



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 04:21 PM UTC

PDB ID : 8WKL / pdb_00008wkl
Title : Rauvolfia serpentina strictosidine synthase (RsSTR) in complex with a non-reactive tryptamine substitute crystallized in P1211 space group
Authors : Nitin, K.; Rajakumara, E.
Deposited on : 2023-09-28
Resolution : 2.67 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

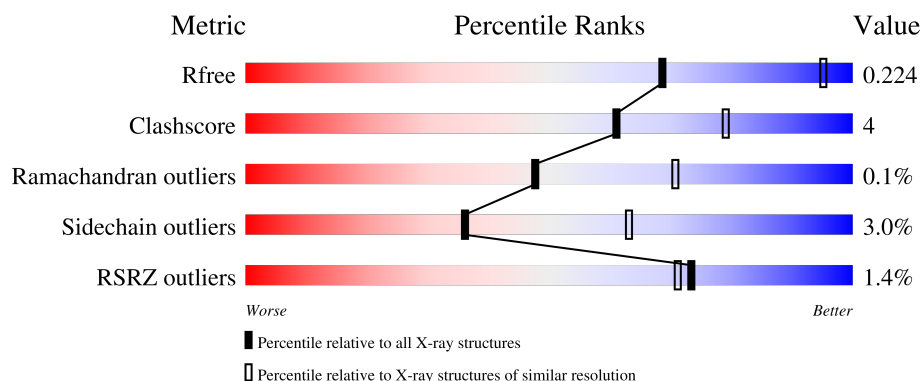
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.67 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	5070 (2.70-2.66)
Clashscore	190562	5409 (2.70-2.66)
Ramachandran outliers	187476	5324 (2.70-2.66)
Sidechain outliers	187428	5324 (2.70-2.66)
RSRZ outliers	180081	5070 (2.70-2.66)

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	318	% 82% 12% • 5%
1	B	318	3% 81% 13% • 5%
1	C	318	% 86% 8% • 5%
1	D	318	2% 83% 11% • 5%
1	E	318	% 84% 10% • 5%

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Mol	Chain	Length	Quality of chain
1	F	318	2% 82% 12% . .
1	G	318	% 83% 13% . .
1	H	318	% 82% 12% . .

2 Entry composition

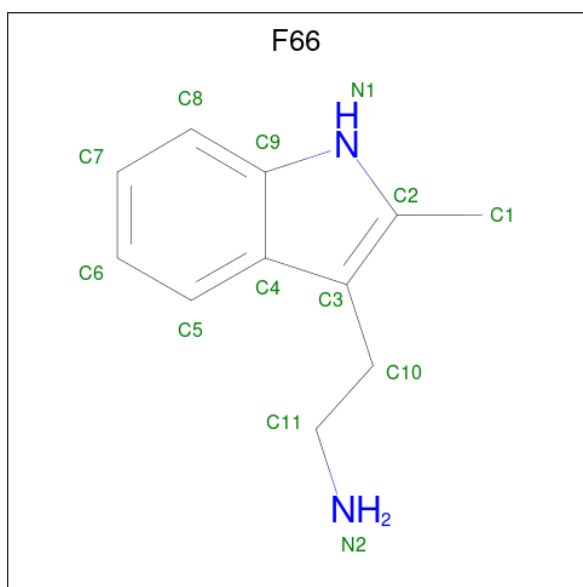
There are 4 unique types of molecules in this entry. The entry contains 19548 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Strictosidine synthase.

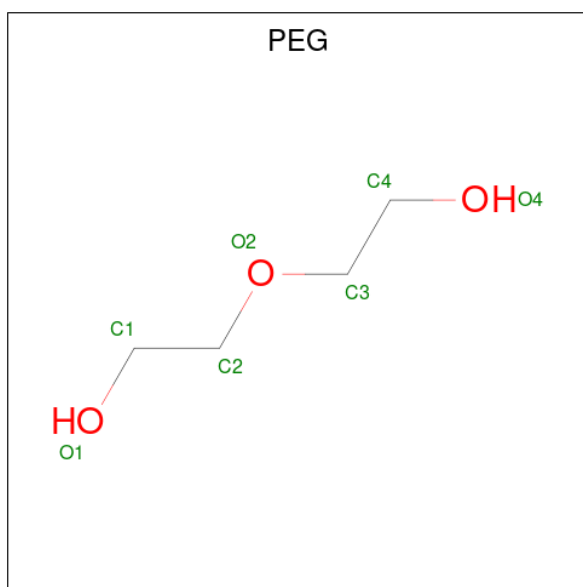
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	303	Total	C	N	O	S	0	1	0
			2389	1535	387	462	5			
1	B	302	Total	C	N	O	S	0	2	0
			2386	1533	388	461	4			
1	C	302	Total	C	N	O	S	0	1	0
			2380	1529	386	460	5			
1	D	302	Total	C	N	O	S	0	2	0
			2395	1538	391	461	5			
1	E	302	Total	C	N	O	S	0	1	0
			2381	1529	387	460	5			
1	F	304	Total	C	N	O	S	0	1	0
			2391	1534	389	463	5			
1	G	307	Total	C	N	O	S	0	0	0
			2407	1546	391	465	5			
1	H	304	Total	C	N	O	S	0	0	0
			2383	1529	387	462	5			

- Molecule 2 is 2-(2-methyl-1H-indol-3-yl)ethanamine (CCD ID: F66) (formula: C₁₁H₁₄N₂) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	N	0	0
			13	11	2		
2	B	1	Total	C	N	0	0
			13	11	2		
2	C	1	Total	C	N	0	0
			13	11	2		
2	D	1	Total	C	N	0	0
			13	11	2		
2	E	1	Total	C	N	0	0
			13	11	2		
2	F	1	Total	C	N	0	0
			13	11	2		
2	G	1	Total	C	N	0	0
			13	11	2		
2	H	1	Total	C	N	0	0
			13	11	2		

- Molecule 3 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: C₄H₁₀O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	B	1	Total	C	O	0	0
			7	4	3		
3	D	1	Total	C	O	0	0
			7	4	3		
3	D	1	Total	C	O	0	0
			7	4	3		
3	E	1	Total	C	O	0	0
			7	4	3		
3	F	1	Total	C	O	0	0
			7	4	3		
3	H	1	Total	C	O	0	0
			7	4	3		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	45	Total	O	0	0
			45	45		
4	B	41	Total	O	0	0
			41	41		
4	C	31	Total	O	0	0
			31	31		
4	D	51	Total	O	0	0
			51	51		
4	E	22	Total	O	0	0
			22	22		
4	F	35	Total	O	0	0
			35	35		

