



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 03:47 PM UTC

PDB ID : 6YVB / pdb_00006yvb
Title : Arabidopsis aspartate transcarbamoylase complex with carbamoyl phosphate
Authors : Ramon Maiques, S.; Del Cano Ochoa, F.; Bellin, L.; Mohlmann, T.
Deposited on : 2020-04-28
Resolution : 1.83 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

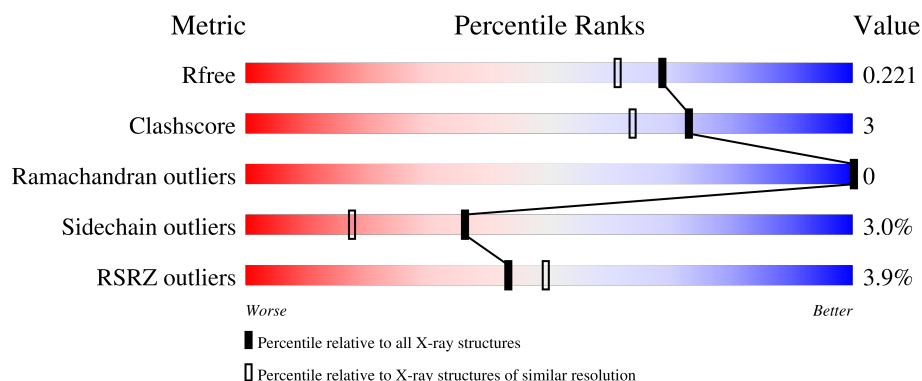
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.83 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	1112 (1.82-1.82)
Clashscore	190562	1148 (1.82-1.82)
Ramachandran outliers	187476	1140 (1.82-1.82)
Sidechain outliers	187428	1140 (1.82-1.82)
RSRZ outliers	180081	1112 (1.82-1.82)

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	332	3% 87% 6% 6%
1	B	332	4% 86% 7% 6%
1	C	332	5% 91% 5% ••
1	D	332	4% 86% 10% •
1	E	332	4% 81% 13% 6%

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Mol	Chain	Length	Quality of chain
1	F	332	

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	GOL	E	1104	-	-	X	-

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 16723 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 PYRB.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	311	Total	C	N	O	S	0	16	0
			2558	1612	436	497	13			
1	B	312	Total	C	N	O	S	0	8	0
			2495	1577	422	483	13			
1	C	324	Total	C	N	O	S	5	14	0
			2628	1659	449	507	13			
1	D	319	Total	C	N	O	S	0	8	0
			2552	1614	435	490	13			
1	E	312	Total	C	N	O	S	0	9	0
			2503	1582	425	481	15			
1	F	311	Total	C	N	O	S	0	4	0
			2451	1549	415	473	14			

There are 138 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	59	MET	-	initiating methionine	UNP A0A178VJE3
A	60	GLY	-	expression tag	UNP A0A178VJE3
A	61	SER	-	expression tag	UNP A0A178VJE3
A	62	SER	-	expression tag	UNP A0A178VJE3
A	63	HIS	-	expression tag	UNP A0A178VJE3
A	64	HIS	-	expression tag	UNP A0A178VJE3
A	65	HIS	-	expression tag	UNP A0A178VJE3
A	66	HIS	-	expression tag	UNP A0A178VJE3
A	67	HIS	-	expression tag	UNP A0A178VJE3
A	68	HIS	-	expression tag	UNP A0A178VJE3
A	69	SER	-	expression tag	UNP A0A178VJE3
A	70	SER	-	expression tag	UNP A0A178VJE3
A	71	GLY	-	expression tag	UNP A0A178VJE3
A	72	LEU	-	expression tag	UNP A0A178VJE3
A	73	GLU	-	expression tag	UNP A0A178VJE3
A	74	VAL	-	expression tag	UNP A0A178VJE3
A	75	LEU	-	expression tag	UNP A0A178VJE3

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Chain	Residue	Modelled	Actual	Comment	Reference
A	76	PHE	-	expression tag	UNP A0A178VJE3
A	77	GLN	-	expression tag	UNP A0A178VJE3
A	78	GLY	-	expression tag	UNP A0A178VJE3
A	79	PRO	-	expression tag	UNP A0A178VJE3
A	80	HIS	-	expression tag	UNP A0A178VJE3
A	81	MET	-	expression tag	UNP A0A178VJE3
B	59	MET	-	initiating methionine	UNP A0A178VJE3
B	60	GLY	-	expression tag	UNP A0A178VJE3
B	61	SER	-	expression tag	UNP A0A178VJE3
B	62	SER	-	expression tag	UNP A0A178VJE3
B	63	HIS	-	expression tag	UNP A0A178VJE3
B	64	HIS	-	expression tag	UNP A0A178VJE3
B	65	HIS	-	expression tag	UNP A0A178VJE3
B	66	HIS	-	expression tag	UNP A0A178VJE3
B	67	HIS	-	expression tag	UNP A0A178VJE3
B	68	HIS	-	expression tag	UNP A0A178VJE3
B	69	SER	-	expression tag	UNP A0A178VJE3
B	70	SER	-	expression tag	UNP A0A178VJE3
B	71	GLY	-	expression tag	UNP A0A178VJE3
B	72	LEU	-	expression tag	UNP A0A178VJE3
B	73	GLU	-	expression tag	UNP A0A178VJE3
B	74	VAL	-	expression tag	UNP A0A178VJE3
B	75	LEU	-	expression tag	UNP A0A178VJE3
B	76	PHE	-	expression tag	UNP A0A178VJE3
B	77	GLN	-	expression tag	UNP A0A178VJE3
B	78	GLY	-	expression tag	UNP A0A178VJE3
B	79	PRO	-	expression tag	UNP A0A178VJE3
B	80	HIS	-	expression tag	UNP A0A178VJE3
B	81	MET	-	expression tag	UNP A0A178VJE3
C	59	MET	-	initiating methionine	UNP A0A178VJE3
C	60	GLY	-	expression tag	UNP A0A178VJE3
C	61	SER	-	expression tag	UNP A0A178VJE3
C	62	SER	-	expression tag	UNP A0A178VJE3
C	63	HIS	-	expression tag	UNP A0A178VJE3
C	64	HIS	-	expression tag	UNP A0A178VJE3
C	65	HIS	-	expression tag	UNP A0A178VJE3
C	66	HIS	-	expression tag	UNP A0A178VJE3
C	67	HIS	-	expression tag	UNP A0A178VJE3
C	68	HIS	-	expression tag	UNP A0A178VJE3
C	69	SER	-	expression tag	UNP A0A178VJE3
C	70	SER	-	expression tag	UNP A0A178VJE3
C	71	GLY	-	expression tag	UNP A0A178VJE3

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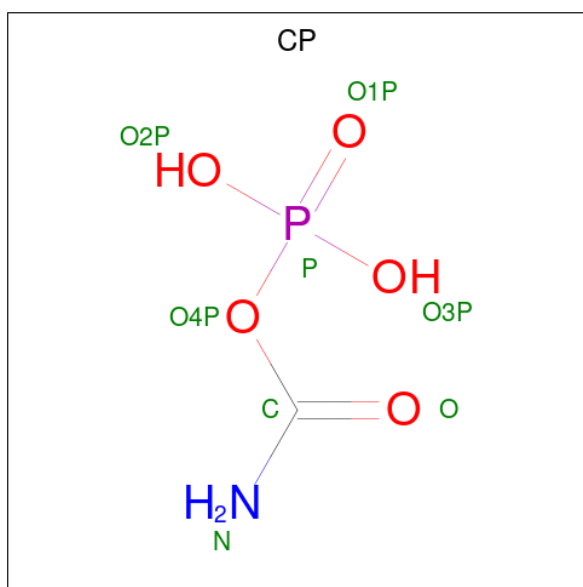
Chain	Residue	Modelled	Actual	Comment	Reference
C	72	LEU	-	expression tag	UNP A0A178VJE3
C	73	GLU	-	expression tag	UNP A0A178VJE3
C	74	VAL	-	expression tag	UNP A0A178VJE3
C	75	LEU	-	expression tag	UNP A0A178VJE3
C	76	PHE	-	expression tag	UNP A0A178VJE3
C	77	GLN	-	expression tag	UNP A0A178VJE3
C	78	GLY	-	expression tag	UNP A0A178VJE3
C	79	PRO	-	expression tag	UNP A0A178VJE3
C	80	HIS	-	expression tag	UNP A0A178VJE3
C	81	MET	-	expression tag	UNP A0A178VJE3
D	59	MET	-	initiating methionine	UNP A0A178VJE3
D	60	GLY	-	expression tag	UNP A0A178VJE3
D	61	SER	-	expression tag	UNP A0A178VJE3
D	62	SER	-	expression tag	UNP A0A178VJE3
D	63	HIS	-	expression tag	UNP A0A178VJE3
D	64	HIS	-	expression tag	UNP A0A178VJE3
D	65	HIS	-	expression tag	UNP A0A178VJE3
D	66	HIS	-	expression tag	UNP A0A178VJE3
D	67	HIS	-	expression tag	UNP A0A178VJE3
D	68	HIS	-	expression tag	UNP A0A178VJE3
D	69	SER	-	expression tag	UNP A0A178VJE3
D	70	SER	-	expression tag	UNP A0A178VJE3
D	71	GLY	-	expression tag	UNP A0A178VJE3
D	72	LEU	-	expression tag	UNP A0A178VJE3
D	73	GLU	-	expression tag	UNP A0A178VJE3
D	74	VAL	-	expression tag	UNP A0A178VJE3
D	75	LEU	-	expression tag	UNP A0A178VJE3
D	76	PHE	-	expression tag	UNP A0A178VJE3
D	77	GLN	-	expression tag	UNP A0A178VJE3
D	78	GLY	-	expression tag	UNP A0A178VJE3
D	79	PRO	-	expression tag	UNP A0A178VJE3
D	80	HIS	-	expression tag	UNP A0A178VJE3
D	81	MET	-	expression tag	UNP A0A178VJE3
E	59	MET	-	initiating methionine	UNP A0A178VJE3
E	60	GLY	-	expression tag	UNP A0A178VJE3
E	61	SER	-	expression tag	UNP A0A178VJE3
E	62	SER	-	expression tag	UNP A0A178VJE3
E	63	HIS	-	expression tag	UNP A0A178VJE3
E	64	HIS	-	expression tag	UNP A0A178VJE3
E	65	HIS	-	expression tag	UNP A0A178VJE3
E	66	HIS	-	expression tag	UNP A0A178VJE3
E	67	HIS	-	expression tag	UNP A0A178VJE3

