



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 05:35 PM UTC

PDB ID : 5TZW / pdb_00005tzw
Title : CRYSTAL STRUCTURE OF HUMAN PHOSPHODIESTERASE 2A IN COMPLEX WITH 1-[(3,4-difluorophenyl)carbonyl]-3,3-difluoro-5-{5-methyl-[1,2,4]triazolo[1,5-a]pyrimidin-7-yl}piperidine
Authors : Xu, R.; Aertgeerts, K.
Deposited on : 2016-11-22
Resolution : 1.59 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

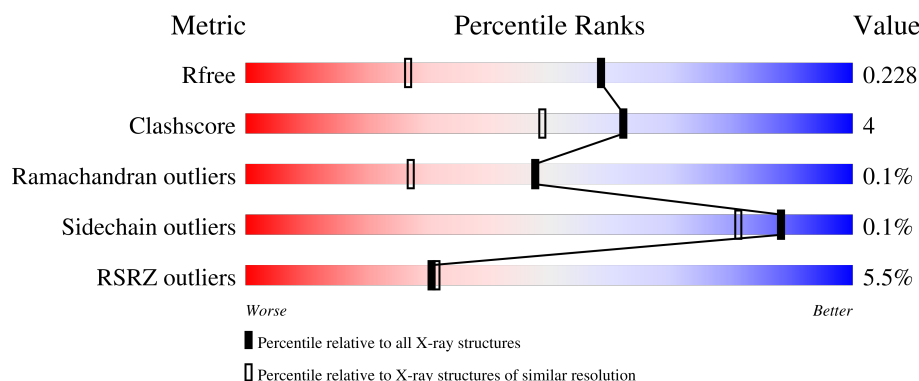
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.59 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	4673 (1.60-1.60)
Clashscore	190562	4931 (1.60-1.60)
Ramachandran outliers	187476	4831 (1.60-1.60)
Sidechain outliers	187428	4830 (1.60-1.60)
RSRZ outliers	180081	4672 (1.60-1.60)

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	344	4% 93% 7%
1	B	344	4% 90% 8%
1	C	344	10% 85% 10% 5%
1	D	344	3% 88% 7% 5%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 12183 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.

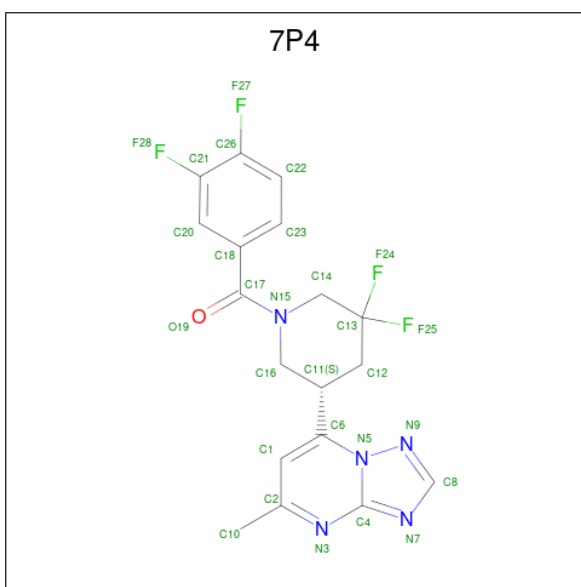
- Molecule 1 is a protein called cGMP-dependent 3',5'-cyclic phosphodiesterase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	342	Total	C	N	O	S	0	0	0
			2794	1778	478	512	26			
1	B	339	Total	C	N	O	S	0	0	0
			2775	1768	475	506	26			
1	C	328	Total	C	N	O	S	0	0	0
			2680	1709	461	485	25			
1	D	327	Total	C	N	O	S	0	0	0
			2676	1707	460	484	25			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	576	SER	-	expression tag	UNP O00408
A	577	ALA	-	expression tag	UNP O00408
A	578	MET	-	expression tag	UNP O00408
B	576	SER	-	expression tag	UNP O00408
B	577	ALA	-	expression tag	UNP O00408
B	578	MET	-	expression tag	UNP O00408
C	576	SER	-	expression tag	UNP O00408
C	577	ALA	-	expression tag	UNP O00408
C	578	MET	-	expression tag	UNP O00408
D	576	SER	-	expression tag	UNP O00408
D	577	ALA	-	expression tag	UNP O00408
D	578	MET	-	expression tag	UNP O00408

- Molecule 2 is [(5S)-3,3-difluoro-5-(5-methyl[1,2,4]triazolo[1,5-a]pyrimidin-7-yl)piperidin-1-yl] (3,4-difluorophenyl)methanone (CCD ID: 7P4) (formula: C₁₈H₁₅F₄N₅O).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	F	N	O	0	1
			56	36	8	10	2		
2	B	1	Total	C	F	N	O	0	0
			28	18	4	5	1		
2	C	1	Total	C	F	N	O	0	0
			28	18	4	5	1		
2	D	1	Total	C	F	N	O	0	0
			28	18	4	5	1		

- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Zn	0	0
			1	1		
3	B	1	Total	Zn	0	0
			1	1		
3	C	1	Total	Zn	0	0
			1	1		
3	D	1	Total	Zn	0	0
			1	1		

- Molecule 4 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Mg	0	0
			1	1		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	1	Total 1	Mg 1	0	0
4	C	1	Total 1	Mg 1	0	0
4	D	1	Total 1	Mg 1	0	0

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	317	Total 317	O 317	0	0
5	B	284	Total 284	O 284	0	0
5	C	232	Total 232	O 232	0	0
5	D	277	Total 277	O 277	0	0

3 Residue-property plots

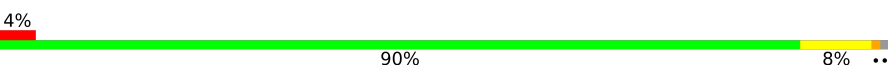
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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.

