/4447
1	C	0.74	1/3285 (0.0%)	0.85	0/4455
2	D	0.75	0/790	0.86	0/1074
2	E	0.77	0/807	0.88	0/1097
2	F	0.80	1/799 (0.1%)	0.88	0/1086
All	All	0.74	3/12203 (0.0%)	0.85	1/16565 (0.0%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	F	43	GLU	CD-OE1	5.56	1.31	1.25
1	A	360	GLU	CD-OE1	5.31	1.31	1.25
1	C	360	GLU	CD-OE1	5.14	1.31	1.25

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	224	ARG	CG-CD-NE	-5.58	100.08	111.80

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	3147	0	3049	32	0
1	B	3168	0	3071	29	0
1	C	3174	0	3088	27	0
2	D	771	0	750	4	0
2	E	788	0	769	11	0
2	F	780	0	755	8	0
3	A	4	0	0	0	0
3	B	4	0	0	0	0
3	C	4	0	0	0	0
3	D	4	0	0	0	0
3	E	4	0	0	1	0
3	F	4	0	0	1	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
4	C	1	0	0	0	0
5	A	30	0	0	3	0
5	B	15	0	0	2	0
5	C	15	0	0	3	0
6	A	24	0	36	4	0
6	B	16	0	24	6	0
6	C	16	0	24	6	0
6	D	4	0	6	1	0
6	E	4	0	6	0	0
6	F	4	0	6	0	0
7	A	12	0	16	1	0
7	B	6	0	8	0	0
7	C	6	0	8	5	0
8	A	10	0	14	3	0
9	B	7	0	10	2	0
10	A	371	0	0	10	0
10	B	378	0	0	11	0
10	C	376	0	0	7	0
10	D	32	0	0	1	0
10	E	68	0	0	1	0
10	F	72	0	0	2	0
All	All	13321	0	11640	122	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 5.

