



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 20, 2026 – 10:07 AM UTC

PDB ID : 7A9V / pdb_00007a9v
Title : Crystal structure of human phosphodiesterase 4D2 catalytic domain with inhibitor NPD-635
Authors : Singh, A.K.; Blaazer, A.R.; Zara, L.; de Esch, I.J.P.; Leurs, R.; Brown, D.G.
Deposited on : 2020-09-02
Resolution : 2.17 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

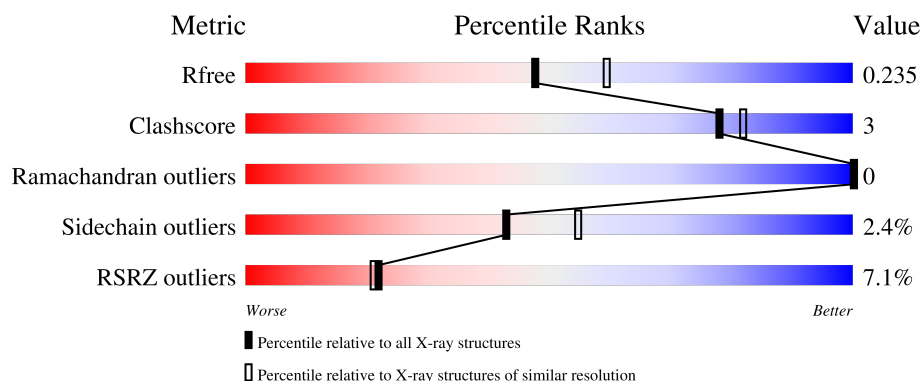
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.17 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	8975 (2.20-2.16)
Clashscore	190562	9786 (2.20-2.16)
Ramachandran outliers	187476	9664 (2.20-2.16)
Sidechain outliers	187428	9664 (2.20-2.16)
RSRZ outliers	180081	8979 (2.20-2.16)

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	364	3% 83% 7% 10%
1	B	364	13% 82% 7% 11%
1	C	364	4% 82% 7% 11%
1	D	364	5% 82% 7% 11%

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	R5Z	B	508	X	-	-	-
6	R5Z	C	509	X	-	-	-
6	R5Z	D	513	X	-	-	-

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 11373 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 cAMP-specific 3',5'-cyclic phosphodiesterase 4D.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	329	Total	C	N	O	S	0	0	0
			2658	1681	454	509	14			
1	B	324	Total	C	N	O	S	0	0	0
			2622	1659	448	501	14			
1	C	325	Total	C	N	O	S	0	0	0
			2631	1664	449	504	14			
1	D	325	Total	C	N	O	S	0	0	0
			2631	1664	450	503	14			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	75	GLY	-	expression tag	UNP Q08499
A	76	SER	-	expression tag	UNP Q08499
A	77	HIS	-	expression tag	UNP Q08499
A	78	MET	-	expression tag	UNP Q08499
B	75	GLY	-	expression tag	UNP Q08499
B	76	SER	-	expression tag	UNP Q08499
B	77	HIS	-	expression tag	UNP Q08499
B	78	MET	-	expression tag	UNP Q08499
C	75	GLY	-	expression tag	UNP Q08499
C	76	SER	-	expression tag	UNP Q08499
C	77	HIS	-	expression tag	UNP Q08499
C	78	MET	-	expression tag	UNP Q08499
D	75	GLY	-	expression tag	UNP Q08499
D	76	SER	-	expression tag	UNP Q08499
D	77	HIS	-	expression tag	UNP Q08499
D	78	MET	-	expression tag	UNP Q08499

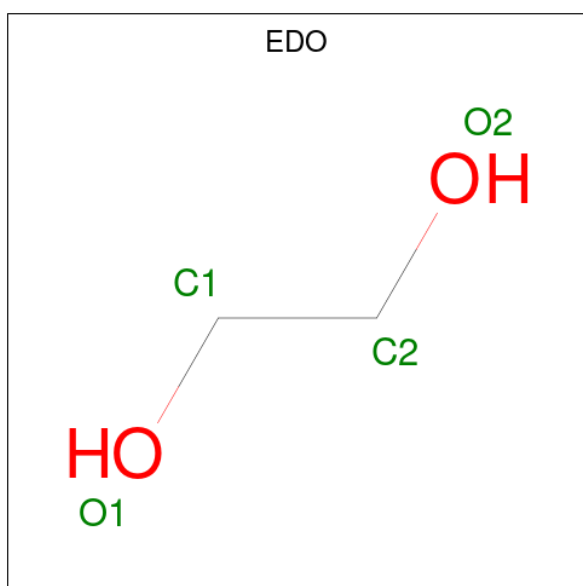
- Molecule 2 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

- Molecule 3 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

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

- Molecule 4 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



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		

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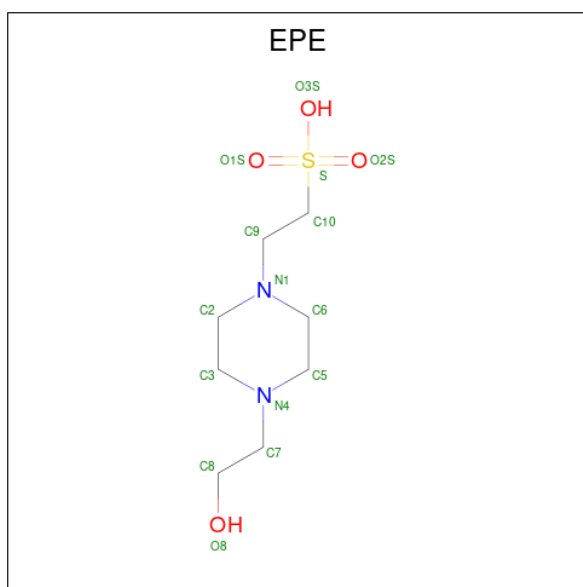
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			4	2	2		
4	A	1	Total	C	O	0	0
			4	2	2		
4	A	1	Total	C	O	0	0
			4	2	2		
4	A	1	Total	C	O	0	0
			4	2	2		
4	A	1	Total	C	O	0	0
			4	2	2		
4	A	1	Total	C	O	0	0
			4	2	2		
4	B	1	Total	C	O	0	0
			4	2	2		
4	B	1	Total	C	O	0	0
			4	2	2		
4	B	1	Total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

- Molecule 5 is 4-(2-HYDROXYETHYL)-1-PIPERAZINE ETHANESULFONIC ACID (CCD ID: EPE) (formula: $C_8H_{18}N_2O_4S$).