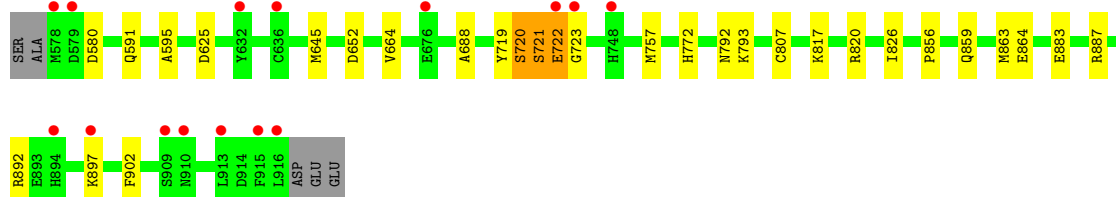
- Molecule 1: cGMP-dependent 3',5'-cyclic phosphodiesterase

Chain A: 



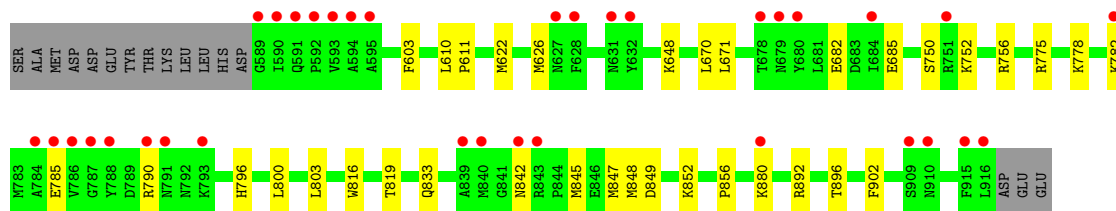
- Molecule 1: cGMP-dependent 3',5'-cyclic phosphodiesterase

Chain B: 



- Molecule 1: cGMP-dependent 3',5'-cyclic phosphodiesterase

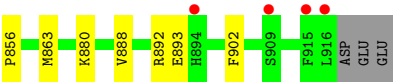
Chain C: 



- Molecule 1: cGMP-dependent 3',5'-cyclic phosphodiesterase

Chain D: 





4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	55.81Å 73.00Å 91.00Å 109.22° 90.96° 91.07°	Depositor
Resolution (Å)	68.91 – 1.59 68.91 – 1.59	Depositor EDS
% Data completeness (in resolution range)	94.6 (68.91-1.59) 94.9 (68.91-1.59)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.53 (at 1.59Å)	Xtriage
Refinement program	PHENIX (1.10.1-2155_1692: ???)	Depositor
R, R_{free}	0.188 , 0.225 0.191 , 0.228	Depositor DCC
R_{free} test set	8534 reflections (4.92%)	wwPDB-VP
Wilson B-factor (Å ²)	16.4	Xtriage
Anisotropy	0.266	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 45.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.013 for h,-k,-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	12183	wwPDB-VP
Average B, all atoms (Å ²)	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 9.59% 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: 7P4, MG, ZN

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	0.32	0/2861	0.50	0/3860
1	B	0.30	0/2842	0.50	2/3834 (0.1%)
1	C	0.28	0/2745	0.46	0/3703
1	D	0.30	0/2741	0.47	0/3698
All	All	0.30	0/11189	0.49	2/15095 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	721	SER	CA-C-N	5.45	131.95	121.54
1	B	721	SER	C-N-CA	5.45	131.95	121.54

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	2794	0	2732	21	0
1	B	2775	0	2718	22	0
1	C	2680	0	2633	30	0
1	D	2676	0	2630	18	0
2	A	56	0	0	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	28	0	0	2	0
2	C	28	0	0	0	0
2	D	28	0	0	1	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
4	C	1	0	0	0	0
4	D	1	0	0	0	0
5	A	317	0	0	4	0
5	B	284	0	0	6	0
5	C	232	0	0	6	0
5	D	277	0	0	5	0
All	All	12183	0	10713	89	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 4.