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Chain	Residue	Modelled	Actual	Comment	Reference
E	68	HIS	-	expression tag	UNP A0A178VJE3
E	69	SER	-	expression tag	UNP A0A178VJE3
E	70	SER	-	expression tag	UNP A0A178VJE3
E	71	GLY	-	expression tag	UNP A0A178VJE3
E	72	LEU	-	expression tag	UNP A0A178VJE3
E	73	GLU	-	expression tag	UNP A0A178VJE3
E	74	VAL	-	expression tag	UNP A0A178VJE3
E	75	LEU	-	expression tag	UNP A0A178VJE3
E	76	PHE	-	expression tag	UNP A0A178VJE3
E	77	GLN	-	expression tag	UNP A0A178VJE3
E	78	GLY	-	expression tag	UNP A0A178VJE3
E	79	PRO	-	expression tag	UNP A0A178VJE3
E	80	HIS	-	expression tag	UNP A0A178VJE3
E	81	MET	-	expression tag	UNP A0A178VJE3
F	59	MET	-	initiating methionine	UNP A0A178VJE3
F	60	GLY	-	expression tag	UNP A0A178VJE3
F	61	SER	-	expression tag	UNP A0A178VJE3
F	62	SER	-	expression tag	UNP A0A178VJE3
F	63	HIS	-	expression tag	UNP A0A178VJE3
F	64	HIS	-	expression tag	UNP A0A178VJE3
F	65	HIS	-	expression tag	UNP A0A178VJE3
F	66	HIS	-	expression tag	UNP A0A178VJE3
F	67	HIS	-	expression tag	UNP A0A178VJE3
F	68	HIS	-	expression tag	UNP A0A178VJE3
F	69	SER	-	expression tag	UNP A0A178VJE3
F	70	SER	-	expression tag	UNP A0A178VJE3
F	71	GLY	-	expression tag	UNP A0A178VJE3
F	72	LEU	-	expression tag	UNP A0A178VJE3
F	73	GLU	-	expression tag	UNP A0A178VJE3
F	74	VAL	-	expression tag	UNP A0A178VJE3
F	75	LEU	-	expression tag	UNP A0A178VJE3
F	76	PHE	-	expression tag	UNP A0A178VJE3
F	77	GLN	-	expression tag	UNP A0A178VJE3
F	78	GLY	-	expression tag	UNP A0A178VJE3
F	79	PRO	-	expression tag	UNP A0A178VJE3
F	80	HIS	-	expression tag	UNP A0A178VJE3
F	81	MET	-	expression tag	UNP A0A178VJE3

- Molecule 2 is PHOSPHORIC ACID MONO(FORMAMIDE)ESTER (CCD ID: CP) (formula: $\text{CH}_4\text{NO}_5\text{P}$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			8	1	1	5	1		
2	B	1	Total	C	N	O	P	0	0
			8	1	1	5	1		
2	C	1	Total	C	N	O	P	0	0
			8	1	1	5	1		
2	D	1	Total	C	N	O	P	0	0
			8	1	1	5	1		
2	E	1	Total	C	N	O	P	0	0
			8	1	1	5	1		
2	F	1	Total	C	N	O	P	0	0
			8	1	1	5	1		

- Molecule 3 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



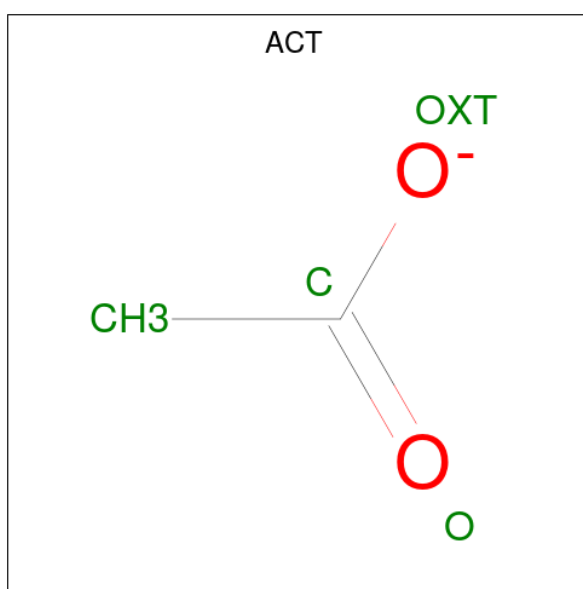
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	1
			12	6	6		
3	A	1	Total	C	O	0	0
			6	3	3		
3	A	1	Total	C	O	0	0
			6	3	3		
3	A	1	Total	C	O	0	0
			6	3	3		
3	A	1	Total	C	O	0	0
			6	3	3		
3	B	1	Total	C	O	0	0
			6	3	3		
3	B	1	Total	C	O	0	0
			6	3	3		
3	B	1	Total	C	O	0	0
			6	3	3		
3	B	1	Total	C	O	0	0
			6	3	3		
3	C	1	Total	C	O	0	0
			6	3	3		
3	C	1	Total	C	O	0	0
			6	3	3		
3	D	1	Total	C	O	0	0
			6	3	3		
3	E	1	Total	C	O	0	0
			6	3	3		
3	E	1	Total	C	O	0	0
			6	3	3		

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

- Molecule 4 is ACETATE ION (CCD ID: ACT) (formula: $C_2H_3O_2$).



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	B	1	Total	C	O	0	0
			4	2	2		
4	B	1	Total	C	O	0	0
			4	2	2		
4	C	1	Total	C	O	0	0
			4	2	2		
4	C	1	Total	C	O	0	0
			4	2	2		
4	C	1	Total	C	O	0	0
			4	2	2		

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

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	296	Total	O	0	0
			296	296		
5	B	195	Total	O	0	0
			195	195		
5	C	247	Total	O	0	0
			247	247		
5	D	223	Total	O	0	0
			223	223		
5	E	222	Total	O	0	0
			222	222		
5	F	151	Total	O	0	0
			151	151		

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.

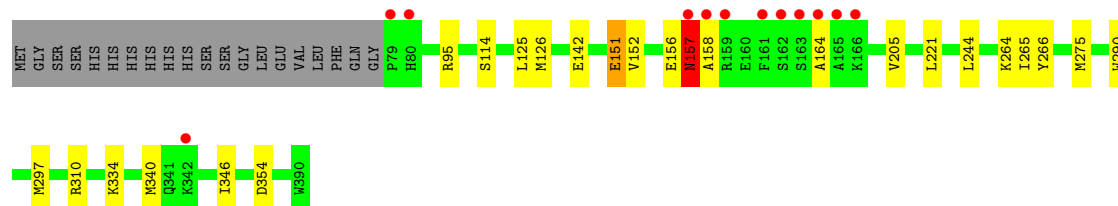
• Molecule 1: PYRB

Chain A: 



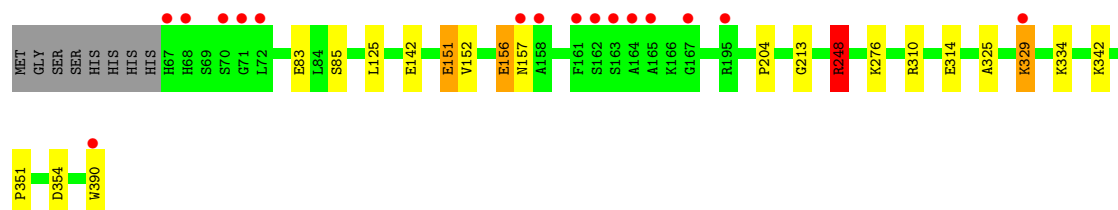
• Molecule 1: PYRB

Chain B: 



• Molecule 1: PYRB

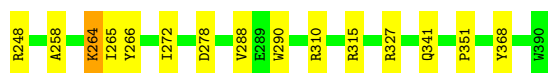
Chain C: 



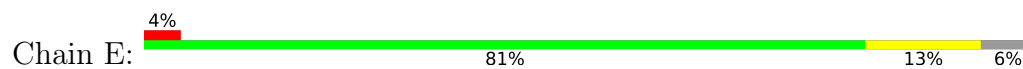
• Molecule 1: PYRB

Chain D: 

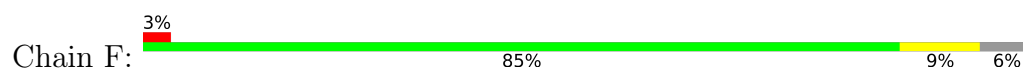




• Molecule 1: PYRB



• Molecule 1: PYRB



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	103.27Å 109.48Å 212.04Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	76.28 – 1.83 76.28 – 1.83	Depositor EDS
% Data completeness (in resolution range)	99.9 (76.28-1.83) 99.9 (76.28-1.83)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.63 (at 1.83Å)	Xtriage
Refinement program	REFMAC 5.8.0258	Depositor
R, R_{free}	0.172 , 0.213 0.180 , 0.221	Depositor DCC
R_{free} test set	10813 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å ²)	34.7	Xtriage
Anisotropy	0.017	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 30.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	16723	wwPDB-VP
Average B, all atoms (Å ²)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.50% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: CP, GOL, ACT

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	1.09	0/2601	1.26	1/3499 (0.0%)
1	B	1.10	1/2538 (0.0%)	1.33	1/3416 (0.0%)
1	C	1.09	1/2680 (0.0%)	1.31	1/3606 (0.0%)
1	D	1.09	0/2594	1.33	1/3492 (0.0%)
1	E	1.12	1/2544 (0.0%)	1.34	4/3426 (0.1%)
1	F	1.12	0/2487	1.38	1/3349 (0.0%)
All	All	1.10	3/15444 (0.0%)	1.32	9/20788 (0.0%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	205	VAL	C-O	5.71	1.29	1.24
1	C	204	PRO	C-O	5.11	1.29	1.23
1	E	388	VAL	N-CA	5.06	1.50	1.46