All (122) 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)
5:C:403:WBP:CA2	10:C:501:HOH:O	2.08	1.01
1:B:68:ARG:HH11	6:B:405:EDO:H11	1.37	0.87
1:A:218:ASP:OD1	1:A:218:ASP:O	1.90	0.87
1:A:79:LYS:HE3	10:A:832:HOH:O	1.82	0.78
6:B:407:EDO:H21	10:B:714:HOH:O	1.82	0.77
1:B:141:ASP:OD2	10:B:501:HOH:O	2.04	0.75
2:E:3:GLN:HG2	2:E:4:ILE:H	1.51	0.74
2:F:7:LYS:HG2	2:F:101:TYR:CE2	2.24	0.72
2:E:3:GLN:NE2	10:E:301:HOH:O	2.23	0.72
6:A:406:EDO:H11	10:A:829:HOH:O	1.90	0.71
5:B:403:WBP:CA2	10:B:569:HOH:O	2.38	0.69
5:B:403:WBP:CA3	10:B:569:HOH:O	2.40	0.68
1:A:44:LYS:HG3	10:A:801:HOH:O	1.95	0.67
1:C:39:ASN:HB2	1:C:42[B]:GLU:CD	2.15	0.66
1:A:229:ASP:O	8:A:408:PGE:H4	1.97	0.65
2:F:7:LYS:HD3	2:F:101:TYR:CZ	2.32	0.65
1:C:120:LYS:H	7:C:408:GOL:H32	1.63	0.64
1:C:120:LYS:N	7:C:408:GOL:H32	2.12	0.63
2:F:7:LYS:HG2	2:F:101:TYR:CD2	2.34	0.63
1:C:120:LYS:H	7:C:408:GOL:C3	2.12	0.62
5:A:403[A]:WBP:OA2	10:A:501:HOH:O	2.11	0.62
1:B:320:LYS:HE2	1:B:324:MET:CE	2.29	0.62
1:B:320:LYS:HE2	1:B:324:MET:HE2	1.82	0.61
5:C:403:WBP:OA2	10:C:501:HOH:O	2.13	0.60
1:B:68:ARG:NH1	6:B:405:EDO:H11	2.14	0.59
5:C:403:WBP:CA3	10:C:501:HOH:O	2.42	0.59
7:C:408:GOL:H2	2:E:86:VAL:CG2	2.32	0.59
2:F:7:LYS:CG	2:F:101:TYR:CE2	2.85	0.59
1:B:281:MET:HE3	1:B:283:PHE:CZ	2.37	0.58
1:B:291:GLU:OE2	10:B:502:HOH:O	2.17	0.58
1:A:219:ASP:OD1	1:A:223:GLY:HA2	2.03	0.57
1:C:65:LEU:HD23	1:C:123:THR:HG22	1.87	0.57
1:C:107:ILE:H	6:C:406:EDO:H12	1.70	0.57
1:C:107:ILE:N	6:C:406:EDO:H12	2.20	0.56
2:E:14:MET:HE2	2:E:34:ARG:HB2	1.87	0.56
6:D:202:EDO:C2	10:D:304:HOH:O	2.53	0.56
1:A:2:ALA:N	10:A:505:HOH:O	2.37	0.56
7:C:408:GOL:H2	2:E:86:VAL:HG22	1.87	0.56
5:A:403[B]:WBP:OA2	5:A:403[B]:WBP:OB2	2.24	0.55
1:C:2:ALA:CB	10:C:560:HOH:O	2.54	0.55
1:C:107:ILE:H	6:C:406:EDO:C1	2.21	0.54
7:A:407:GOL:H12	10:A:684:HOH:O	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:2:ALA:HB3	10:C:560:HOH:O	2.07	0.53
1:B:320:LYS:CG	1:B:324:MET:HE2	2.37	0.52
1:A:232:GLY:H	8:A:408:PGE:H42	1.74	0.52
1:A:262:ILE:HD12	8:A:408:PGE:H6	1.92	0.52
1:A:168:LYS:HE2	10:A:806:HOH:O	2.08	0.52
1:B:224:ARG:NH2	10:B:518:HOH:O	2.42	0.52
1:A:38:ILE:CD1	1:A:55:VAL:HG12	2.39	0.52
1:B:68:ARG:HH11	6:B:405:EDO:C1	2.16	0.51
2:F:92:GLU:HG3	2:F:107:LYS:HE2	1.92	0.51
1:B:163:LYS:HD3	6:B:407:EDO:O2	2.11	0.51
1:C:83:LYS:HD3	10:C:800:HOH:O	2.11	0.50
1:C:94:ALA:HB1	1:C:108:LEU:HB2	1.93	0.49
1:C:287:VAL:HB	1:C:295:TYR:HB2	1.94	0.49
2:D:10:ALA:O	2:D:13:ASP:HB2	2.13	0.49
1:B:218:ASP:OD2	10:B:503:HOH:O	2.20	0.49
1:B:320:LYS:HG2	1:B:324:MET:HE2	1.95	0.48
1:A:218:ASP:OD1	1:A:218:ASP:C	2.51	0.48
1:A:68:ARG:HH11	6:A:406:EDO:C2	2.27	0.48
1:B:171:TRP:CE2	1:B:172:ARG:HG3	2.49	0.47
1:A:249:ARG:HG3	1:A:250:GLU:N	2.30	0.47
2:E:3:GLN:HG2	2:E:4:ILE:N	2.26	0.47
2:D:51:ALA:HB2	2:D:67:PHE:CG	2.50	0.47
1:A:330:ASN:HD21	5:A:403[A]:WBP:CA4	2.28	0.46
1:C:79[A]:LYS:HD3	6:C:405:EDO:H22	1.97	0.46
2:D:90:VAL:HG23	2:D:107:LYS:HG2	1.96	0.46
1:A:174:ALA:HB2	1:A:337:ARG:HD3	1.97	0.46
1:B:122:LYS:HA	6:B:409:EDO:H22	1.98	0.46
1:C:194:LYS:HB2	10:C:550:HOH:O	2.15	0.46
1:A:159:GLU:CD	6:A:404:EDO:H22	2.36	0.45
1:A:287:VAL:HB	1:A:295:TYR:HB2	1.98	0.45
1:A:219:ASP:O	10:A:502:HOH:O	2.21	0.45
2:E:95:VAL:HA	2:E:99:GLU:O	2.16	0.45
1:A:65:LEU:HD23	1:A:123:THR:HG22	1.98	0.44
1:B:64:CYS:HB2	1:B:126[A]:VAL:CG2	2.47	0.44
1:C:91:TRP:O	6:C:405:EDO:O1	2.27	0.44
2:F:68:HIS:HB2	3:F:201:FES:S1	2.57	0.44
1:B:174:ALA:HB1	1:B:286:TYR:CD1	2.52	0.44
1:C:174:ALA:HB1	1:C:286:TYR:CD2	2.53	0.44
1:A:10:LYS:HG3	10:A:522:HOH:O	2.17	0.43
1:C:115:GLN:HA	1:C:115:GLN:OE1	2.18	0.43
1:A:166:ILE:HG23	1:A:293[B]:THR:HG22	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:68:HIS:HB2	3:E:201:FES:S1	2.58	0.43
9:B:404:PEG:H41	10:B:813:HOH:O	2.18	0.43
1:A:307:ASP:OD1	1:A:310:ARG:NH1	2.51	0.43
1:B:273:ASN:OD1	1:B:281:MET:HG2	2.19	0.43
1:A:343:PHE:CG	1:B:73:GLY:HA3	2.54	0.43
1:C:175:VAL:HG11	1:C:365:TRP:CE2	2.54	0.43
1:A:143:PRO:HG3	1:A:147:ARG:CZ	2.49	0.43
1:B:332:ASP:HA	1:B:335:TRP:NE1	2.34	0.43
2:D:4:ILE:O	2:D:104:GLY:N	2.50	0.42
1:B:94:ALA:HB1	1:B:108:LEU:HB2	2.01	0.42
1:C:137:LEU:HD22	1:C:137:LEU:HA	1.93	0.42
1:A:68:ARG:HH11	6:A:406:EDO:H22	1.84	0.42
9:B:404:PEG:C4	10:B:813:HOH:O	2.68	0.42
1:C:94:ALA:CB	1:C:108:LEU:HB2	2.49	0.42
1:A:185:TYR:OH	1:B:83:LYS:HE2	2.19	0.42
1:C:143:PRO:HG3	1:C:147:ARG:CZ	2.50	0.42
1:B:158:MET:CE	1:B:281:MET:CE	2.98	0.41
1:C:18:TYR:CE2	1:C:366:ARG:HG2	2.55	0.41
1:C:14:GLY:HA3	10:F:329:HOH:O	2.20	0.41
2:F:12:SER:OG	10:F:301:HOH:O	2.21	0.41
1:B:118[B]:ARG:NE	10:B:520:HOH:O	2.46	0.41
1:B:90:CYS:O	1:B:94:ALA:HA	2.20	0.41
1:B:275:PHE:CG	1:B:276:PRO:HA	2.55	0.41
2:E:3:GLN:CG	2:E:4:ILE:H	2.28	0.41
1:B:65:LEU:HD23	1:B:123:THR:HG22	2.03	0.41
1:B:111:PRO:HG3	10:B:753:HOH:O	2.21	0.41
1:C:160:ILE:HG23	1:C:299:THR:HB	2.02	0.41
1:A:367[A]:LYS:CE	10:A:506:HOH:O	2.68	0.41
1:C:16:ALA:N	1:C:17:PRO:CD	2.84	0.41
1:A:94:ALA:HB1	1:A:108:LEU:HB2	2.03	0.41
1:A:242:THR:HA	1:A:246:GLU:O	2.20	0.41
1:B:242:THR:O	6:C:406:EDO:H21	2.21	0.41
1:C:273:ASN:HA	1:C:274:PRO:HA	1.89	0.41
2:E:19:ILE:HG21	2:E:54[A]:SER:HA	2.03	0.40
1:A:273:ASN:HA	1:A:274:PRO:HA	1.93	0.40
2:E:31:ALA:O	2:E:41:ALA:HA	2.21	0.40
1:A:159:GLU:O	1:A:301:GLY:HA2	2.22	0.40
1:A:171:TRP:CE2	1:A:172:ARG:HG3	2.56	0.40
2:F:8:VAL:CG2	2:F:102:VAL:HG12	2.50	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	390/392 (100%)	370 (95%)	19 (5%)	1 (0%)	41	32
1	B	393/392 (100%)	375 (95%)	17 (4%)	1 (0%)	41	32
1	C	394/392 (100%)	373 (95%)	20 (5%)	1 (0%)	41	32
2	D	103/115 (90%)	99 (96%)	4 (4%)	0	100	100
2	E	105/115 (91%)	103 (98%)	2 (2%)	0	100	100
2	F	104/115 (90%)	100 (96%)	4 (4%)	0	100	100
All	All	1489/1521 (98%)	1420 (95%)	66 (4%)	3 (0%)	47	39

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	268	GLY
1	A	268	GLY
1	C	268	GLY

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	339/339 (100%)	332 (98%)	7 (2%)	53	41
1	B	342/339 (101%)	336 (98%)	6 (2%)	59	47
1	C	343/339 (101%)	334 (97%)	9 (3%)	46	32
2	D	83/93 (89%)	83 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	E	85/93 (91%)	83 (98%)	2 (2%)	49	36
2	F	84/93 (90%)	81 (96%)	3 (4%)	35	20
All	All	1276/1296 (98%)	1249 (98%)	27 (2%)	52	41