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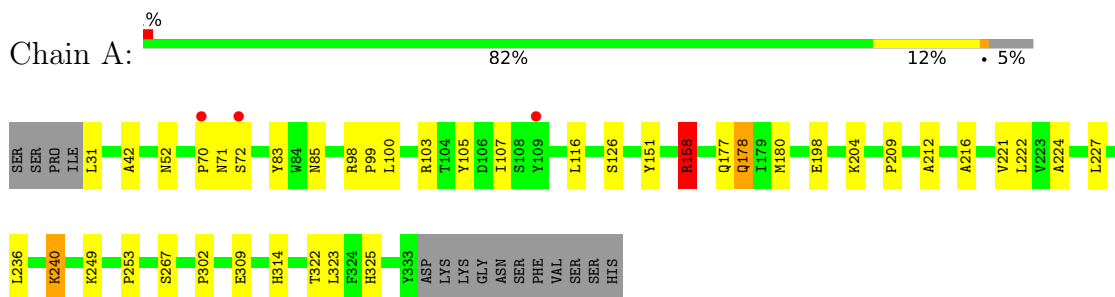
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	G	20	Total	O	0	0
			20	20		
4	H	45	Total	O	0	0
			45	45		

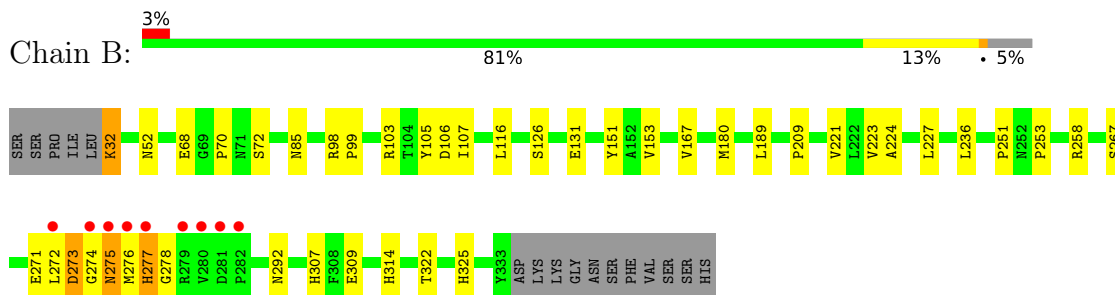
3 Residue-property plots [i](#)

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.

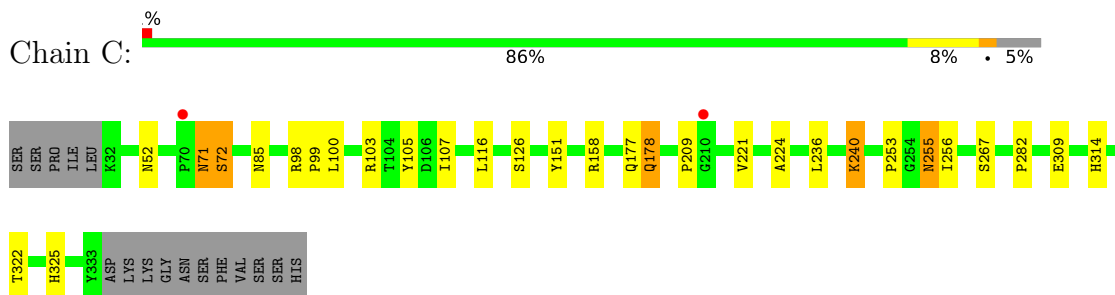
- Molecule 1: Strictosidine synthase



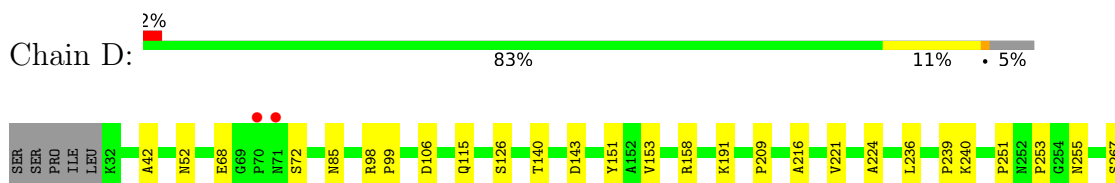
- Molecule 1: Strictosidine synthase

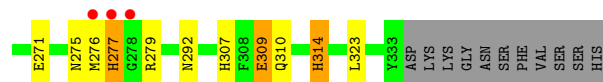


- Molecule 1: Strictosidine synthase

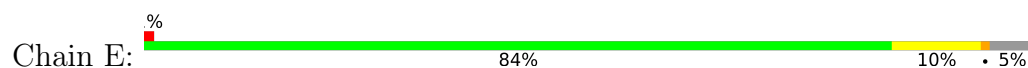


- Molecule 1: Strictosidine synthase

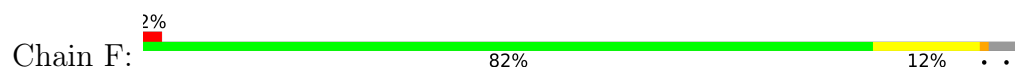




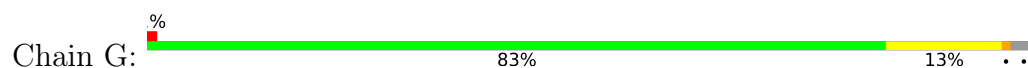
• Molecule 1: Strictosidine synthase



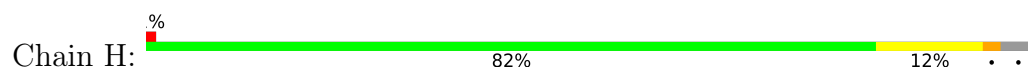
• Molecule 1: Strictosidine synthase



• Molecule 1: Strictosidine synthase



• Molecule 1: Strictosidine synthase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	88.49Å 82.64Å 171.84Å 90.00° 98.52° 90.00°	Depositor
Resolution (Å)	26.43 – 2.67 26.43 – 2.67	Depositor EDS
% Data completeness (in resolution range)	99.9 (26.43-2.67) 99.9 (26.43-2.67)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.76 (at 2.68Å)	Xtriage
Refinement program	REFMAC 5.8.0419	Depositor
R, R_{free}	0.196 , 0.218 0.201 , 0.224	Depositor DCC
R_{free} test set	3459 reflections (4.95%)	wwPDB-VP
Wilson B-factor (Å ²)	40.1	Xtriage
Anisotropy	0.316	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 35.0	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	0.94	EDS
Total number of atoms	19548	wwPDB-VP
Average B, all atoms (Å ²)	49.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 25.90 % 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 2.9080e-03. 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: PEG, F66

