



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 05:52 PM UTC

PDB ID : 6H12 / pdb_00006h12
Title : Crystal structure of TcACHE complexed to 1-(6-Oxo-1,2,3,4,6,10b-hexahydro pyrido[2,1-a]isoindol-10-yl)-3-(4-(((1-(2-((1,2,3,4-tetrahydroacridin-9-yl)amino)ethyl)-1H-1,2,3-triazol-4-yl)methoxy)methyl)pyridin-2-yl)urea
Authors : Coquelle, N.; Colletier, J.P.
Deposited on : 2018-07-10
Resolution : 2.20 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

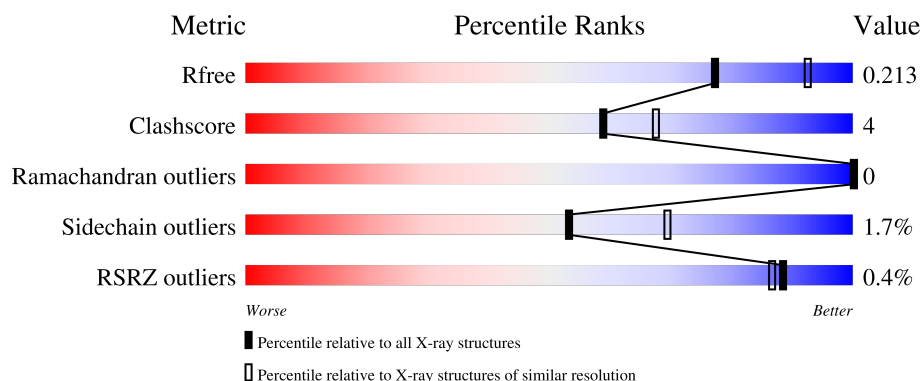
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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	6164 (2.20-2.20)
Clashscore	190562	6851 (2.20-2.20)
Ramachandran outliers	187476	6768 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)
RSRZ outliers	180081	6166 (2.20-2.20)

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	565	 85% 9% 6%
1	B	565	 87% 7% 6%

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
10	FJK	A	626	X	-	-	-
10	FJK	B	619	X	-	-	-
2	MES	A	611	-	-	X	-
7	PEG	B	613	-	-	X	-

2 Entry composition [i](#)

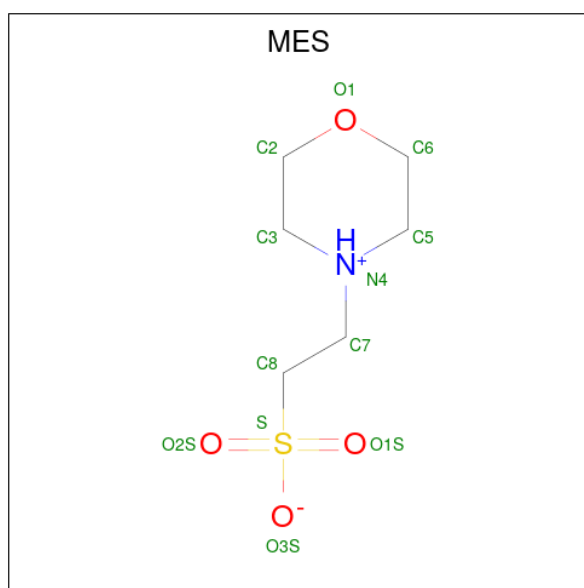
There are 11 unique types of molecules in this entry. The entry contains 9735 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Acetylcholinesterase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	532	Total	C	N	O	S	0	11	0
			4311	2765	736	788	22			
1	B	532	Total	C	N	O	S	0	9	0
			4295	2755	732	786	22			

- Molecule 2 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (CCD ID: MES) (formula: $C_6H_{13}NO_4S$).



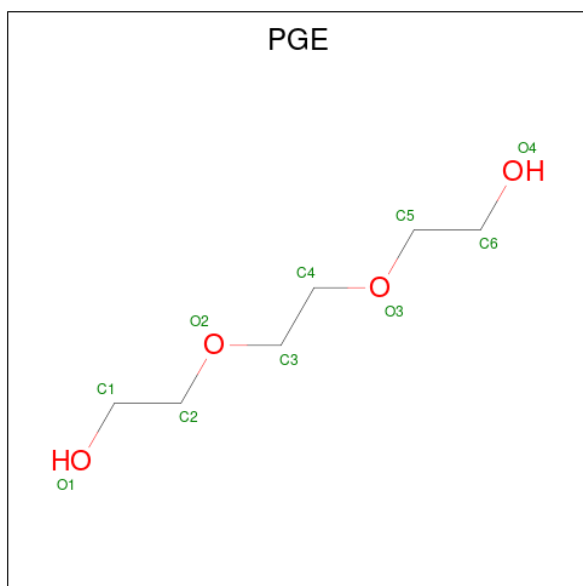
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	S	0	0
			12	6	1	4	1		
2	A	1	Total	C	N	O	S	0	0
			12	6	1	4	1		
2	A	1	Total	C	N	O	S	0	0
			12	6	1	4	1		
2	A	1	Total	C	N	O	S	0	0
			12	6	1	4	1		

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



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

- Molecule 4 is TRIETHYLENE GLYCOL (CCD ID: PGE) (formula: $C_6H_{14}O_4$).



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

- Molecule 5 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



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

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

- Molecule 6 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	O	S	0	0
			5	4	1		
6	A	1	Total	O	S	0	0
			5	4	1		
6	B	1	Total	O	S	0	0
			5	4	1		

- Molecule 7 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: C₄H₁₀O₃).



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

- Molecule 8 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).

