



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 22, 2026 – 05:55 PM UTC

PDB ID : 7B9H / pdb_00007b9h
Title : Crystal structure of the PDE4D catalytic domain in complex with GEBR-42a
Authors : Torretta, A.; Abbate, S.; Parisini, E.
Deposited on : 2020-12-14
Resolution : 1.50 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

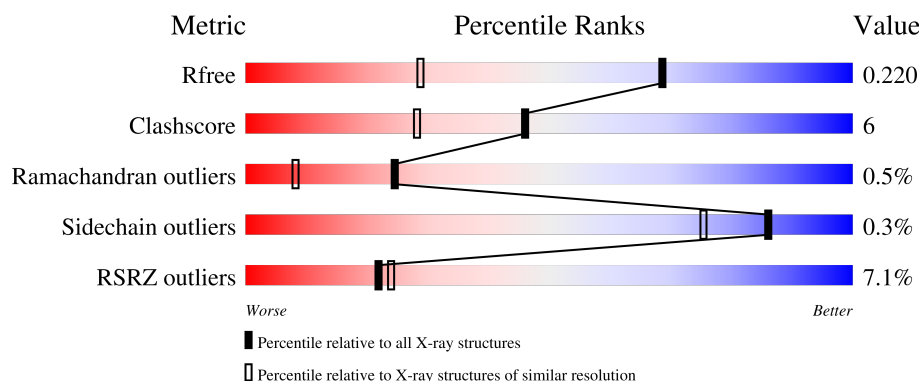
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.50 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	4037 (1.50-1.50)
Clashscore	190562	4235 (1.50-1.50)
Ramachandran outliers	187476	4153 (1.50-1.50)
Sidechain outliers	187428	4150 (1.50-1.50)
RSRZ outliers	180081	4039 (1.50-1.50)

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	343	6% 84% 12% •
1	B	343	8% 85% 10% • 5%

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
4	EDO	A	517	-	-	X	-

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 6328 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	332	Total	C	N	O	S	0	14	0
			2754	1748	464	525	17			
1	B	327	Total	C	N	O	S	0	11	0
			2706	1722	456	511	17			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	77	MET	-	initiating methionine	UNP Q08499
A	413	ALA	-	expression tag	UNP Q08499
A	414	HIS	-	expression tag	UNP Q08499
A	415	HIS	-	expression tag	UNP Q08499
A	416	HIS	-	expression tag	UNP Q08499
A	417	HIS	-	expression tag	UNP Q08499
A	418	HIS	-	expression tag	UNP Q08499
A	419	HIS	-	expression tag	UNP Q08499
B	77	MET	-	initiating methionine	UNP Q08499
B	413	ALA	-	expression tag	UNP Q08499
B	414	HIS	-	expression tag	UNP Q08499
B	415	HIS	-	expression tag	UNP Q08499
B	416	HIS	-	expression tag	UNP Q08499
B	417	HIS	-	expression tag	UNP Q08499
B	418	HIS	-	expression tag	UNP Q08499
B	419	HIS	-	expression tag	UNP Q08499

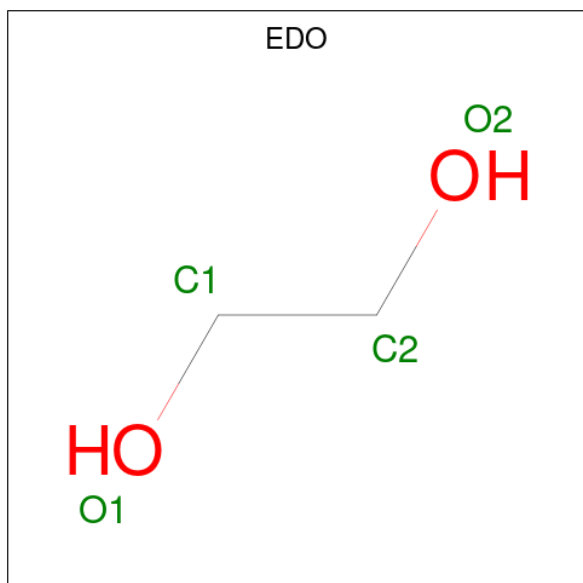
- Molecule 2 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	5	Total	Mg	0	0
			5	5		
3	B	3	Total	Mg	0	0
			3	3		

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



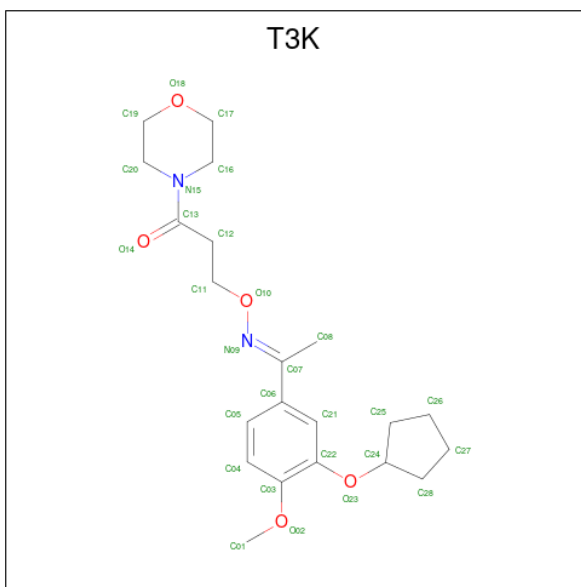
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			4	2	2		
4	A	1	Total	C	O	0	0
			4	2	2		
4	A	1	Total	C	O	0	0
			4	2	2		
4	A	1	Total	C	O	0	0
			4	2	2		
4	A	1	Total	C	O	0	0
			4	2	2		
4	A	1	Total	C	O	0	0
			4	2	2		
4	A	1	Total	C	O	0	1
			8	4	4		