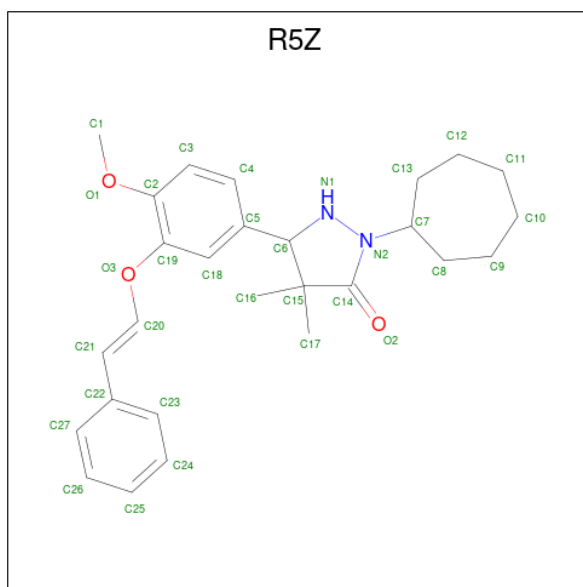
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	A	1	Total	C	N	O	S	0	0
			15	8	2	4	1		

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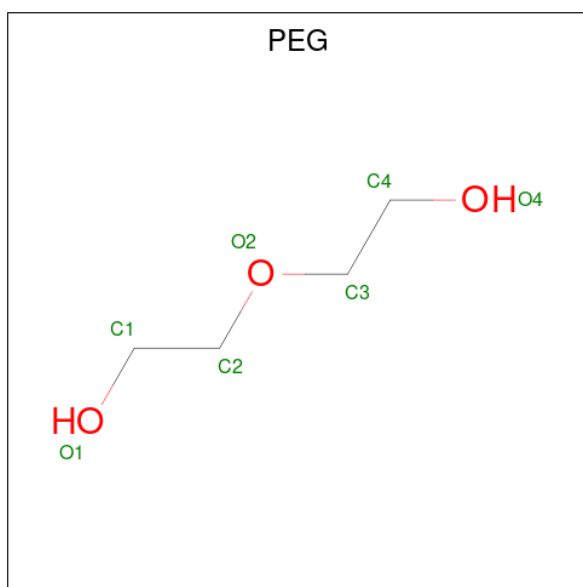
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	C	1	Total	C	N	O	S	0	0
			15	8	2	4	1		
5	D	1	Total	C	N	O	S	0	0
			15	8	2	4	1		

- Molecule 6 is 1-cycloheptyl-3-[4-methoxy-3-(2-phenylethoxy)phenyl]-4,4-dimethyl-4,5-dihydro-1H-pyrazol-5-one (CCD ID: R5Z) (formula: $C_{27}H_{34}N_2O_3$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	B	1	Total	C	N	O	0	0
			32	27	2	3		
6	C	1	Total	C	N	O	0	0
			32	27	2	3		
6	D	1	Total	C	N	O	0	0
			32	27	2	3		

- Molecule 7 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: $C_4H_{10}O_3$).



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

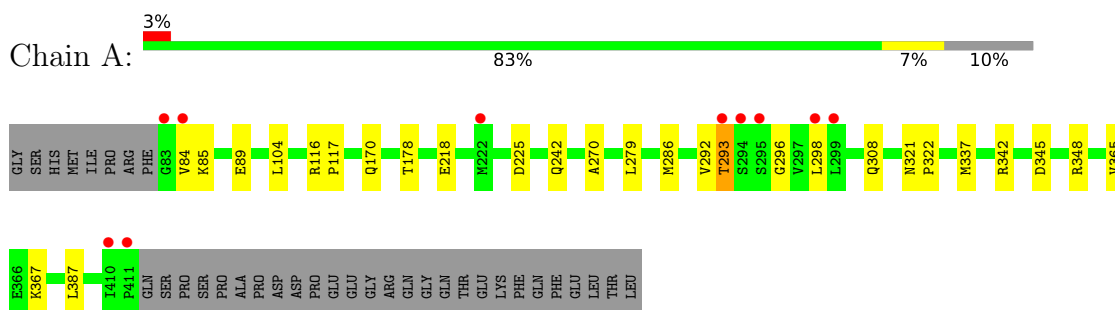
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	145	Total	O	0	0
			145	145		
8	B	111	Total	O	0	0
			111	111		
8	C	108	Total	O	0	0
			108	108		
8	D	172	Total	O	0	0
			172	172		

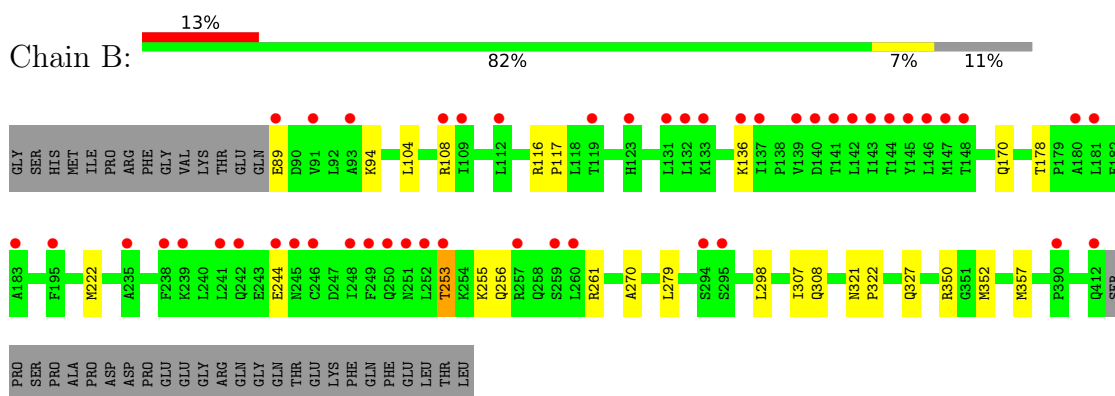
3 Residue-property plots

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.

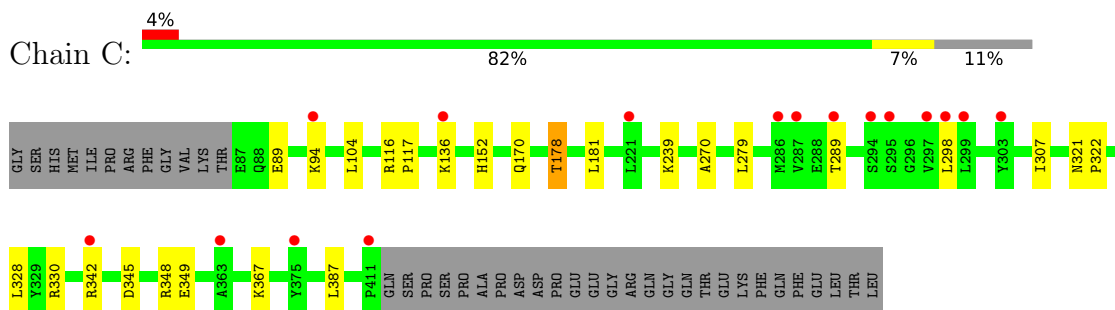
- Molecule 1: cAMP-specific 3',5'-cyclic phosphodiesterase 4D



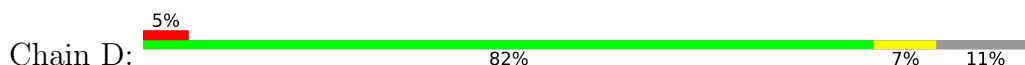
- Molecule 1: cAMP-specific 3',5'-cyclic phosphodiesterase 4D