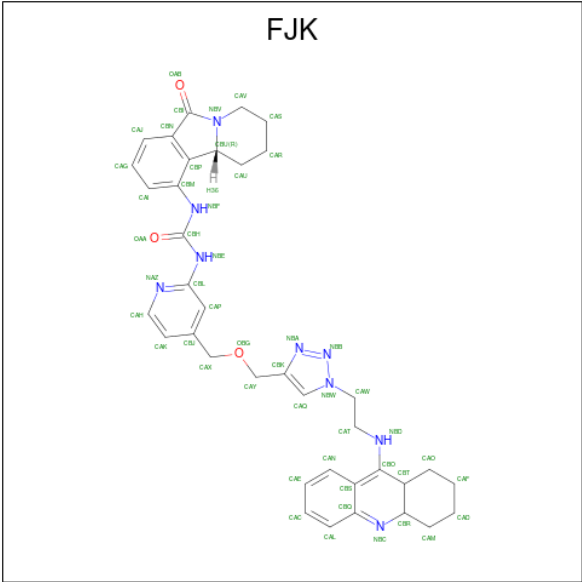


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
8	A	1	Total	C	N	O	0	0
			14	8	1	5		
8	A	1	Total	C	N	O	0	0
			14	8	1	5		
8	B	1	Total	C	N	O	0	0
			14	8	1	5		
8	B	1	Total	C	N	O	0	0
			14	8	1	5		
8	B	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 9 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	5	Total	Cl	0	0
			5	5		
9	B	1	Total	Cl	0	0
			1	1		

- Molecule 10 is 1-[4-[[1-[2-(1,2,3,4,4 {a},9 {a}-hexahydroacridin-9-ylamino)ethyl]-1,2,3-triazol-4-yl]methoxymethyl]pyridin-2-yl]-3-[(10 {b} {R})-6-oxidanylidene-2,3,4,10 {b}-tetrahydro-1 {H}-pyrido[2,1-a]isoindol-10-yl]urea (CCD ID: FJK) (formula: C₃₇H₄₁N₉O₃).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
10	A	1	Total	C	N	O	0	0
			49	37	9	3		
10	B	1	Total	C	N	O	0	0
			49	37	9	3		

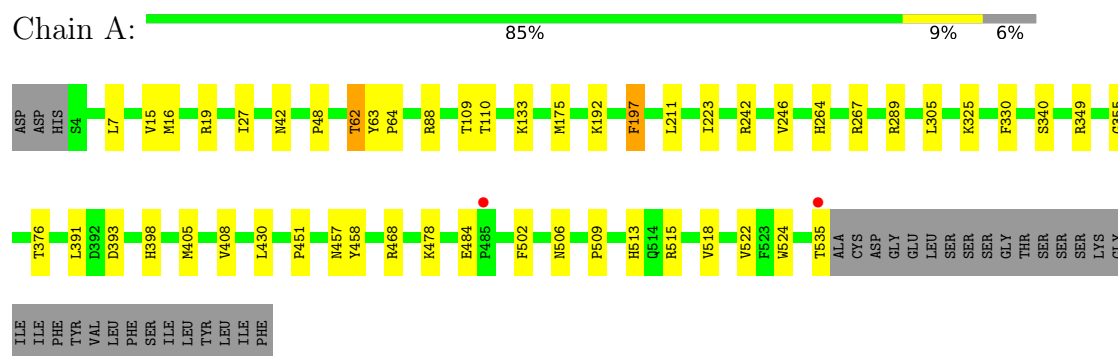
- Molecule 11 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
11	A	362	Total	O	0	0
			362	362		
11	B	384	Total	O	0	0
			384	384		

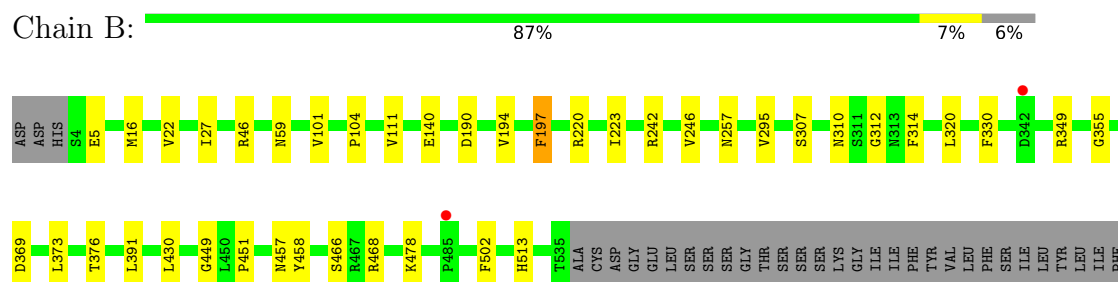
3 Residue-property plots [i](#)

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: Acetylcholinesterase



• Molecule 1: Acetylcholinesterase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	91.27Å 105.09Å 149.69Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.84 – 2.20 19.84 – 2.20	Depositor EDS
% Data completeness (in resolution range)	99.8 (19.84-2.20) 99.7 (19.84-2.20)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.68 (at 2.19Å)	Xtrriage
Refinement program	PHENIX (1.10.1_2155: ???)	Depositor
R, R_{free}	0.171 , 0.212 0.172 , 0.213	Depositor DCC
R_{free} test set	2000 reflections (2.72%)	wwPDB-VP
Wilson B-factor (Å ²)	27.4	Xtrriage
Anisotropy	0.628	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 48.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	9735	wwPDB-VP
Average B, all atoms (Å ²)	31.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 44.97 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.4139e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: CL, NAG, PEG, EDO, FJK, GOL, SO4, MES, PGE

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	0.30	0/4467	0.49	0/6061
1	B	0.32	0/4445	0.50	0/6033
All	All	0.31	0/8912	0.50	0/12094