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	94	ASP	CA-CB-CG	6.54	119.14	112.60
1	B	157	ASN	N-CA-C	-6.10	102.82	111.24
1	E	284	THR	CA-CB-OG1	-5.89	100.76	109.60
1	E	95	ARG	CG-CD-NE	-5.81	99.22	112.00
1	D	278	ASP	CA-CB-CG	5.73	118.33	112.60
1	A	318	GLU	CB-CG-CD	5.51	121.97	112.60
1	C	248	ARG	CG-CD-NE	5.50	124.09	112.00
1	E	214	GLU	CA-C-N	5.02	128.37	122.85
1	E	214	GLU	C-N-CA	5.02	128.37	122.85

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	2558	0	2551	14	0
1	B	2495	0	2496	14	0
1	C	2628	0	2629	12	0
1	D	2552	0	2532	18	0
1	E	2503	0	2489	28	0
1	F	2451	0	2455	15	0
2	A	8	0	2	0	0
2	B	8	0	2	0	0
2	C	8	0	2	0	0
2	D	8	0	2	0	0
2	E	8	0	2	0	0
2	F	8	0	2	0	0
3	A	36	0	48	2	0
3	B	24	0	32	0	0
3	C	12	0	16	1	0
3	D	6	0	8	0	0
3	E	18	0	24	4	0
3	F	18	0	24	1	0
4	A	8	0	6	0	0
4	B	8	0	6	1	0
4	C	12	0	9	0	0
4	D	4	0	3	0	0
4	E	4	0	3	0	0
4	F	4	0	3	0	0
5	A	296	0	0	2	0
5	B	195	0	0	0	0
5	C	247	0	0	1	0
5	D	223	0	0	4	0
5	E	222	0	0	2	0
5	F	151	0	0	0	0
All	All	16723	0	15346	98	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 3.

All (98) 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:E:314[B]:GLU:HG3	5:E:1363:HOH:O	1.77	0.83
3:C:403:GOL:H31	5:D:623:HOH:O	1.80	0.81
1:B:142[B]:GLU:HG2	1:B:152:VAL:HG11	1.66	0.77
1:B:264:LYS:HE3	1:B:266:TYR:CZ	2.22	0.75
3:A:402[A]:GOL:H32	5:A:604:HOH:O	1.86	0.74
1:E:324:GLU:OE2	1:E:327:ARG:NH2	2.23	0.72
1:B:310:ARG:NH1	1:B:354:ASP:OD1	2.23	0.72
1:A:142[B]:GLU:HG2	1:A:152:VAL:HG11	1.71	0.70
1:F:376:LEU:HG	1:F:380[B]:MET:HE2	1.75	0.69
1:A:126[A]:MET:HE2	1:A:152:VAL:HG22	1.76	0.67
1:D:138:ARG:HD2	5:D:531:HOH:O	1.94	0.67
1:A:272[A]:ILE:HG13	5:A:708:HOH:O	1.95	0.67
1:D:142[A]:GLU:HG2	1:D:152:VAL:HG11	1.75	0.67
1:C:310[B]:ARG:NH1	1:C:351:PRO:O	2.28	0.65
1:F:280:LYS:NZ	1:F:292:GLU:OE2	2.25	0.65
1:C:142[B]:GLU:HG2	1:C:152:VAL:HG11	1.79	0.64
1:E:227:GLN:HE21	3:E:1104:GOL:C1	2.12	0.63
1:D:310[B]:ARG:NH2	1:D:351:PRO:O	2.32	0.62
1:A:192:GLY:CA	1:E:320:LEU:HD11	2.29	0.62
1:F:337:LEU:HD11	1:F:360:VAL:HG13	1.81	0.62
1:E:227:GLN:HE21	3:E:1104:GOL:H11	1.63	0.62
1:F:310:ARG:NH2	1:F:354:ASP:OD1	2.31	0.61
1:C:157:ASN:HA	5:C:705:HOH:O	2.00	0.61
1:D:68:HIS:HD2	1:D:103:ASP:OD2	1.83	0.61
1:D:82:PHE:CD2	1:D:97[B]:MET:HE3	2.36	0.61
1:D:310[B]:ARG:HB2	1:D:310[B]:ARG:CZ	2.28	0.60
1:F:377:PHE:HA	1:F:380[B]:MET:HE3	1.85	0.59
1:E:376:LEU:HG	1:E:380[B]:MET:HE3	1.85	0.58
1:E:248:ARG:HG3	5:E:1353:HOH:O	2.04	0.58
1:A:243:ASP:OD2	1:A:246[A]:ASN:HB2	2.03	0.57
1:E:243:ASP:OD2	1:E:246[B]:ASN:HB2	2.04	0.57
1:F:126[B]:MET:HE2	1:F:185:VAL:HG21	1.86	0.56
1:A:126[A]:MET:HE1	1:A:142[A]:GLU:HA	1.88	0.56
1:C:125:LEU:CD2	1:C:151:GLU:HB3	2.37	0.55
1:E:125:LEU:HD22	1:E:153:LEU:HG	1.87	0.55
1:F:312:GLN:HA	1:F:312:GLN:HE21	1.71	0.55
1:B:264:LYS:HE3	1:B:266:TYR:OH	2.07	0.54
1:F:147:ARG:HD2	3:F:405:GOL:H2	1.91	0.52
1:A:96:GLU:HB3	3:A:404:GOL:H12	1.92	0.52
1:A:126[A]:MET:HE2	1:A:152:VAL:CG2	2.40	0.52
1:C:156:GLU:O	1:C:157:ASN:C	2.52	0.52
1:D:68:HIS:CD2	1:D:103:ASP:OD2	2.63	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:264:LYS:HE3	1:D:266:TYR:CZ	2.44	0.52
1:E:310[B]:ARG:NH1	1:E:351:PRO:O	2.43	0.51
1:B:158:ALA:O	1:B:164:ALA:HB3	2.10	0.51
1:C:310[A]:ARG:NH2	1:C:354:ASP:OD1	2.44	0.51
1:E:126[A]:MET:HE2	1:E:152:VAL:HG22	1.92	0.50
1:B:126[A]:MET:HE2	1:B:152:VAL:HG22	1.92	0.49
1:E:126[A]:MET:HE1	1:E:142:GLU:HA	1.94	0.49
1:C:314[A]:GLU:H	1:C:314[A]:GLU:CD	2.20	0.48
1:E:265:ILE:O	1:E:290:TRP:HA	2.14	0.48
1:F:126[B]:MET:HE2	1:F:185:VAL:CG2	2.44	0.48
1:F:212:PRO:HA	1:F:248:ARG:HD3	1.96	0.47
1:C:83[B]:GLU:OE2	1:C:85[B]:SER:OG	2.18	0.47
1:A:310[B]:ARG:NH1	1:A:312:GLN:HE22	2.13	0.47
1:C:213:GLY:O	1:C:248:ARG:HG3	2.15	0.47
1:E:112:GLU:HB2	1:E:380[B]:MET:HE1	1.97	0.47
1:B:125:LEU:HD22	1:B:151[A]:GLU:HB3	1.97	0.46
1:B:340:MET:SD	1:B:346:ILE:HD11	2.55	0.46
1:D:265:ILE:O	1:D:290:TRP:HA	2.14	0.46
1:D:106:ARG:NH2	5:D:516:HOH:O	2.49	0.45
1:B:265:ILE:O	1:B:290:TRP:HA	2.15	0.45
1:B:297:MET:HG2	4:B:405:ACT:H1	1.99	0.45
1:E:227:GLN:NE2	3:E:1104:GOL:H11	2.31	0.45
1:D:142[B]:GLU:HG3	1:D:152:VAL:HG21	1.99	0.45
1:F:297:MET:HE3	1:F:339:VAL:HG11	1.99	0.45
1:D:310[A]:ARG:HH21	1:D:310[A]:ARG:HG3	1.82	0.44
1:F:128:THR:OG1	1:F:154:THR:HA	2.17	0.44
1:E:227:GLN:NE2	3:E:1104:GOL:C1	2.79	0.44
1:E:213:GLY:O	1:E:248:ARG:NH1	2.43	0.44
1:B:157:ASN:HD22	1:B:157:ASN:HA	1.55	0.44
1:F:337:LEU:HD13	1:F:363:ASP:OD2	2.18	0.43
1:B:221:LEU:C	1:B:221:LEU:HD12	2.44	0.43
1:D:341[A]:GLN:HG3	5:D:562:HOH:O	2.18	0.43
1:C:276:LYS:HE3	1:D:272:ILE:HG13	2.00	0.43
1:A:192:GLY:N	1:E:320:LEU:HD11	2.34	0.43
1:A:156:GLU:O	1:A:157:ASN:C	2.60	0.43
1:E:344:ALA:O	1:E:365:ARG:HG2	2.19	0.43
1:D:128:THR:OG1	1:D:154:THR:HA	2.19	0.42
1:D:221:LEU:HD12	1:D:221:LEU:C	2.44	0.42
1:C:314[A]:GLU:CD	1:C:314[A]:GLU:N	2.77	0.42
1:E:310[B]:ARG:CZ	1:E:310[B]:ARG:HB2	2.40	0.42
1:A:192:GLY:HA2	1:E:320:LEU:HD11	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:136:ARG:HG3	1:F:176:THR:HG21	2.01	0.42
1:E:268:VAL:HA	1:E:293:SER:O	2.20	0.42
1:C:325:ALA:O	1:C:329[A]:LYS:HD3	2.20	0.41
1:E:194:ALA:HB1	1:E:207:ASN:HB2	2.02	0.41
1:F:221:LEU:C	1:F:221:LEU:HD12	2.46	0.41
1:B:156:GLU:O	1:B:157:ASN:C	2.64	0.41
1:D:141:PHE:CZ	1:D:206:ILE:HG21	2.55	0.41
1:E:310[A]:ARG:HG2	1:E:355:GLU:CD	2.46	0.41
1:A:125:LEU:CD2	1:A:151[B]:GLU:HB3	2.50	0.41
1:E:82:PHE:CE1	1:E:97[A]:MET:HE2	2.55	0.41
1:E:83:GLU:OE1	1:E:97[B]:MET:HE1	2.20	0.41
1:B:244:LEU:HB3	1:B:275:MET:HE2	2.03	0.40
1:E:175:ARG:HG3	1:E:200:THR:HG22	2.03	0.40
1:A:272[A]:ILE:HD11	1:A:316:PHE:CE1	2.56	0.40
1:D:258:ALA:HA	1:D:288:VAL:HG21	2.04	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	325/332 (98%)	316 (97%)	9 (3%)	0	100	100
1	B	318/332 (96%)	309 (97%)	9 (3%)	0	100	100
1	C	336/332 (101%)	326 (97%)	10 (3%)	0	100	100
1	D	321/332 (97%)	314 (98%)	7 (2%)	0	100	100
1	E	319/332 (96%)	312 (98%)	7 (2%)	0	100	100
1	F	313/332 (94%)	303 (97%)	10 (3%)	0	100	100
All	All	1932/1992 (97%)	1880 (97%)	52 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	273/280 (98%)	260 (95%)	13 (5%)	23	6
1	B	265/280 (95%)	259 (98%)	6 (2%)	44	28
1	C	281/280 (100%)	273 (97%)	8 (3%)	38	21
1	D	270/280 (96%)	260 (96%)	10 (4%)	30	12
1	E	264/280 (94%)	257 (97%)	7 (3%)	39	22
1	F	260/280 (93%)	252 (97%)	8 (3%)	35	17
All	All	1613/1680 (96%)	1561 (97%)	52 (3%)	36	16