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

- Molecule 5 is 3-[(E))-1-(3-cyclopentyloxy-4-methoxy-phenyl)ethylideneamino]oxy-1-morpholin-4-yl-propan-1-one (CCD ID: T3K) (formula: C₂₁H₃₀N₂O₅) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	N	O	0	0
			28	21	2	5		
5	B	1	Total	C	N	O	0	0
			28	21	2	5		

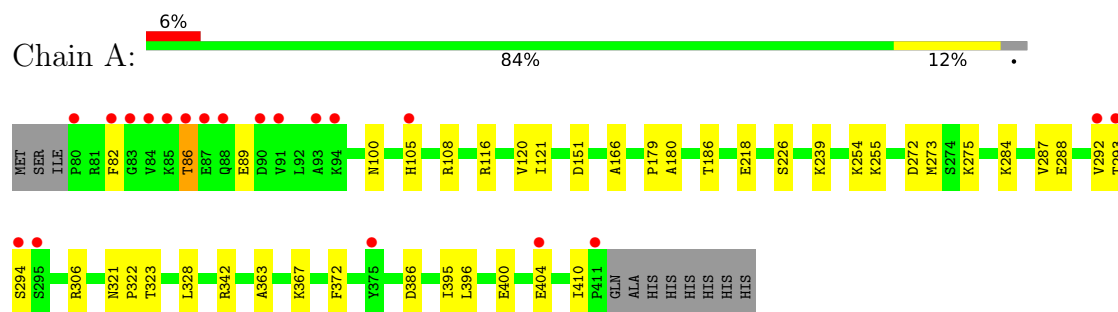
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	371	Total	O	0	0
			371	371		
6	B	315	Total	O	0	0
			315	315		

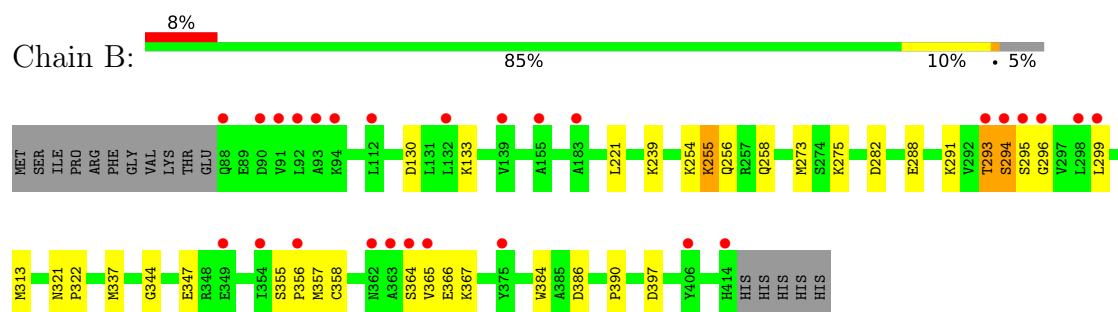
3 Residue-property plots [i](#)

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: 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	64.75Å 98.63Å 119.82Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	54.13 – 1.50 54.13 – 1.50	Depositor EDS
% Data completeness (in resolution range)	99.6 (54.13-1.50) 91.5 (54.13-1.50)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.68 (at 1.50Å)	Xtriage
Refinement program	PHENIX 1.19rc7_4070	Depositor
R, R_{free}	0.194 , 0.221 0.194 , 0.220	Depositor DCC
R_{free} test set	6209 reflections (4.65%)	wwPDB-VP
Wilson B-factor (Å ²)	16.3	Xtriage
Anisotropy	0.398	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 31.3	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	6328	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 4.13% 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: T3K, EDO, ZN, MG

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	0.43	0/2852	0.61	0/3869
1	B	0.39	0/2795	0.61	0/3793
All	All	0.41	0/5647	0.61	0/7662

There are no bond length outliers.

There are no bond angle outliers.

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	2754	0	2743	38	1
1	B	2706	0	2697	26	2
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	5	0	0	0	0
3	B	3	0	0	0	0
4	A	72	0	108	13	1
4	B	44	0	66	6	0
5	A	28	0	0	2	0
5	B	28	0	0	0	0
6	A	371	0	0	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	B	315	0	0	3	0
All	All	6328	0	5614	65	2

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 6.