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	4311	0	4192	42	0
1	B	4295	0	4165	32	0
2	A	48	0	49	15	0
3	A	12	0	15	2	0
3	B	6	0	8	2	0
4	A	10	0	12	0	0
4	B	10	0	14	0	0
5	A	24	0	36	3	0
5	B	28	0	42	7	0
6	A	10	0	0	0	0
6	B	5	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	A	28	0	38	2	0
7	B	28	0	36	11	0
8	A	28	0	26	0	0
8	B	42	0	39	0	0
9	A	5	0	0	0	0
9	B	1	0	0	0	0
10	A	49	0	0	1	0
10	B	49	0	0	0	0
11	A	362	0	0	3	0
11	B	384	0	0	7	0
All	All	9735	0	8672	78	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 (78) 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:A:398:HIS:HD1	5:A:610:EDO:H22	1.38	0.86
10:A:626:FJK:NBF	10:A:626:FJK:NAZ	2.17	0.85
1:A:242[A]:ARG:HH11	2:A:614:MES:H81	1.43	0.83
7:B:614:PEG:H12	11:B:735:HOH:O	1.79	0.83
1:B:242:ARG:HH11	7:B:611:PEG:H31	1.47	0.78
1:B:59:ASN:H	5:B:609:EDO:H11	1.49	0.77
1:A:478:LYS:HD2	2:A:611:MES:H32	1.69	0.74
1:A:478:LYS:HE3	2:A:611:MES:H72	1.71	0.71
1:A:267:ARG:HD2	2:A:601:MES:H21	1.75	0.67
1:B:373:LEU:HB2	5:B:607:EDO:H22	1.77	0.66
1:B:140:GLU:OE1	11:B:701:HOH:O	2.14	0.66
1:A:398:HIS:ND1	5:A:610:EDO:H22	2.10	0.65
1:B:310:ASN:HD22	7:B:613:PEG:H12	1.63	0.64
1:A:289:ARG:HE	3:A:609:GOL:H11	1.63	0.63
1:A:246:VAL:HG21	2:A:614:MES:H82	1.82	0.61
1:B:246:VAL:HG21	7:B:611:PEG:H41	1.82	0.60
1:A:349:ARG:NH2	1:A:376:THR:OG1	2.33	0.60
1:A:110:THR:OG1	2:A:611:MES:H71	2.03	0.59
1:A:242[A]:ARG:HG2	2:A:614:MES:H51	1.84	0.58
1:A:264:HIS:HA	2:A:601:MES:H22	1.86	0.57
1:A:62:THR:HG23	1:A:88[B]:ARG:NH2	2.21	0.56
1:A:506:ASN:HB2	3:A:602:GOL:H11	1.88	0.55
1:A:109:THR:HA	2:A:611:MES:H82	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:349:ARG:NH2	1:B:376:THR:OG1	2.37	0.55
1:A:393:ASP:OD1	7:A:615:PEG:H31	2.07	0.55
1:B:307:SER:HB3	7:B:613:PEG:H11	1.89	0.54
1:A:524:TRP:HB3	5:A:610:EDO:H21	1.89	0.53
1:B:369:ASP:HB3	5:B:607:EDO:H12	1.91	0.53
1:B:59:ASN:N	5:B:609:EDO:H11	2.21	0.52
1:A:63:TYR:HB2	1:A:88[B]:ARG:HE	1.74	0.52
1:A:451:PRO:HA	1:A:458:TYR:CD1	2.44	0.52
1:B:451:PRO:HA	1:B:458:TYR:CD2	2.45	0.52
1:A:48:PRO:HB2	1:A:175:MET:HE2	1.92	0.51
3:B:604:GOL:H31	11:B:894:HOH:O	2.10	0.51
1:A:64:PRO:O	1:A:88[B]:ARG:HG2	2.10	0.51
1:A:246:VAL:HG11	2:A:614:MES:H21	1.91	0.50
1:B:242:ARG:HD3	7:B:611:PEG:H42	1.93	0.50
1:B:197:PHE:HB3	1:B:223:ILE:HB	1.94	0.49
1:A:110:THR:HB	2:A:611:MES:H31	1.94	0.49
1:A:42:ASN:HB3	2:A:601:MES:H51	1.95	0.49
1:B:190:ASP:OD2	3:B:604:GOL:H12	2.12	0.49
1:A:468[A]:ARG:NH1	11:A:701:HOH:O	2.17	0.49
1:A:478:LYS:NZ	2:A:611:MES:H52	2.28	0.48
1:B:59:ASN:H	5:B:609:EDO:C1	2.23	0.48
1:A:355:GLY:HA3	1:A:391:LEU:HD21	1.95	0.48
1:B:5:GLU:OE2	1:B:104:PRO:HA	2.14	0.48
1:B:355:GLY:HA3	1:B:391:LEU:HD21	1.95	0.48
1:B:478:LYS:NZ	5:B:603:EDO:H22	2.28	0.48
1:A:325:LYS:HG3	7:A:615:PEG:H12	1.95	0.48
1:A:211:LEU:HD13	1:A:305:LEU:HD22	1.96	0.47
1:A:7:LEU:HD13	1:A:16:MET:HE2	1.96	0.47
1:A:502:PHE:CZ	1:A:513:HIS:HB2	2.50	0.47
1:B:220:ARG:NH1	11:B:714:HOH:O	2.38	0.47
1:B:468[A]:ARG:NH2	11:B:708:HOH:O	2.33	0.47
5:B:606:EDO:O1	7:B:614:PEG:H22	2.15	0.46
1:A:457:ASN:ND2	11:A:724:HOH:O	2.48	0.46
1:A:509:PRO:HG2	1:B:46[B]:ARG:NH1	2.31	0.46
1:B:502:PHE:CZ	1:B:513:HIS:HB2	2.49	0.46
1:A:518:VAL:O	1:A:522:VAL:HG23	2.15	0.45
1:A:197:PHE:HB3	1:A:223:ILE:HB	1.99	0.45
1:A:110:THR:CB	2:A:611:MES:H31	2.45	0.44
1:B:27:ILE:HG12	1:B:101:VAL:O	2.17	0.44
1:B:197:PHE:CB	1:B:223:ILE:HB	2.48	0.44
1:B:310:ASN:ND2	7:B:613:PEG:H12	2.32	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:257:ASN:ND2	11:B:704:HOH:O	2.30	0.43
1:A:515:ARG:HB3	1:A:518:VAL:HB	2.00	0.43
1:B:223:ILE:HA	1:B:320:LEU:O	2.18	0.43
1:A:197:PHE:CB	1:A:223:ILE:HB	2.49	0.42
1:B:111:VAL:HB	1:B:194:VAL:HG22	2.02	0.42
1:A:19[A]:ARG:NH1	11:A:704:HOH:O	2.27	0.42
1:B:307:SER:HA	7:B:613:PEG:H11	2.01	0.42
1:A:27:ILE:HD11	1:A:133:LYS:HB2	2.01	0.41
1:B:307:SER:CB	7:B:613:PEG:H11	2.49	0.41
7:B:613:PEG:H22	11:B:898:HOH:O	2.21	0.41
1:B:449:GLY:HA2	1:B:466:SER:OG	2.21	0.41
1:A:242[A]:ARG:NH1	2:A:614:MES:H81	2.23	0.41
1:B:312:GLY:HA2	1:B:314:PHE:CE2	2.55	0.41
1:A:405:MET:HA	1:A:408:VAL:HG12	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	541/565 (96%)	521 (96%)	20 (4%)	0	100	100
1	B	539/565 (95%)	519 (96%)	20 (4%)	0	100	100
All	All	1080/1130 (96%)	1040 (96%)	40 (4%)	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	475/494 (96%)	465 (98%)	10 (2%)	47	63
1	B	472/494 (96%)	465 (98%)	7 (2%)	57	73
All	All	947/988 (96%)	930 (98%)	17 (2%)	53	68