All (27) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	46	LEU
1	A	92	TYR
1	A	137	LEU
1	A	211	LYS
1	A	286	TYR
1	A	356	PHE
1	A	388	HIS
1	B	46	LEU
1	B	92	TYR
1	B	137	LEU
1	B	312	LYS
1	B	356	PHE
1	B	388	HIS
1	C	46	LEU
1	C	92	TYR
1	C	137	LEU
1	C	219	ASP
1	C	222	VAL
1	C	286	TYR
1	C	307	ASP
1	C	312	LYS
1	C	356	PHE
2	E	6	LEU
2	E	107	LYS
2	F	6	LEU
2	F	7	LYS
2	F	105	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	234	HIS
1	B	388	HIS

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Mol	Chain	Res	Type
2	F	38	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 monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 36 ligands modelled in this entry, 3 are monoatomic - leaving 33 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	$\#\|Z\| > 2$
7	GOL	A	407	-	5,5,5	0.10	0	5,5,5	0.37	0
6	EDO	E	202	-	3,3,3	0.18	0	2,2,2	0.36	0
6	EDO	A	404	-	3,3,3	0.29	0	2,2,2	0.67	0
3	FES	E	201	2	0,4,4	-	-	-		
7	GOL	C	408	-	5,5,5	0.21	0	5,5,5	0.64	0
8	PGE	A	408	-	9,9,9	0.34	0	8,8,8	0.20	0
6	EDO	A	406	-	3,3,3	0.25	0	2,2,2	0.31	0
6	EDO	A	405	-	3,3,3	0.11	0	2,2,2	0.12	0
3	FES	B	401	1	0,4,4	-	-	-		
7	GOL	A	412	-	5,5,5	0.12	0	5,5,5	0.31	0
6	EDO	A	410	-	3,3,3	0.13	0	2,2,2	0.27	0
5	WBP	C	403	-	16,16,16	2.70	3 (18%)	22,22,22	0.95	1 (4%)
6	EDO	C	407	-	3,3,3	0.16	0	2,2,2	0.27	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
6	EDO	C	406	-	3,3,3	0.66	0	2,2,2	0.50	0
6	EDO	F	202	-	3,3,3	0.12	0	2,2,2	0.24	0
6	EDO	C	404	-	3,3,3	0.21	0	2,2,2	0.24	0
6	EDO	C	405	-	3,3,3	0.42	0	2,2,2	0.59	0
6	EDO	B	409	-	3,3,3	0.26	0	2,2,2	0.65	0
9	PEG	B	404	-	6,6,6	0.19	0	5,5,5	0.43	0
6	EDO	B	407	-	3,3,3	0.39	0	2,2,2	0.36	0
6	EDO	B	405	-	3,3,3	0.35	0	2,2,2	0.08	0
6	EDO	B	408	-	3,3,3	0.06	0	2,2,2	0.40	0
6	EDO	A	409	-	3,3,3	0.13	0	2,2,2	0.31	0
5	WBP	A	403[B]	-	16,16,16	2.38	3 (18%)	22,22,22	1.00	1 (4%)
6	EDO	A	411	-	3,3,3	0.18	0	2,2,2	0.20	0
3	FES	A	401	1	0,4,4	-	-	-		
7	GOL	B	406	-	5,5,5	0.10	0	5,5,5	0.22	0
5	WBP	B	403	-	16,16,16	2.78	3 (18%)	22,22,22	0.84	0
6	EDO	D	202	-	3,3,3	0.36	0	2,2,2	0.22	0
3	FES	D	201	2	0,4,4	-	-	-		
5	WBP	A	403[A]	-	16,16,16	2.40	3 (18%)	22,22,22	1.19	3 (13%)
3	FES	F	201	2	0,4,4	-	-	-		
3	FES	C	401	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
7	GOL	A	407	-	-	2/4/4/4	-
6	EDO	E	202	-	-	1/1/1/1	-
6	EDO	A	404	-	-	1/1/1/1	-
7	GOL	C	408	-	-	0/4/4/4	-
3	FES	E	201	2	-	-	0/1/1/1
8	PGE	A	408	-	-	4/7/7/7	-
6	EDO	A	406	-	-	1/1/1/1	-
6	EDO	A	405	-	-	0/1/1/1	-
3	FES	B	401	1	-	-	0/1/1/1
7	GOL	A	412	-	-	1/4/4/4	-
6	EDO	A	410	-	-	0/1/1/1	-
5	WBP	C	403	-	-	0/4/4/4	0/2/2/2
6	EDO	C	407	-	-	0/1/1/1	-
6	EDO	C	406	-	-	0/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	EDO	F	202	-	-	0/1/1/1	-
6	EDO	C	404	-	-	0/1/1/1	-
6	EDO	C	405	-	-	0/1/1/1	-
6	EDO	B	409	-	-	1/1/1/1	-
9	PEG	B	404	-	-	1/4/4/4	-
6	EDO	B	407	-	-	1/1/1/1	-
6	EDO	B	405	-	-	1/1/1/1	-
6	EDO	B	408	-	-	0/1/1/1	-
6	EDO	A	409	-	-	0/1/1/1	-
5	WBP	A	403[B]	-	-	1/4/4/4	0/2/2/2
6	EDO	A	411	-	-	1/1/1/1	-
7	GOL	B	406	-	-	4/4/4/4	-
3	FES	A	401	1	-	-	0/1/1/1
6	EDO	D	202	-	-	1/1/1/1	-
5	WBP	B	403	-	-	0/4/4/4	0/2/2/2
3	FES	D	201	2	-	-	0/1/1/1
5	WBP	A	403[A]	-	-	0/4/4/4	0/2/2/2
3	FES	F	201	2	-	-	0/1/1/1
3	FES	C	401	1	-	-	0/1/1/1

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	403	WBP	CA3-CA2	8.75	1.50	1.40
5	C	403	WBP	CA3-CA2	7.72	1.49	1.40
5	A	403[A]	WBP	CA3-CA2	7.31	1.48	1.40
5	A	403[B]	WBP	CA3-CA2	6.57	1.47	1.40
5	C	403	WBP	CA1-CA2	6.37	1.51	1.40
5	A	403[B]	WBP	CA1-CA2	6.02	1.50	1.40
5	B	403	WBP	CA1-CA2	5.54	1.50	1.40
5	A	403[A]	WBP	CA1-CA2	5.12	1.49	1.40
5	B	403	WBP	CB1-CB2	3.53	1.50	1.40
5	C	403	WBP	CB1-CB2	3.34	1.50	1.40
5	A	403[A]	WBP	CB1-CB2	2.81	1.48	1.40
5	A	403[B]	WBP	CB1-CB2	2.50	1.47	1.40

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	A	403[A]	WBP	CB6-CB1-CA1	3.12	125.18	118.74
5	A	403[A]	WBP	CA1-CB1-CB2	-2.69	117.00	123.14
5	A	403[B]	WBP	CA1-CA2-CA3	-2.38	118.51	120.03

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	A	403[A]	WBP	CA4-CA3-CA2	-2.18	117.83	120.06
5	C	403	WBP	CA1-CA2-CA3	-2.02	118.73	120.03

There are no chirality outliers.