All (52) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	81	MET
1	A	89[A]	GLU
1	A	89[B]	GLU
1	A	115	SER
1	A	151[A]	GLU
1	A	151[B]	GLU
1	A	157	ASN
1	A	159	ARG
1	A	272[A]	ILE
1	A	272[B]	ILE
1	A	314	GLU
1	A	343	LYS
1	A	352	ARG
1	B	95	ARG
1	B	114	SER
1	B	151[A]	GLU
1	B	151[B]	GLU
1	B	157	ASN
1	B	334	LYS
1	C	151	GLU
1	C	156	GLU
1	C	248	ARG

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Mol	Chain	Res	Type
1	C	329[A]	LYS
1	C	329[B]	LYS
1	C	334	LYS
1	C	342	LYS
1	C	390	TRP
1	D	77	GLN
1	D	115	SER
1	D	116	SER
1	D	119	GLU
1	D	232	LYS
1	D	248	ARG
1	D	264	LYS
1	D	315	ARG
1	D	327	ARG
1	D	368	TYR
1	E	156	GLU
1	E	159	ARG
1	E	264	LYS
1	E	310[A]	ARG
1	E	310[B]	ARG
1	E	352	ARG
1	E	368	TYR
1	F	116	SER
1	F	159	ARG
1	F	261	LYS
1	F	264	LYS
1	F	312	GLN
1	F	327	ARG
1	F	352	ARG
1	F	368	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	157	ASN
1	A	312	GLN
1	B	157	ASN
1	B	312	GLN
1	C	312	GLN
1	D	67	HIS
1	D	68	HIS
1	D	77	GLN

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Mol	Chain	Res	Type
1	D	312	GLN
1	F	157	ASN
1	F	312	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

35 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	$\# Z > 2$
4	ACT	C	406	-	3,3,3	0.97	0	3,3,3	0.84	0
3	GOL	A	405	-	5,5,5	0.11	0	5,5,5	0.37	0
3	GOL	B	406	-	5,5,5	0.25	0	5,5,5	0.43	0
2	CP	A	401	-	6,7,7	0.91	0	7,10,10	2.05	2 (28%)
3	GOL	E	1101	-	5,5,5	0.14	0	5,5,5	0.43	0
2	CP	B	401	-	6,7,7	1.30	1 (16%)	7,10,10	1.50	1 (14%)
3	GOL	F	405	-	5,5,5	0.25	0	5,5,5	0.54	0
3	GOL	F	402	-	5,5,5	0.10	0	5,5,5	0.39	0
2	CP	F	401	-	6,7,7	1.56	2 (33%)	7,10,10	1.09	0
4	ACT	A	407	-	3,3,3	1.36	0	3,3,3	0.67	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	ACT	A	408	-	3,3,3	1.25	0	3,3,3	1.12	0
4	ACT	C	405	-	3,3,3	0.99	0	3,3,3	1.07	0
3	GOL	A	404	-	5,5,5	0.15	0	5,5,5	0.47	0
4	ACT	C	404	-	3,3,3	1.44	1 (33%)	3,3,3	0.79	0
3	GOL	F	403	-	5,5,5	0.10	0	5,5,5	0.23	0
4	ACT	B	405	-	3,3,3	1.33	0	3,3,3	0.88	0
4	ACT	B	407	-	3,3,3	1.00	0	3,3,3	1.07	0
3	GOL	A	403	-	5,5,5	0.10	0	5,5,5	1.00	0
3	GOL	B	402	-	5,5,5	0.20	0	5,5,5	0.43	0
3	GOL	B	404	-	5,5,5	0.12	0	5,5,5	0.25	0
2	CP	E	1102	-	6,7,7	1.30	1 (16%)	7,10,10	1.36	0
4	ACT	E	1105	-	3,3,3	1.09	0	3,3,3	0.76	0
3	GOL	A	402[A]	-	5,5,5	0.08	0	5,5,5	0.24	0
4	ACT	F	404	-	3,3,3	1.14	0	3,3,3	0.68	0
3	GOL	E	1104	-	5,5,5	0.14	0	5,5,5	0.39	0
2	CP	C	401	-	6,7,7	0.62	0	7,10,10	1.18	0
3	GOL	A	402[B]	-	5,5,5	0.09	0	5,5,5	0.24	0
3	GOL	B	403	-	5,5,5	0.09	0	5,5,5	0.36	0
3	GOL	C	402	-	5,5,5	0.22	0	5,5,5	0.54	0
3	GOL	E	1103	-	5,5,5	0.26	0	5,5,5	0.85	0
3	GOL	A	406	-	5,5,5	0.19	0	5,5,5	0.14	0
2	CP	D	401	-	6,7,7	0.66	0	7,10,10	1.76	2 (28%)
3	GOL	C	403	-	5,5,5	0.48	0	5,5,5	1.15	0
3	GOL	D	402	-	5,5,5	0.17	0	5,5,5	0.34	0
4	ACT	D	403	-	3,3,3	1.23	0	3,3,3	0.83	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
3	GOL	A	405	-	-	0/4/4/4	-
3	GOL	B	406	-	-	2/4/4/4	-
2	CP	A	401	-	-	0/3/5/5	-
3	GOL	E	1101	-	-	0/4/4/4	-
2	CP	B	401	-	-	0/3/5/5	-
3	GOL	F	405	-	-	2/4/4/4	-
3	GOL	F	402	-	-	2/4/4/4	-
2	CP	F	401	-	-	0/3/5/5	-
3	GOL	A	404	-	-	2/4/4/4	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	GOL	F	403	-	-	2/4/4/4	-
3	GOL	A	403	-	-	2/4/4/4	-
3	GOL	B	402	-	-	3/4/4/4	-
3	GOL	B	404	-	-	4/4/4/4	-
2	CP	E	1102	-	-	0/3/5/5	-
3	GOL	A	402[A]	-	-	4/4/4/4	-
3	GOL	E	1104	-	-	1/4/4/4	-
2	CP	C	401	-	-	0/3/5/5	-
3	GOL	A	402[B]	-	-	4/4/4/4	-
3	GOL	B	403	-	-	0/4/4/4	-
3	GOL	C	402	-	-	2/4/4/4	-
3	GOL	E	1103	-	-	3/4/4/4	-
3	GOL	A	406	-	-	0/4/4/4	-
2	CP	D	401	-	-	0/3/5/5	-
3	GOL	C	403	-	-	2/4/4/4	-
3	GOL	D	402	-	-	0/4/4/4	-

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	F	401	CP	O-C	2.24	1.25	1.22
2	B	401	CP	P-O1P	-2.19	1.43	1.50
2	F	401	CP	P-O4P	2.18	1.63	1.59
2	E	1102	CP	P-O4P	2.06	1.63	1.59
4	C	404	ACT	O-C	2.05	1.31	1.22

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	401	CP	O-C-N	4.31	132.39	125.58
2	D	401	CP	O3P-P-O2P	3.85	122.26	107.80
2	B	401	CP	O2P-P-O4P	-2.63	97.66	105.32
2	D	401	CP	O3P-P-O4P	-2.42	98.28	105.32
2	A	401	CP	O2P-P-O1P	2.32	119.88	110.83

There are no chirality outliers.

All (35) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	402[A]	GOL	O1-C1-C2-C3
3	A	402[B]	GOL	O1-C1-C2-O2
3	A	402[B]	GOL	O1-C1-C2-C3
3	A	402[B]	GOL	C1-C2-C3-O3
3	A	403	GOL	C1-C2-C3-O3
3	A	404	GOL	C1-C2-C3-O3
3	B	402	GOL	O1-C1-C2-C3
3	B	404	GOL	O1-C1-C2-O2
3	B	404	GOL	O1-C1-C2-C3
3	C	402	GOL	O1-C1-C2-C3
3	C	403	GOL	O1-C1-C2-C3
3	F	402	GOL	C1-C2-C3-O3
3	F	403	GOL	C1-C2-C3-O3
3	A	402[A]	GOL	C1-C2-C3-O3
3	B	404	GOL	C1-C2-C3-O3
3	E	1103	GOL	O1-C1-C2-C3
3	E	1104	GOL	O1-C1-C2-C3
3	F	405	GOL	O1-C1-C2-C3
3	A	402[A]	GOL	O1-C1-C2-O2
3	A	402[B]	GOL	O2-C2-C3-O3
3	A	404	GOL	O2-C2-C3-O3
3	C	402	GOL	O1-C1-C2-O2
3	F	403	GOL	O2-C2-C3-O3
3	A	403	GOL	O2-C2-C3-O3
3	B	402	GOL	O1-C1-C2-O2
3	C	403	GOL	O1-C1-C2-O2
3	E	1103	GOL	O1-C1-C2-O2
3	F	402	GOL	O2-C2-C3-O3
3	F	405	GOL	O1-C1-C2-O2
3	B	402	GOL	O2-C2-C3-O3
3	B	404	GOL	O2-C2-C3-O3
3	B	406	GOL	O1-C1-C2-C3
3	A	402[A]	GOL	O2-C2-C3-O3
3	E	1103	GOL	O2-C2-C3-O3
3	B	406	GOL	O1-C1-C2-O2

There are no ring outliers.