All (17) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	15[A]	VAL
1	A	15[B]	VAL
1	A	62	THR
1	A	192	LYS
1	A	197	PHE
1	A	330	PHE
1	A	340	SER
1	A	430	LEU
1	A	484	GLU
1	A	535	THR
1	B	16	MET
1	B	22	VAL
1	B	197	PHE
1	B	295	VAL
1	B	330	PHE
1	B	430	LEU
1	B	457	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	310	ASN
1	B	525	ASN

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 46 ligands modelled in this entry, 6 are monoatomic - leaving 40 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	$\# Z > 2$
10	FJK	B	619	-	53,56,56	5.99	22 (41%)	62,79,79	2.56	22 (35%)
5	EDO	A	610	-	3,3,3	0.47	0	2,2,2	0.40	0
7	PEG	A	618	-	6,6,6	0.63	0	5,5,5	0.26	0
6	SO4	B	608	-	4,4,4	0.30	0	6,6,6	0.10	0
5	EDO	A	605	-	3,3,3	0.40	0	2,2,2	0.70	0
4	PGE	B	605	-	9,9,9	0.39	0	8,8,8	0.28	0
5	EDO	A	606	-	3,3,3	0.48	0	2,2,2	0.16	0
7	PEG	B	613	-	6,6,6	0.58	0	5,5,5	0.35	0
8	NAG	A	619	1	14,14,15	0.45	0	17,19,21	0.77	1 (5%)
5	EDO	A	604	-	3,3,3	0.53	0	2,2,2	0.26	0
5	EDO	B	606	-	3,3,3	0.36	0	2,2,2	0.44	0
5	EDO	B	603	-	3,3,3	0.40	0	2,2,2	0.54	0
7	PEG	A	616	-	6,6,6	0.56	0	5,5,5	0.20	0
5	EDO	B	601	-	3,3,3	0.40	0	2,2,2	0.40	0
8	NAG	B	616	1	14,14,15	0.40	0	17,19,21	0.58	0
7	PEG	B	611	-	6,6,6	0.63	0	5,5,5	0.74	0
6	SO4	A	613	-	4,4,4	0.29	0	6,6,6	0.08	0
7	PEG	B	614	-	6,6,6	0.63	0	5,5,5	0.41	0
5	EDO	A	607	-	3,3,3	0.41	0	2,2,2	0.42	0
2	MES	A	601	-	12,12,12	2.27	1 (8%)	15,16,16	1.68	4 (26%)
3	GOL	A	609	-	5,5,5	0.46	0	5,5,5	0.87	0
7	PEG	A	617	-	6,6,6	0.62	0	5,5,5	0.32	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	GOL	A	602	-	5,5,5	0.29	0	5,5,5	0.68	0
10	FJK	A	626	-	53,56,56	6.03	25 (47%)	62,79,79	2.86	25 (40%)
4	PGE	A	603	-	9,9,9	0.38	0	8,8,8	0.38	0
5	EDO	B	602	-	3,3,3	0.59	0	2,2,2	0.04	0
5	EDO	B	609	-	3,3,3	0.32	0	2,2,2	0.71	0
7	PEG	B	612	-	6,6,6	0.60	0	5,5,5	0.35	0
7	PEG	A	615	-	6,6,6	0.66	0	5,5,5	0.85	0
2	MES	A	611	-	12,12,12	1.97	1 (8%)	15,16,16	1.83	2 (13%)
3	GOL	B	604	-	5,5,5	0.27	0	5,5,5	0.86	0
2	MES	A	614	-	12,12,12	2.30	1 (8%)	15,16,16	2.04	4 (26%)
8	NAG	B	617	-	14,14,15	0.69	1 (7%)	17,19,21	0.68	1 (5%)
5	EDO	B	607	-	3,3,3	0.44	0	2,2,2	0.20	0
6	SO4	A	627	-	4,4,4	0.25	0	6,6,6	0.25	0
8	NAG	B	615	1	14,14,15	0.76	1 (7%)	17,19,21	0.70	1 (5%)
5	EDO	A	608	-	3,3,3	0.41	0	2,2,2	0.63	0
8	NAG	A	620	1	14,14,15	0.43	0	17,19,21	0.59	0
2	MES	A	612	-	12,12,12	2.39	1 (8%)	15,16,16	1.83	1 (6%)
5	EDO	B	610	-	3,3,3	0.39	0	2,2,2	0.88	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
10	FJK	B	619	-	2/2/7/10	6/20/66/66	0/7/8/8
5	EDO	A	610	-	-	1/1/1/1	-
7	PEG	A	618	-	-	1/4/4/4	-
5	EDO	A	605	-	-	1/1/1/1	-
4	PGE	B	605	-	-	4/7/7/7	-
5	EDO	A	606	-	-	0/1/1/1	-
7	PEG	B	613	-	-	1/4/4/4	-
8	NAG	A	619	1	-	2/6/23/26	0/1/1/1
5	EDO	A	604	-	-	0/1/1/1	-
5	EDO	B	606	-	-	0/1/1/1	-
5	EDO	B	603	-	-	0/1/1/1	-
7	PEG	A	616	-	-	3/4/4/4	-
5	EDO	B	601	-	-	1/1/1/1	-
8	NAG	B	616	1	-	0/6/23/26	0/1/1/1
7	PEG	B	611	-	-	1/4/4/4	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	PEG	B	614	-	-	3/4/4/4	-
5	EDO	A	607	-	-	1/1/1/1	-
2	MES	A	601	-	-	5/6/14/14	0/1/1/1
3	GOL	A	609	-	-	3/4/4/4	-
10	FJK	A	626	-	2/2/7/10	3/20/66/66	0/7/8/8
3	GOL	A	602	-	-	4/4/4/4	-
7	PEG	A	617	-	-	2/4/4/4	-
4	PGE	A	603	-	-	4/7/7/7	-
5	EDO	B	602	-	-	0/1/1/1	-
5	EDO	B	609	-	-	0/1/1/1	-
7	PEG	B	612	-	-	1/4/4/4	-
7	PEG	A	615	-	-	3/4/4/4	-
2	MES	A	611	-	-	3/6/14/14	0/1/1/1
3	GOL	B	604	-	-	0/4/4/4	-
2	MES	A	614	-	-	3/6/14/14	0/1/1/1
8	NAG	B	617	-	-	2/6/23/26	0/1/1/1
5	EDO	B	607	-	-	0/1/1/1	-
8	NAG	B	615	1	-	2/6/23/26	0/1/1/1
5	EDO	A	608	-	-	1/1/1/1	-
8	NAG	A	620	1	-	0/6/23/26	0/1/1/1
2	MES	A	612	-	-	4/6/14/14	0/1/1/1
5	EDO	B	610	-	-	1/1/1/1	-