All (21) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	A	407	GOL	C1-C2-C3-O3
8	A	408	PGE	O3-C5-C6-O4
7	A	412	GOL	C1-C2-C3-O3
7	B	406	GOL	O1-C1-C2-C3
7	B	406	GOL	C1-C2-C3-O3
7	A	407	GOL	O2-C2-C3-O3
6	A	404	EDO	O1-C1-C2-O2
6	B	405	EDO	O1-C1-C2-O2
7	B	406	GOL	O1-C1-C2-O2
6	A	406	EDO	O1-C1-C2-O2
6	A	411	EDO	O1-C1-C2-O2
6	B	409	EDO	O1-C1-C2-O2
8	A	408	PGE	C3-C4-O3-C5
8	A	408	PGE	C1-C2-O2-C3
9	B	404	PEG	C4-C3-O2-C2
8	A	408	PGE	C6-C5-O3-C4
5	A	403[B]	WBP	CA6-CA1-CB1-CB6
6	B	407	EDO	O1-C1-C2-O2
6	D	202	EDO	O1-C1-C2-O2
6	E	202	EDO	O1-C1-C2-O2
7	B	406	GOL	O2-C2-C3-O3

There are no ring outliers.

18 monomers are involved in 38 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	A	407	GOL	1	0
6	A	404	EDO	1	0
3	E	201	FES	1	0
7	C	408	GOL	5	0
8	A	408	PGE	3	0
6	A	406	EDO	3	0
5	C	403	WBP	3	0
6	C	406	EDO	4	0

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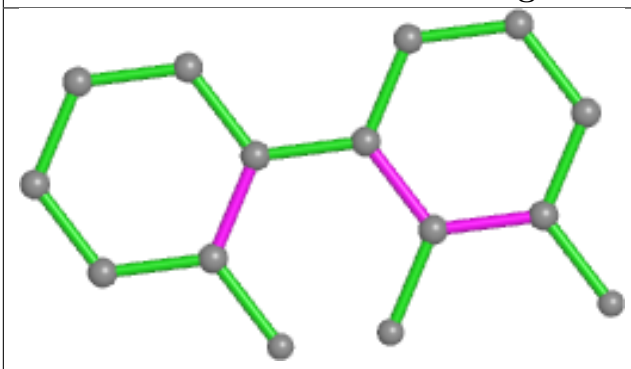
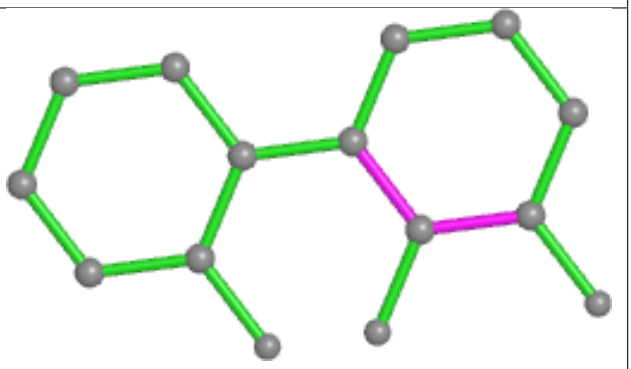
Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	C	405	EDO	2	0
6	B	409	EDO	1	0
9	B	404	PEG	2	0
6	B	407	EDO	2	0
6	B	405	EDO	3	0
5	A	403[B]	WBP	1	0
5	B	403	WBP	2	0
6	D	202	EDO	1	0
5	A	403[A]	WBP	2	0
3	F	201	FES	1	0

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.

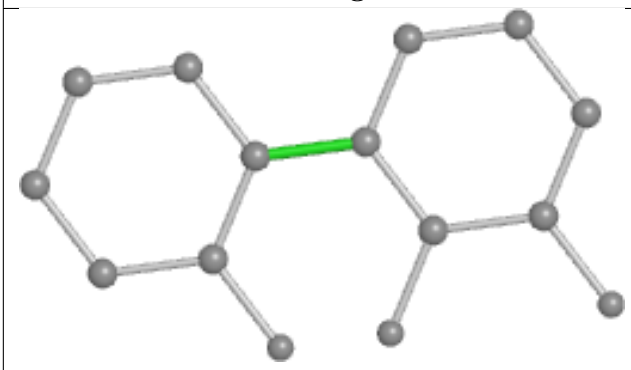
Ligand WBP C 403



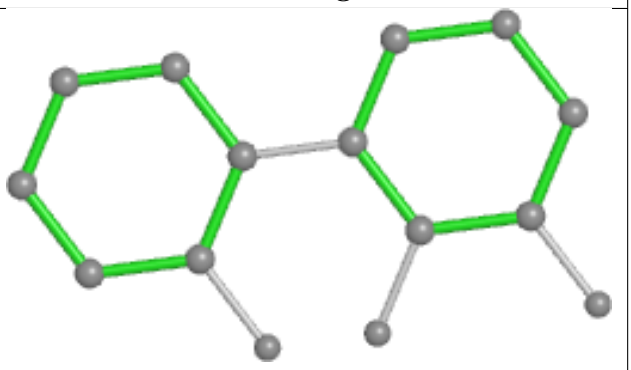
Bond lengths



Bond angles

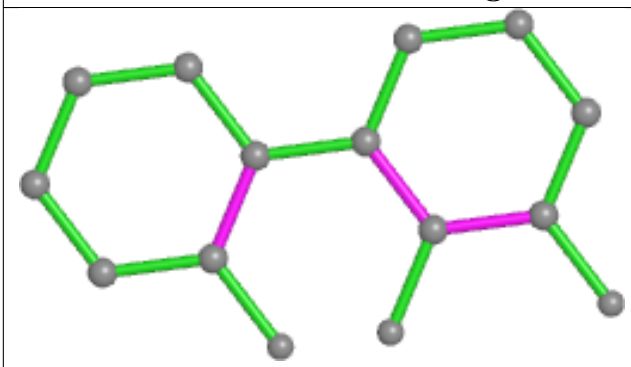


Torsions

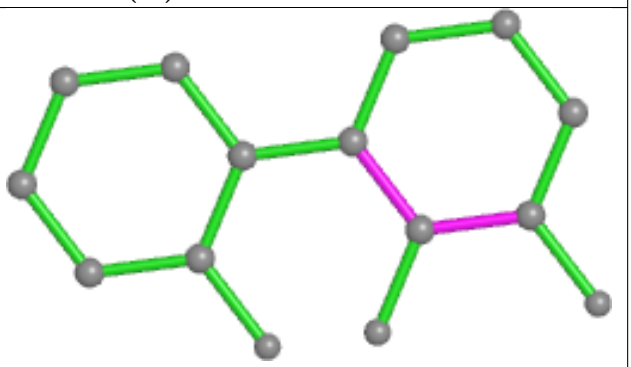


Rings

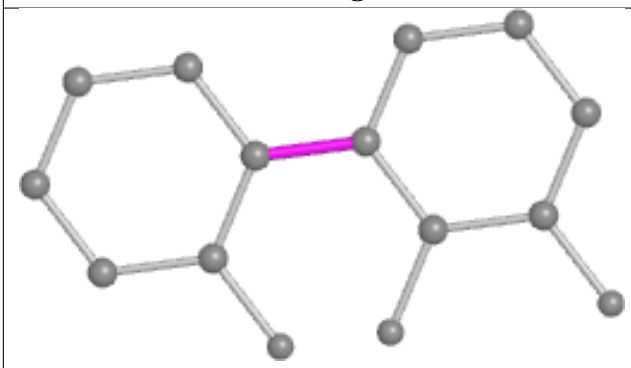
Ligand WBP A 403 (B)