6 monomers are involved in 9 short contacts:

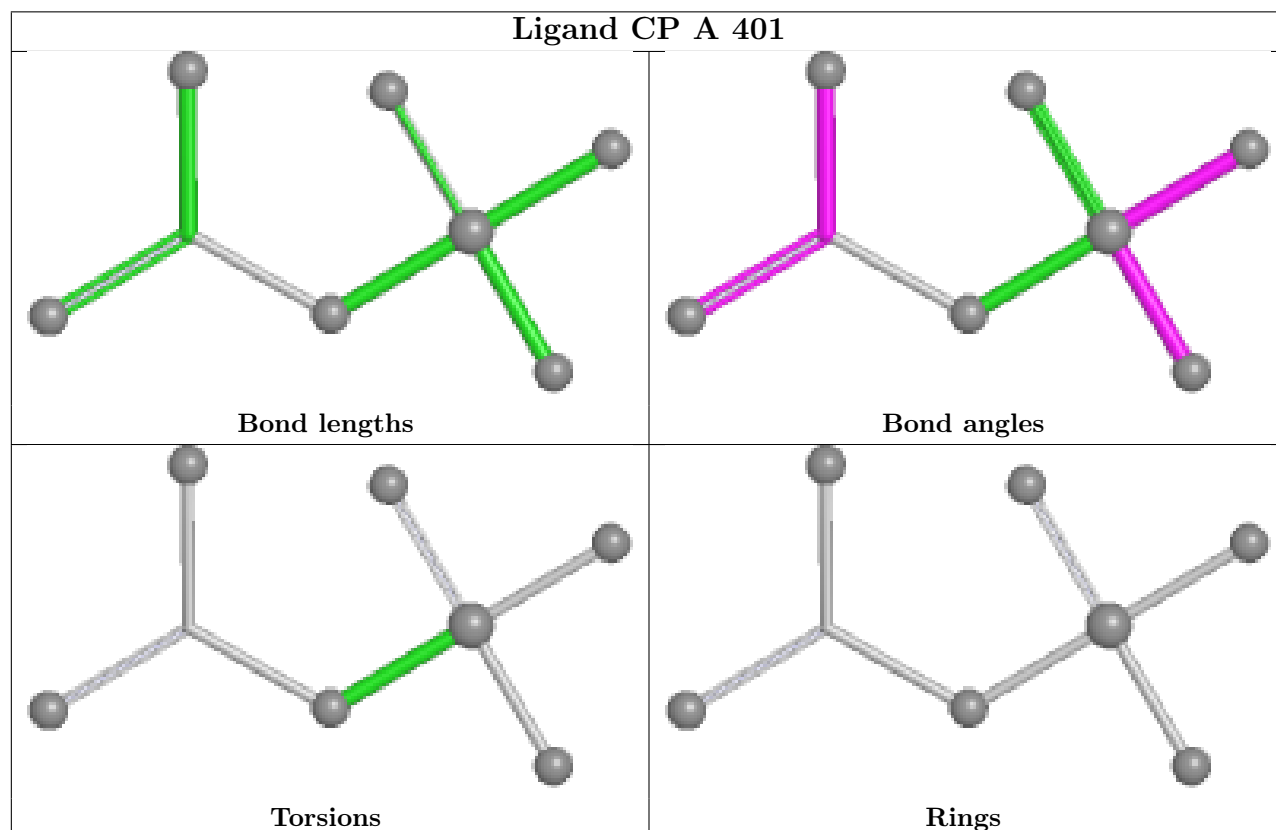
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	F	405	GOL	1	0
3	A	404	GOL	1	0
4	B	405	ACT	1	0

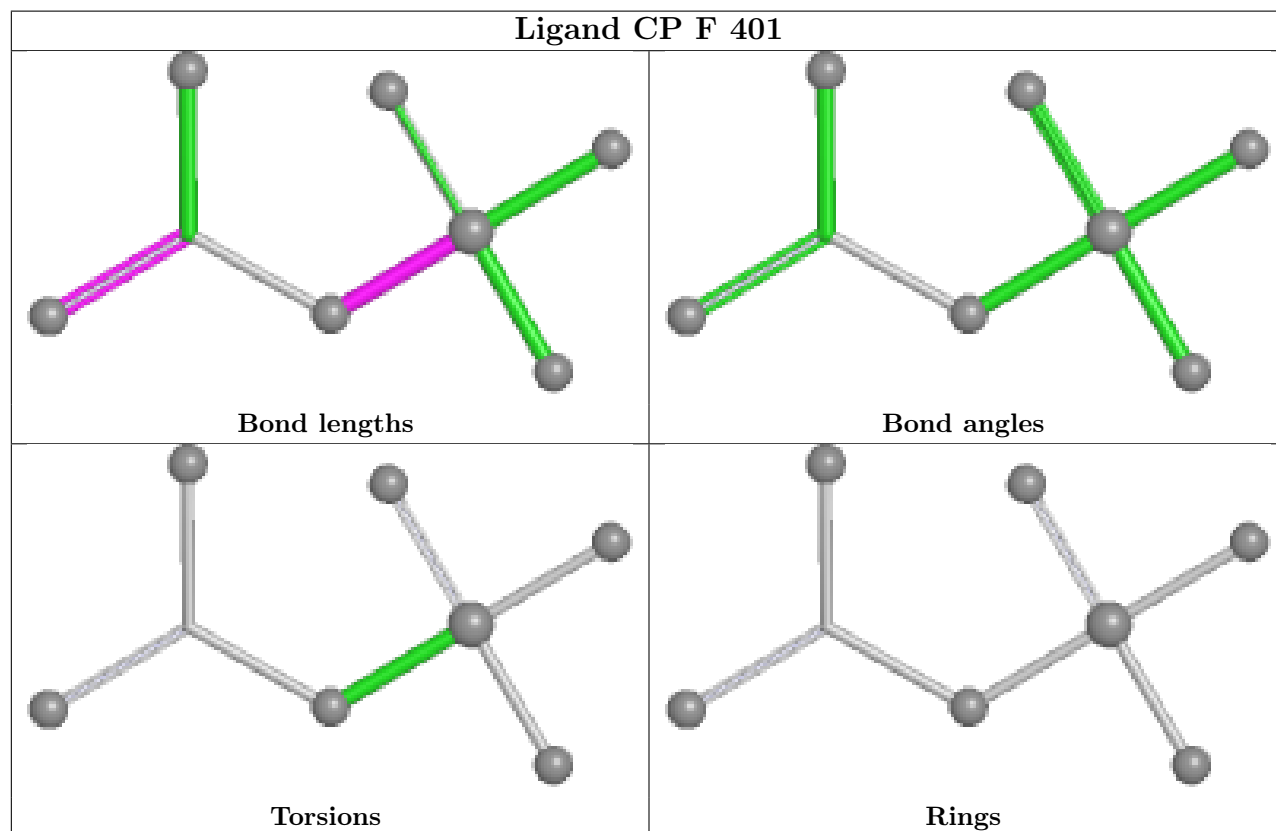
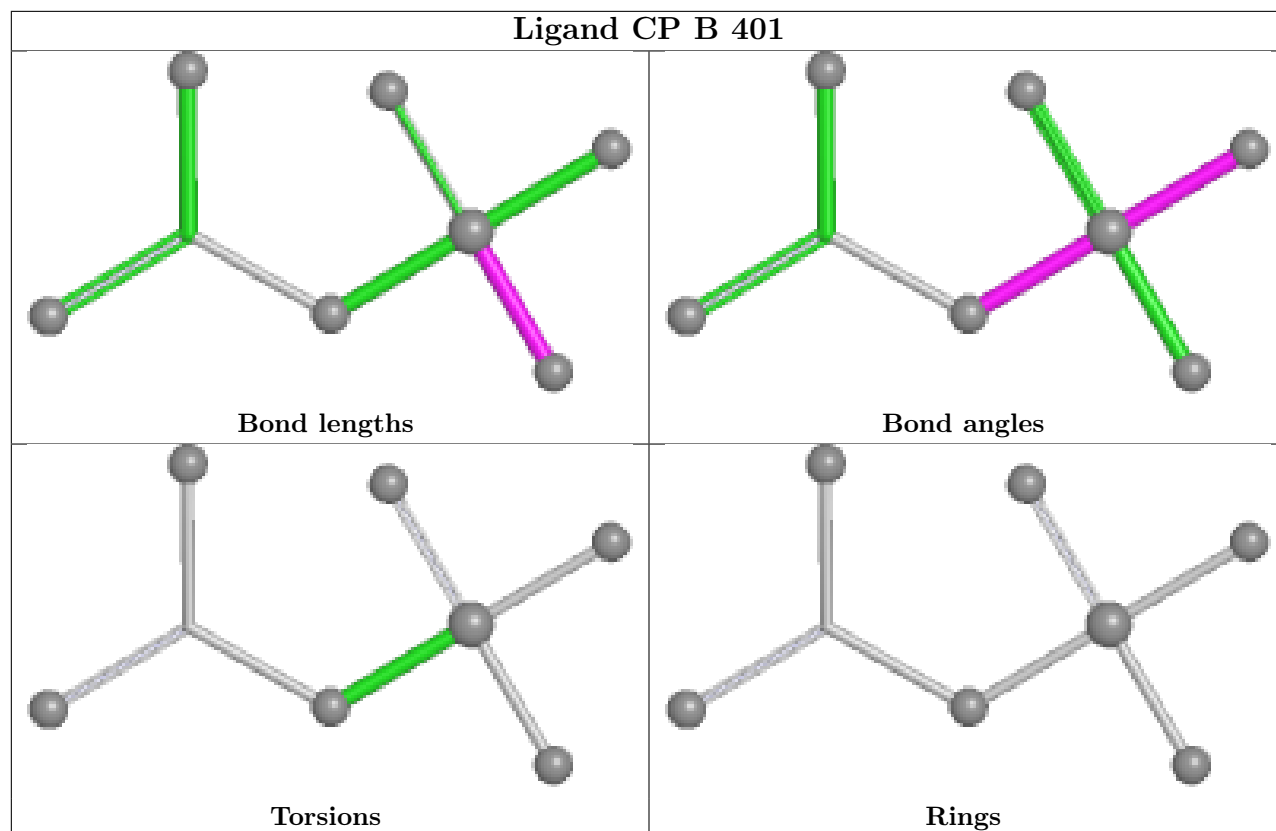
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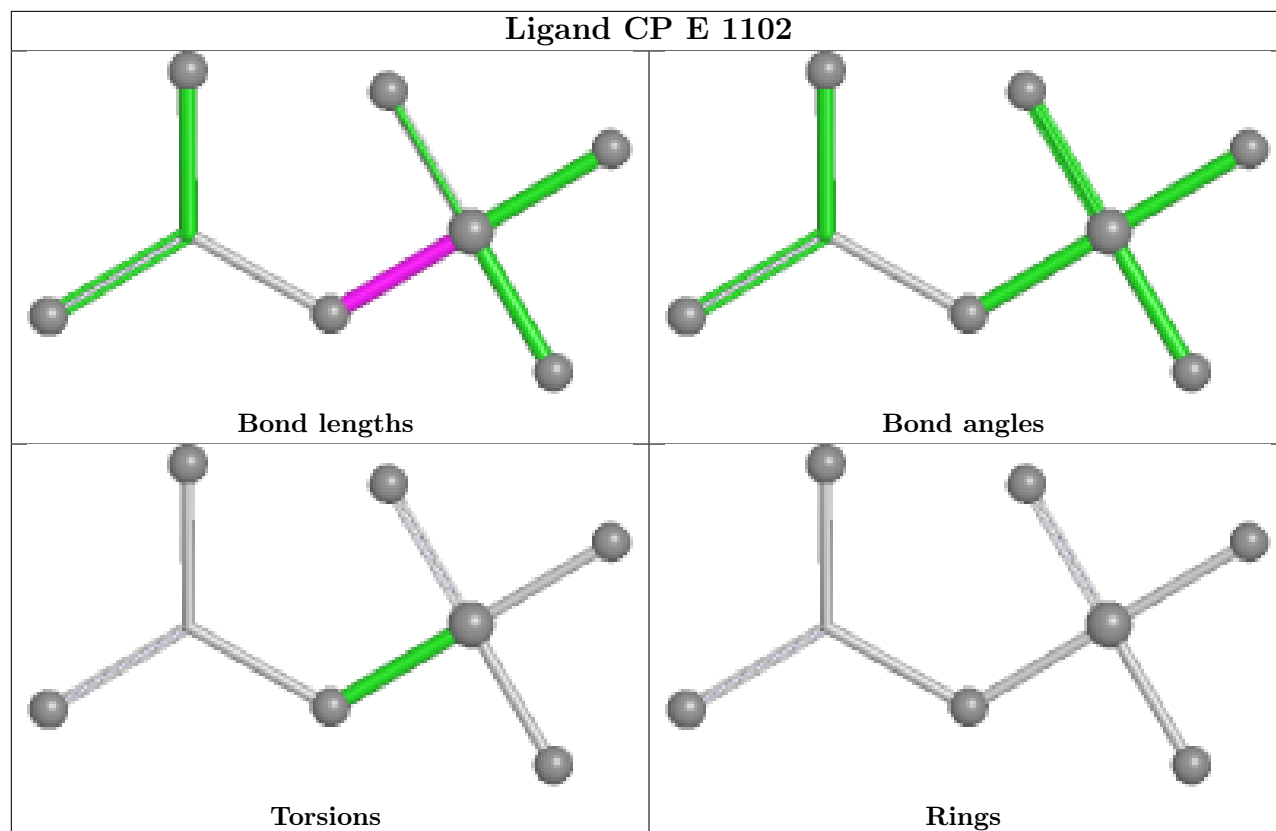
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	402[A]	GOL	1	0
3	E	1104	GOL	4	0
3	C	403	GOL	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less 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.