All (53) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
10	A	626	FJK	CAO-CBT	-20.79	1.15	1.53
10	B	619	FJK	CAO-CBT	-20.67	1.15	1.53
10	B	619	FJK	CAM-CBR	-17.59	1.16	1.53
10	A	626	FJK	CAM-CBR	-16.79	1.18	1.53
10	B	619	FJK	CBT-CBR	-14.94	1.35	1.53
10	A	626	FJK	CBT-CBR	-14.78	1.35	1.53
10	B	619	FJK	CAF-CAO	-14.47	1.16	1.53
10	A	626	FJK	CAF-CAO	-14.09	1.17	1.53
10	B	619	FJK	CAD-CAM	-13.79	1.18	1.53
10	A	626	FJK	CAD-CAM	-13.76	1.18	1.53
10	A	626	FJK	CBN-CBI	-9.27	1.34	1.48
10	B	619	FJK	CBN-CBI	-9.25	1.34	1.48
10	B	619	FJK	CBR-NBC	-8.91	1.35	1.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
10	B	619	FJK	CAF-CAD	-8.89	1.19	1.51
10	A	626	FJK	CAF-CAD	-8.70	1.19	1.51
10	A	626	FJK	CBR-NBC	-8.66	1.35	1.47
2	A	612	MES	C8-S	-8.00	1.66	1.77
2	A	614	MES	C8-S	-7.66	1.66	1.77
2	A	601	MES	C8-S	-7.56	1.67	1.77
10	B	619	FJK	CBT-CBO	-7.38	1.40	1.50
10	A	626	FJK	CBQ-NBC	7.03	1.35	1.29
10	B	619	FJK	CBQ-NBC	6.78	1.35	1.29
10	A	626	FJK	CBT-CBO	-6.74	1.40	1.50
2	A	611	MES	C8-S	-6.57	1.68	1.77
10	A	626	FJK	CBP-CBU	-6.17	1.40	1.51
10	A	626	FJK	CAX-CBJ	-5.20	1.38	1.50
10	A	626	FJK	CBU-NBV	-5.07	1.40	1.47
10	B	619	FJK	CAX-CBJ	-5.04	1.38	1.50
10	A	626	FJK	CBN-CBP	-4.98	1.32	1.39
10	A	626	FJK	CBM-CBP	-4.83	1.32	1.39
10	B	619	FJK	CBM-NBF	-4.61	1.32	1.41
10	A	626	FJK	CBM-NBF	-4.59	1.32	1.41
10	B	619	FJK	CBP-CBU	-4.49	1.43	1.51
10	A	626	FJK	NBW-NBB	-4.47	1.27	1.34
10	B	619	FJK	CAJ-CBN	-4.26	1.33	1.39
10	B	619	FJK	CBO-CBS	3.83	1.41	1.36
10	A	626	FJK	CBI-NBV	-3.79	1.32	1.36
10	B	619	FJK	CBI-NBV	-3.65	1.32	1.36
10	A	626	FJK	CAJ-CBN	-3.59	1.34	1.39
10	B	619	FJK	CAY-CBK	3.42	1.55	1.49
10	A	626	FJK	NBA-NBB	-3.42	1.26	1.32
10	A	626	FJK	CBO-CBS	3.40	1.41	1.36
10	B	619	FJK	NBA-NBB	-3.26	1.26	1.32
10	B	619	FJK	CAH-NAZ	3.19	1.41	1.34
10	A	626	FJK	CAH-NAZ	3.00	1.40	1.34
10	B	619	FJK	CBN-CBP	-2.92	1.35	1.39
10	A	626	FJK	CBL-NBE	-2.92	1.33	1.40
10	B	619	FJK	CBM-CBP	-2.66	1.36	1.39
10	B	619	FJK	CBL-NBE	-2.58	1.34	1.40
10	A	626	FJK	CAY-CBK	2.47	1.53	1.49
10	A	626	FJK	CAQ-CBK	-2.39	1.32	1.36
8	B	615	NAG	O5-C1	2.38	1.47	1.43
8	B	617	NAG	O5-C1	2.16	1.47	1.43