All (89) 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:C:752:LYS:NZ	5:C:1102:HOH:O	2.05	0.89
1:A:789:ASP:H	1:A:795:HIS:HD2	1.19	0.88
1:C:880:LYS:NZ	5:C:1101:HOH:O	1.92	0.88
1:D:676:GLU:OE2	1:D:880:LYS:NZ	2.09	0.84
1:B:883:GLU:OE1	1:B:887:ARG:NH2	2.15	0.79
1:C:682:GLU:OE2	1:C:756:ARG:NH2	2.20	0.75
1:A:864:GLU:OE1	1:A:892:ARG:NH2	2.23	0.71
1:B:652:ASP:OD2	5:B:1101:HOH:O	2.11	0.66
1:D:756:ARG:NH1	5:D:1102:HOH:O	2.28	0.65
1:A:893:GLU:HG2	1:A:897:LYS:NZ	2.12	0.63
1:B:772:HIS:HD2	5:B:1204:HOH:O	1.82	0.61
1:C:892:ARG:HH12	1:C:896:THR:CG2	2.13	0.61
1:D:892:ARG:NH1	1:D:893:GLU:OE1	2.34	0.60
1:A:789:ASP:H	1:A:795:HIS:CD2	2.11	0.59
1:B:792:ASN:HA	5:B:1112:HOH:O	2.03	0.59
1:C:880:LYS:N	1:C:880:LYS:HD3	2.19	0.58
1:A:817:LYS:NZ	5:A:1101:HOH:O	2.34	0.58
1:C:610:LEU:HD12	1:C:611:PRO:HD2	1.86	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:750:SER:HB2	5:C:1259:HOH:O	2.02	0.58
1:C:845:MET:HE2	1:C:847:MET:HE3	1.86	0.57
1:D:772:HIS:HD2	5:D:1160:HOH:O	1.88	0.56
1:C:778:LYS:NZ	5:C:1107:HOH:O	2.36	0.55
1:C:880:LYS:HD3	1:C:880:LYS:H	1.73	0.54
1:A:744:ASN:HD22	1:A:746:PHE:H	1.54	0.54
1:B:580:ASP:OD2	1:C:842:ASN:ND2	2.41	0.54
1:B:721:SER:O	1:B:723:GLY:N	2.42	0.52
1:C:782:LYS:HE3	1:C:785:GLU:OE2	2.10	0.52
1:A:587:HIS:HE1	5:A:1365:HOH:O	1.92	0.52
1:D:824:GLU:HG2	1:D:828:LYS:HE3	1.91	0.51
1:B:720:SER:C	1:B:722:GLU:H	2.19	0.51
1:D:679:ASN:HD21	1:D:790:ARG:HH21	1.58	0.51
1:B:864:GLU:OE1	1:B:892:ARG:NH2	2.44	0.50
1:B:719:TYR:O	1:B:722:GLU:OE1	2.30	0.50
1:C:892:ARG:HH12	1:C:896:THR:HG21	1.76	0.50
1:B:591:GLN:HG2	1:B:595:ALA:HB3	1.94	0.50
1:C:849:ASP:OD1	1:C:852:LYS:HD2	2.11	0.50
1:A:744:ASN:HD22	1:A:744:ASN:C	2.21	0.49
1:C:845:MET:HG2	1:C:848:MET:HG3	1.95	0.48
1:A:795:HIS:HE1	5:A:1368:HOH:O	1.96	0.48
1:A:671:LEU:HD13	1:A:803:LEU:HD22	1.96	0.48
1:C:833:GLN:CD	1:C:848:MET:HE1	2.39	0.48
1:B:817:LYS:HG2	1:B:820:ARG:HH12	1.78	0.47
1:D:633:LYS:N	1:D:633:LYS:HD2	2.29	0.47
1:C:790:ARG:HH11	1:C:796:HIS:HE1	1.62	0.47
1:A:860:ILE:O	1:A:864:GLU:HG3	2.15	0.47
1:D:856:PRO:HG3	1:D:902:PHE:CD1	2.49	0.47
1:A:854:TYR:HD2	1:A:857:GLU:HB3	1.80	0.46
1:D:782:LYS:HE3	5:D:1354:HOH:O	2.15	0.46
1:A:752:LYS:HA	1:A:752:LYS:HE2	1.97	0.46
1:D:746:PHE:CZ	1:D:757:MET:HE2	2.50	0.46
1:B:856:PRO:HG3	1:B:902:PHE:CD1	2.51	0.46
1:D:794:GLN:HA	1:D:794:GLN:OE1	2.16	0.45
1:B:625:ASP:O	1:C:778:LYS:HE2	2.17	0.45
1:C:880:LYS:HB2	1:C:880:LYS:HE2	1.58	0.45
1:A:859:GLN:O	1:A:863:MET:HG2	2.17	0.45
1:D:660:HIS:HD2	5:D:1115:HOH:O	1.99	0.45
1:B:793:LYS:NZ	5:B:1112:HOH:O	2.50	0.44
1:D:816:TRP:CD1	1:D:817:LYS:HD3	2.53	0.44
1:A:826:ILE:HD13	2:A:1001[B]:7P4:C4	2.48	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:845:MET:CG	1:C:848:MET:HG3	2.48	0.44
1:C:880:LYS:NZ	5:C:1105:HOH:O	2.32	0.43
1:C:685:GLU:HB3	1:C:800:LEU:HD11	2.00	0.43
1:B:645:MET:HG2	5:B:1180:HOH:O	2.17	0.43
1:C:816:TRP:HA	1:C:819:THR:HG22	2.00	0.43
1:C:603:PHE:HA	1:C:670:LEU:HD13	2.00	0.43
1:C:622:MET:O	1:C:626:MET:HG3	2.18	0.43
5:B:1264:HOH:O	1:C:775:ARG:HG2	2.18	0.43
1:C:648:LYS:HE2	5:C:1146:HOH:O	2.19	0.43
1:D:863:MET:CE	1:D:888:VAL:HG13	2.50	0.42
1:B:580:ASP:OD1	1:B:580:ASP:N	2.52	0.42
1:A:826:ILE:HD13	2:A:1001[A]:7P4:C4	2.50	0.42
1:B:826:ILE:CD1	2:B:1001:7P4:C6	2.98	0.42
1:D:644:LEU:HD23	1:D:644:LEU:HA	1.88	0.42
1:A:815:GLY:N	5:A:1101:HOH:O	2.52	0.42
1:B:688:ALA:HA	1:B:757:MET:HE1	2.01	0.42
1:A:893:GLU:HG2	1:A:897:LYS:HZ3	1.81	0.41
1:B:897:LYS:O	1:B:897:LYS:NZ	2.48	0.41
1:C:833:GLN:OE1	1:C:848:MET:HE1	2.20	0.41
1:C:856:PRO:HG3	1:C:902:PHE:CD1	2.56	0.41
1:D:790:ARG:HG3	5:D:1261:HOH:O	2.20	0.41
1:C:671:LEU:HD13	1:C:803:LEU:HD22	2.02	0.41
1:B:664:VAL:HG13	1:B:807:CYS:HB3	2.03	0.41
1:A:673:LYS:HE3	1:A:673:LYS:HB3	1.96	0.41
1:B:859:GLN:O	1:B:863:MET:HG2	2.21	0.41
1:D:679:ASN:ND2	1:D:790:ARG:HH21	2.18	0.41
1:A:892:ARG:C	1:A:892:ARG:HD3	2.46	0.40
1:B:826:ILE:HD13	2:B:1001:7P4:C6	2.52	0.40
1:D:826:ILE:HD13	2:D:1001:7P4:N5	2.37	0.40
1:A:626:MET:HG2	1:A:672:TYR:CD1	2.57	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	340/344 (99%)	338 (99%)	2 (1%)	0	100	100
1	B	337/344 (98%)	331 (98%)	5 (2%)	1 (0%)	36	20
1	C	326/344 (95%)	321 (98%)	5 (2%)	0	100	100
1	D	325/344 (94%)	324 (100%)	1 (0%)	0	100	100
All	All	1328/1376 (96%)	1314 (99%)	13 (1%)	1 (0%)	48	27

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	722	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	308/310 (99%)	308 (100%)	0	100	100
1	B	306/310 (99%)	305 (100%)	1 (0%)	86	78
1	C	295/310 (95%)	295 (100%)	0	100	100
1	D	295/310 (95%)	295 (100%)	0	100	100
All	All	1204/1240 (97%)	1203 (100%)	1 (0%)	88	81

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	720	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (29) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	587	HIS

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Mol	Chain	Res	Type
1	A	591	GLN
1	A	599	ASN
1	A	744	ASN
1	A	795	HIS
1	A	812	GLN
1	A	875	GLN
1	A	911	ASN
1	B	660	HIS
1	B	741	HIS
1	B	748	HIS
1	B	772	HIS
1	B	812	GLN
1	B	865	HIS
1	B	894	HIS
1	C	791	ASN
1	C	812	GLN
1	C	842	ASN
1	D	591	GLN
1	D	599	ASN
1	D	660	HIS
1	D	679	ASN
1	D	708	GLN
1	D	772	HIS
1	D	781	GLN
1	D	791	ASN
1	D	812	GLN
1	D	842	ASN
1	D	894	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 13 ligands modelled in this entry, 8 are monoatomic - leaving 5 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
2	7P4	A	1001[B]	-	29,31,31	1.23	4 (13%)	40,47,47	1.14	3 (7%)
2	7P4	C	1001	-	29,31,31	1.20	2 (6%)	40,47,47	1.32	7 (17%)
2	7P4	A	1001[A]	-	29,31,31	1.25	4 (13%)	40,47,47	1.15	3 (7%)
2	7P4	B	1001	-	29,31,31	1.15	3 (10%)	40,47,47	1.00	1 (2%)
2	7P4	D	1001	-	29,31,31	1.17	3 (10%)	40,47,47	1.18	3 (7%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	7P4	A	1001[B]	-	-	0/12/26/26	0/4/4/4
2	7P4	C	1001	-	-	0/12/26/26	0/4/4/4
2	7P4	A	1001[A]	-	-	0/12/26/26	0/4/4/4
2	7P4	B	1001	-	-	0/12/26/26	0/4/4/4
2	7P4	D	1001	-	-	0/12/26/26	0/4/4/4