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	1.19	3/2457 (0.1%)	0.85	1/3344 (0.0%)
1	B	1.17	8/2458 (0.3%)	0.83	1/3346 (0.0%)
1	C	1.14	2/2448 (0.1%)	0.85	0/3332
1	D	1.20	6/2467 (0.2%)	0.87	3/3356 (0.1%)
1	E	1.11	2/2449 (0.1%)	0.83	0/3333
1	F	1.15	4/2459 (0.2%)	0.86	1/3347 (0.0%)
1	G	1.15	4/2473 (0.2%)	0.83	2/3368 (0.1%)
1	H	1.17	3/2448 (0.1%)	0.88	1/3334 (0.0%)
All	All	1.16	32/19659 (0.2%)	0.85	9/26760 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2

All (32) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	H	32	LYS	C-O	-8.05	1.13	1.24
1	H	107	ILE	C-O	-7.45	1.16	1.23
1	D	309	GLU	CD-OE2	7.08	1.38	1.25
1	D	307	HIS	CD2-NE2	6.59	1.45	1.37
1	B	275	ASN	C-O	-6.34	1.16	1.24
1	B	278	GLY	C-O	-5.96	1.15	1.23
1	A	240	LYS	CB-CG	5.87	1.70	1.52
1	F	158	ARG	NE-CZ	5.86	1.39	1.33
1	B	274	GLY	C-N	5.80	1.41	1.33
1	D	307	HIS	CB-CG	-5.78	1.42	1.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	131	GLU	CD-OE2	5.78	1.36	1.25
1	A	158	ARG	NE-CZ	-5.75	1.26	1.33
1	D	271	GLU	CD-OE2	-5.65	1.14	1.25
1	F	134	HIS	CE1-NE2	5.65	1.38	1.32
1	C	240	LYS	CB-CG	5.61	1.69	1.52
1	B	278	GLY	C-N	5.57	1.40	1.33
1	G	32	LYS	C-O	-5.52	1.17	1.23
1	D	239	PRO	CA-CB	5.47	1.61	1.53
1	G	207	HIS	CE1-NE2	-5.40	1.27	1.32
1	A	198	GLU	CG-CD	5.38	1.65	1.52
1	D	279	ARG	NE-CZ	5.36	1.39	1.33
1	G	333	TYR	C-N	5.33	1.41	1.33
1	F	37	GLU	CD-OE1	5.28	1.35	1.25
1	H	45	SER	CA-CB	-5.28	1.44	1.54
1	C	71	ASN	C-N	-5.26	1.26	1.33
1	B	258	ARG	CZ-NH2	-5.25	1.26	1.33
1	B	271	GLU	C-O	-5.25	1.17	1.23
1	F	107	ILE	C-O	-5.20	1.18	1.23
1	B	32	LYS	CD-CE	5.11	1.67	1.52
1	E	158	ARG	CZ-NH2	-5.11	1.26	1.33
1	G	263	HIS	CD2-NE2	-5.11	1.32	1.37
1	E	306	GLU	CD-OE1	5.02	1.34	1.25

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	314	HIS	CB-CG-CD2	6.45	139.59	131.20
1	D	143	ASP	CA-CB-CG	6.09	118.69	112.60
1	D	314	HIS	CB-CG-ND1	-5.40	114.60	122.70
1	G	85	ASN	CB-CA-C	5.26	118.73	109.80
1	G	61	ASP	CA-CB-CG	5.24	117.84	112.60
1	B	277	HIS	CB-CA-C	5.21	120.78	110.42
1	A	249	LYS	CG-CD-CE	5.04	122.90	111.30
1	H	193	ASP	CA-CB-CG	5.01	117.61	112.60
1	F	193	ASP	CA-CB-CG	5.00	117.60	112.60

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	158	ARG	Sidechain
1	A	72	SER	Peptide