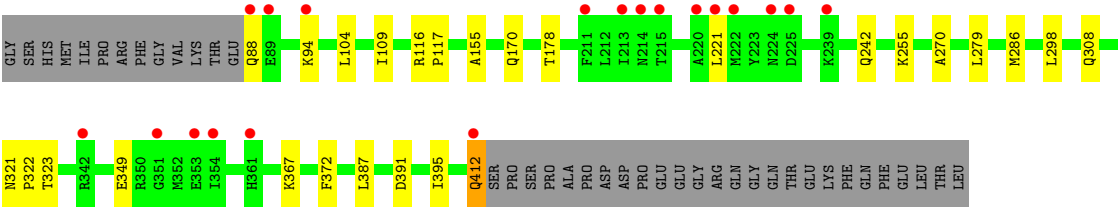


- Molecule 1: cAMP-specific 3',5'-cyclic phosphodiesterase 4D



- Molecule 1: cAMP-specific 3',5'-cyclic phosphodiesterase 4D





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	99.20Å 111.16Å 159.68Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	91.29 – 2.17 91.23 – 2.17	Depositor EDS
% Data completeness (in resolution range)	100.0 (91.29-2.17) 100.0 (91.23-2.17)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.18 (at 2.16Å)	Xtriage
Refinement program	REFMAC 5.8.0258	Depositor
R, R_{free}	0.189 , 0.229 0.195 , 0.235	Depositor DCC
R_{free} test set	4819 reflections (5.12%)	wwPDB-VP
Wilson B-factor (Å ²)	40.8	Xtriage
Anisotropy	0.110	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 37.4	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	0.96	EDS
Total number of atoms	11373	wwPDB-VP
Average B, all atoms (Å ²)	50.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.04% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: EPE, PEG, EDO, R5Z, 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	1.04	0/2712	1.32	0/3684
1	B	1.02	0/2676	1.34	0/3636
1	C	1.02	0/2685	1.32	1/3648 (0.0%)
1	D	1.03	0/2685	1.31	2/3648 (0.1%)
All	All	1.03	0/10758	1.32	3/14616 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	349	GLU	CB-CA-C	-6.74	98.17	110.63
1	D	349	GLU	CB-CA-C	-5.21	101.83	110.68
1	D	391	ASP	CA-CB-CG	5.12	117.72	112.60

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	2658	0	2616	19	0
1	B	2622	0	2578	14	0
1	C	2631	0	2584	13	0
1	D	2631	0	2586	16	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	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	36	0	54	5	0
4	B	24	0	36	3	0
4	C	28	0	42	1	0
4	D	44	0	66	0	0
5	A	15	0	18	0	0
5	C	15	0	18	1	0
5	D	15	0	17	0	0
6	B	32	0	0	1	0
6	C	32	0	0	1	0
6	D	32	0	0	2	0
7	D	14	0	20	2	0
8	A	145	0	0	3	0
8	B	111	0	0	1	0
8	C	108	0	0	0	0
8	D	172	0	0	0	0
All	All	11373	0	10635	61	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 (61) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:352:MET:HE2	4:B:505:EDO:C2	2.13	0.79
1:D:412:GLN:H	1:D:412:GLN:CD	1.93	0.77
1:A:218:GLU:OE1	4:A:506:EDO:H11	1.85	0.76
1:A:218:GLU:OE1	4:A:506:EDO:C1	2.36	0.74
1:B:352:MET:HE2	4:B:505:EDO:H21	1.68	0.73
1:A:286:MET:HE3	8:A:616:HOH:O	1.91	0.70
1:C:345:ASP:OD1	1:C:348:ARG:NH2	2.30	0.64
1:A:321:ASN:HB2	1:A:322:PRO:HD3	1.80	0.63
1:A:286:MET:CE	8:A:616:HOH:O	2.47	0.62
1:D:286:MET:HE3	1:D:308:GLN:OE1	2.06	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:85:LYS:HB2	1:A:89:GLU:HB3	1.87	0.56
1:A:242:GLN:OE1	1:D:242:GLN:OE1	2.25	0.54
1:A:292:VAL:HG12	1:A:293:THR:O	2.09	0.53
1:D:155:ALA:HB2	7:D:515:PEG:H32	1.91	0.52
1:B:357:MET:SD	6:B:508:R5Z:C21	2.98	0.52
1:D:372:PHE:HB2	6:D:513:R5Z:C22	2.40	0.52
4:A:512:EDO:H21	1:B:222:MET:HE1	1.92	0.51
1:A:298:LEU:HD11	1:A:387:LEU:HG	1.94	0.50
1:D:286:MET:CE	1:D:308:GLN:OE1	2.60	0.50
1:A:225:ASP:CG	1:B:261:ARG:HH12	2.19	0.49
1:C:270:ALA:HB1	1:C:279:LEU:HD11	1.93	0.49
1:A:345:ASP:OD1	1:A:348:ARG:NH2	2.46	0.49
1:B:270:ALA:HB1	1:B:279:LEU:HD11	1.95	0.49
1:D:395:ILE:HG13	7:D:514:PEG:H32	1.95	0.49
1:C:289:THR:O	1:C:289:THR:HG22	2.13	0.48
1:A:218:GLU:OE1	4:A:506:EDO:H12	2.10	0.48
1:A:270:ALA:HB1	1:A:279:LEU:HD11	1.96	0.48
1:C:116:ARG:N	1:C:117:PRO:CD	2.78	0.47
1:A:116:ARG:N	1:A:117:PRO:CD	2.78	0.47
1:C:321:ASN:HB2	1:C:322:PRO:HD3	1.96	0.47
1:B:104:LEU:HD22	1:B:170:GLN:HG3	1.96	0.47
1:D:270:ALA:HB1	1:D:279:LEU:HD11	1.97	0.47
1:D:104:LEU:HD22	1:D:170:GLN:HG3	1.97	0.47
1:C:330:ARG:HH11	1:C:330:ARG:HG2	1.80	0.47
1:D:116:ARG:N	1:D:117:PRO:CD	2.79	0.46
1:B:116:ARG:N	1:B:117:PRO:CD	2.79	0.46
1:C:104:LEU:HD22	1:C:170:GLN:HG3	1.97	0.46
1:A:337:MET:HE2	1:A:365:VAL:HG22	1.97	0.46
1:D:298:LEU:HD11	1:D:387:LEU:HG	1.98	0.46
1:A:292:VAL:CG1	1:A:296:GLY:HA2	2.46	0.46
1:C:328:LEU:HD23	5:C:511:EPE:O2S	2.16	0.45
1:C:298:LEU:HD11	1:C:387:LEU:HG	1.99	0.45
1:C:152:HIS:HE1	4:C:506:EDO:C1	2.30	0.45
1:A:308:GLN:HB3	8:A:616:HOH:O	2.17	0.45
6:C:509:R5Z:C21	6:C:509:R5Z:C18	2.96	0.44
1:D:321:ASN:HB2	1:D:322:PRO:HD3	1.98	0.43
4:A:512:EDO:C2	1:B:222:MET:HE1	2.48	0.43
1:D:372:PHE:HB2	6:D:513:R5Z:C21	2.47	0.43
1:B:321:ASN:HB2	1:B:322:PRO:HD3	2.00	0.43
1:C:178:THR:HG22	1:C:181:LEU:HD12	2.00	0.43
1:D:323:THR:HB	1:D:395:ILE:HG23	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:253:THR:HG23	1:B:256:GLN:HG3	2.01	0.42
1:B:352:MET:HE2	4:B:505:EDO:C1	2.49	0.42
1:B:350:ARG:HB3	8:B:614:HOH:O	2.18	0.42
1:C:330:ARG:HG2	1:C:330:ARG:NH1	2.35	0.41
1:A:104:LEU:HD22	1:A:170:GLN:HG3	2.01	0.41
1:B:307:ILE:HD12	1:B:307:ILE:HA	1.94	0.41
1:D:279:LEU:HD23	1:D:279:LEU:HA	1.97	0.41
1:A:84:VAL:HG22	1:A:85:LYS:H	1.86	0.40
1:C:307:ILE:HD12	1:C:307:ILE:HA	1.97	0.40
1:D:104:LEU:HD11	1:D:109:ILE:HD11	2.03	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	327/364 (90%)	321 (98%)	6 (2%)	0	100	100
1	B	322/364 (88%)	317 (98%)	5 (2%)	0	100	100
1	C	323/364 (89%)	318 (98%)	5 (2%)	0	100	100
1	D	323/364 (89%)	317 (98%)	6 (2%)	0	100	100
All	All	1295/1456 (89%)	1273 (98%)	22 (2%)	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	300/331 (91%)	296 (99%)	4 (1%)	61	74
1	B	296/331 (89%)	285 (96%)	11 (4%)	30	38
1	C	297/331 (90%)	290 (98%)	7 (2%)	43	55
1	D	297/331 (90%)	290 (98%)	7 (2%)	43	55
All	All	1190/1324 (90%)	1161 (98%)	29 (2%)	43	55