All (16) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	1001	7P4	C1-C2	2.78	1.47	1.41
2	A	1001[A]	7P4	C1-C2	2.75	1.47	1.41
2	C	1001	7P4	C2-N3	-2.73	1.29	1.33
2	A	1001[B]	7P4	C1-C2	2.72	1.47	1.41
2	A	1001[B]	7P4	C2-N3	-2.71	1.29	1.33
2	D	1001	7P4	C1-C2	2.63	1.47	1.41
2	D	1001	7P4	C2-N3	-2.63	1.29	1.33
2	A	1001[A]	7P4	C2-N3	-2.60	1.29	1.33
2	B	1001	7P4	C2-N3	-2.58	1.29	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1001	7P4	C1-C2	2.56	1.46	1.41
2	A	1001[A]	7P4	C16-N15	-2.53	1.44	1.46
2	B	1001	7P4	C16-N15	-2.48	1.44	1.46
2	A	1001[B]	7P4	C16-N15	-2.36	1.44	1.46
2	A	1001[B]	7P4	N5-N9	-2.20	1.34	1.37
2	A	1001[A]	7P4	N5-N9	-2.13	1.34	1.37
2	D	1001	7P4	N5-N9	-2.11	1.34	1.37

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1001[A]	7P4	C10-C2-C1	-2.70	116.91	120.44
2	A	1001[B]	7P4	C10-C2-C1	-2.67	116.95	120.44
2	C	1001	7P4	C10-C2-C1	-2.65	116.98	120.44
2	D	1001	7P4	C8-N9-N5	2.55	102.94	100.86
2	D	1001	7P4	C12-C11-C6	2.53	116.08	111.78
2	B	1001	7P4	C12-C11-C6	2.50	116.03	111.78
2	A	1001[B]	7P4	C1-C2-N3	2.46	125.13	122.71
2	C	1001	7P4	C12-C13-C14	-2.41	112.01	114.30
2	D	1001	7P4	C1-C2-N3	2.39	125.05	122.71
2	A	1001[A]	7P4	C1-C2-N3	2.34	125.01	122.71
2	C	1001	7P4	C23-C18-C20	2.34	121.95	119.25
2	C	1001	7P4	C12-C11-C6	2.25	115.60	111.78
2	A	1001[B]	7P4	C8-N9-N5	2.23	102.68	100.86
2	C	1001	7P4	C1-C2-N3	2.21	124.88	122.71
2	C	1001	7P4	C8-N9-N5	2.11	102.59	100.86
2	C	1001	7P4	O19-C17-C18	-2.06	116.21	120.29
2	A	1001[A]	7P4	C12-C11-C6	2.02	115.21	111.78

There are no chirality outliers.

There are no torsion outliers.

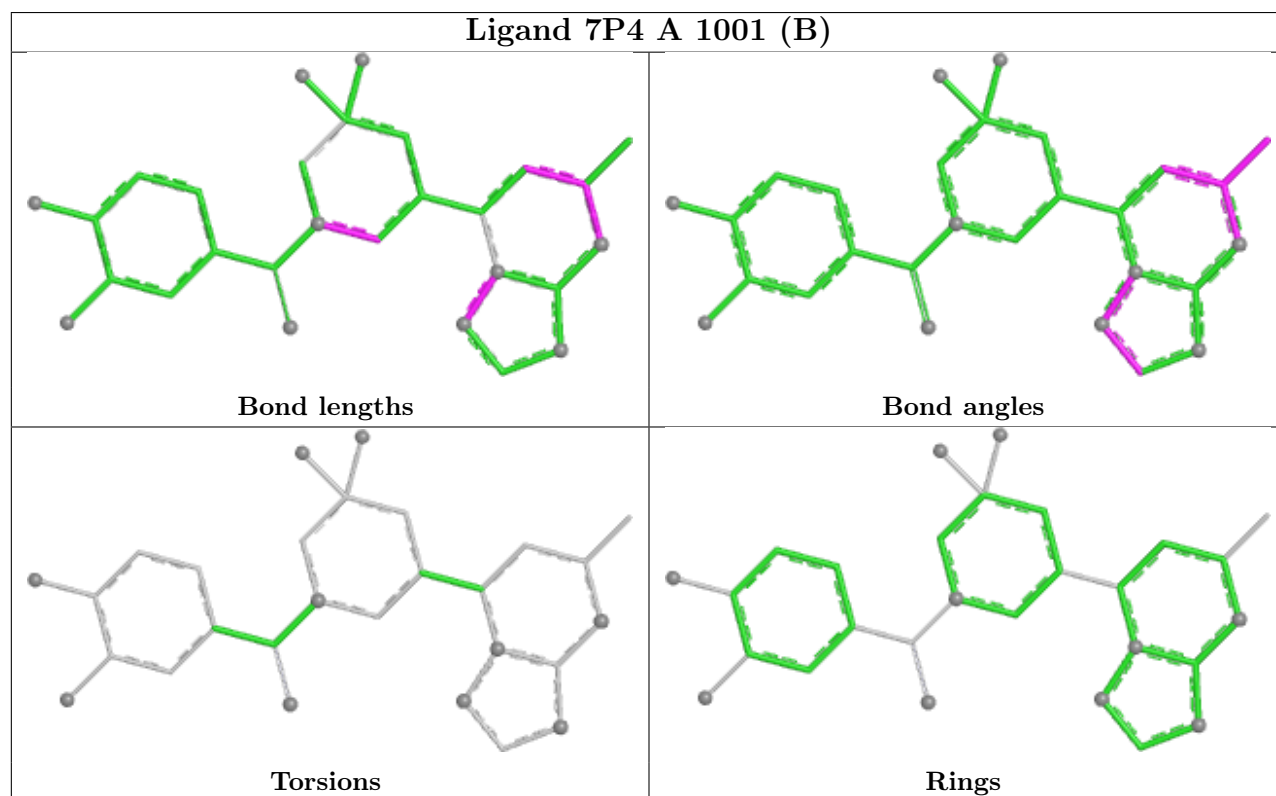
There are no ring outliers.