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	2389	0	2289	19	0
1	B	2386	0	2284	23	0
1	C	2380	0	2275	17	0
1	D	2395	0	2302	16	0
1	E	2381	0	2280	17	0
1	F	2391	0	2285	26	0
1	G	2407	0	2299	18	0
1	H	2383	0	2264	28	0
2	A	13	0	0	0	0
2	B	13	0	0	0	0
2	C	13	0	0	1	0
2	D	13	0	0	0	0
2	E	13	0	0	0	0
2	F	13	0	0	0	0
2	G	13	0	0	0	0
2	H	13	0	0	0	0
3	B	7	0	10	0	0
3	D	14	0	20	2	0
3	E	7	0	10	0	0
3	F	7	0	10	1	0
3	H	7	0	10	0	0
4	A	45	0	0	1	0
4	B	41	0	0	0	0
4	C	31	0	0	1	0
4	D	51	0	0	1	0
4	E	22	0	0	2	0
4	F	35	0	0	1	0
4	G	20	0	0	0	0
4	H	45	0	0	0	0
All	All	19548	0	18338	158	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 (158) 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:D:277:HIS:HE1	4:D:528:HOH:O	1.55	0.87
1:A:151:TYR:OH	1:A:309:GLU:OE1	2.10	0.70
1:F:134:HIS:CD2	3:F:402:PEG:H32	2.26	0.69
1:F:151:TYR:OH	1:F:309:GLU:OE1	2.11	0.68
1:G:151:TYR:OH	1:G:309:GLU:OE1	2.12	0.68
1:D:151:TYR:OH	1:D:309:GLU:OE1	2.11	0.68
1:E:151:TYR:OH	1:E:309:GLU:OE1	2.12	0.67
1:C:151:TYR:OH	1:C:309:GLU:OE1	2.12	0.67
1:D:255:ASN:HD22	1:D:310:GLN:HB2	1.60	0.66
1:A:83:TYR:O	1:A:83:TYR:CD2	2.49	0.66
1:B:151:TYR:OH	1:B:309:GLU:OE1	2.12	0.66
1:H:151:TYR:OH	1:H:309:GLU:OE1	2.14	0.65
1:C:282:PRO:HD2	4:C:525:HOH:O	1.96	0.65
1:F:285:ILE:HD12	1:F:296:VAL:HG22	1.79	0.64
1:B:272:LEU:O	1:B:273:ASP:HB2	1.97	0.64
1:C:158:ARG:CB	1:C:158:ARG:HH11	2.10	0.64
1:F:285:ILE:CD1	1:F:296:VAL:HG22	2.28	0.63
1:B:277:HIS:ND1	1:B:307:HIS:CE1	2.66	0.63
1:H:158:ARG:HH11	1:H:158:ARG:CB	2.12	0.63
1:D:158:ARG:NE	1:D:216:ALA:O	2.31	0.62
1:G:68:GLU:HB2	1:G:72:SER:HB2	1.81	0.61
1:F:68:GLU:HB2	1:F:72:SER:HB2	1.82	0.61
1:D:68:GLU:HB2	1:D:72:SER:HB2	1.83	0.61
1:H:189:LEU:HD22	1:H:223:VAL:CG2	2.31	0.61
1:H:180:MET:HG3	1:H:276:MET:HE2	1.83	0.60
1:B:277:HIS:HA	1:B:307:HIS:HE1	1.68	0.59
1:E:219:SER:HA	1:E:237:GLU:HG2	1.85	0.59
1:H:68:GLU:HB2	1:H:72:SER:HB2	1.86	0.58
1:H:148:LYS:HE3	1:H:148:LYS:HA	1.84	0.58
1:E:68:GLU:HB2	1:E:72:SER:HB2	1.85	0.58
1:B:68:GLU:HB2	1:B:72:SER:HB2	1.87	0.57
1:D:251:PRO:HG3	1:F:83:TYR:CE2	2.40	0.57
1:C:255:ASN:HD22	1:C:256:ILE:H	1.53	0.56
1:H:322:THR:HG21	1:H:325:HIS:HB2	1.86	0.56
1:G:255:ASN:HD22	1:G:256:ILE:H	1.54	0.56
1:F:180:MET:HG3	1:F:276:MET:CE	2.36	0.55
1:E:103:ARG:HD2	1:E:105:TYR:CE1	2.42	0.55
1:H:255:ASN:HD22	1:H:256:ILE:H	1.54	0.54
1:A:209:PRO:HA	1:A:224:ALA:O	2.09	0.53
1:B:103:ARG:HD2	1:B:105:TYR:CE1	2.43	0.52
1:H:209:PRO:HA	1:H:224:ALA:O	2.10	0.52
1:B:209:PRO:HA	1:B:224:ALA:O	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:209:PRO:HA	1:D:224:ALA:O	2.09	0.52
1:H:189:LEU:HD22	1:H:223:VAL:HG21	1.90	0.52
1:C:209:PRO:HA	1:C:224:ALA:O	2.09	0.52
1:E:209:PRO:HA	1:E:224:ALA:O	2.09	0.52
1:F:209:PRO:HA	1:F:224:ALA:O	2.09	0.52
1:G:209:PRO:HA	1:G:224:ALA:O	2.09	0.52
1:D:255:ASN:HD22	1:D:310:GLN:HE21	1.57	0.52
1:F:103:ARG:HD2	1:F:105:TYR:CE1	2.44	0.51
1:G:334:ASP:O	1:G:335:LYS:C	2.52	0.51
1:H:180:MET:HG3	1:H:276:MET:CE	2.40	0.51
1:E:219:SER:HA	1:E:237:GLU:CG	2.42	0.50
1:D:292:ASN:HB3	1:F:87:ALA:CB	2.42	0.49
1:E:158:ARG:NH2	1:E:216:ALA:O	2.42	0.49
1:F:189:LEU:HD22	1:F:223:VAL:CG2	2.44	0.47
1:F:52:ASN:OD1	1:F:314:HIS:NE2	2.47	0.47
2:C:401:F66:N2	2:C:401:F66:C5	2.77	0.47
1:A:158:ARG:NH2	1:A:216:ALA:O	2.48	0.47
1:C:52:ASN:OD1	1:C:314:HIS:NE2	2.47	0.47
1:C:158:ARG:HH11	1:C:158:ARG:HB2	1.79	0.47
1:G:300:PRO:HB2	1:H:31:LEU:HD12	1.96	0.47
1:E:322:THR:HG22	4:E:502:HOH:O	2.15	0.47
1:A:180:MET:HE1	1:A:227:LEU:HD21	1.96	0.46
1:B:189:LEU:HD22	1:B:223:VAL:CG2	2.46	0.46
1:A:177:GLN:HB3	1:A:178:GLN:HE21	1.79	0.46
1:B:322:THR:HG21	1:B:325[A]:HIS:HB2	1.98	0.46
1:C:177:GLN:HB3	1:C:178:GLN:HE21	1.80	0.46
1:A:70:PRO:O	1:A:71:ASN:CB	2.64	0.46
1:B:52:ASN:OD1	1:B:314:HIS:NE2	2.47	0.45
1:A:52:ASN:OD1	1:A:314:HIS:NE2	2.47	0.45
1:E:177:GLN:HB3	1:E:178:GLN:HE21	1.82	0.45
1:G:177:GLN:HB3	1:G:178:GLN:HE21	1.81	0.45
1:G:98:ARG:N	1:G:99:PRO:CD	2.80	0.45
1:F:221:VAL:CG2	1:F:236:LEU:HD11	2.47	0.45
1:E:180:MET:HE1	1:E:227:LEU:HD21	1.99	0.45
1:E:221:VAL:CG2	1:E:236:LEU:HD11	2.47	0.45