All (29) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	178	THR
1	A	293	THR
1	A	342	ARG
1	A	367	LYS
1	B	89	GLU
1	B	94	LYS
1	B	108	ARG
1	B	136	LYS
1	B	178	THR
1	B	244	GLU
1	B	253	THR
1	B	255	LYS
1	B	298	LEU
1	B	308	GLN
1	B	327	GLN
1	C	89	GLU
1	C	94	LYS
1	C	136	LYS
1	C	178	THR
1	C	239	LYS
1	C	342	ARG
1	C	367	LYS
1	D	88	GLN
1	D	94	LYS
1	D	178	THR
1	D	221	LEU
1	D	255	LYS
1	D	367	LYS
1	D	412	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	308	GLN
1	A	331	GLN
1	A	369	GLN
1	A	389	HIS
1	B	250	GLN
1	B	369	GLN
1	B	389	HIS
1	C	152	HIS
1	C	210	GLN
1	C	231	ASN
1	C	250	GLN
1	C	258	GLN
1	D	210	GLN
1	D	224	ASN
1	D	258	GLN
1	D	308	GLN
1	D	312	ASN

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](#)

Of 49 ligands modelled in this entry, 8 are monoatomic - leaving 41 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the

expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
4	EDO	A	509	-	3,3,3	0.22	0	2,2,2	0.35	0
4	EDO	C	505	-	3,3,3	0.13	0	2,2,2	0.13	0
4	EDO	D	506	-	3,3,3	0.15	0	2,2,2	0.09	0
6	R5Z	B	508	-	32,35,35	1.63	5 (15%)	36,49,49	1.30	4 (11%)
4	EDO	D	507	-	3,3,3	0.14	0	2,2,2	0.32	0
4	EDO	C	503	-	3,3,3	0.12	0	2,2,2	0.08	0
4	EDO	A	507	-	3,3,3	0.20	0	2,2,2	0.51	0
6	R5Z	C	509	-	32,35,35	1.62	5 (15%)	36,49,49	1.25	2 (5%)
4	EDO	D	512	-	3,3,3	0.75	0	2,2,2	0.63	0
4	EDO	B	503	-	3,3,3	0.19	0	2,2,2	0.17	0
4	EDO	D	508	-	3,3,3	0.25	0	2,2,2	0.41	0
4	EDO	C	507	-	3,3,3	0.30	0	2,2,2	0.37	0
4	EDO	A	508	-	3,3,3	0.47	0	2,2,2	0.43	0
4	EDO	A	505	-	3,3,3	0.53	0	2,2,2	0.49	0
4	EDO	D	505	-	3,3,3	0.21	0	2,2,2	0.21	0
4	EDO	B	509	-	3,3,3	0.35	0	2,2,2	0.69	0
4	EDO	A	510	-	3,3,3	0.18	0	2,2,2	0.19	0
4	EDO	B	507	-	3,3,3	0.14	0	2,2,2	0.32	0
4	EDO	D	511	-	3,3,3	0.27	0	2,2,2	0.16	0
4	EDO	C	510	-	3,3,3	0.21	0	2,2,2	0.17	0
5	EPE	A	511	-	15,15,15	1.67	1 (6%)	19,20,20	1.31	2 (10%)
4	EDO	A	504	-	3,3,3	0.30	0	2,2,2	0.33	0
4	EDO	D	504	-	3,3,3	0.18	0	2,2,2	0.41	0
4	EDO	C	508	-	3,3,3	0.16	0	2,2,2	0.07	0
4	EDO	D	503	-	3,3,3	0.14	0	2,2,2	0.11	0
4	EDO	A	512	-	3,3,3	0.10	0	2,2,2	0.21	0
7	PEG	D	514	-	6,6,6	0.72	0	5,5,5	0.43	0
4	EDO	A	506	-	3,3,3	0.20	0	2,2,2	0.22	0
4	EDO	D	510	-	3,3,3	0.07	0	2,2,2	0.09	0
4	EDO	B	505	-	3,3,3	0.43	0	2,2,2	0.89	0
4	EDO	C	504	-	3,3,3	0.24	0	2,2,2	0.52	0
4	EDO	C	506	-	3,3,3	0.34	0	2,2,2	0.42	0
4	EDO	B	506	-	3,3,3	0.17	0	2,2,2	0.26	0
4	EDO	B	504	-	3,3,3	0.11	0	2,2,2	0.16	0
7	PEG	D	515	-	6,6,6	0.32	0	5,5,5	0.21	0
4	EDO	D	516	-	3,3,3	0.44	0	2,2,2	0.64	0
4	EDO	A	503	-	3,3,3	0.09	0	2,2,2	0.15	0
5	EPE	D	517	-	15,15,15	1.77	1 (6%)	19,20,20	1.64	1 (5%)
4	EDO	D	509	-	3,3,3	0.10	0	2,2,2	0.25	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	R5Z	D	513	-	32,35,35	1.61	5 (15%)	36,49,49	1.10	1 (2%)
5	EPE	C	511	-	15,15,15	1.82	2 (13%)	19,20,20	1.89	4 (21%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	EDO	A	509	-	-	1/1/1/1	-
4	EDO	C	505	-	-	1/1/1/1	-
4	EDO	D	506	-	-	1/1/1/1	-
6	R5Z	B	508	-	1/1/5/8	7/12/45/45	0/4/4/4
4	EDO	D	507	-	-	0/1/1/1	-
4	EDO	C	503	-	-	0/1/1/1	-
4	EDO	A	507	-	-	0/1/1/1	-
6	R5Z	C	509	-	1/1/5/8	6/12/45/45	0/4/4/4
4	EDO	D	512	-	-	0/1/1/1	-
4	EDO	B	503	-	-	0/1/1/1	-
4	EDO	D	508	-	-	0/1/1/1	-
4	EDO	C	507	-	-	1/1/1/1	-
4	EDO	A	508	-	-	1/1/1/1	-
4	EDO	A	505	-	-	1/1/1/1	-
4	EDO	D	505	-	-	1/1/1/1	-
4	EDO	B	509	-	-	1/1/1/1	-
4	EDO	A	510	-	-	0/1/1/1	-
4	EDO	B	507	-	-	1/1/1/1	-
4	EDO	D	511	-	-	1/1/1/1	-
4	EDO	C	510	-	-	0/1/1/1	-
5	EPE	A	511	-	-	6/9/19/19	0/1/1/1
4	EDO	A	504	-	-	0/1/1/1	-
4	EDO	D	504	-	-	0/1/1/1	-
4	EDO	C	508	-	-	0/1/1/1	-
4	EDO	D	503	-	-	0/1/1/1	-
4	EDO	A	512	-	-	1/1/1/1	-
7	PEG	D	514	-	-	2/4/4/4	-
4	EDO	A	506	-	-	1/1/1/1	-
4	EDO	D	510	-	-	1/1/1/1	-
4	EDO	B	505	-	-	1/1/1/1	-
4	EDO	C	504	-	-	0/1/1/1	-
4	EDO	C	506	-	-	1/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	EDO	B	506	-	-	0/1/1/1	-
4	EDO	B	504	-	-	1/1/1/1	-
7	PEG	D	515	-	-	3/4/4/4	-
4	EDO	D	516	-	-	1/1/1/1	-
4	EDO	A	503	-	-	1/1/1/1	-
5	EPE	D	517	-	-	3/9/19/19	0/1/1/1
4	EDO	D	509	-	-	1/1/1/1	-
6	R5Z	D	513	-	1/1/5/8	5/12/45/45	0/4/4/4
5	EPE	C	511	-	-	2/9/19/19	0/1/1/1