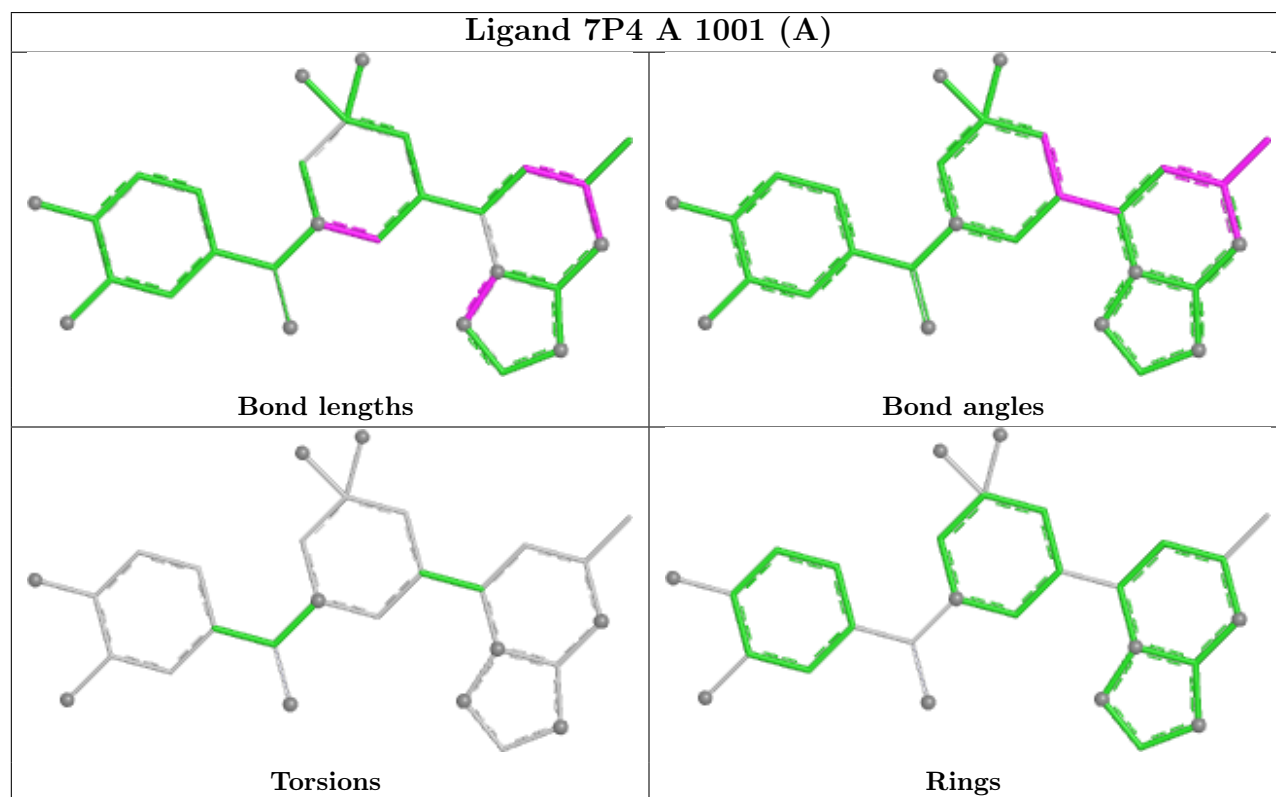
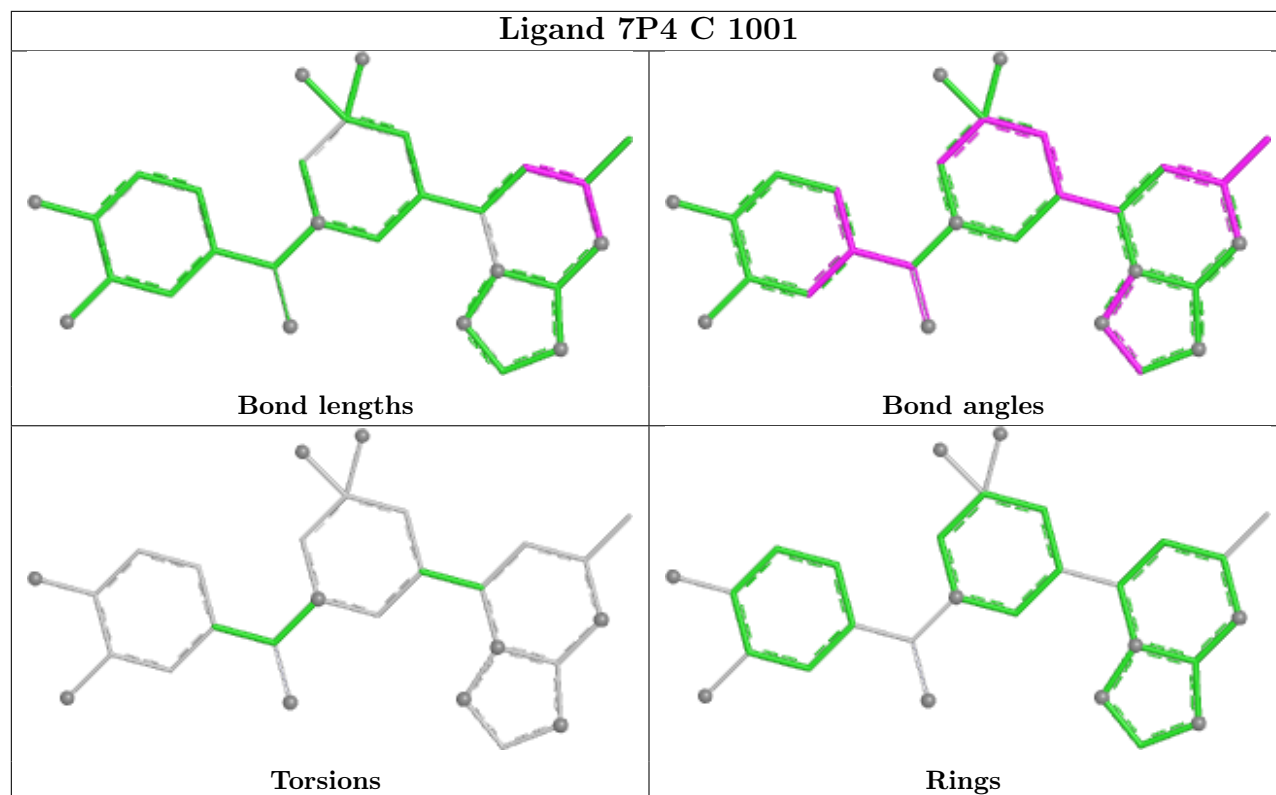
4 monomers are involved in 5 short contacts:

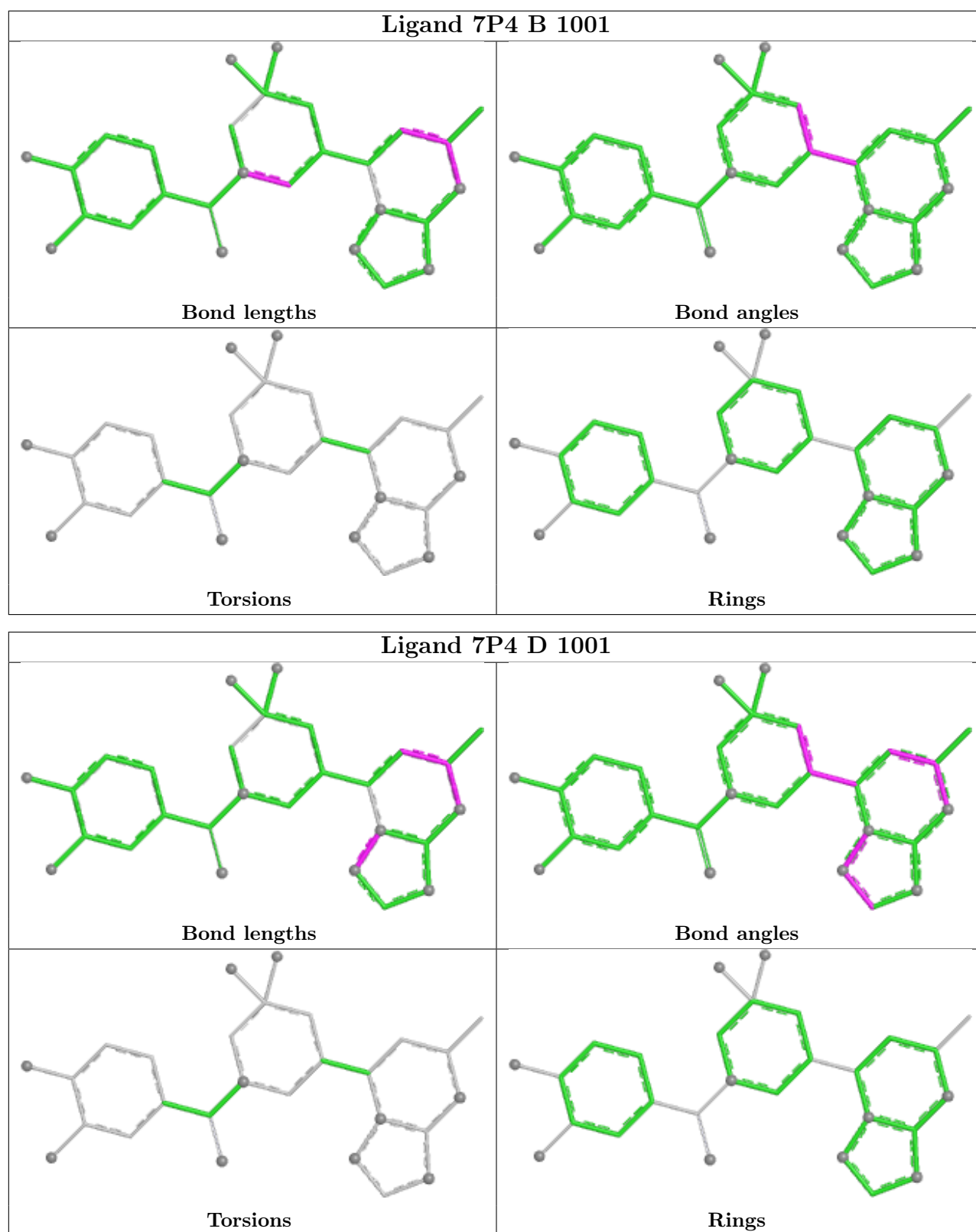
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1001[B]	7P4	1	0
2	A	1001[A]	7P4	1	0
2	B	1001	7P4	2	0
2	D	1001	7P4	1	0

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.







5.7 Other polymers [\(i\)](#)

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

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	342/344 (99%)	0.22	13 (3%)	44	46	11, 22, 44, 59	0
1	B	339/344 (98%)	0.34	15 (4%)	39	40	11, 24, 43, 57	0
1	C	328/344 (95%)	0.64	34 (10%)	11	11	13, 28, 50, 64	0
1	D	327/344 (95%)	0.25	12 (3%)	45	47	12, 24, 43, 57	0
All	All	1336/1376 (97%)	0.36	74 (5%)	30	31	11, 25, 45, 64	0

All (74) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	723	GLY	5.5
1	C	680	TYR	5.2
1	C	786	VAL	5.1
1	B	722	GLU	4.7
1	C	593	VAL	4.5
1	B	578	MET	4.3
1	D	915	PHE	4.1
1	D	590	ILE	3.9
1	C	589	GLY	3.9
1	B	915	PHE	3.8
1	C	916	LEU	3.6
1	B	916	LEU	3.4
1	A	817	LYS	3.3
1	A	843	ARG	3.3
1	C	628	PHE	3.2
1	C	843	ARG	3.1
1	A	839	ALA	3.1
1	A	598	SER	3.0
1	C	784	ALA	2.9
1	A	909	SER	2.9
1	C	910	ASN	2.8

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Mol	Chain	Res	Type	RSRZ
1	C	595	ALA	2.8
1	C	627	ASN	2.7
1	D	894	HIS	2.7
1	D	916	LEU	2.7
1	C	915	PHE	2.7
1	C	793	LYS	2.7
1	C	839	ALA	2.6
1	D	909	SER	2.6
1	B	748	HIS	2.6
1	B	894	HIS	2.5
1	C	880	LYS	2.5
1	A	599	ASN	2.5
1	C	751	ARG	2.5
1	C	790	ARG	2.5
1	C	590	ILE	2.5
1	C	785	GLU	2.5
1	C	787	GLY	2.5
1	B	676	GLU	2.4
1	C	909	SER	2.4
1	C	684	ILE	2.4
1	C	788	TYR	2.4
1	A	577	ALA	2.4
1	D	594	ALA	2.4
1	D	595	ALA	2.4
1	B	897	LYS	2.4
1	B	632	TYR	2.4
1	B	636	CYS	2.3
1	D	751	ARG	2.3
1	A	917	ASP	2.3
1	B	910	ASN	2.2
1	D	630	ASN	2.2
1	A	892	ARG	2.2
1	C	791	ASN	2.2
1	B	579	ASP	2.2
1	C	632	TYR	2.2
1	C	782	LYS	2.2
1	C	679	ASN	2.2
1	D	628	PHE	2.2
1	A	916	LEU	2.1
1	B	913	LEU	2.1
1	C	678	THR	2.1
1	D	632	TYR	2.1