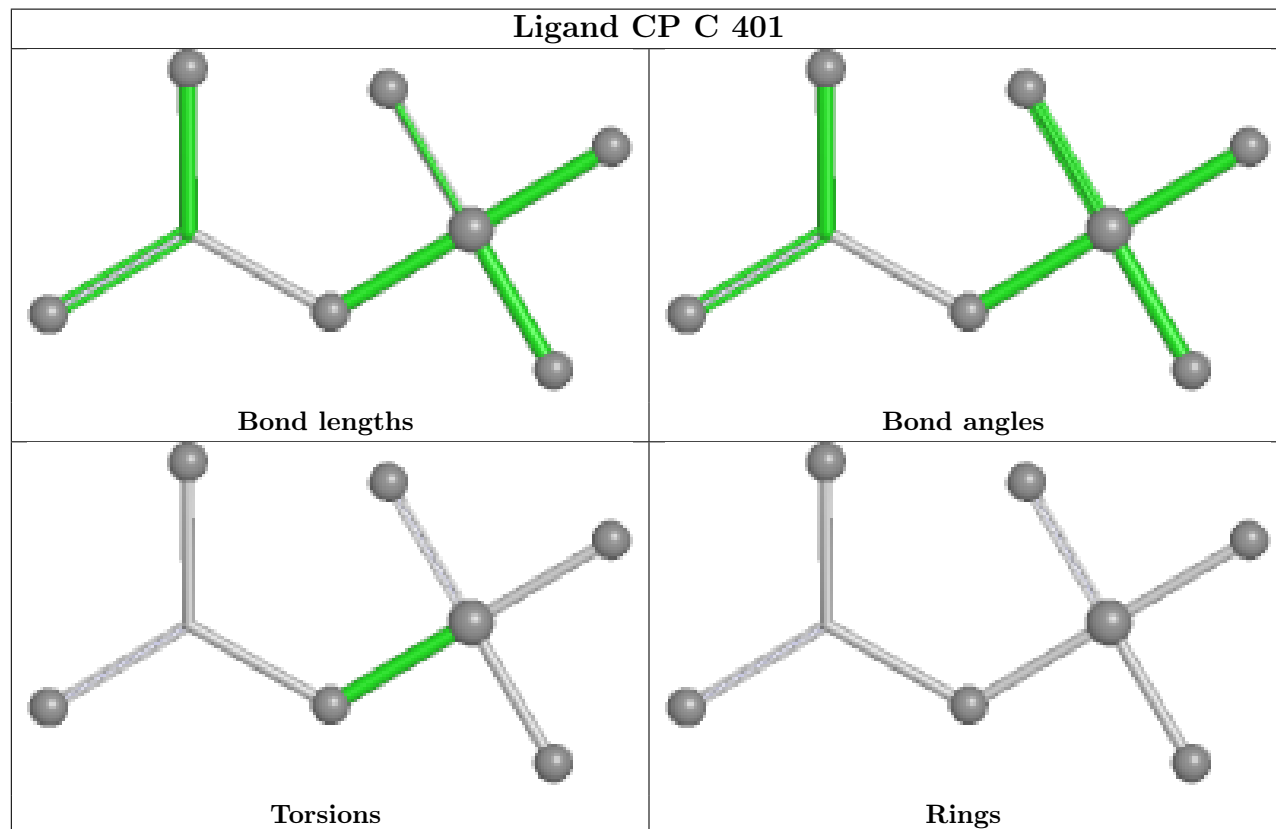


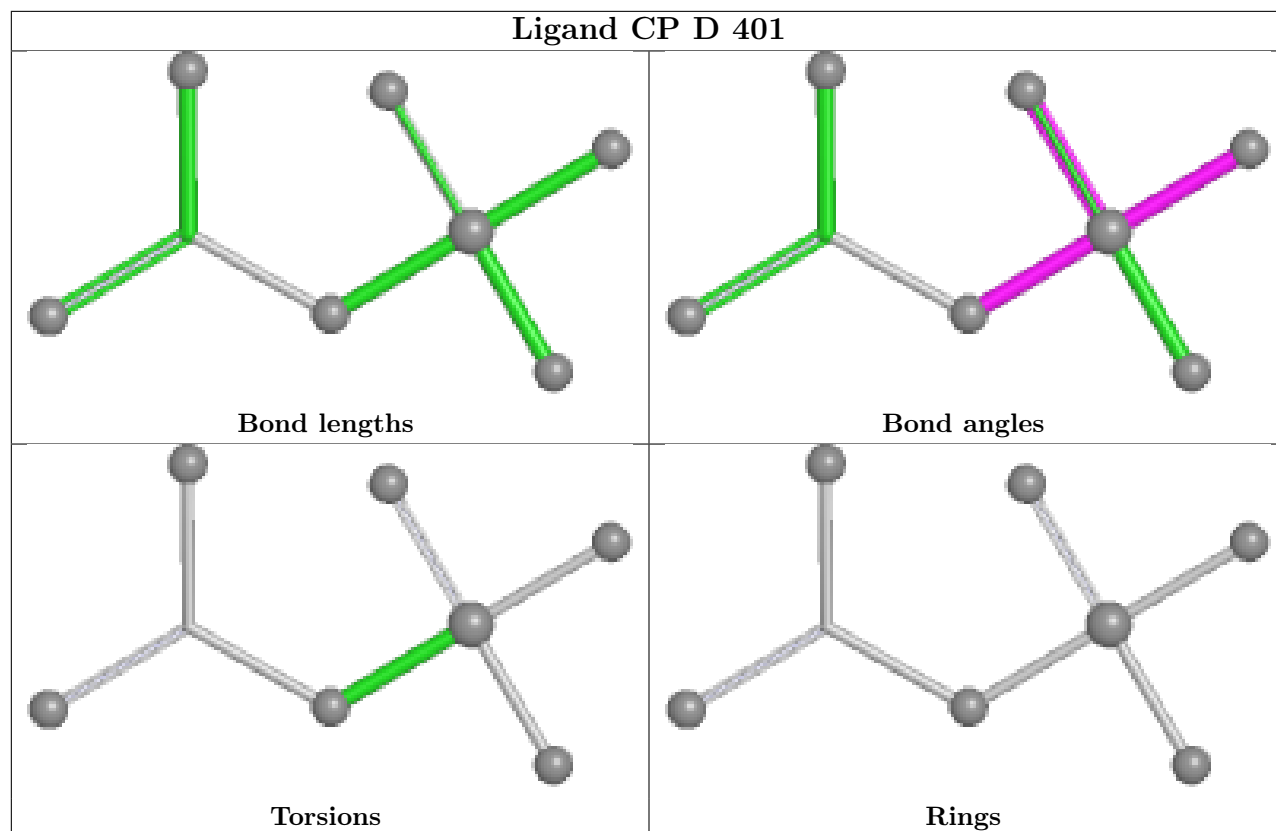


Ligand CP E 1102



Ligand CP C 401





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	311/332 (93%)	-0.21	11 (3%) 47 54	13, 29, 52, 84	16 (5%)
1	B	312/332 (93%)	0.19	12 (3%) 44 50	16, 38, 61, 81	8 (2%)
1	C	324/332 (97%)	0.09	16 (4%) 35 41	15, 35, 65, 95	14 (4%)
1	D	319/332 (96%)	0.17	12 (3%) 44 50	17, 37, 61, 97	8 (2%)
1	E	312/332 (93%)	0.32	13 (4%) 40 46	14, 39, 61, 93	9 (2%)
1	F	311/332 (93%)	0.58	10 (3%) 50 57	18, 46, 63, 78	4 (1%)
All	All	1889/1992 (94%)	0.19	74 (3%) 43 49	13, 37, 63, 97	59 (3%)