All (65) 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:397:ASP:HB3	4:B:510:EDO:H11	1.65	0.78
1:A:367:LYS:HG3	1:A:410:ILE:HD13	1.67	0.77
1:A:363:ALA:H	4:A:510:EDO:H12	1.48	0.77
1:A:275:LYS:NZ	4:A:523:EDO:H11	2.01	0.75
1:B:364:SER:HB3	1:B:367:LYS:HE2	1.68	0.74
1:B:294:SER:O	1:B:296:GLY:N	2.22	0.73
1:A:328:LEU:HD21	4:A:517:EDO:H12	1.71	0.72
1:A:273[B]:MET:HB2	5:A:524:T3K:C19	2.20	0.71
1:A:275:LYS:HZ3	4:A:523:EDO:H11	1.60	0.66
1:B:239[A]:LYS:NZ	6:B:607:HOH:O	2.29	0.66
1:A:100[B]:ASN:ND2	6:A:607:HOH:O	2.32	0.61
1:A:186:THR:HG22	4:A:519:EDO:H11	1.85	0.59
1:B:347:GLU:OE2	1:B:355:SER:OG	2.20	0.59
1:A:323:THR:HB	1:A:395:ILE:HG23	1.87	0.56
1:B:337[B]:MET:SD	1:B:365:VAL:HG22	2.44	0.56
1:B:275:LYS:HD3	4:B:513:EDO:H21	1.86	0.56
1:A:82:PHE:HB3	1:A:120[B]:VAL:HG23	1.88	0.56
1:A:179:PRO:HB2	4:A:520:EDO:H11	1.88	0.55
1:B:130:ASP:OD1	1:B:133:LYS:HE3	2.05	0.55
1:A:180:ALA:HB2	4:A:520:EDO:H21	1.91	0.53
1:B:321:ASN:HB2	1:B:322:PRO:HD3	1.91	0.52
1:A:396:LEU:O	1:A:400[B]:GLU:HG3	2.11	0.50
1:A:292:VAL:HG12	1:A:293:THR:O	2.12	0.50
1:A:328:LEU:CD2	4:A:517:EDO:H12	2.41	0.50
1:A:306:ARG:NH1	6:A:610:HOH:O	2.39	0.49
1:B:386[B]:ASP:OD2	6:B:601:HOH:O	2.20	0.49
1:A:239:LYS:HD3	1:B:221:LEU:HD21	1.95	0.49
1:A:342:ARG:NH1	6:A:603:HOH:O	2.27	0.49
1:A:105:HIS:CB	4:A:517:EDO:H11	2.42	0.48
1:A:254:LYS:HE2	1:A:254:LYS:HB2	1.65	0.48
1:A:273[B]:MET:HE2	5:A:524:T3K:C19	2.43	0.48
1:A:284:LYS:O	1:A:288:GLU:HG3	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:294:SER:C	1:B:296:GLY:H	2.22	0.47
1:B:357:MET:HE3	1:B:357:MET:HB2	1.76	0.47
1:A:105:HIS:ND1	1:A:108:ARG:NH1	2.61	0.47
4:A:521:EDO:C1	4:A:523:EDO:H12	2.44	0.47
1:B:254:LYS:O	1:B:258:GLN:HG3	2.14	0.47
1:B:356:PRO:O	1:B:357:MET:HB2	2.15	0.46
1:A:294:SER:N	6:A:618:HOH:O	2.46	0.46
1:A:342:ARG:HG3	6:A:839:HOH:O	2.16	0.46
1:B:313:MET:HB2	1:B:384:TRP:CH2	2.51	0.45
1:A:372:PHE:HA	4:A:518:EDO:H21	1.98	0.45
1:A:86:THR:HG23	1:A:89:GLU:HG2	1.99	0.44
1:B:293:THR:HG22	1:B:299[B]:LEU:HD21	2.01	0.43
1:B:344:GLY:HA3	1:B:358:CYS:O	2.18	0.43
1:B:282:ASP:OD1	4:B:507:EDO:H11	2.18	0.42
1:A:226[B]:SER:OG	6:A:601:HOH:O	2.21	0.42
1:B:255[A]:LYS:HG3	1:B:256:GLN:N	2.33	0.42
1:A:272:ASP:HB3	1:A:275:LYS:HD2	2.01	0.42
1:B:337[A]:MET:HA	1:B:337[A]:MET:HE3	2.01	0.42
1:B:390:PRO:HG3	4:B:512:EDO:H11	2.01	0.42
1:A:151:ASP:HB3	4:A:512:EDO:H22	2.02	0.42
1:A:255:LYS:H	1:A:255:LYS:HE2	1.85	0.42
1:B:273:MET:HB3	1:B:273:MET:HE3	1.75	0.41
1:A:121:ILE:HD12	1:A:166:ALA:HB1	2.02	0.41
1:B:291:LYS:HA	1:B:291:LYS:HD3	1.75	0.41
1:A:105:HIS:CG	4:A:517:EDO:H11	2.56	0.41
1:A:321:ASN:HB2	1:A:322:PRO:HD3	2.03	0.41
1:B:366:GLU:H	1:B:366:GLU:CD	2.29	0.41
1:A:116:ARG:O	1:A:120[B]:VAL:HG12	2.20	0.40
1:B:275:LYS:CD	4:B:513:EDO:H21	2.50	0.40
1:A:287:VAL:HG11	1:A:386[B]:ASP:HB3	2.04	0.40
4:B:508:EDO:O2	6:B:602:HOH:O	2.22	0.40

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:288:GLU:OE1	4:A:517:EDO:O2[3_645]	2.09	0.11
1:A:218[A]:GLU:OE2	1:B:367:LYS:NZ[3_555]	2.10	0.10