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Mol	Chain	Res	Type	RSRZ
1	C	631	ASN	2.1
1	C	591	GLN	2.1
1	C	592	PRO	2.1
1	A	816	TRP	2.1
1	C	594	ALA	2.0
1	A	636	CYS	2.0
1	A	576	SER	2.0
1	C	840	MET	2.0
1	D	842	ASN	2.0
1	B	909	SER	2.0
1	C	842	ASN	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(Å ²)	Q<0.9
2	7P4	A	1001[A]	28/28	0.89	0.09	13,21,30,34	28
2	7P4	A	1001[B]	28/28	0.89	0.09	12,21,29,33	28
2	7P4	B	1001	28/28	0.94	0.08	15,22,33,36	0
2	7P4	D	1001	28/28	0.94	0.07	15,20,29,40	0
2	7P4	C	1001	28/28	0.95	0.08	13,22,42,52	0
4	MG	A	1003	1/1	0.99	0.02	11,11,11,11	0
3	ZN	B	1002	1/1	1.00	0.01	15,15,15,15	0
3	ZN	C	1002	1/1	1.00	0.01	16,16,16,16	0
3	ZN	D	1002	1/1	1.00	0.01	16,16,16,16	0
3	ZN	A	1002	1/1	1.00	0.02	14,14,14,14	0
4	MG	B	1003	1/1	1.00	0.02	14,14,14,14	0
4	MG	C	1003	1/1	1.00	0.02	13,13,13,13	0

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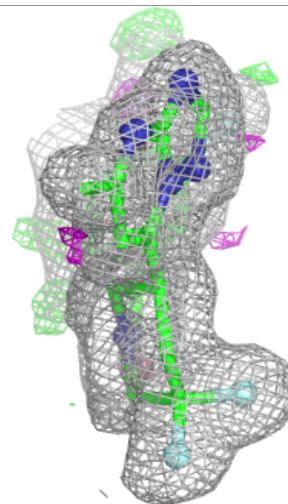
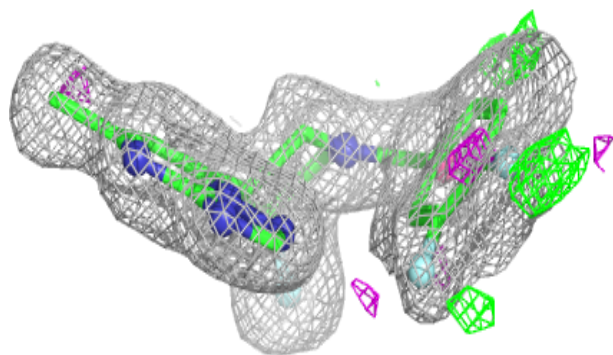
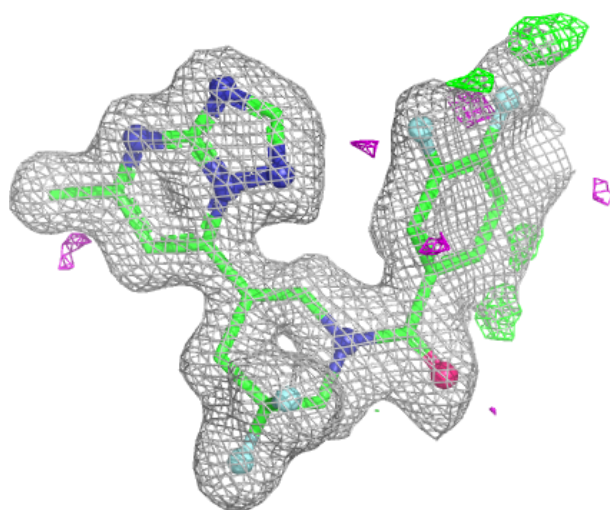
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	MG	D	1003	1/1	1.00	0.01	12,12,12,12	0

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.

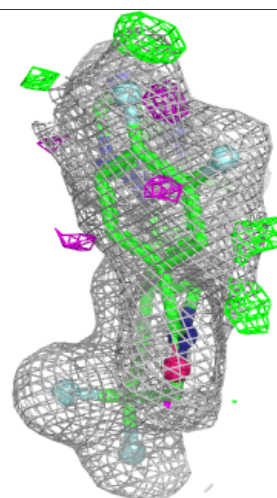
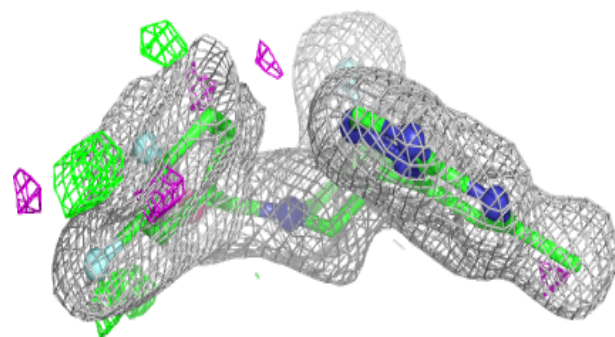
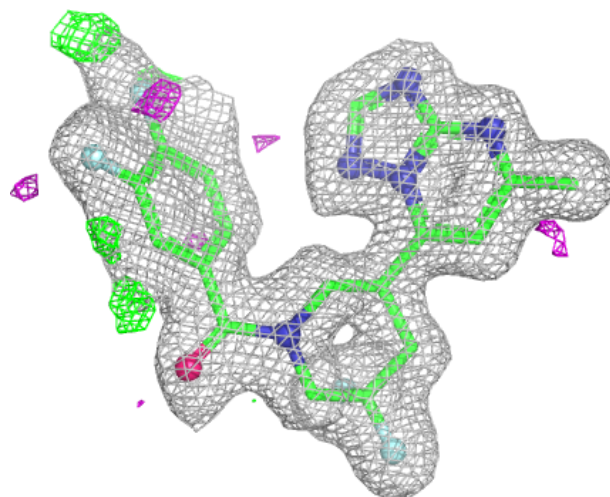
Electron density around 7P4 A 1001 (A):