All (61) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	A	626	FJK	CBN-CBI-NBV	10.40	113.04	106.42
10	B	619	FJK	CBN-CBI-NBV	7.32	111.08	106.42
10	A	626	FJK	CBL-NBE-CBH	-7.18	116.51	129.91
10	A	626	FJK	CAV-NBV-CBI	6.77	134.69	124.50
10	A	626	FJK	CAX-OBG-CAY	-5.68	105.86	112.36
10	B	619	FJK	CAM-CBR-NBC	5.53	121.46	110.47
10	B	619	FJK	CAV-NBV-CBI	5.53	132.82	124.50
10	A	626	FJK	CAM-CBR-NBC	5.48	121.37	110.47
10	B	619	FJK	CAX-OBG-CAY	5.27	118.39	112.36
10	B	619	FJK	CBM-NBF-CBH	-5.21	113.20	125.34
10	A	626	FJK	CBU-NBV-CBI	-5.19	105.83	112.86
2	A	612	MES	C5-N4-C3	5.17	119.97	108.84
10	B	619	FJK	CBL-NBE-CBH	-5.14	120.31	129.91
2	A	614	MES	C5-N4-C3	4.90	119.40	108.84
10	A	626	FJK	CAO-CBT-CBO	4.77	122.83	112.04
10	A	626	FJK	OAB-CBI-NBV	-4.74	121.57	125.34
10	B	619	FJK	CAO-CBT-CBO	4.55	122.32	112.04
10	A	626	FJK	CBP-CBM-NBF	-4.39	109.83	119.89
2	A	611	MES	C5-N4-C3	4.14	117.75	108.84
10	B	619	FJK	CBU-NBV-CBI	-4.01	107.43	112.86
10	B	619	FJK	CAW-NBW-NBB	3.82	128.46	120.78
10	B	619	FJK	CAK-CAH-NAZ	-3.50	119.69	123.97
2	A	614	MES	O2S-S-C8	3.47	111.98	106.73
10	B	619	FJK	NBE-CBL-NAZ	3.46	125.26	114.87
10	B	619	FJK	NBW-NBB-NBA	3.44	110.11	107.02
2	A	601	MES	C5-N4-C3	3.38	116.12	108.84
10	A	626	FJK	CAK-CAH-NAZ	-3.35	119.87	123.97
10	A	626	FJK	NBW-NBB-NBA	3.32	110.01	107.02
2	A	611	MES	O3S-S-C8	3.27	112.41	106.00
10	B	619	FJK	CAW-NBW-CAQ	-3.16	122.94	128.83
10	B	619	FJK	CBJ-CAP-CBL	3.02	120.73	118.14
10	A	626	FJK	CAY-CBK-CAQ	-2.76	125.45	130.22
10	B	619	FJK	CAP-CBL-NBE	-2.76	115.13	122.53
10	A	626	FJK	CBP-CBU-NBV	2.69	104.76	102.08
10	B	619	FJK	NBF-CBH-NBE	2.66	117.58	112.44
10	A	626	FJK	CAT-CAW-NBW	-2.60	107.35	111.61
10	B	619	FJK	CAH-NAZ-CBL	2.58	120.90	117.21
10	A	626	FJK	CAJ-CBN-CBI	2.58	133.91	129.59
10	A	626	FJK	CAH-NAZ-CBL	2.57	120.88	117.21
10	B	619	FJK	CAP-CBL-NAZ	-2.56	119.56	122.92
10	B	619	FJK	CAS-CAV-NBV	-2.56	106.69	110.65
10	A	626	FJK	CBJ-CAP-CBL	2.54	120.32	118.14
10	A	626	FJK	CAY-CBK-NBA	2.52	125.66	121.49

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	A	626	FJK	CAI-CBM-NBF	2.49	127.58	121.82
10	A	626	FJK	NBE-CBL-NAZ	2.46	122.25	114.87
10	A	626	FJK	CAW-NBW-NBB	2.45	125.69	120.78
8	A	619	NAG	C1-O5-C5	2.44	115.45	112.19
2	A	614	MES	C7-N4-C5	2.42	117.68	111.24
2	A	601	MES	C6-C5-N4	-2.41	106.46	110.12
10	A	626	FJK	CAW-NBW-CAQ	-2.41	124.34	128.83
10	A	626	FJK	CAP-CBL-NAZ	-2.39	119.78	122.92
10	B	619	FJK	OAA-CBH-NBF	-2.36	119.45	123.64
2	A	614	MES	C7-N4-C3	2.31	117.39	111.24
2	A	601	MES	O2S-S-C8	2.30	110.20	106.73
8	B	617	NAG	C1-O5-C5	2.21	115.15	112.19
10	B	619	FJK	CAQ-NBW-NBB	-2.21	108.61	110.75
2	A	601	MES	O3S-S-C8	2.17	110.25	106.00
10	B	619	FJK	CAF-CAD-CAM	2.17	115.87	111.42
8	B	615	NAG	C1-O5-C5	2.16	115.08	112.19
10	A	626	FJK	CAF-CAD-CAM	2.10	115.73	111.42
10	A	626	FJK	CAD-CAM-CBR	2.08	114.69	111.29

All (4) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
10	A	626	FJK	CBT
10	A	626	FJK	CBR
10	B	619	FJK	CBT
10	B	619	FJK	CBR

All (66) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	601	MES	C8-C7-N4-C5
2	A	611	MES	C7-C8-S-O1S
2	A	611	MES	C7-C8-S-O3S
2	A	612	MES	C8-C7-N4-C5
2	A	612	MES	C7-C8-S-O2S
2	A	612	MES	C7-C8-S-O3S
2	A	614	MES	N4-C7-C8-S
3	A	602	GOL	O1-C1-C2-O2
3	A	602	GOL	O1-C1-C2-C3
3	A	602	GOL	C1-C2-C3-O3
3	A	609	GOL	C1-C2-C3-O3
10	A	626	FJK	CBT-CBO-NBD-CAT

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Mol	Chain	Res	Type	Atoms
10	B	619	FJK	CBK-CAY-OBG-CAX
10	B	619	FJK	CBT-CBO-NBD-CAT
8	B	617	NAG	O5-C5-C6-O6
10	A	626	FJK	NBD-CAT-CAW-NBW
10	B	619	FJK	NBD-CAT-CAW-NBW
4	A	603	PGE	O2-C3-C4-O3
8	B	617	NAG	C4-C5-C6-O6
8	A	619	NAG	C8-C7-N2-C2
8	A	619	NAG	O7-C7-N2-C2
8	B	615	NAG	C8-C7-N2-C2
8	B	615	NAG	O7-C7-N2-C2
7	B	613	PEG	O2-C3-C4-O4
7	B	614	PEG	O1-C1-C2-O2
4	B	605	PGE	O3-C5-C6-O4
3	A	609	GOL	O1-C1-C2-C3
7	A	615	PEG	O1-C1-C2-O2
3	A	609	GOL	O2-C2-C3-O3
4	A	603	PGE	O3-C5-C6-O4
7	B	612	PEG	O2-C3-C4-O4
7	A	616	PEG	O2-C3-C4-O4
7	A	617	PEG	O1-C1-C2-O2
7	A	618	PEG	O2-C3-C4-O4
3	A	602	GOL	O2-C2-C3-O3
5	B	601	EDO	O1-C1-C2-O2
2	A	614	MES	C8-C7-N4-C3
2	A	614	MES	C8-C7-N4-C5
10	B	619	FJK	CBJ-CAX-OBG-CAY
10	B	619	FJK	CAI-CBM-NBF-CBH
2	A	601	MES	C7-C8-S-O3S
5	A	607	EDO	O1-C1-C2-O2
10	B	619	FJK	CBP-CBM-NBF-CBH
2	A	601	MES	C7-C8-S-O1S
2	A	601	MES	C7-C8-S-O2S
2	A	611	MES	C7-C8-S-O2S
2	A	612	MES	C7-C8-S-O1S
7	B	611	PEG	O1-C1-C2-O2
7	A	616	PEG	C4-C3-O2-C2
4	B	605	PGE	C3-C4-O3-C5
4	A	603	PGE	C3-C4-O3-C5
4	B	605	PGE	O2-C3-C4-O3
4	A	603	PGE	C6-C5-O3-C4
7	A	615	PEG	O2-C3-C4-O4