1:F:158:ARG:HD3	1:F:216:ALA:O	2.17	0.45
1:G:52:ASN:OD1	1:G:314:HIS:NE2	2.48	0.45
1:A:322:THR:HG21	1:A:325:HIS:HB2	1.98	0.44
1:F:98:ARG:N	1:F:99:PRO:CD	2.81	0.44
1:C:322:THR:HG21	1:C:325:HIS:HB2	1.99	0.44
1:D:98:ARG:N	1:D:99:PRO:CD	2.80	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:255:ASN:HD22	1:H:256:ILE:N	2.16	0.44
1:A:98:ARG:N	1:A:99:PRO:CD	2.80	0.44
1:B:180:MET:HE2	1:B:276:MET:CB	2.47	0.44
1:B:251:PRO:HG3	1:H:83:TYR:CE2	2.52	0.44
1:E:253:PRO:HA	1:E:267:SER:O	2.18	0.44
1:H:98:ARG:N	1:H:99:PRO:CD	2.81	0.44
1:B:221:VAL:CG2	1:B:236:LEU:HD11	2.48	0.44
1:B:253:PRO:HA	1:B:267:SER:O	2.18	0.44
1:G:253:PRO:HA	1:G:267:SER:O	2.18	0.44
1:H:253:PRO:HA	1:H:267:SER:O	2.18	0.44
1:B:98:ARG:N	1:B:99:PRO:CD	2.81	0.44
1:E:98:ARG:N	1:E:99:PRO:CD	2.81	0.44
1:H:44:ASN:HD22	1:H:44:ASN:H	1.66	0.44
1:A:253:PRO:HA	1:A:267:SER:O	2.18	0.43
1:C:255:ASN:HD22	1:C:256:ILE:N	2.16	0.43
1:B:180:MET:HE1	1:B:227:LEU:HD21	2.00	0.43
1:D:42:ALA:HB1	1:D:323:LEU:HA	2.00	0.43
1:H:31:LEU:HD23	1:H:32:LYS:H	1.83	0.43
1:B:292:ASN:OD1	1:H:87:ALA:HB2	2.18	0.43
1:C:221:VAL:CG2	1:C:236:LEU:HD11	2.47	0.43
1:C:253:PRO:HA	1:C:267:SER:O	2.18	0.43
1:F:180:MET:HE1	1:F:227:LEU:HD21	2.00	0.43
1:F:285:ILE:CD1	1:F:296:VAL:HG13	2.48	0.43
1:A:83:TYR:O	1:A:83:TYR:CG	2.71	0.43
1:C:71:ASN:O	1:C:72:SER:CB	2.66	0.43
1:D:253:PRO:HA	1:D:267:SER:O	2.19	0.43
1:G:255:ASN:HD22	1:G:256:ILE:N	2.17	0.43
1:C:98:ARG:N	1:C:99:PRO:CD	2.81	0.43
1:D:221:VAL:CG2	1:D:236:LEU:HD11	2.48	0.43
1:H:52:ASN:OD1	1:H:314:HIS:NE2	2.48	0.43
1:C:158:ARG:HH11	1:C:158:ARG:HB3	1.80	0.43
1:F:42:ALA:HB1	1:F:323:LEU:HA	2.01	0.43
1:G:221:VAL:CG2	1:G:236:LEU:HD11	2.49	0.43
1:H:221:VAL:CG2	1:H:236:LEU:HD11	2.48	0.43
1:F:189:LEU:HD22	1:F:223:VAL:HG21	2.00	0.43
1:G:322:THR:HG21	1:G:325:HIS:HB2	2.01	0.43
1:A:302:PRO:HB3	1:B:70:PRO:HG2	2.00	0.42
1:A:221:VAL:CG2	1:A:236:LEU:HD11	2.49	0.42
1:E:151:TYR:HE2	4:E:517:HOH:O	2.02	0.42
1:F:107:ILE:HB	1:F:116:LEU:HD11	2.02	0.42
1:D:52:ASN:OD1	1:D:314:HIS:NE2	2.48	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:253:PRO:HA	1:F:267:SER:O	2.18	0.42
1:H:158:ARG:HH11	1:H:158:ARG:HB2	1.80	0.42
1:E:42:ALA:HB1	1:E:323:LEU:HA	2.01	0.42
1:D:292:ASN:OD1	1:F:87:ALA:HB2	2.19	0.42
1:F:151:TYR:HB2	1:F:167:VAL:HG23	2.02	0.42
1:G:180:MET:HE1	1:G:227:LEU:HD21	2.01	0.42
1:F:180:MET:HB2	1:F:276:MET:HE1	2.01	0.42
1:H:44:ASN:ND2	1:H:103:ARG:HH12	2.17	0.42
1:B:189:LEU:HD22	1:B:223:VAL:HG21	2.01	0.41
1:D:106:ASP:HB3	1:D:153:VAL:HG12	2.03	0.41
3:D:402:PEG:H12	1:F:87:ALA:HB1	2.01	0.41
1:B:277:HIS:CA	1:B:307:HIS:HE1	2.32	0.41
1:A:100:LEU:HB2	4:A:530:HOH:O	2.20	0.41
1:E:107:ILE:HB	1:E:116:LEU:HD11	2.03	0.41
1:A:107:ILE:HB	1:A:116:LEU:HD11	2.03	0.41
1:C:103:ARG:HD2	1:C:105:TYR:CE2	2.55	0.41
1:G:42:ALA:HB1	1:G:323:LEU:HA	2.02	0.41
1:B:107:ILE:HB	1:B:116:LEU:HD11	2.03	0.41
1:G:230:GLN:HB3	1:G:249:LYS:HD3	2.02	0.41
1:H:103:ARG:HD2	1:H:105:TYR:CE2	2.55	0.41
1:C:107:ILE:HB	1:C:116:LEU:HD11	2.03	0.41
1:H:31:LEU:HD23	1:H:32:LYS:N	2.36	0.41
1:H:158:ARG:HH11	1:H:158:ARG:HB3	1.83	0.41
3:D:402:PEG:H11	4:F:528:HOH:O	2.21	0.40
1:E:70:PRO:HG2	1:F:302:PRO:HB3	2.03	0.40
1:H:107:ILE:HB	1:H:116:LEU:HD11	2.03	0.40
1:A:42:ALA:HB1	1:A:323:LEU:HA	2.03	0.40
1:H:295:GLU:OE2	1:H:333:TYR:OH	2.37	0.40
1:A:103:ARG:HD2	1:A:105:TYR:CE2	2.55	0.40
1:B:151:TYR:HB2	1:B:167:VAL:HG23	2.03	0.40
1:G:107:ILE:HB	1:G:116:LEU:HD11	2.03	0.40
1:A:212:ALA:HA	1:A:222:LEU:O	2.22	0.40
1:B:106:ASP:HB3	1:B:153:VAL:HG12	2.03	0.40
1:G:212:ALA:HA	1:G:222:LEU:O	2.21	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	302/318 (95%)	289 (96%)	13 (4%)	0	100	100
1	B	302/318 (95%)	287 (95%)	14 (5%)	1 (0%)	36	57
1	C	301/318 (95%)	289 (96%)	11 (4%)	1 (0%)	36	57
1	D	302/318 (95%)	290 (96%)	12 (4%)	0	100	100
1	E	301/318 (95%)	290 (96%)	11 (4%)	0	100	100
1	F	303/318 (95%)	291 (96%)	12 (4%)	0	100	100
1	G	305/318 (96%)	294 (96%)	11 (4%)	0	100	100
1	H	302/318 (95%)	291 (96%)	11 (4%)	0	100	100
All	All	2418/2544 (95%)	2321 (96%)	95 (4%)	2 (0%)	48	71