All (74) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	161	PHE	7.0
1	B	161	PHE	6.9
1	D	161	PHE	6.8
1	A	164	ALA	6.2
1	C	161	PHE	5.8
1	A	165	ALA	5.5
1	C	162	SER	5.5
1	F	161	PHE	5.4
1	A	162	SER	5.2
1	C	70	SER	5.2
1	B	164	ALA	4.9
1	C	67	HIS	4.9
1	C	390	TRP	4.7
1	D	72	LEU	4.5
1	E	161	PHE	4.5
1	A	160	GLU	4.5
1	D	66	HIS	4.3
1	F	80	HIS	4.3
1	A	163	SER	4.2

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Mol	Chain	Res	Type	RSRZ
1	C	165	ALA	4.2
1	B	162	SER	4.0
1	C	72	LEU	4.0
1	C	164	ALA	3.8
1	E	79	PRO	3.8
1	B	165	ALA	3.8
1	B	158	ALA	3.7
1	F	164	ALA	3.7
1	D	70	SER	3.6
1	F	165	ALA	3.5
1	A	166	LYS	3.4
1	E	164	ALA	3.3
1	B	163	SER	3.2
1	A	157	ASN	3.2
1	D	157	ASN	3.2
1	E	162	SER	3.2
1	E	165	ALA	3.1
1	C	163	SER	3.1
1	D	160	GLU	3.1
1	B	80	HIS	3.1
1	E	156	GLU	3.0
1	F	160	GLU	3.0
1	C	157	ASN	3.0
1	F	166	LYS	2.8
1	B	79	PRO	2.8
1	E	93	PHE	2.7
1	D	156	GLU	2.7
1	E	115	SER	2.6
1	D	68	HIS	2.6
1	E	116	SER	2.6
1	B	159	ARG	2.5
1	F	158	ALA	2.5
1	E	80	HIS	2.5
1	B	157	ASN	2.4
1	F	157	ASN	2.4
1	E	81	MET	2.3
1	E	114	SER	2.3
1	D	67	HIS	2.3
1	C	71	GLY	2.3
1	C	329[A]	LYS	2.3
1	D	159	ARG	2.2
1	A	80	HIS	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	342[A]	LYS	2.2
1	C	158	ALA	2.2
1	A	158	ALA	2.2
1	C	167	GLY	2.2
1	F	162	SER	2.1
1	A	167	GLY	2.1
1	B	166	LYS	2.1
1	C	68	HIS	2.1
1	F	81	MET	2.1
1	D	167	GLY	2.1
1	E	236	ILE	2.0
1	D	71	GLY	2.0
1	C	195[A]	ARG	2.0

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
4	ACT	B	407	4/4	0.68	0.28	69,76,78,81	0
3	GOL	A	405	6/6	0.72	0.22	50,62,68,73	0
3	GOL	F	405	6/6	0.73	0.22	44,72,75,75	0
3	GOL	B	406	6/6	0.77	0.22	60,72,77,78	0
4	ACT	D	403	4/4	0.77	0.21	65,66,68,77	0
3	GOL	C	403	6/6	0.79	0.23	33,62,70,72	0
4	ACT	A	407	4/4	0.81	0.16	42,47,56,63	0
3	GOL	D	402	6/6	0.81	0.20	60,72,74,78	0
3	GOL	B	404	6/6	0.81	0.15	67,69,74,75	0
4	ACT	A	408	4/4	0.82	0.15	38,49,52,59	0

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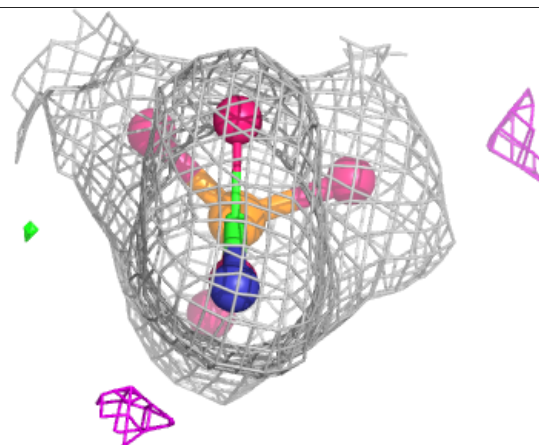
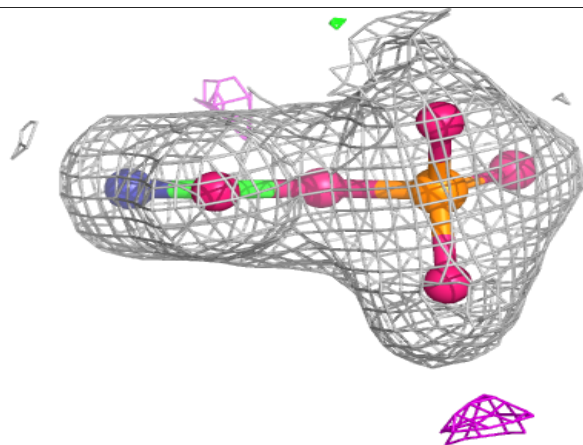
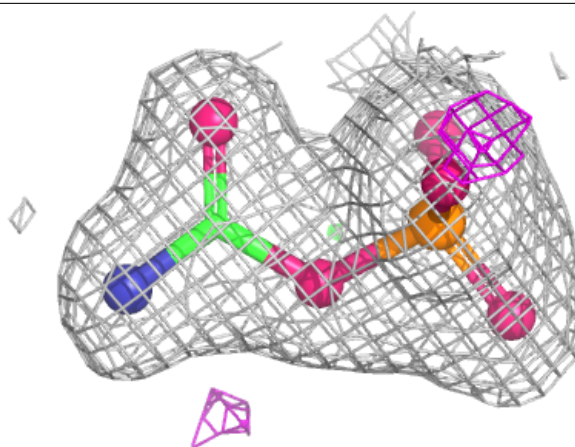
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	ACT	B	405	4/4	0.83	0.17	48,58,68,69	0
4	ACT	F	404	4/4	0.83	0.16	68,71,80,81	0
3	GOL	B	403	6/6	0.84	0.15	47,60,64,75	0
4	ACT	C	404	4/4	0.84	0.18	43,54,55,63	0
4	ACT	C	405	4/4	0.87	0.14	61,62,66,69	0
3	GOL	F	403	6/6	0.88	0.14	62,68,70,71	0
3	GOL	A	404	6/6	0.88	0.14	50,61,64,65	0
3	GOL	E	1101	6/6	0.89	0.16	50,58,61,73	0
3	GOL	E	1104	6/6	0.89	0.12	45,51,52,58	0
3	GOL	A	402[B]	6/6	0.89	0.18	42,49,50,50	6
4	ACT	E	1105	4/4	0.89	0.14	45,56,61,61	0
3	GOL	A	402[A]	6/6	0.89	0.18	46,57,61,66	6
3	GOL	A	406	6/6	0.92	0.10	39,42,47,48	0
3	GOL	F	402	6/6	0.93	0.09	44,47,48,48	0
4	ACT	C	406	4/4	0.93	0.14	64,64,68,71	0
3	GOL	B	402	6/6	0.93	0.10	41,46,50,50	0
3	GOL	E	1103	6/6	0.93	0.10	43,44,52,55	0
3	GOL	C	402	6/6	0.93	0.11	37,40,53,53	0
3	GOL	A	403	6/6	0.96	0.07	30,33,38,39	0
2	CP	F	401	8/8	0.98	0.06	35,37,39,42	0
2	CP	A	401	8/8	0.98	0.05	27,29,31,32	0
2	CP	C	401	8/8	0.98	0.05	30,31,33,34	0
2	CP	B	401	8/8	0.99	0.05	32,35,37,39	0
2	CP	D	401	8/8	0.99	0.04	28,30,31,32	0
2	CP	E	1102	8/8	0.99	0.04	31,33,37,38	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.

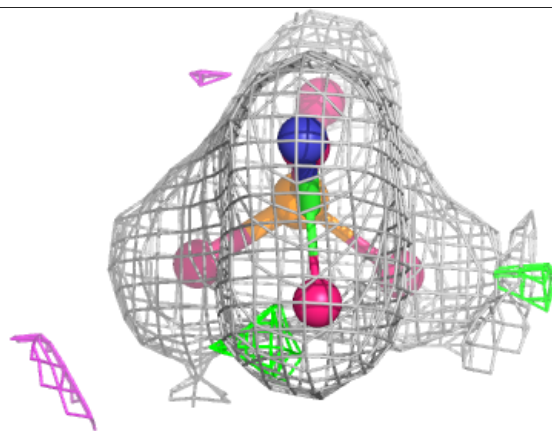
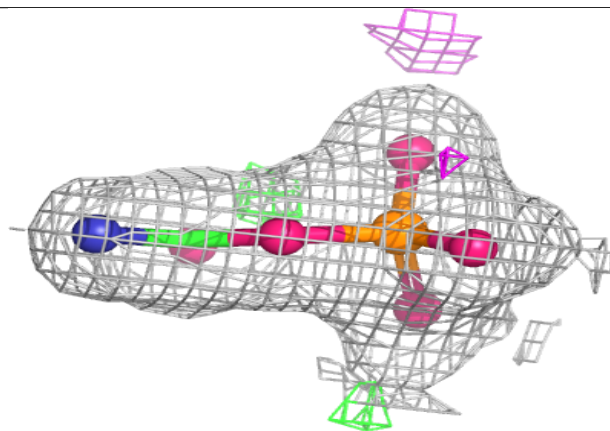
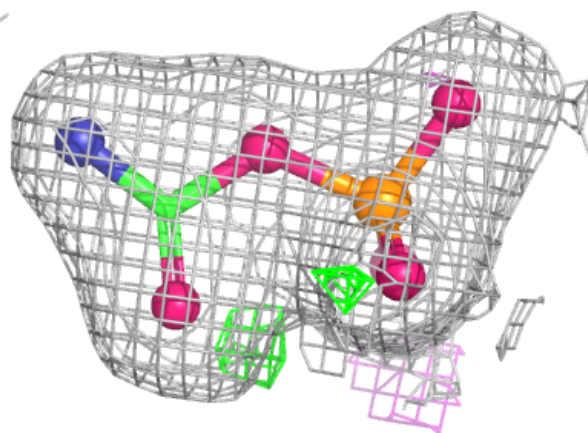
Electron density around CP F 401:

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

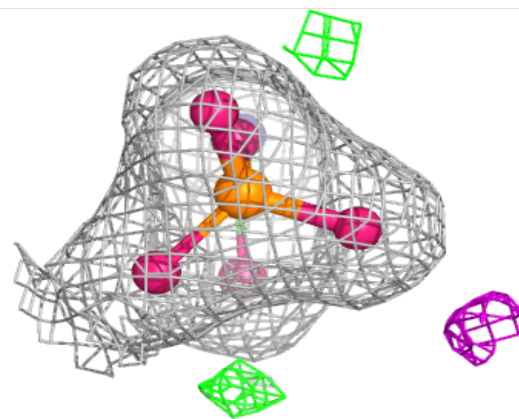
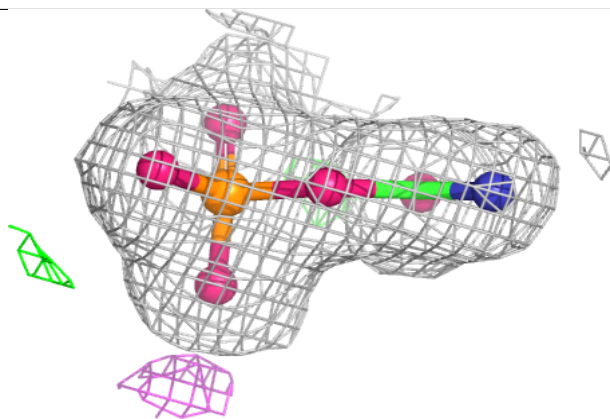
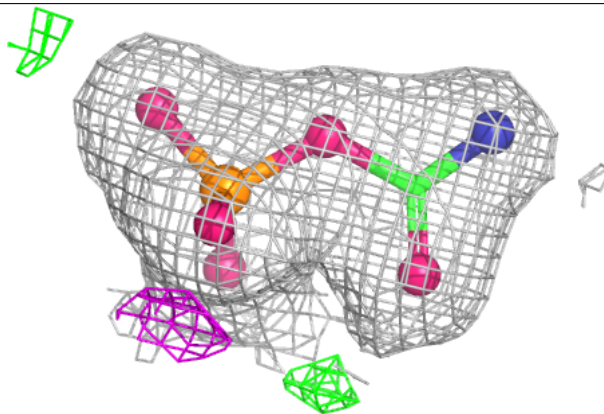


Electron density around CP A 401:

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

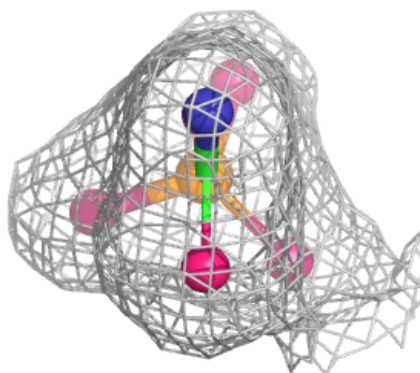
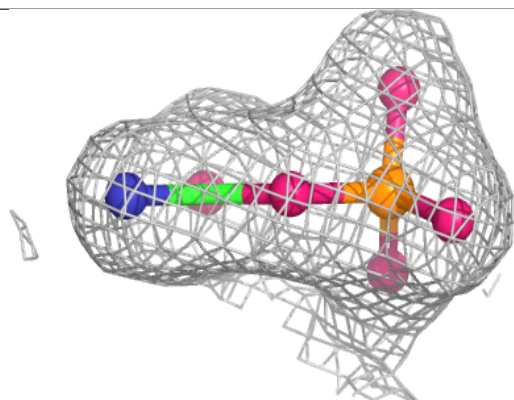
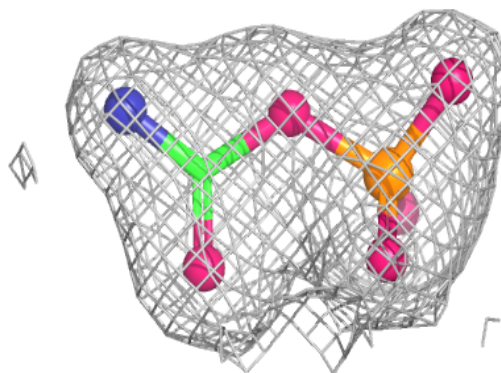
**Electron density around CP C 401:**

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



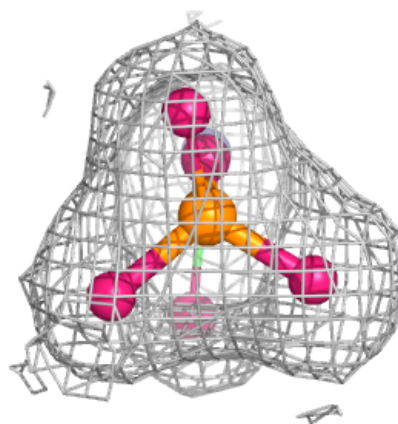
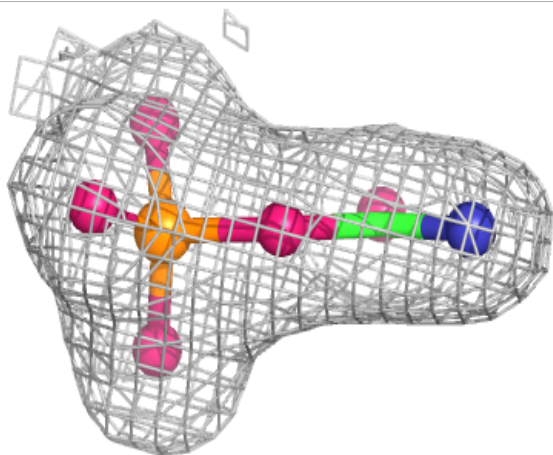
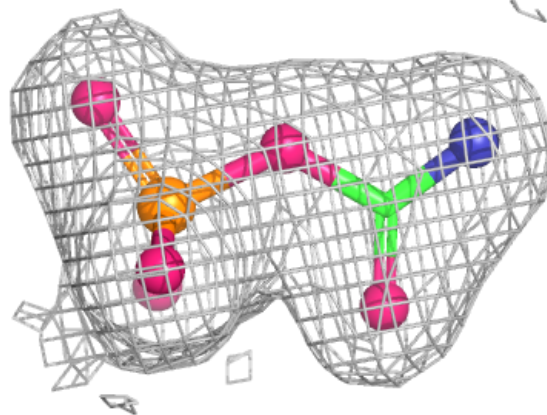
Electron density around CP B 401:

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



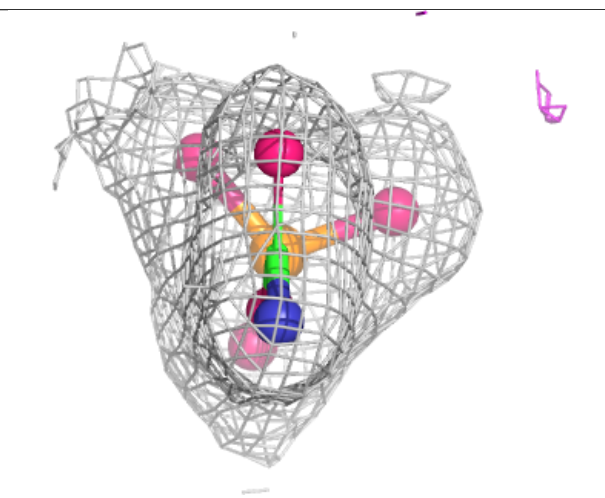
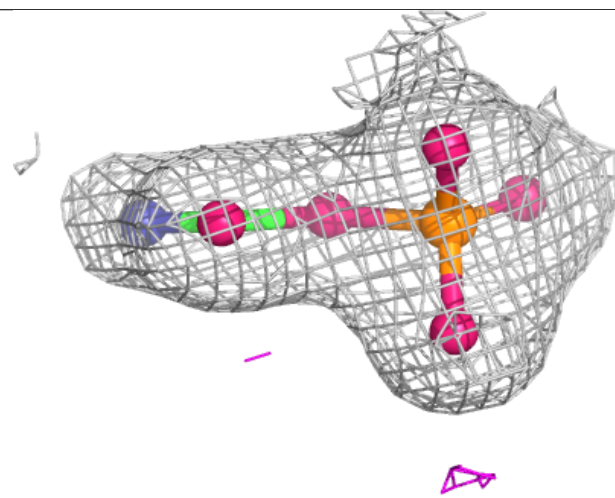
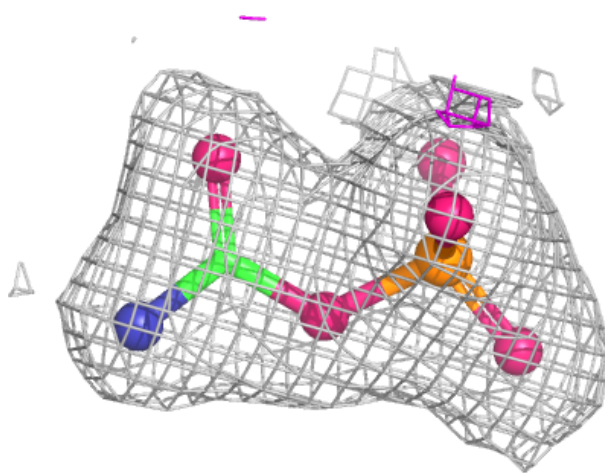
Electron density around CP D 401:

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



Electron density around CP E 1102:

$2mF_o-DF_c$ (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.