All (19) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	C	511	EPE	C10-S	-6.35	1.68	1.77
6	C	509	R5Z	C21-C20	6.21	1.52	1.32
6	B	508	R5Z	C21-C20	6.14	1.52	1.32
5	A	511	EPE	C10-S	-6.06	1.69	1.77
6	D	513	R5Z	C21-C20	6.00	1.52	1.32
5	D	517	EPE	C10-S	-5.86	1.69	1.77
6	C	509	R5Z	O3-C20	4.06	1.49	1.38
6	D	513	R5Z	O3-C20	4.03	1.49	1.38
6	B	508	R5Z	C5-C6	-3.80	1.47	1.52
6	C	509	R5Z	C5-C6	-3.68	1.47	1.52
6	B	508	R5Z	O3-C20	3.60	1.48	1.38
6	D	513	R5Z	C5-C6	-3.48	1.47	1.52
6	B	508	R5Z	C15-C6	-2.58	1.52	1.57
6	D	513	R5Z	C15-C6	-2.44	1.52	1.57
6	B	508	R5Z	C22-C21	2.41	1.54	1.47
6	C	509	R5Z	C15-C6	-2.37	1.52	1.57
6	D	513	R5Z	C22-C21	2.29	1.54	1.47
6	C	509	R5Z	C22-C21	2.22	1.53	1.47
5	C	511	EPE	O1S-S	2.04	1.50	1.45

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	C	511	EPE	O1S-S-C10	6.01	115.81	106.73
6	C	509	R5Z	O2-C14-N2	5.21	129.00	124.48
5	D	517	EPE	O3S-S-C10	4.93	115.66	106.00
6	B	508	R5Z	O2-C14-N2	4.51	128.40	124.48
6	D	513	R5Z	O2-C14-N2	4.14	128.08	124.48

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	511	EPE	O1S-S-C10	3.49	112.00	106.73
5	C	511	EPE	O2S-S-C10	-2.98	102.23	106.73
5	A	511	EPE	C9-N1-C2	2.58	118.12	111.24
6	B	508	R5Z	O3-C19-C2	2.49	124.73	117.04
5	C	511	EPE	O3S-S-C10	2.47	110.83	106.00
5	C	511	EPE	O3S-S-O2S	-2.45	105.28	111.40
6	C	509	R5Z	C19-O3-C20	2.33	122.60	118.38
6	B	508	R5Z	C18-C5-C6	-2.21	116.46	120.31
6	B	508	R5Z	O3-C19-C18	-2.19	116.20	122.08

All (3) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
6	B	508	R5Z	C6
6	C	509	R5Z	C6
6	D	513	R5Z	C6

All (53) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	511	EPE	C10-C9-N1-C2
5	A	511	EPE	C9-C10-S-O1S
5	A	511	EPE	C9-C10-S-O3S
6	B	508	R5Z	C18-C5-C6-C15
6	B	508	R5Z	C4-C5-C6-C15
6	B	508	R5Z	C21-C20-O3-C19
6	B	508	R5Z	C20-C21-C22-C23
6	C	509	R5Z	C18-C5-C6-C15
6	C	509	R5Z	C4-C5-C6-C15
6	C	509	R5Z	O3-C20-C21-C22
6	C	509	R5Z	C21-C20-O3-C19
6	D	513	R5Z	C18-C5-C6-C15
6	D	513	R5Z	C4-C5-C6-C15
6	D	513	R5Z	O3-C20-C21-C22
5	A	511	EPE	N4-C7-C8-O8
5	C	511	EPE	C8-C7-N4-C5
7	D	514	PEG	O2-C3-C4-O4
7	D	515	PEG	O2-C3-C4-O4
4	A	505	EDO	O1-C1-C2-O2
4	B	504	EDO	O1-C1-C2-O2
4	B	505	EDO	O1-C1-C2-O2
4	C	505	EDO	O1-C1-C2-O2

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Mol	Chain	Res	Type	Atoms
4	C	507	EDO	O1-C1-C2-O2
4	D	509	EDO	O1-C1-C2-O2
4	D	511	EDO	O1-C1-C2-O2
5	A	511	EPE	C10-C9-N1-C6
4	A	506	EDO	O1-C1-C2-O2
6	C	509	R5Z	C18-C5-C6-N1
5	A	511	EPE	C9-C10-S-O2S
6	B	508	R5Z	C20-C21-C22-C27
6	C	509	R5Z	C4-C5-C6-N1
5	D	517	EPE	C8-C7-N4-C5
7	D	515	PEG	O1-C1-C2-O2
5	D	517	EPE	C10-C9-N1-C6
6	D	513	R5Z	C4-C5-C6-N1
5	C	511	EPE	C9-C10-S-O3S
7	D	515	PEG	C1-C2-O2-C3
7	D	514	PEG	C1-C2-O2-C3
5	D	517	EPE	C8-C7-N4-C3
4	A	503	EDO	O1-C1-C2-O2
4	A	512	EDO	O1-C1-C2-O2
4	B	509	EDO	O1-C1-C2-O2
4	C	506	EDO	O1-C1-C2-O2
4	D	510	EDO	O1-C1-C2-O2
4	D	516	EDO	O1-C1-C2-O2
6	B	508	R5Z	C18-C19-O3-C20
6	B	508	R5Z	C18-C5-C6-N1
6	D	513	R5Z	C18-C5-C6-N1
4	A	509	EDO	O1-C1-C2-O2
4	B	507	EDO	O1-C1-C2-O2
4	D	506	EDO	O1-C1-C2-O2
4	A	508	EDO	O1-C1-C2-O2
4	D	505	EDO	O1-C1-C2-O2

There are no ring outliers.