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	72	SER
1	B	273	ASP

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	260/275 (94%)	253 (97%)	7 (3%)	39	67
1	B	260/275 (94%)	256 (98%)	4 (2%)	57	79
1	C	258/275 (94%)	252 (98%)	6 (2%)	44	71

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	D	262/275 (95%)	253 (97%)	9 (3%)	32	59
1	E	259/275 (94%)	249 (96%)	10 (4%)	28	54
1	F	260/275 (94%)	251 (96%)	9 (4%)	32	58
1	G	261/275 (95%)	254 (97%)	7 (3%)	39	67
1	H	257/275 (94%)	246 (96%)	11 (4%)	26	51
All	All	2077/2200 (94%)	2014 (97%)	63 (3%)	36	63

All (63) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	31	LEU
1	A	85	ASN
1	A	126	SER
1	A	158	ARG
1	A	178	GLN
1	A	204	LYS
1	A	240	LYS
1	B	32	LYS
1	B	85	ASN
1	B	126	SER
1	B	275	ASN
1	C	85	ASN
1	C	100	LEU
1	C	126	SER
1	C	178	GLN
1	C	240	LYS
1	C	255	ASN
1	D	85	ASN
1	D	115	GLN
1	D	126	SER
1	D	140	THR
1	D	191	LYS
1	D	240	LYS
1	D	275	ASN
1	D	276	MET
1	D	277	HIS
1	E	68	GLU
1	E	85	ASN
1	E	113	ASN
1	E	126	SER

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Mol	Chain	Res	Type
1	E	158	ARG
1	E	178	GLN
1	E	204	LYS
1	E	237	GLU
1	E	240	LYS
1	E	250	ILE
1	F	85	ASN
1	F	113	ASN
1	F	126	SER
1	F	140	THR
1	F	158	ARG
1	F	191	LYS
1	F	204	LYS
1	F	223	VAL
1	F	283	LYS
1	G	85	ASN
1	G	100	LEU
1	G	126	SER
1	G	178	GLN
1	G	250	ILE
1	G	255	ASN
1	G	295	GLU
1	H	44	ASN
1	H	85	ASN
1	H	126	SER
1	H	140	THR
1	H	148	LYS
1	H	191	LYS
1	H	223	VAL
1	H	249	LYS
1	H	255	ASN
1	H	275	ASN
1	H	306	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (36) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	178	GLN
1	A	255	ASN
1	A	307	HIS
1	A	312	GLN
1	B	114	ASN

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Mol	Chain	Res	Type
1	B	255	ASN
1	B	307	HIS
1	B	312	GLN
1	C	114	ASN
1	C	137	GLN
1	C	178	GLN
1	C	255	ASN
1	C	307	HIS
1	C	312	GLN
1	D	255	ASN
1	D	312	GLN
1	E	113	ASN
1	E	114	ASN
1	E	178	GLN
1	E	255	ASN
1	E	312	GLN
1	F	112	GLN
1	F	113	ASN
1	F	114	ASN
1	F	134	HIS
1	F	255	ASN
1	F	312	GLN
1	G	114	ASN
1	G	178	GLN
1	G	255	ASN
1	G	312	GLN
1	H	44	ASN
1	H	114	ASN
1	H	177	GLN
1	H	255	ASN
1	H	312	GLN

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 [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

14 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	F66	A	401	-	14,14,14	1.17	1 (7%)	19,19,19	0.71	0
2	F66	F	401	-	14,14,14	0.61	0	19,19,19	0.60	0
3	PEG	E	402	-	6,6,6	0.81	0	5,5,5	0.08	0
2	F66	G	401	-	14,14,14	1.01	0	19,19,19	0.65	0
3	PEG	F	402	-	6,6,6	1.34	0	5,5,5	0.15	0
3	PEG	H	402	-	6,6,6	0.99	0	5,5,5	0.10	0
2	F66	D	401	-	14,14,14	1.33	1 (7%)	19,19,19	0.76	0
2	F66	C	401	-	14,14,14	1.61	2 (14%)	19,19,19	1.03	1 (5%)
3	PEG	D	402	-	6,6,6	1.00	0	5,5,5	0.14	0
2	F66	H	401	-	14,14,14	1.21	1 (7%)	19,19,19	0.76	1 (5%)
3	PEG	D	403	-	6,6,6	0.80	0	5,5,5	0.08	0
2	F66	B	401	-	14,14,14	1.21	1 (7%)	19,19,19	0.71	0
2	F66	E	401	-	14,14,14	1.03	2 (14%)	19,19,19	0.81	1 (5%)
3	PEG	B	402	-	6,6,6	0.93	0	5,5,5	0.08	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
2	F66	A	401	-	-	3/3/3/3	0/2/2/2
2	F66	F	401	-	-	1/3/3/3	0/2/2/2
3	PEG	E	402	-	-	2/4/4/4	-
2	F66	G	401	-	-	1/3/3/3	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	PEG	F	402	-	-	4/4/4/4	-
3	PEG	H	402	-	-	2/4/4/4	-
2	F66	D	401	-	-	1/3/3/3	0/2/2/2
2	F66	C	401	-	-	0/3/3/3	0/2/2/2
3	PEG	D	402	-	-	2/4/4/4	-
2	F66	H	401	-	-	0/3/3/3	0/2/2/2
3	PEG	D	403	-	-	4/4/4/4	-
2	F66	B	401	-	-	1/3/3/3	0/2/2/2
2	F66	E	401	-	-	0/3/3/3	0/2/2/2
3	PEG	B	402	-	-	1/4/4/4	-

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	401	F66	C10-C3	-4.65	1.44	1.51
2	A	401	F66	C5-C4	2.71	1.44	1.39
2	H	401	F66	C10-C3	-2.70	1.47	1.51
2	D	401	F66	C5-C4	2.66	1.44	1.39
2	B	401	F66	C5-C4	2.17	1.43	1.39
2	E	401	F66	C5-C4	2.15	1.43	1.39
2	E	401	F66	C10-C3	-2.05	1.48	1.51
2	C	401	F66	C5-C4	2.03	1.43	1.39

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	401	F66	C4-C3-C2	3.36	108.36	106.98
2	E	401	F66	C4-C3-C2	2.28	107.92	106.98
2	H	401	F66	C4-C3-C2	2.00	107.80	106.98

There are no chirality outliers.