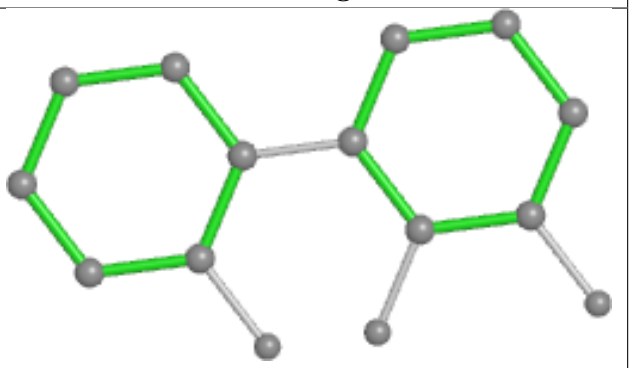
Bond lengths



Bond angles

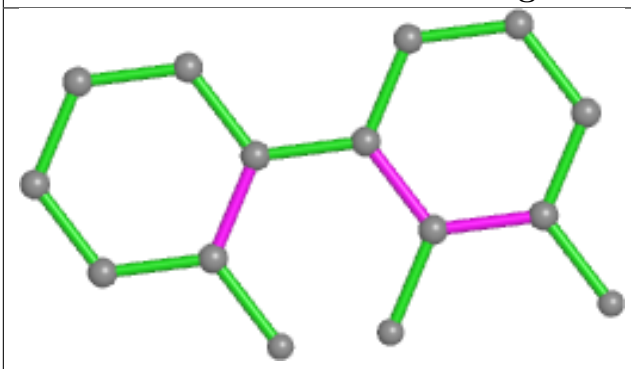


Torsions

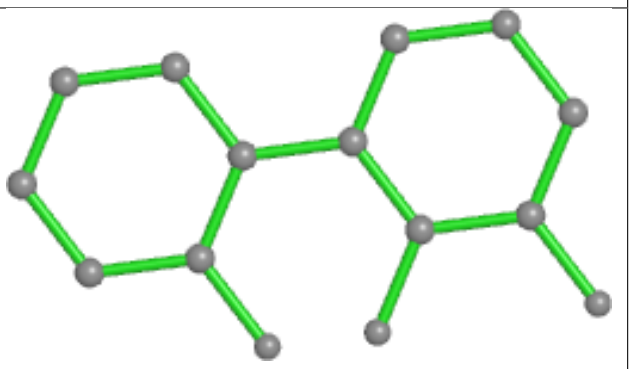


Rings

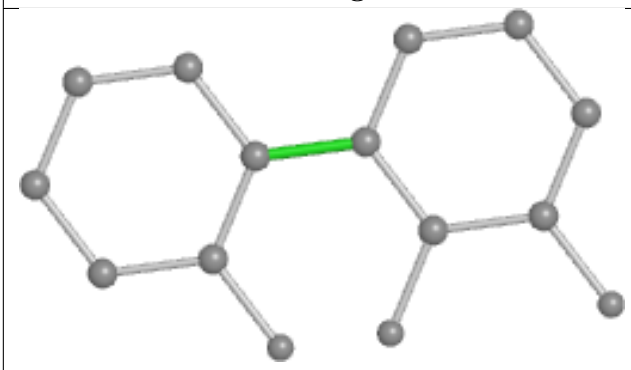
Ligand WBP B 403



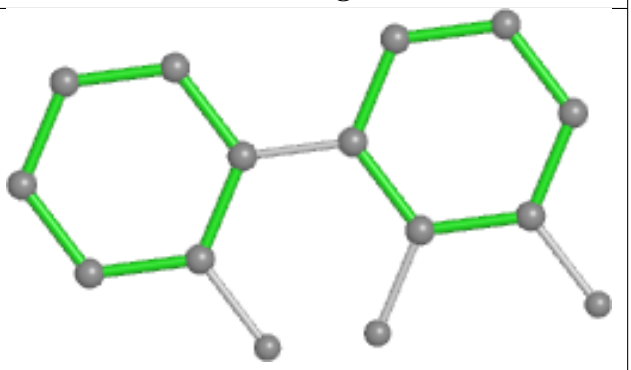
Bond lengths



Bond angles

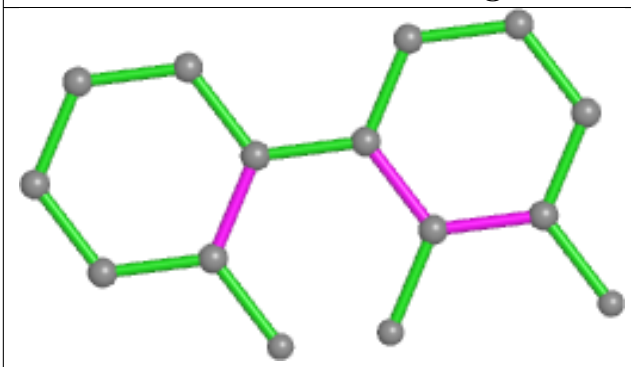


Torsions

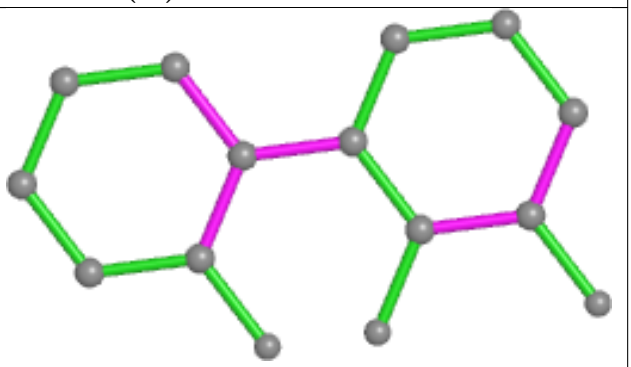


Rings

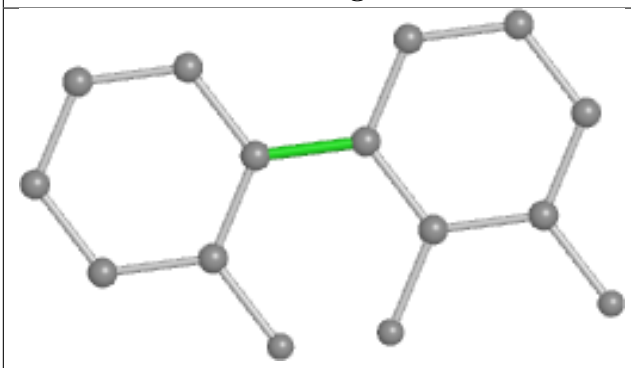
Ligand WBP A 403 (A)