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Mol	Chain	Res	Type	Atoms
2	A	601	MES	C8-C7-N4-C3
7	B	614	PEG	C1-C2-O2-C3
7	B	614	PEG	C4-C3-O2-C2
10	A	626	FJK	CBS-CBO-NBD-CAT
4	B	605	PGE	C4-C3-O2-C2
7	A	616	PEG	O1-C1-C2-O2
7	A	615	PEG	C1-C2-O2-C3
5	B	610	EDO	O1-C1-C2-O2
5	A	610	EDO	O1-C1-C2-O2
5	A	605	EDO	O1-C1-C2-O2
5	A	608	EDO	O1-C1-C2-O2
7	A	617	PEG	O2-C3-C4-O4

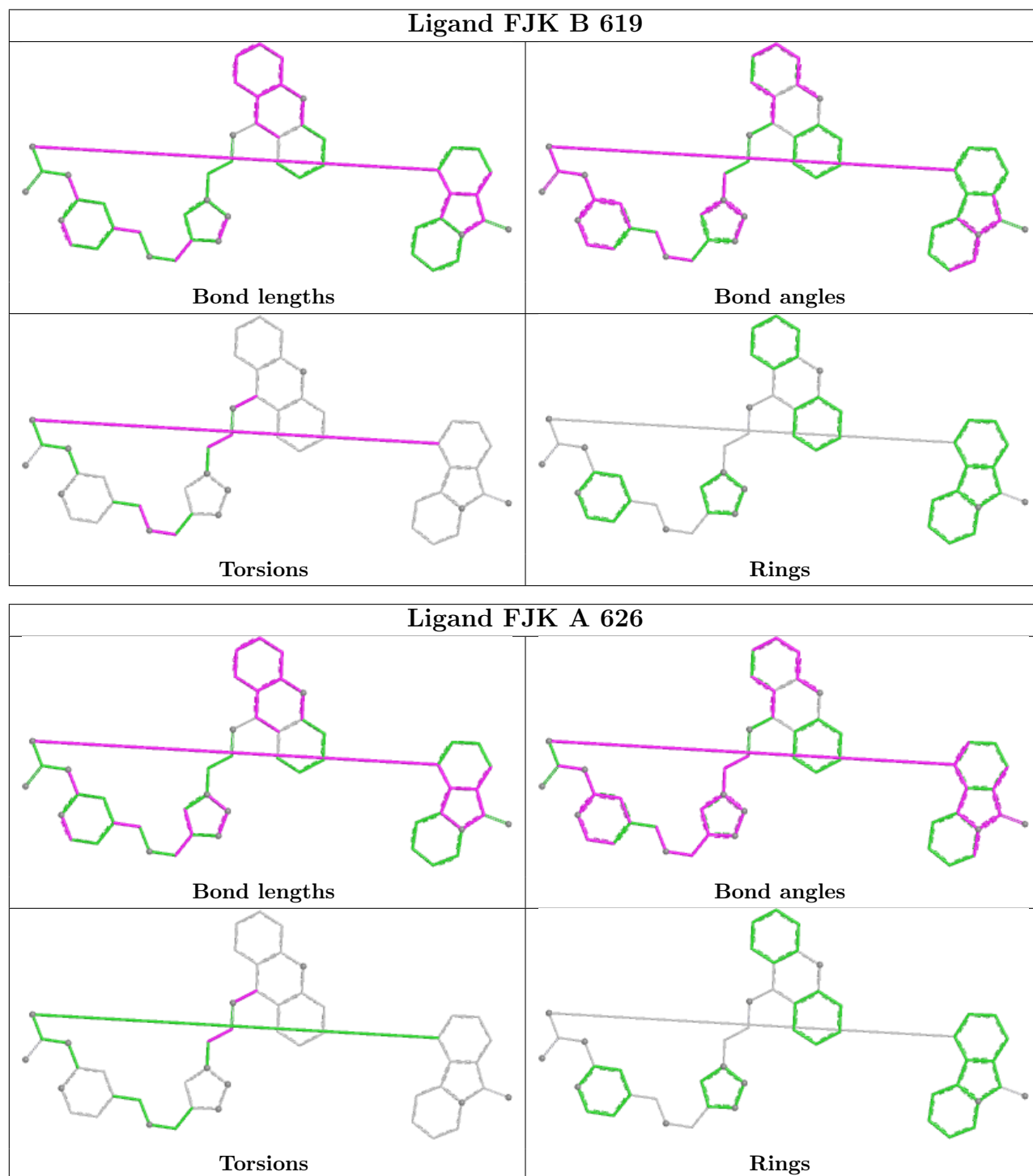
There are no ring outliers.

16 monomers are involved in 42 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	610	EDO	3	0
7	B	613	PEG	6	0
5	B	606	EDO	1	0
5	B	603	EDO	1	0
7	B	611	PEG	3	0
7	B	614	PEG	2	0
2	A	601	MES	3	0
3	A	609	GOL	1	0
3	A	602	GOL	1	0
10	A	626	FJK	1	0
5	B	609	EDO	3	0
7	A	615	PEG	2	0
2	A	611	MES	7	0
3	B	604	GOL	2	0
2	A	614	MES	5	0
5	B	607	EDO	2	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 ⓘ

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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	532/565 (94%)	-0.59	2 (0%) 88 87	15, 28, 46, 80	13 (2%)
1	B	532/565 (94%)	-0.63	2 (0%) 88 87	16, 27, 45, 88	12 (2%)
All	All	1064/1130 (94%)	-0.61	4 (0%) 88 87	15, 27, 46, 88	25 (2%)