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	344/343 (100%)	339 (98%)	5 (2%)	0	100	100
1	B	336/343 (98%)	326 (97%)	7 (2%)	3 (1%)	14	3
All	All	680/686 (99%)	665 (98%)	12 (2%)	3 (0%)	24	12

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	295	SER
1	B	294	SER
1	B	293	THR

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	317/313 (101%)	316 (100%)	1 (0%)	86	75
1	B	309/313 (99%)	307 (99%)	2 (1%)	78	62
All	All	626/626 (100%)	623 (100%)	3 (0%)	86	66

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	86	THR
1	B	255[A]	LYS
1	B	255[B]	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	250	GLN
1	A	321	ASN
1	B	115	ASN
1	B	250	GLN
1	B	258	GLN
1	B	321	ASN
1	B	331	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](#)

Of 41 ligands modelled in this entry, 10 are monoatomic - leaving 31 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	517	-	3,3,3	0.27	0	2,2,2	0.71	0
4	EDO	A	519	-	3,3,3	0.40	0	2,2,2	0.52	0
4	EDO	B	506	-	3,3,3	0.41	0	2,2,2	0.48	0
4	EDO	A	515[A]	-	3,3,3	0.46	0	2,2,2	0.44	0
4	EDO	B	515	-	3,3,3	0.46	0	2,2,2	0.29	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	EDO	B	507	-	3,3,3	0.46	0	2,2,2	0.15	0
4	EDO	A	513	-	3,3,3	0.44	0	2,2,2	0.48	0
4	EDO	B	512	-	3,3,3	0.55	0	2,2,2	0.12	0
4	EDO	B	509	-	3,3,3	0.40	0	2,2,2	0.43	0
4	EDO	A	507	-	3,3,3	0.48	0	2,2,2	0.53	0
4	EDO	A	518	-	3,3,3	0.40	0	2,2,2	0.55	0
4	EDO	A	512	-	3,3,3	0.50	0	2,2,2	0.47	0
4	EDO	A	514	-	3,3,3	0.42	0	2,2,2	0.27	0
4	EDO	B	505	-	3,3,3	0.38	0	2,2,2	0.83	0
4	EDO	A	523	-	3,3,3	0.54	0	2,2,2	0.27	0
4	EDO	B	513	-	3,3,3	0.53	0	2,2,2	0.33	0
4	EDO	A	509	-	3,3,3	0.39	0	2,2,2	0.70	0
4	EDO	A	516	-	3,3,3	0.43	0	2,2,2	0.73	0
4	EDO	A	515[B]	-	3,3,3	0.50	0	2,2,2	0.31	0
4	EDO	A	522	-	3,3,3	0.50	0	2,2,2	0.29	0
4	EDO	B	514	-	3,3,3	0.45	0	2,2,2	0.44	0
5	T3K	A	524	-	30,30,30	2.09	8 (26%)	38,39,39	2.28	8 (21%)
4	EDO	B	510	-	3,3,3	0.48	0	2,2,2	0.34	0
4	EDO	A	508	-	3,3,3	0.41	0	2,2,2	0.47	0
4	EDO	A	520	-	3,3,3	0.48	0	2,2,2	0.28	0
4	EDO	A	511	-	3,3,3	0.45	0	2,2,2	0.71	0
4	EDO	B	511	-	3,3,3	0.49	0	2,2,2	0.51	0
4	EDO	A	510	-	3,3,3	0.43	0	2,2,2	0.37	0
5	T3K	B	516	-	30,30,30	2.00	7 (23%)	38,39,39	2.36	9 (23%)
4	EDO	B	508	-	3,3,3	0.49	0	2,2,2	0.46	0
4	EDO	A	521	-	3,3,3	0.55	0	2,2,2	0.14	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
4	EDO	A	517	-	-	0/1/1/1	-
4	EDO	A	519	-	-	0/1/1/1	-
4	EDO	B	506	-	-	0/1/1/1	-
4	EDO	A	515[A]	-	-	0/1/1/1	-
4	EDO	B	515	-	-	1/1/1/1	-
4	EDO	B	507	-	-	1/1/1/1	-
4	EDO	A	513	-	-	0/1/1/1	-
4	EDO	B	512	-	-	0/1/1/1	-
4	EDO	B	509	-	-	0/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	EDO	A	507	-	-	0/1/1/1	-
4	EDO	A	518	-	-	0/1/1/1	-
4	EDO	A	512	-	-	1/1/1/1	-
4	EDO	A	514	-	-	0/1/1/1	-
4	EDO	B	505	-	-	0/1/1/1	-
4	EDO	A	523	-	-	1/1/1/1	-
4	EDO	B	513	-	-	1/1/1/1	-
4	EDO	A	509	-	-	1/1/1/1	-
4	EDO	A	516	-	-	0/1/1/1	-
4	EDO	A	515[B]	-	-	0/1/1/1	-
4	EDO	A	522	-	-	1/1/1/1	-
4	EDO	B	514	-	-	1/1/1/1	-
5	T3K	A	524	-	-	8/21/36/36	0/3/3/3
4	EDO	B	510	-	-	0/1/1/1	-
4	EDO	A	508	-	-	0/1/1/1	-
4	EDO	A	520	-	-	0/1/1/1	-
4	EDO	A	511	-	-	0/1/1/1	-
4	EDO	B	511	-	-	0/1/1/1	-
4	EDO	A	510	-	-	1/1/1/1	-
5	T3K	B	516	-	-	4/21/36/36	0/3/3/3
4	EDO	B	508	-	-	0/1/1/1	-
4	EDO	A	521	-	-	1/1/1/1	-