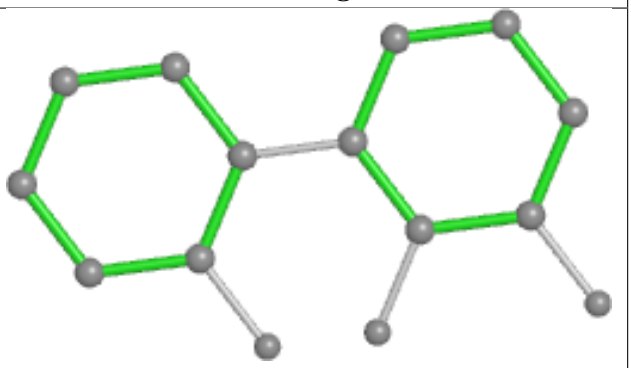
Bond lengths



Bond angles



Torsions



Rings

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data (i)

6.1 Protein, DNA and RNA chains (i)

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å^2)	Q<0.9
1	A	388/392 (98%)	-0.42	3 (0%)	86	89	10, 17, 41, 58	0
1	B	389/392 (99%)	-0.36	4 (1%)	82	86	11, 21, 47, 78	0
1	C	388/392 (98%)	-0.54	1 (0%)	94	96	12, 20, 41, 65	0
2	D	104/115 (90%)	0.80	21 (20%)	1	1	15, 38, 74, 79	0
2	E	106/115 (92%)	-0.00	2 (1%)	66	72	16, 29, 50, 64	0
2	F	104/115 (90%)	0.07	6 (5%)	23	29	15, 29, 52, 75	0
All	All	1479/1521 (97%)	-0.29	37 (2%)	57	64	10, 21, 50, 79	0

All (37) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	93	VAL	4.9
2	D	4	ILE	4.5
2	D	38	GLN	4.4
2	D	98	GLY	4.2
2	D	37	ASP	3.9
1	B	221	VAL	3.8
1	A	221	VAL	3.7
2	D	101	TYR	3.7
1	B	390	HIS	3.7
2	D	104	GLY	3.4
2	D	97	GLU	3.3
2	D	12	SER	3.2
2	D	36	GLY	3.1
2	F	25	VAL	3.0
2	D	40	TYR	3.0
2	F	6	LEU	2.9
2	D	16	PRO	2.9
2	D	39	PHE	2.9
2	D	35	VAL	2.8

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Mol	Chain	Res	Type	RSRZ
2	D	96	LYS	2.7
2	D	92	GLU	2.7
2	D	95	VAL	2.7
2	F	101	TYR	2.6
1	B	389	HIS	2.6
2	D	26	GLY	2.5
2	E	37	ASP	2.5
1	A	389	HIS	2.4
2	F	4	ILE	2.4
2	F	95	VAL	2.4
2	F	107	LYS	2.3
2	E	25	VAL	2.3
2	D	5	TRP	2.3
1	B	305	ALA	2.3
1	A	220	ASP	2.3
2	D	25	VAL	2.2
1	C	389	HIS	2.1
2	D	94	GLU	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 monosaccharides 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	EDO	A	405	4/4	0.81	0.14	45,47,47,49	0
6	EDO	A	409	4/4	0.81	0.20	54,58,60,63	0
8	PGE	A	408	10/10	0.82	0.17	28,40,47,49	0
6	EDO	E	202	4/4	0.84	0.12	47,57,57,59	0
6	EDO	B	405	4/4	0.85	0.16	38,38,40,45	0

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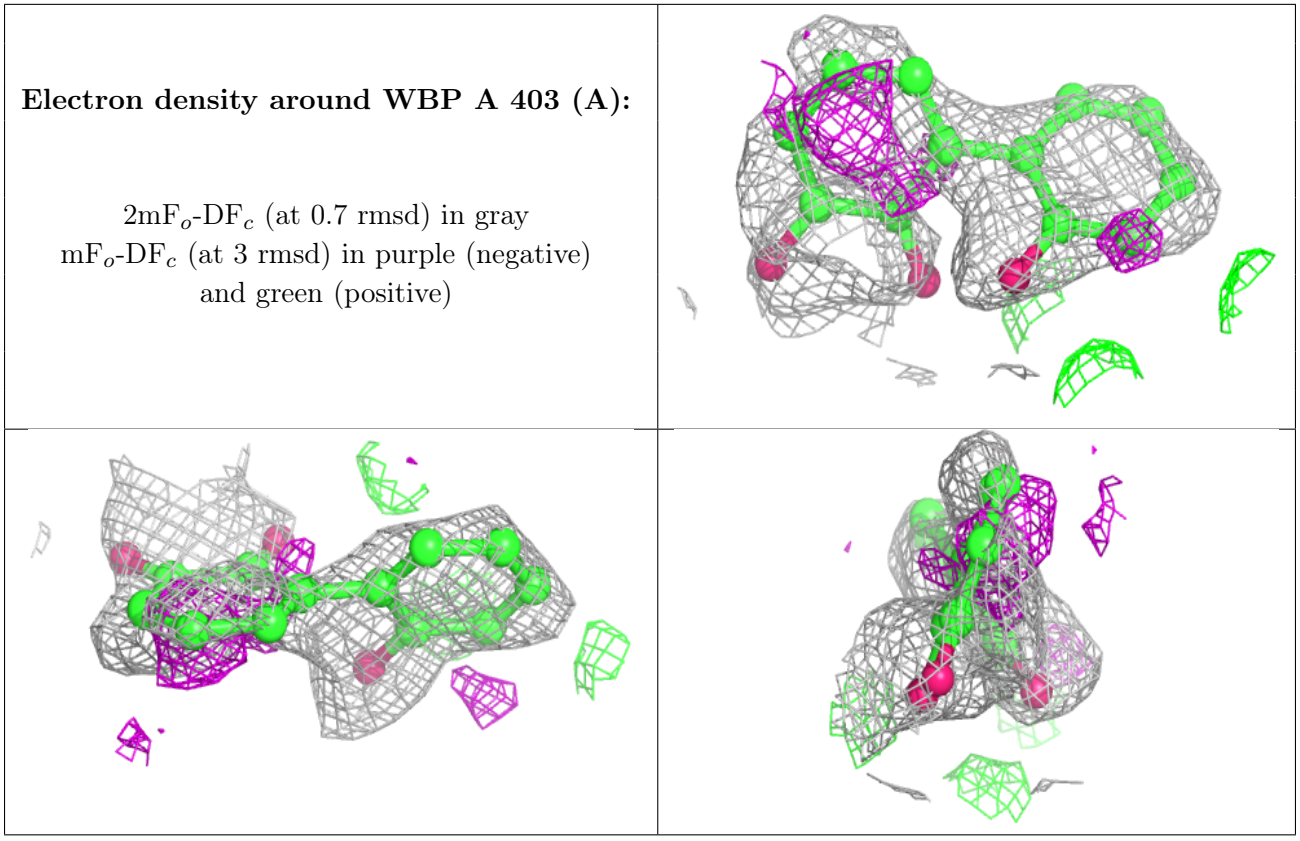
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
5	WBP	A	403[A]	15/15	0.85	0.29	41,48,50,51	15
5	WBP	A	403[B]	15/15	0.85	0.29	28,31,33,34	15
6	EDO	D	202	4/4	0.86	0.28	35,42,45,46	0
5	WBP	B	403	15/15	0.86	0.20	46,52,63,63	0
7	GOL	B	406	6/6	0.86	0.18	53,54,55,58	0
6	EDO	C	407	4/4	0.86	0.21	49,52,54,54	0
6	EDO	B	408	4/4	0.87	0.30	49,52,54,56	0
6	EDO	A	411	4/4	0.87	0.12	48,49,51,51	0
5	WBP	C	403	15/15	0.88	0.20	39,44,50,60	0
9	PEG	B	404	7/7	0.88	0.14	47,50,53,54	0
6	EDO	A	410	4/4	0.89	0.14	41,49,49,50	0
6	EDO	B	409	4/4	0.89	0.21	47,51,55,56	0
7	GOL	A	412	6/6	0.90	0.15	50,51,52,53	0
6	EDO	A	404	4/4	0.90	0.27	36,37,39,40	0
6	EDO	F	202	4/4	0.91	0.24	58,58,60,63	0
6	EDO	A	406	4/4	0.92	0.20	40,41,43,45	0
7	GOL	A	407	6/6	0.92	0.15	23,46,49,51	0
7	GOL	C	408	6/6	0.93	0.15	27,41,45,54	0
6	EDO	C	404	4/4	0.95	0.10	30,40,40,43	0
6	EDO	B	407	4/4	0.96	0.21	31,34,35,39	0
6	EDO	C	405	4/4	0.97	0.13	31,31,32,33	0
6	EDO	C	406	4/4	0.97	0.15	24,26,27,29	0
4	FE2	B	402	1/1	0.99	0.04	32,32,32,32	0
3	FES	C	401	4/4	0.99	0.07	16,16,18,18	0
4	FE2	C	402	1/1	1.00	0.02	24,24,24,24	0
3	FES	A	401	4/4	1.00	0.09	12,12,12,13	0
3	FES	D	201	4/4	1.00	0.05	16,16,17,19	0
3	FES	E	201	4/4	1.00	0.07	17,17,18,18	0
3	FES	F	201	4/4	1.00	0.05	13,14,14,16	0
4	FE2	A	402	1/1	1.00	0.03	23,23,23,23	0
3	FES	B	401	4/4	1.00	0.09	11,11,12,12	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.