10 monomers are involved in 16 short contacts:

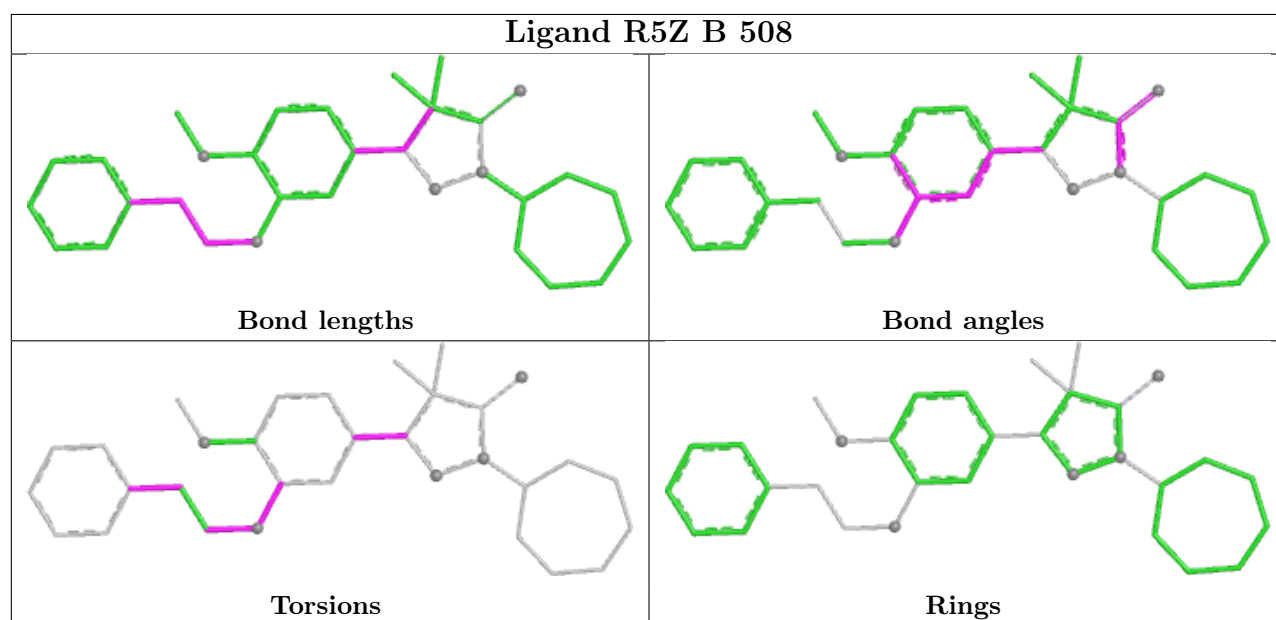
Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	B	508	R5Z	1	0
6	C	509	R5Z	1	0
4	A	512	EDO	2	0
7	D	514	PEG	1	0
4	A	506	EDO	3	0
4	B	505	EDO	3	0

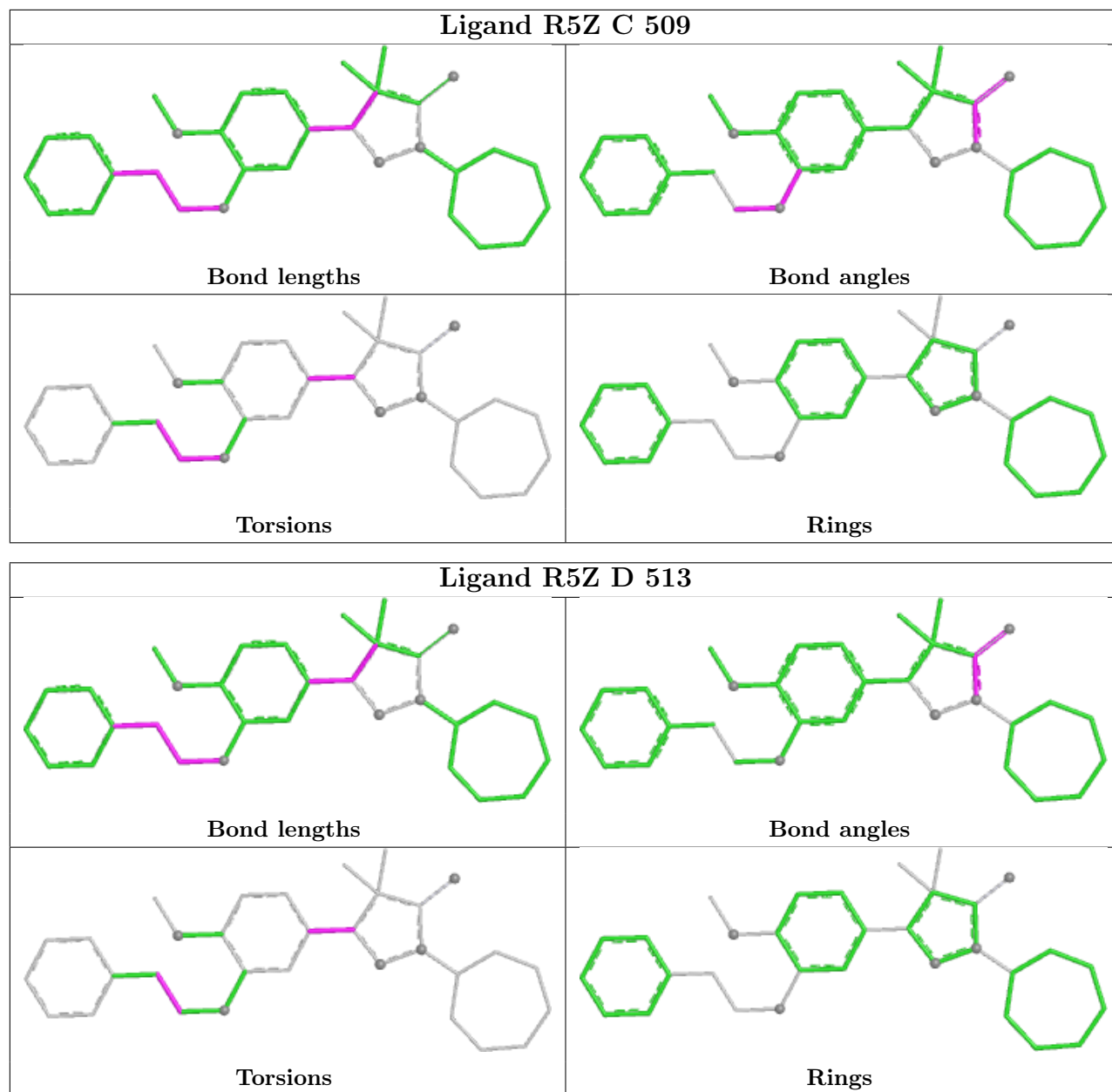
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Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	C	506	EDO	1	0
7	D	515	PEG	1	0
6	D	513	R5Z	2	0
5	C	511	EPE	1	0

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 [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	329/364 (90%)	0.12	10 (3%) 52 52	26, 42, 76, 120	0
1	B	324/364 (89%)	0.91	48 (14%) 5 5	29, 55, 83, 118	0
1	C	325/364 (89%)	0.42	16 (4%) 35 34	29, 50, 83, 115	0
1	D	325/364 (89%)	0.11	19 (5%) 29 28	24, 38, 70, 100	0
All	All	1303/1456 (89%)	0.39	93 (7%) 22 21	24, 47, 79, 120	0