All (15) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	516	T3K	C13-N15	5.82	1.46	1.35
5	A	524	T3K	C13-N15	5.25	1.45	1.35
5	A	524	T3K	C07-N09	-5.24	1.23	1.28
5	A	524	T3K	C26-C25	-3.81	1.36	1.51
5	B	516	T3K	C27-C28	-3.80	1.36	1.51
5	B	516	T3K	C26-C25	-3.76	1.36	1.51
5	A	524	T3K	C27-C28	-3.64	1.37	1.51
5	B	516	T3K	O02-C03	3.02	1.42	1.37
5	B	516	T3K	C06-C07	2.86	1.53	1.49
5	A	524	T3K	C27-C26	2.77	1.67	1.48
5	B	516	T3K	C27-C26	2.74	1.66	1.48
5	A	524	T3K	C20-N15	-2.74	1.42	1.47
5	A	524	T3K	O10-C11	-2.19	1.39	1.43
5	A	524	T3K	O10-N09	-2.14	1.38	1.42
5	B	516	T3K	O14-C13	-2.01	1.18	1.23

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	B	516	T3K	O10-N09-C07	8.83	125.33	111.94
5	A	524	T3K	C21-C06-C07	-7.04	110.83	120.53
5	A	524	T3K	O10-N09-C07	6.53	121.84	111.94
5	A	524	T3K	C11-O10-N09	-5.64	103.40	108.31
5	B	516	T3K	C05-C06-C07	5.38	127.66	121.27
5	B	516	T3K	C21-C06-C07	-5.02	113.61	120.53
5	A	524	T3K	C05-C06-C07	3.79	125.77	121.27
5	B	516	T3K	C12-C13-N15	3.66	123.64	118.09
5	A	524	T3K	C05-C06-C21	3.59	123.40	119.25
5	B	516	T3K	C22-O23-C24	-3.54	108.76	120.14
5	A	524	T3K	C22-O23-C24	-3.12	110.14	120.14
5	B	516	T3K	C19-C20-N15	3.11	116.36	109.82
5	A	524	T3K	C04-C05-C06	-2.81	117.80	120.80
5	B	516	T3K	O23-C22-C21	-2.75	117.69	123.87
5	B	516	T3K	C17-C16-N15	2.71	115.52	109.82
5	B	516	T3K	O14-C13-N15	-2.58	117.53	122.12
5	A	524	T3K	O10-C11-C12	-2.23	102.55	109.14

There are no chirality outliers.

All (22) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	524	T3K	C28-C24-O23-C22
5	A	524	T3K	C25-C24-O23-C22
5	A	524	T3K	C21-C06-C07-N09
5	A	524	T3K	C05-C06-C07-N09
5	A	524	T3K	C12-C11-O10-N09
5	B	516	T3K	C28-C24-O23-C22
5	B	516	T3K	C25-C24-O23-C22
5	B	516	T3K	O10-C11-C12-C13
5	A	524	T3K	C21-C06-C07-C08
5	A	524	T3K	C05-C06-C07-C08
4	A	510	EDO	O1-C1-C2-O2
4	A	521	EDO	O1-C1-C2-O2
5	B	516	T3K	C12-C11-O10-N09
4	A	522	EDO	O1-C1-C2-O2
4	A	523	EDO	O1-C1-C2-O2
4	B	513	EDO	O1-C1-C2-O2
4	B	514	EDO	O1-C1-C2-O2
4	B	515	EDO	O1-C1-C2-O2
5	A	524	T3K	C07-N09-O10-C11

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Mol	Chain	Res	Type	Atoms
4	A	512	EDO	O1-C1-C2-O2
4	B	507	EDO	O1-C1-C2-O2
4	A	509	EDO	O1-C1-C2-O2