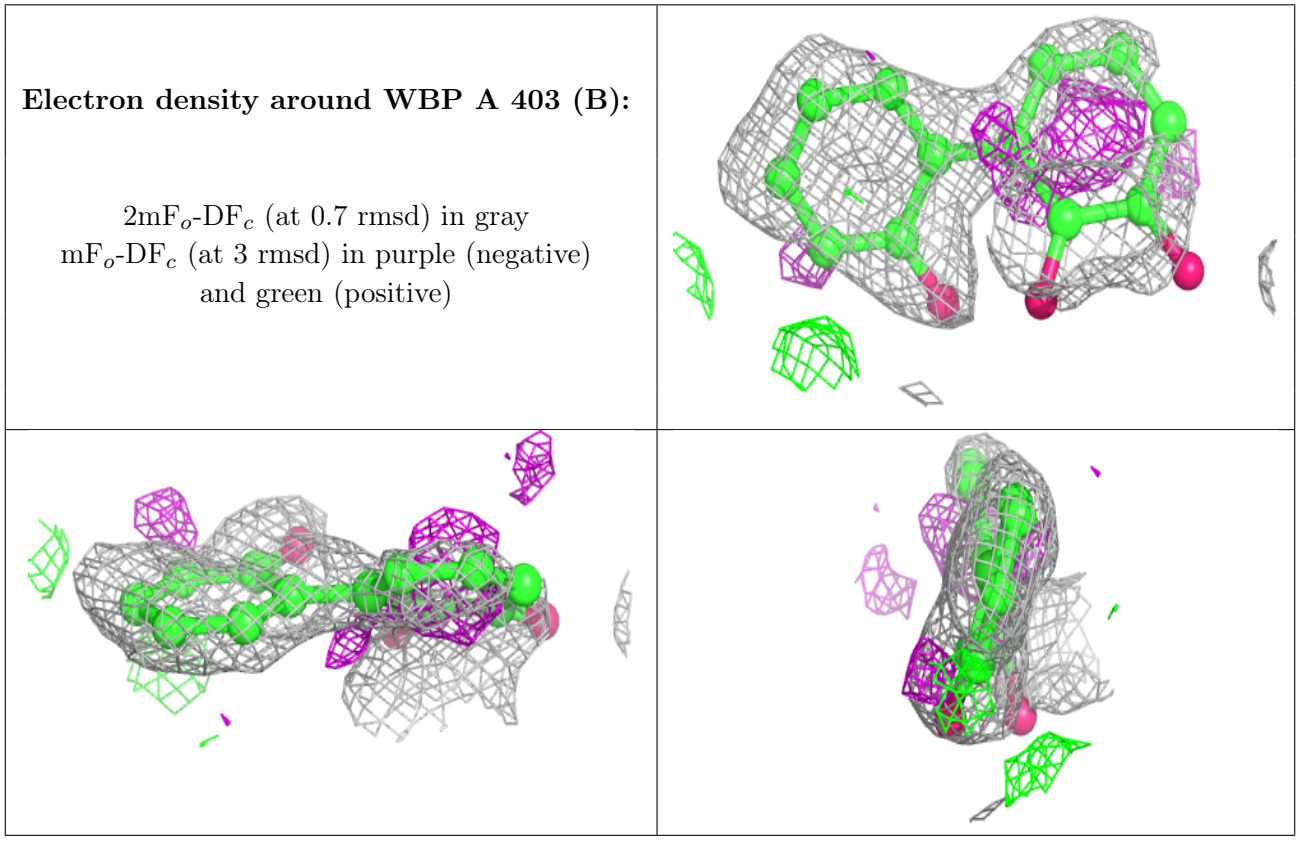
Electron density around WBP A 403 (A):