All (22) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	401	F66	C3-C10-C11-N2
2	A	401	F66	C11-C10-C3-C4
2	F	401	F66	C3-C10-C11-N2
3	E	402	PEG	O2-C3-C4-O4
3	H	402	PEG	O2-C3-C4-O4
3	B	402	PEG	O1-C1-C2-O2

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Mol	Chain	Res	Type	Atoms
3	D	402	PEG	O2-C3-C4-O4
3	E	402	PEG	O1-C1-C2-O2
3	F	402	PEG	O1-C1-C2-O2
3	H	402	PEG	O1-C1-C2-O2
3	D	402	PEG	O1-C1-C2-O2
3	F	402	PEG	O2-C3-C4-O4
3	D	403	PEG	O1-C1-C2-O2
2	D	401	F66	C3-C10-C11-N2
2	G	401	F66	C3-C10-C11-N2
2	A	401	F66	C11-C10-C3-C2
3	F	402	PEG	C1-C2-O2-C3
2	B	401	F66	C3-C10-C11-N2
3	D	403	PEG	C1-C2-O2-C3
3	F	402	PEG	C4-C3-O2-C2
3	D	403	PEG	O2-C3-C4-O4
3	D	403	PEG	C4-C3-O2-C2

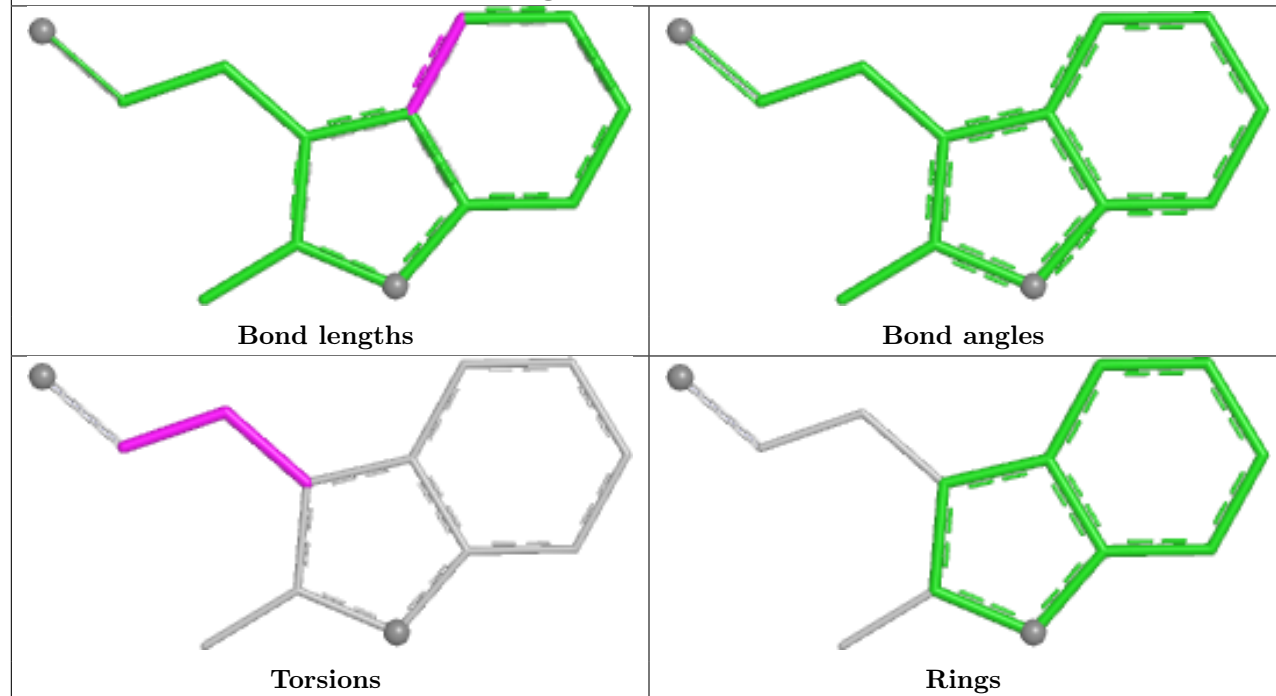
There are no ring outliers.

3 monomers are involved in 4 short contacts:

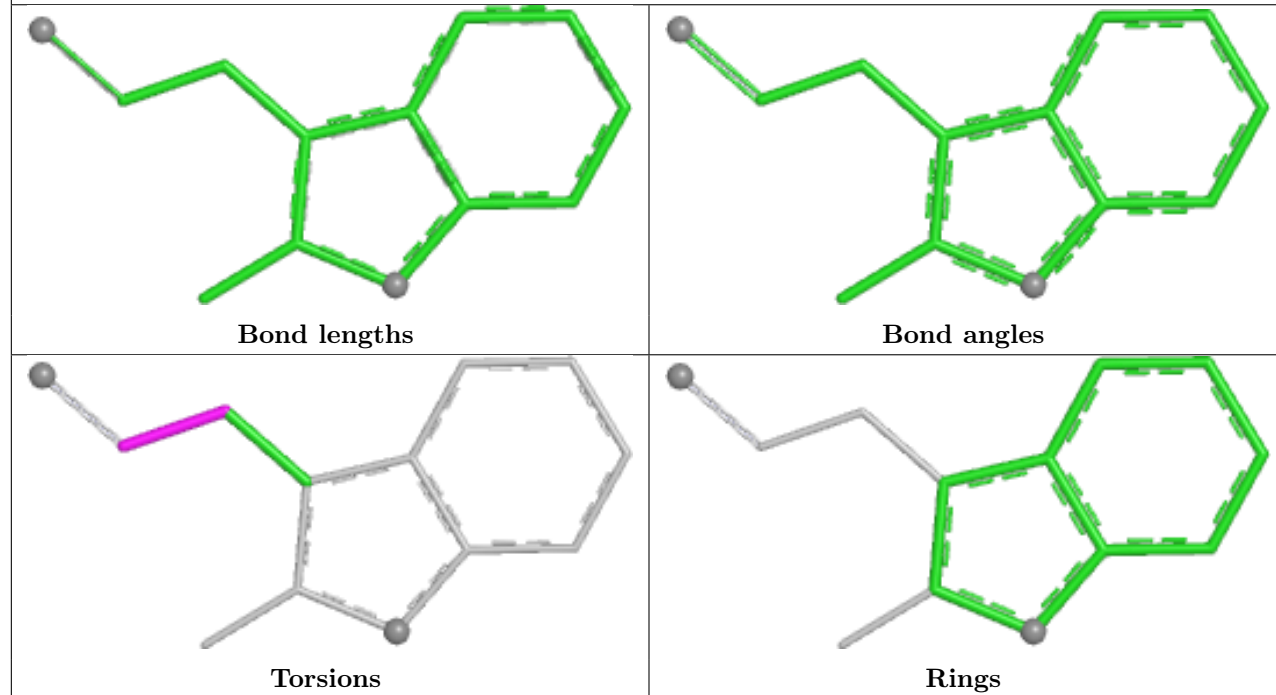
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	F	402	PEG	1	0
2	C	401	F66	1	0
3	D	402	PEG	2	0

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.