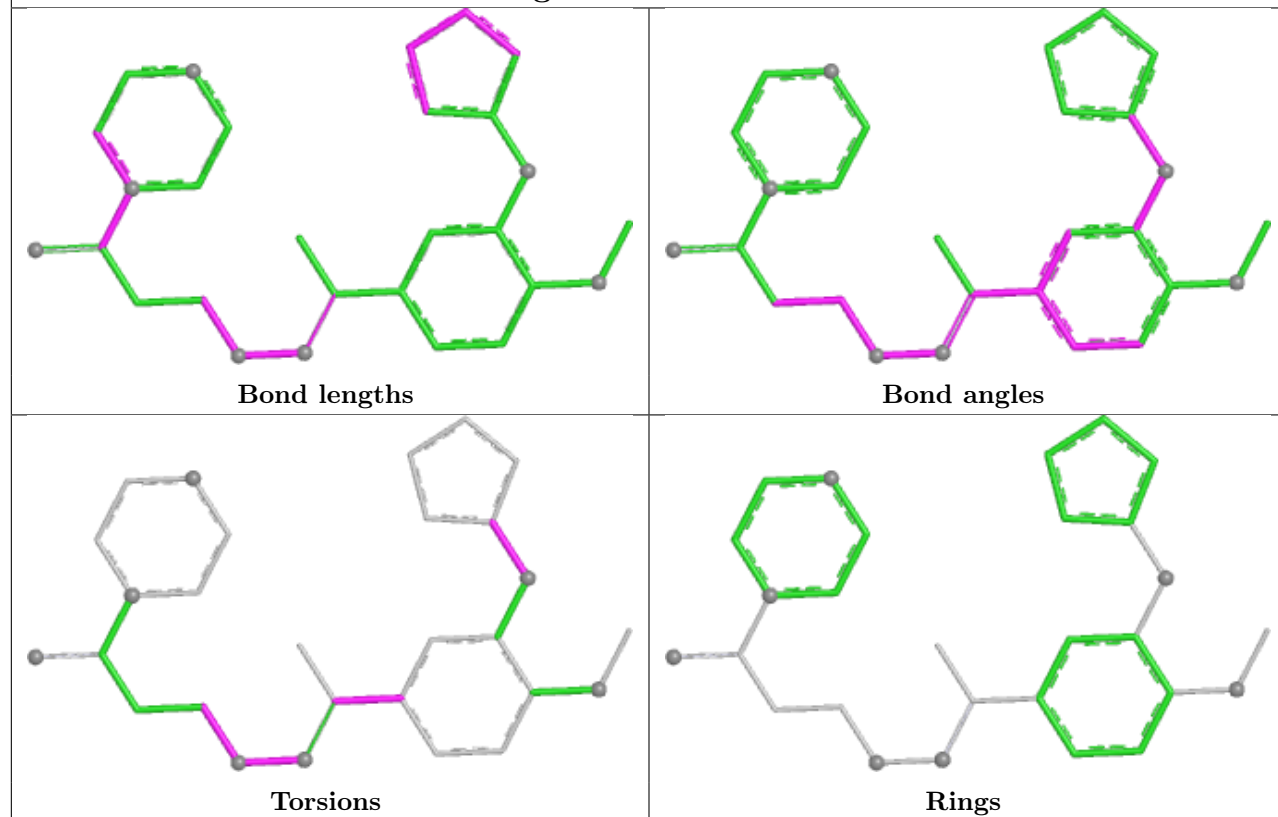
There are no ring outliers.

14 monomers are involved in 22 short contacts:

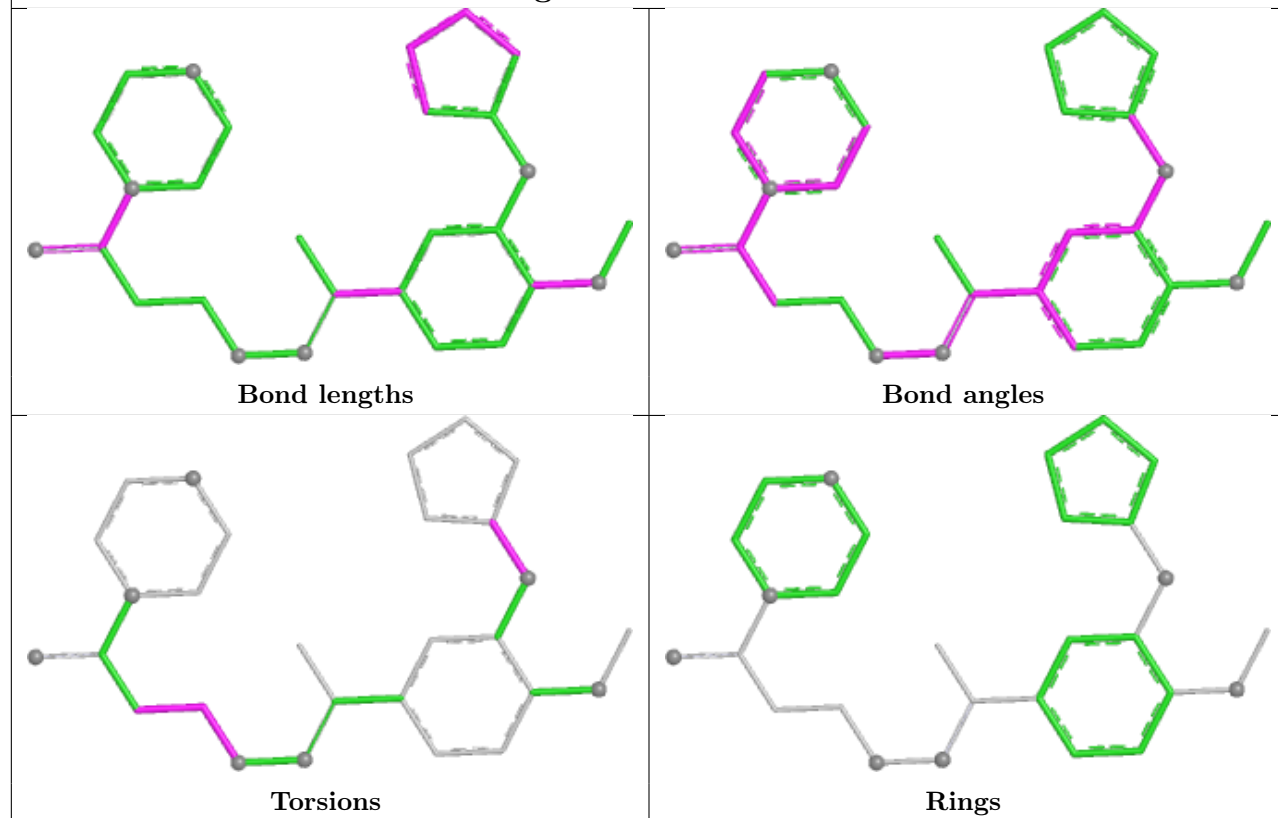
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	517	EDO	4	1
4	A	519	EDO	1	0
4	B	507	EDO	1	0
4	B	512	EDO	1	0
4	A	518	EDO	1	0
4	A	512	EDO	1	0
4	A	523	EDO	3	0
4	B	513	EDO	2	0
5	A	524	T3K	2	0
4	B	510	EDO	1	0
4	A	520	EDO	2	0
4	A	510	EDO	1	0
4	B	508	EDO	1	0
4	A	521	EDO	1	0