All (93) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	221	LEU	5.8
1	D	412	GLN	5.3
1	A	83	GLY	4.9
1	A	411	PRO	4.9
1	D	213	ILE	4.2
1	B	239	LYS	4.2
1	B	137	ILE	4.2
1	B	91	VAL	3.9
1	B	144	THR	3.8
1	B	131	LEU	3.8
1	D	222	MET	3.8
1	A	298	LEU	3.5
1	B	140	ASP	3.5
1	A	293	THR	3.4
1	A	294	SER	3.4
1	B	141	THR	3.3
1	C	411	PRO	3.3
1	B	295	SER	3.2
1	B	294	SER	3.2
1	A	84	VAL	3.1
1	B	143	ILE	3.1

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Mol	Chain	Res	Type	RSRZ
1	D	220	ALA	3.1
1	B	89	GLU	3.0
1	B	142	LEU	2.9
1	B	132	LEU	2.9
1	D	351	GLY	2.9
1	C	297	VAL	2.8
1	D	224	ASN	2.8
1	B	93	ALA	2.8
1	D	89	GLU	2.8
1	B	252	LEU	2.8
1	B	133	LYS	2.8
1	B	148	THR	2.8
1	B	145	TYR	2.7
1	B	146	LEU	2.7
1	B	139	VAL	2.7
1	B	244	GLU	2.7
1	D	88	GLN	2.6
1	B	249	PHE	2.6
1	D	239	LYS	2.6
1	A	295	SER	2.6
1	D	215	THR	2.6
1	C	136	LYS	2.5
1	D	225	ASP	2.5
1	C	295	SER	2.5
1	D	214	ASN	2.5
1	B	242	GLN	2.5
1	B	412	GLN	2.5
1	A	299	LEU	2.4
1	B	250	GLN	2.4
1	C	303	TYR	2.4
1	B	180	ALA	2.4
1	B	257	ARG	2.4
1	B	251	ASN	2.4
1	B	241	LEU	2.4
1	B	253	THR	2.4
1	C	375	TYR	2.3
1	B	112	LEU	2.3
1	B	260	LEU	2.3
1	B	238	PHE	2.3
1	C	94	LYS	2.3
1	D	94	LYS	2.3
1	C	294	SER	2.3

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Mol	Chain	Res	Type	RSRZ
1	D	354	ILE	2.3
1	B	246	CYS	2.3
1	C	287	VAL	2.3
1	C	299	LEU	2.3
1	D	211	PHE	2.3
1	B	147	MET	2.3
1	B	183	ALA	2.2
1	B	235	ALA	2.2
1	B	259	SER	2.2
1	B	248	ILE	2.2
1	A	222	MET	2.2
1	B	181	LEU	2.2
1	C	221	LEU	2.2
1	C	286	MET	2.2
1	B	109	ILE	2.1
1	B	108	ARG	2.1
1	B	195	PHE	2.1
1	D	353	GLU	2.1
1	B	123	HIS	2.1
1	D	361	HIS	2.1
1	D	342	ARG	2.1
1	C	363	ALA	2.1
1	B	245	ASN	2.1
1	C	289	THR	2.1
1	A	410	ILE	2.1
1	B	119	THR	2.0
1	C	298	LEU	2.0
1	C	342	ARG	2.0
1	B	136	LYS	2.0
1	B	390	PRO	2.0

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

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

6.3 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
6	R5Z	B	508	32/32	0.75	0.29	62,94,114,124	0
7	PEG	D	514	7/7	0.76	0.23	51,58,66,74	0
6	R5Z	D	513	32/32	0.77	0.25	54,80,152,161	0
6	R5Z	C	509	32/32	0.78	0.25	58,79,144,150	0
5	EPE	A	511	15/15	0.79	0.24	55,108,142,144	0
4	EDO	A	504	4/4	0.84	0.18	67,68,71,71	0
4	EDO	D	512	4/4	0.85	0.21	46,50,56,58	0
4	EDO	B	504	4/4	0.85	0.17	70,71,74,74	0
4	EDO	B	507	4/4	0.86	0.17	64,65,67,78	0
4	EDO	C	506	4/4	0.86	0.18	65,66,68,68	0
4	EDO	C	507	4/4	0.86	0.18	61,62,70,71	0
4	EDO	C	510	4/4	0.86	0.18	67,73,74,80	0
4	EDO	A	507	4/4	0.86	0.16	47,54,54,58	0
4	EDO	B	509	4/4	0.87	0.22	64,65,66,69	0
4	EDO	B	506	4/4	0.87	0.23	62,64,71,73	0
4	EDO	D	510	4/4	0.87	0.19	64,67,71,73	0
4	EDO	A	505	4/4	0.88	0.17	48,65,67,68	0
4	EDO	C	505	4/4	0.88	0.18	72,73,78,79	0
5	EPE	C	511	15/15	0.88	0.16	55,91,101,101	0
5	EPE	D	517	15/15	0.88	0.21	37,99,110,110	0
4	EDO	C	504	4/4	0.89	0.17	65,66,69,71	0
4	EDO	A	506	4/4	0.89	0.16	61,67,67,68	0
4	EDO	A	508	4/4	0.89	0.15	51,51,57,58	0
4	EDO	D	511	4/4	0.89	0.13	44,55,55,60	0
7	PEG	D	515	7/7	0.89	0.20	71,74,81,82	0
4	EDO	D	505	4/4	0.90	0.18	74,75,78,78	0
4	EDO	A	512	4/4	0.90	0.19	70,75,77,79	0
4	EDO	A	509	4/4	0.90	0.14	50,56,59,66	0
4	EDO	D	507	4/4	0.91	0.11	42,45,49,50	0
4	EDO	D	516	4/4	0.91	0.14	40,53,56,59	0
4	EDO	D	508	4/4	0.91	0.17	59,60,62,65	0
4	EDO	B	505	4/4	0.91	0.24	50,52,57,59	0
4	EDO	D	506	4/4	0.91	0.20	49,52,58,69	0
4	EDO	A	503	4/4	0.92	0.12	57,58,59,60	0
4	EDO	D	504	4/4	0.92	0.13	53,55,55,57	0
4	EDO	D	503	4/4	0.95	0.09	43,44,44,46	0
4	EDO	C	503	4/4	0.95	0.12	61,62,64,67	0