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



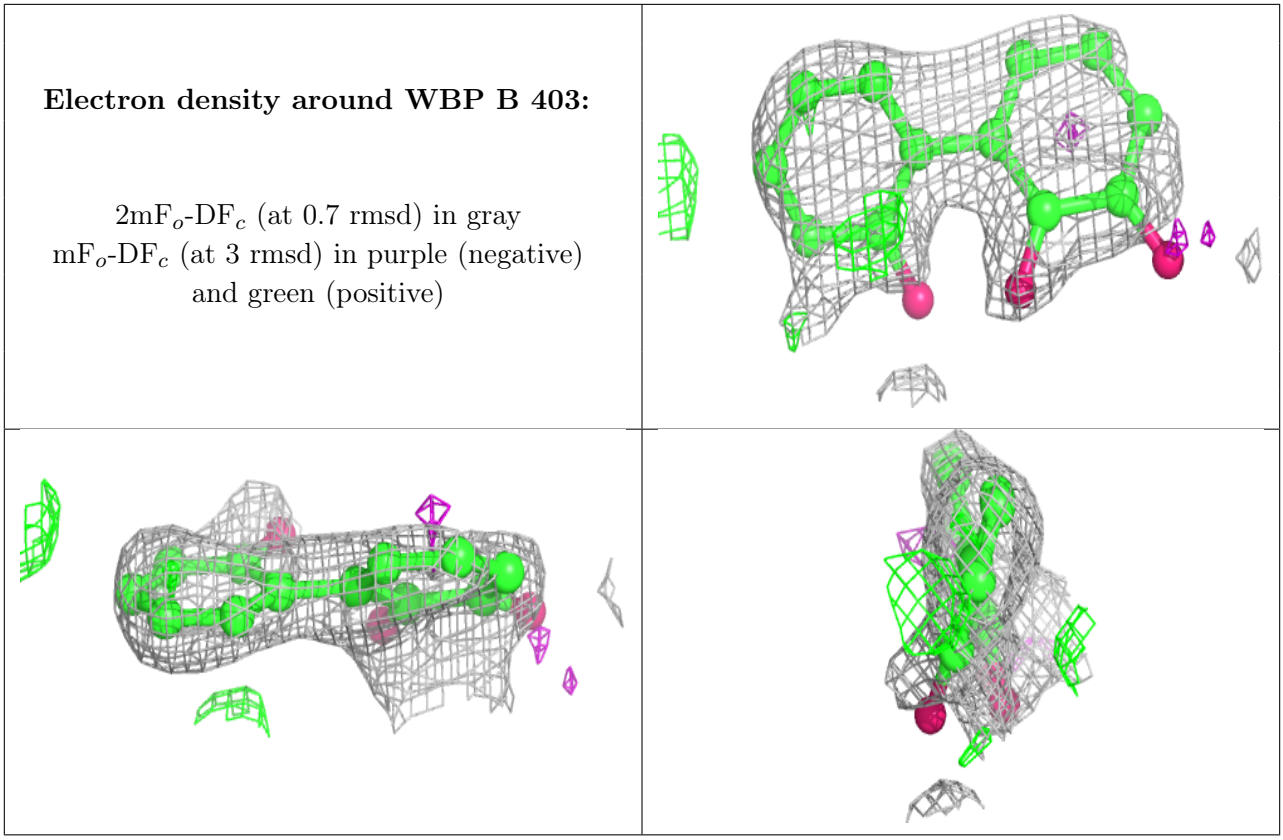
Electron density around WBP A 403 (B):

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



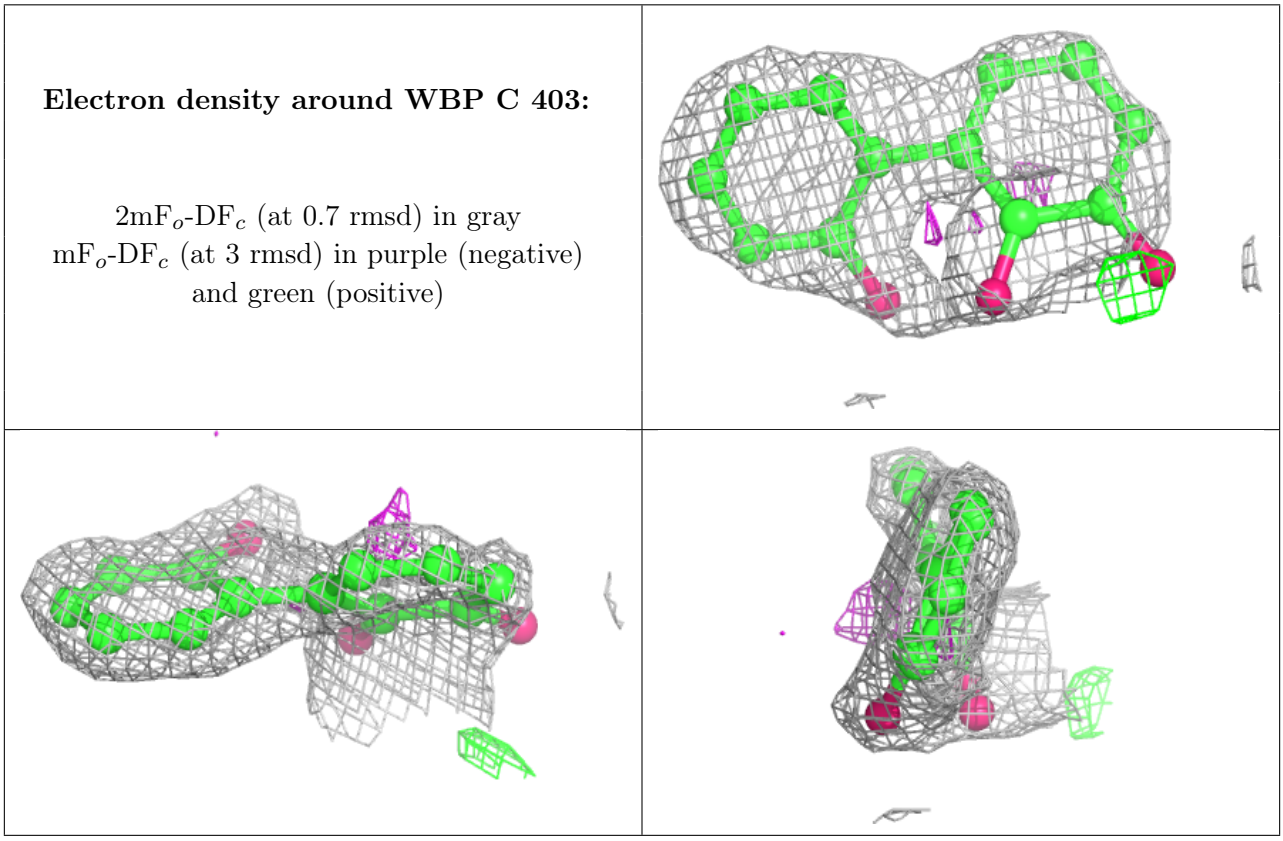
Electron density around WBP B 403:

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



Electron density around WBP C 403:

$2mF_o$-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.