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 T3K A 524



Ligand T3K B 516



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	332/343 (96%)	0.34	20 (6%)	27 30	10, 22, 44, 94	14 (4%)
1	B	327/343 (95%)	0.62	27 (8%)	17 19	10, 25, 49, 73	11 (3%)
All	All	659/686 (96%)	0.48	47 (7%)	22 24	10, 23, 48, 94	25 (3%)

All (47) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	363	ALA	6.3
1	A	82	PHE	5.6
1	A	86	THR	5.0
1	A	80	PRO	4.5
1	B	91	VAL	4.3
1	A	84	VAL	4.2
1	B	294	SER	4.1
1	B	414	HIS	3.9
1	A	83	GLY	3.6
1	A	91	VAL	3.5
1	B	365	VAL	3.5
1	B	295	SER	3.4
1	B	299[A]	LEU	3.1
1	A	85	LYS	3.0
1	A	93	ALA	3.0
1	B	406[A]	TYR	3.0
1	A	411	PRO	2.9
1	A	294	SER	2.9
1	B	364	SER	2.9
1	B	362	ASN	2.8
1	B	88	GLN	2.7
1	B	296	GLY	2.7
1	A	88	GLN	2.7
1	A	87	GLU	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	90	ASP	2.6
1	B	93	ALA	2.6
1	A	105	HIS	2.5
1	B	112	LEU	2.5
1	B	94	LYS	2.5
1	A	375	TYR	2.5
1	B	293	THR	2.4
1	B	183	ALA	2.3
1	B	139	VAL	2.3
1	A	94	LYS	2.3
1	B	354	ILE	2.3
1	A	292	VAL	2.2
1	A	295	SER	2.2
1	A	404	GLU	2.2
1	B	90	ASP	2.2
1	B	375	TYR	2.2
1	B	155	ALA	2.1
1	A	293	THR	2.1
1	B	349	GLU	2.1
1	B	92	LEU	2.0
1	B	132	LEU	2.0
1	B	356	PRO	2.0
1	B	298	LEU	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.