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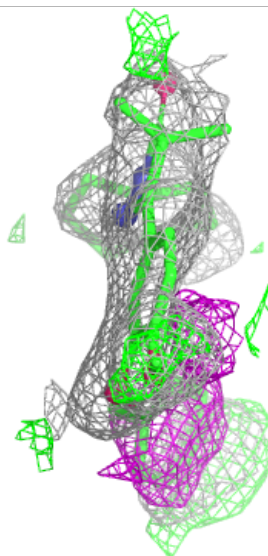
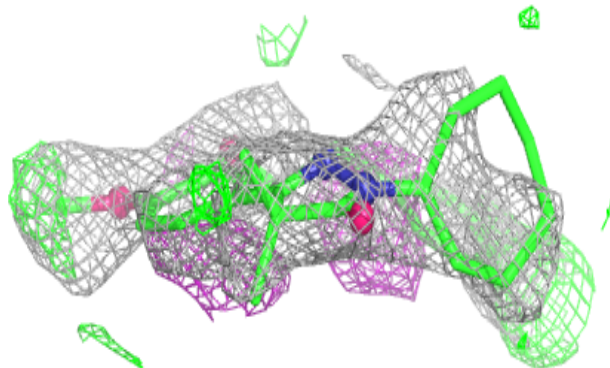
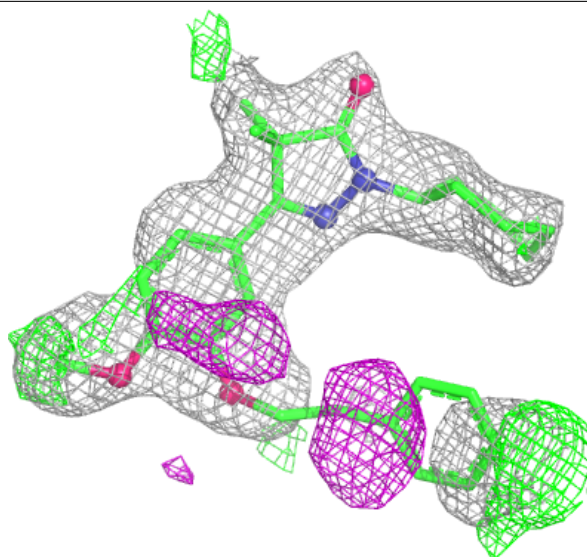
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	EDO	D	509	4/4	0.95	0.10	45,47,48,53	0
4	EDO	C	508	4/4	0.95	0.12	64,71,72,76	0
4	EDO	A	510	4/4	0.95	0.10	42,46,50,50	0
4	EDO	B	503	4/4	0.96	0.07	41,43,49,55	0
2	ZN	B	501	1/1	0.99	0.04	43,43,43,43	0
3	MG	D	502	1/1	1.00	0.03	30,30,30,30	0
2	ZN	A	501	1/1	1.00	0.02	36,36,36,36	0
2	ZN	C	501	1/1	1.00	0.02	41,41,41,41	0
2	ZN	D	501	1/1	1.00	0.01	35,35,35,35	0
3	MG	A	502	1/1	1.00	0.02	27,27,27,27	0
3	MG	B	502	1/1	1.00	0.02	34,34,34,34	0
3	MG	C	502	1/1	1.00	0.01	28,28,28,28	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.

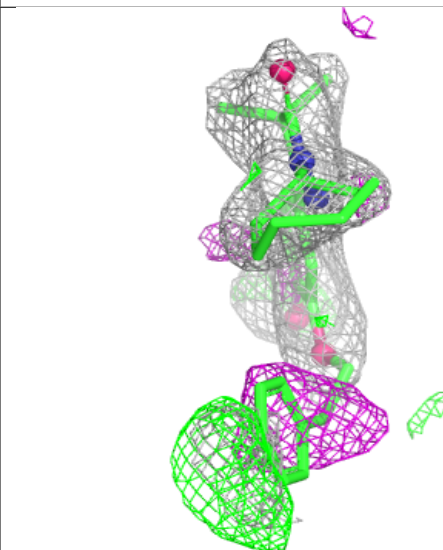
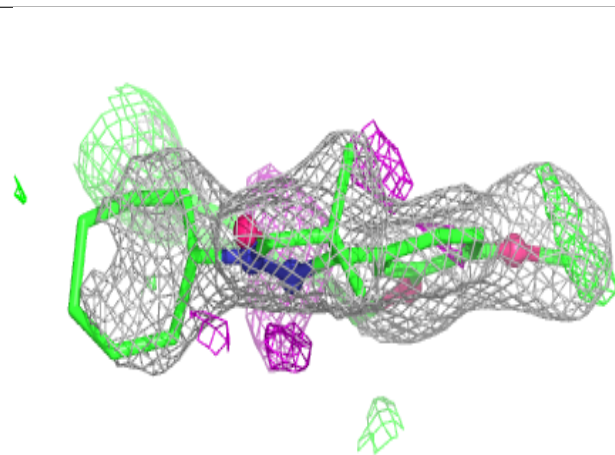
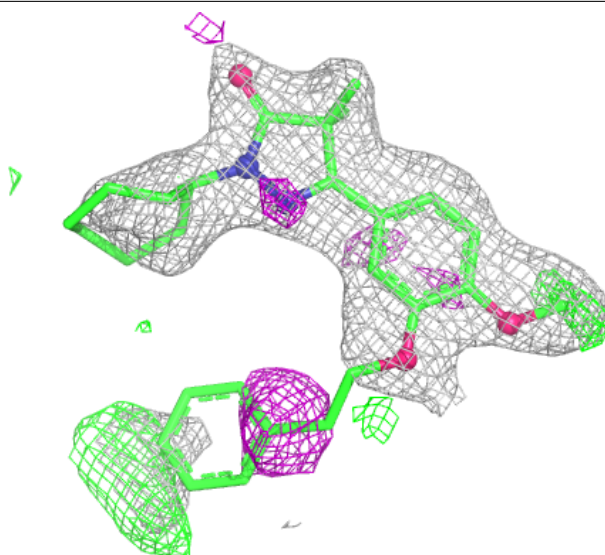
Electron density around R5Z B 508:

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



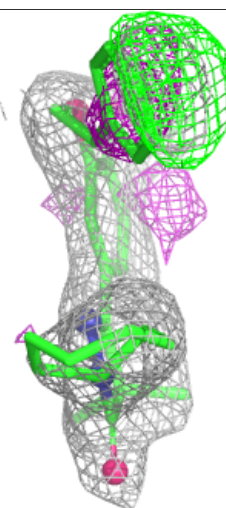
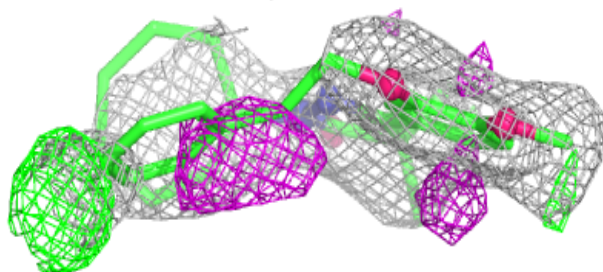
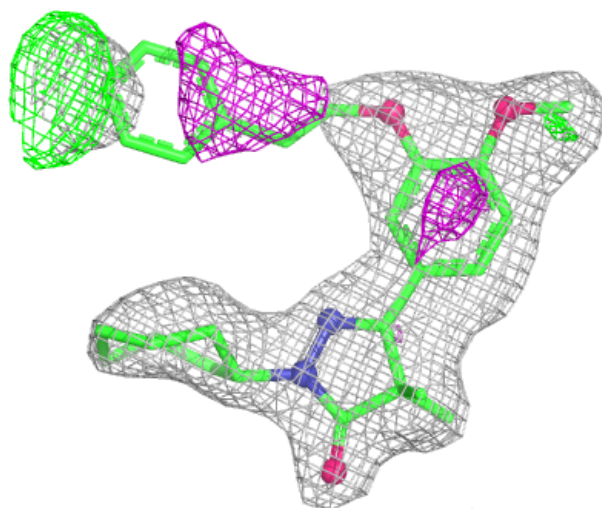
Electron density around R5Z D 513:

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



Electron density around R5Z C 509:

$2mF_o-DF_c$ (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.