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	535	THR	3.5
1	B	485	PRO	3.3
1	A	485	PRO	2.5
1	B	342	ASP	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
8	NAG	B	617	14/15	0.62	0.15	55,68,72,73	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	PGE	A	603	10/10	0.63	0.17	52,58,63,67	0
7	PEG	B	614	7/7	0.64	0.17	46,52,58,59	0
5	EDO	B	602	4/4	0.70	0.18	48,50,52,54	0
10	FJK	B	619	49/49	0.71	0.20	21,44,58,62	49
5	EDO	A	604	4/4	0.72	0.16	48,49,51,53	0
8	NAG	A	619	14/15	0.73	0.12	48,54,60,70	0
5	EDO	B	609	4/4	0.75	0.16	35,39,46,55	0
8	NAG	B	615	14/15	0.75	0.11	50,57,67,68	0
3	GOL	A	609	6/6	0.76	0.17	49,51,53,58	0
2	MES	A	614	12/12	0.76	0.21	45,54,64,64	12
10	FJK	A	626	49/49	0.77	0.19	18,42,58,60	49
7	PEG	A	616	7/7	0.77	0.15	39,49,54,56	0
7	PEG	A	617	7/7	0.78	0.16	45,56,59,60	0
7	PEG	B	613	7/7	0.78	0.16	48,51,60,68	0
7	PEG	A	615	7/7	0.78	0.15	34,38,48,49	0
3	GOL	B	604	6/6	0.78	0.18	39,43,45,54	0
7	PEG	A	618	7/7	0.80	0.13	38,45,49,50	0
2	MES	A	611	12/12	0.82	0.20	38,42,48,49	12
2	MES	A	612	12/12	0.82	0.16	38,56,65,65	12
5	EDO	A	605	4/4	0.83	0.14	29,42,43,44	0
5	EDO	A	608	4/4	0.84	0.12	47,50,51,61	0
5	EDO	A	606	4/4	0.84	0.11	42,47,47,52	0
7	PEG	B	612	7/7	0.85	0.11	39,46,51,55	0
5	EDO	B	606	4/4	0.85	0.12	38,43,51,52	0
5	EDO	A	610	4/4	0.85	0.13	35,38,39,41	0
2	MES	A	601	12/12	0.85	0.12	54,59,67,70	0
5	EDO	B	610	4/4	0.86	0.15	41,42,44,57	0
9	CL	A	624	1/1	0.87	0.13	63,63,63,63	0
5	EDO	B	603	4/4	0.87	0.11	41,46,47,51	0
8	NAG	A	620	14/15	0.87	0.08	30,41,55,59	0
5	EDO	B	607	4/4	0.88	0.12	36,42,43,50	0
8	NAG	B	616	14/15	0.88	0.09	37,46,54,61	0
3	GOL	A	602	6/6	0.88	0.16	30,41,44,62	0
4	PGE	B	605	10/10	0.89	0.10	36,41,52,53	0
7	PEG	B	611	7/7	0.90	0.11	32,36,45,46	0
5	EDO	B	601	4/4	0.91	0.08	31,36,41,46	0
9	CL	A	623	1/1	0.92	0.18	69,69,69,69	0
5	EDO	A	607	4/4	0.92	0.08	36,38,45,48	0
6	SO4	B	608	5/5	0.93	0.11	51,59,66,71	0
9	CL	A	621	1/1	0.93	0.12	57,57,57,57	0
6	SO4	A	627	5/5	0.94	0.12	35,39,46,53	5
9	CL	A	622	1/1	0.94	0.14	63,63,63,63	0

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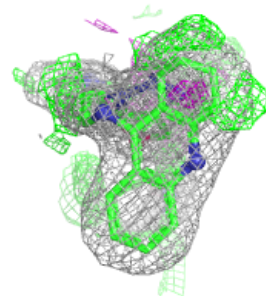
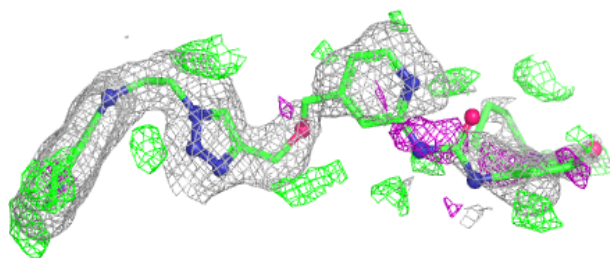
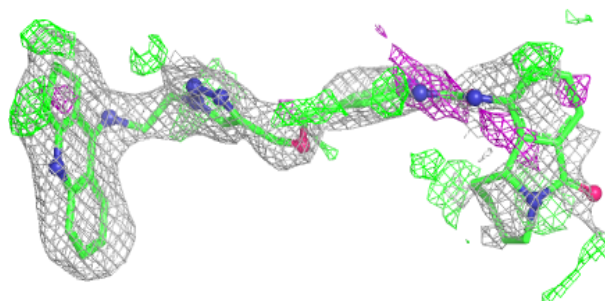
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
6	SO4	A	613	5/5	0.96	0.12	50,50,61,62	0
9	CL	A	625	1/1	0.97	0.11	55,55,55,55	0
9	CL	B	618	1/1	0.99	0.07	50,50,50,50	0

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.

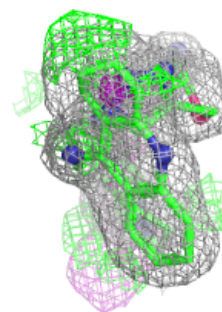
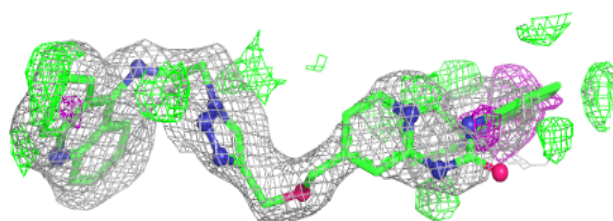
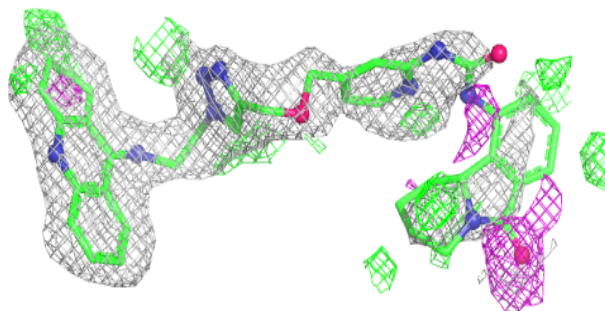
Electron density around FJK B 619:

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 FJK A 626:

$2mF_o-DF_c$ (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.