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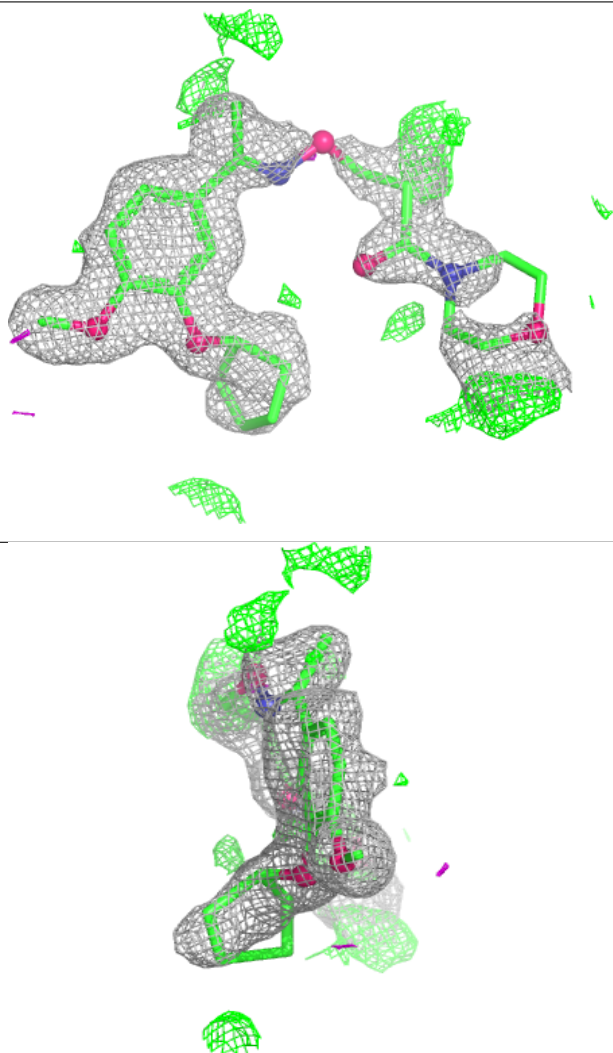
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	EDO	B	508	4/4	0.69	0.17	38,47,51,53	0
4	EDO	B	514	4/4	0.71	0.16	42,44,54,55	0
4	EDO	B	513	4/4	0.72	0.18	31,31,39,44	0
4	EDO	B	510	4/4	0.72	0.17	44,44,48,52	0
4	EDO	A	512	4/4	0.74	0.19	36,42,44,45	0
4	EDO	A	513	4/4	0.74	0.18	43,46,49,55	0
4	EDO	A	515[A]	4/4	0.74	0.19	29,30,31,32	4
4	EDO	A	515[B]	4/4	0.74	0.19	26,29,30,33	4
4	EDO	A	507	4/4	0.75	0.18	34,36,37,41	0
4	EDO	A	522	4/4	0.75	0.17	42,44,46,52	0
4	EDO	A	516	4/4	0.76	0.17	34,37,41,45	0
4	EDO	A	511	4/4	0.76	0.16	35,36,38,47	0
4	EDO	A	523	4/4	0.77	0.17	40,42,47,48	0
4	EDO	B	507	4/4	0.77	0.18	27,38,43,50	0
4	EDO	A	521	4/4	0.78	0.21	28,44,45,48	0
4	EDO	A	509	4/4	0.78	0.16	35,40,41,50	0
4	EDO	A	518	4/4	0.78	0.16	40,41,46,57	0
4	EDO	A	519	4/4	0.78	0.17	32,36,39,46	0
5	T3K	B	516	28/28	0.79	0.20	21,35,44,49	28
4	EDO	B	512	4/4	0.81	0.14	27,38,42,46	0
4	EDO	A	510	4/4	0.81	0.14	40,46,48,51	0
4	EDO	B	506	4/4	0.83	0.17	48,52,52,53	0
4	EDO	B	511	4/4	0.84	0.15	30,37,38,45	0
4	EDO	B	509	4/4	0.85	0.12	38,40,48,49	0
4	EDO	A	517	4/4	0.87	0.22	21,40,41,55	0
4	EDO	A	514	4/4	0.88	0.12	32,37,48,48	0
4	EDO	A	520	4/4	0.88	0.12	36,41,43,43	0
3	MG	B	503	1/1	0.88	0.12	41,41,41,41	0
5	T3K	A	524	28/28	0.90	0.13	20,27,31,33	27
3	MG	A	506	1/1	0.90	0.21	47,47,47,47	0
4	EDO	B	505	4/4	0.92	0.10	29,29,30,30	0
4	EDO	B	515	4/4	0.92	0.17	21,37,48,49	0
4	EDO	A	508	4/4	0.95	0.08	27,30,35,36	0
3	MG	B	504	1/1	0.95	0.14	37,37,37,37	0
3	MG	A	503	1/1	0.95	0.11	33,33,33,33	0
3	MG	A	504	1/1	0.96	0.06	39,39,39,39	0
3	MG	A	505	1/1	0.98	0.15	23,23,23,23	0
3	MG	A	502	1/1	1.00	0.03	11,11,11,11	0
2	ZN	A	501	1/1	1.00	0.03	16,16,16,16	0
3	MG	B	502	1/1	1.00	0.05	12,12,12,12	0
2	ZN	B	501	1/1	1.00	0.01	17,17,17,17	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.

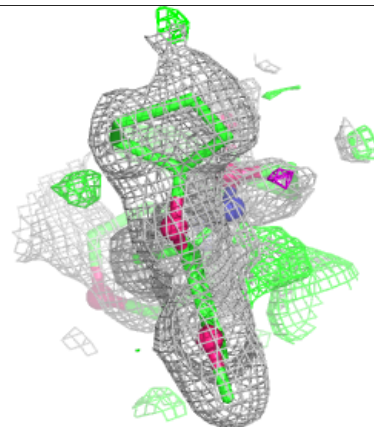
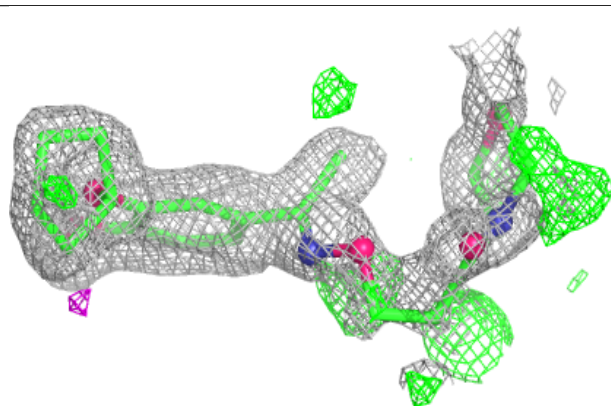
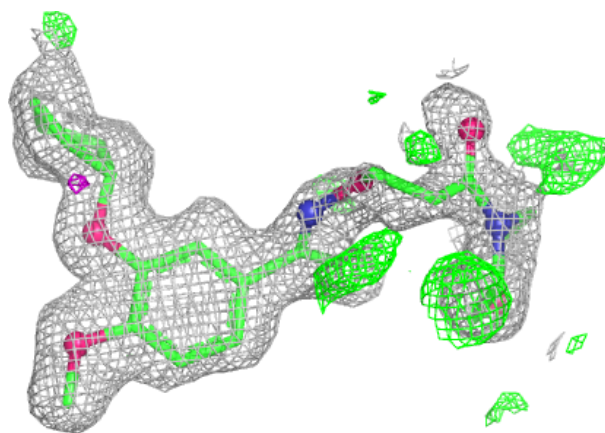
Electron density around T3K B 516:

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



Electron density around T3K A 524:

$2mF_o-DF_c$ (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.