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



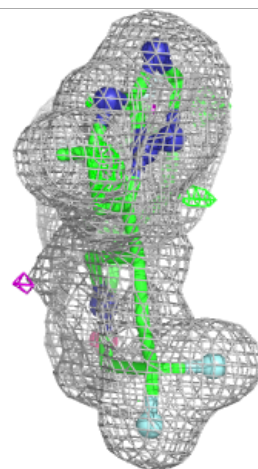
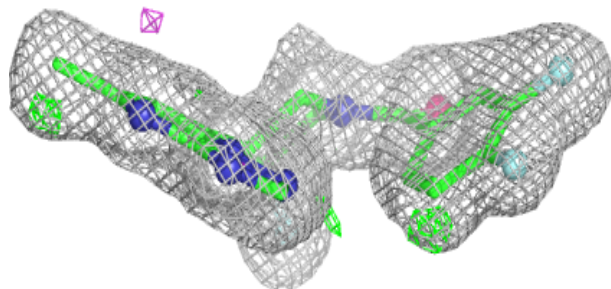
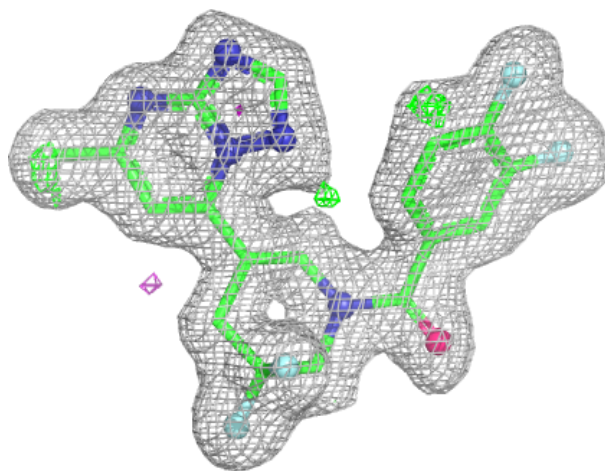
Electron density around 7P4 A 1001 (B):

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



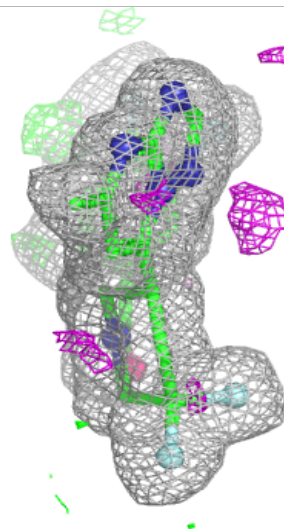
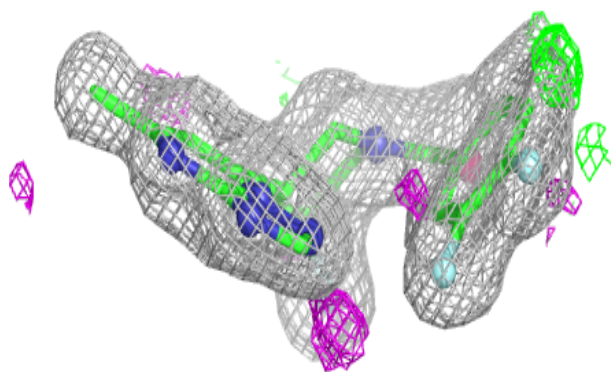
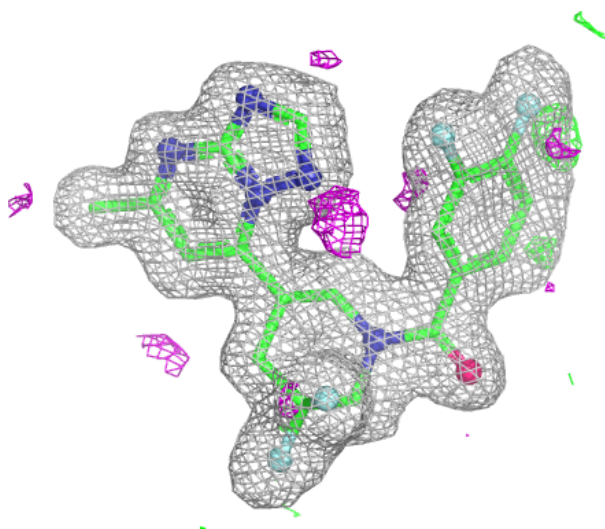
Electron density around 7P4 B 1001:

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



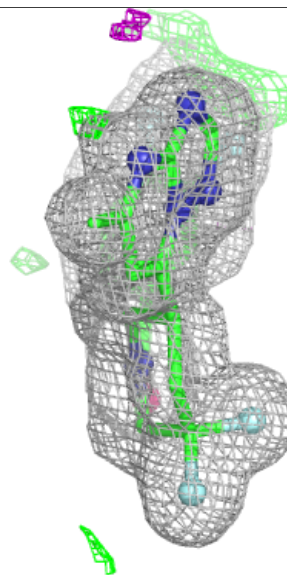
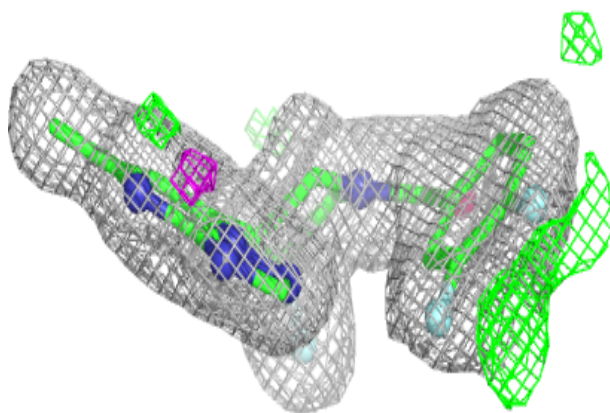
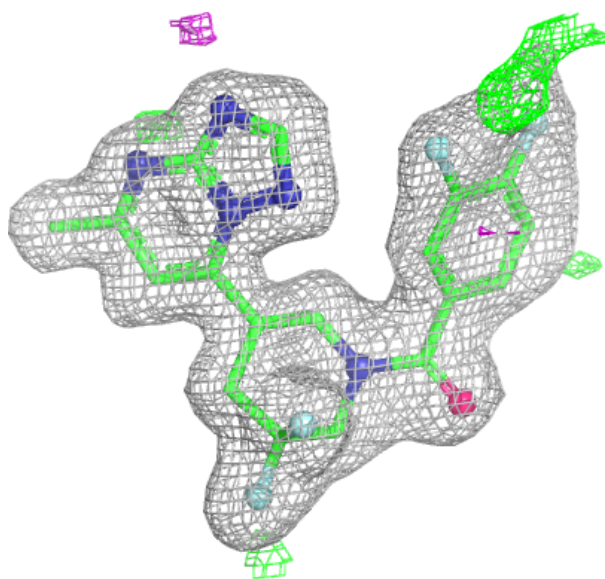
Electron density around 7P4 D 1001:

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



Electron density around 7P4 C 1001:

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



6.5 Other polymers ⓘ

There are no such residues in this entry.