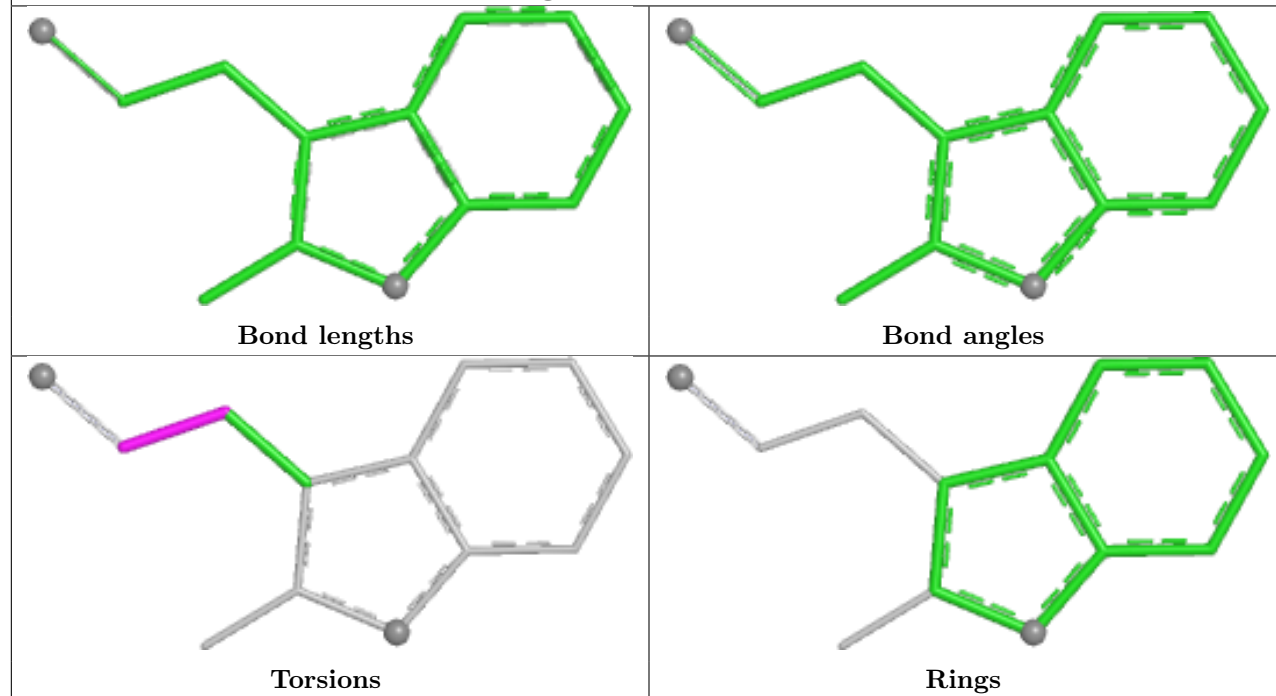
Ligand F66 A 401



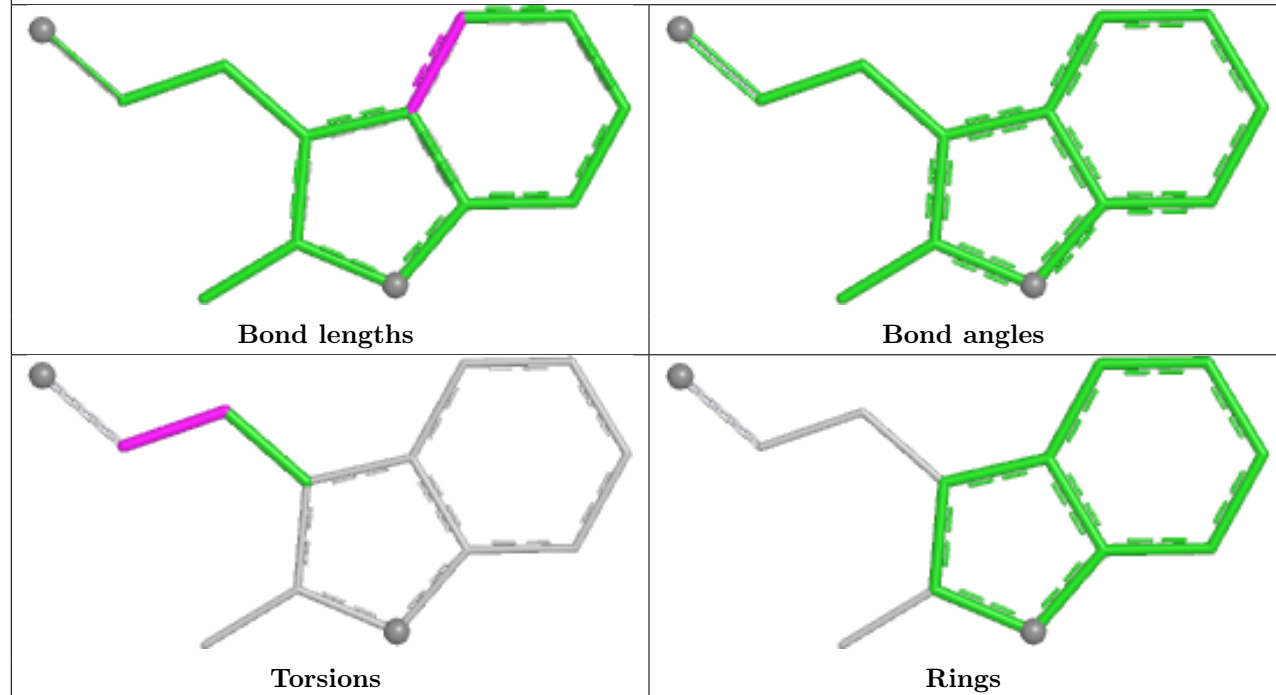
Ligand F66 F 401



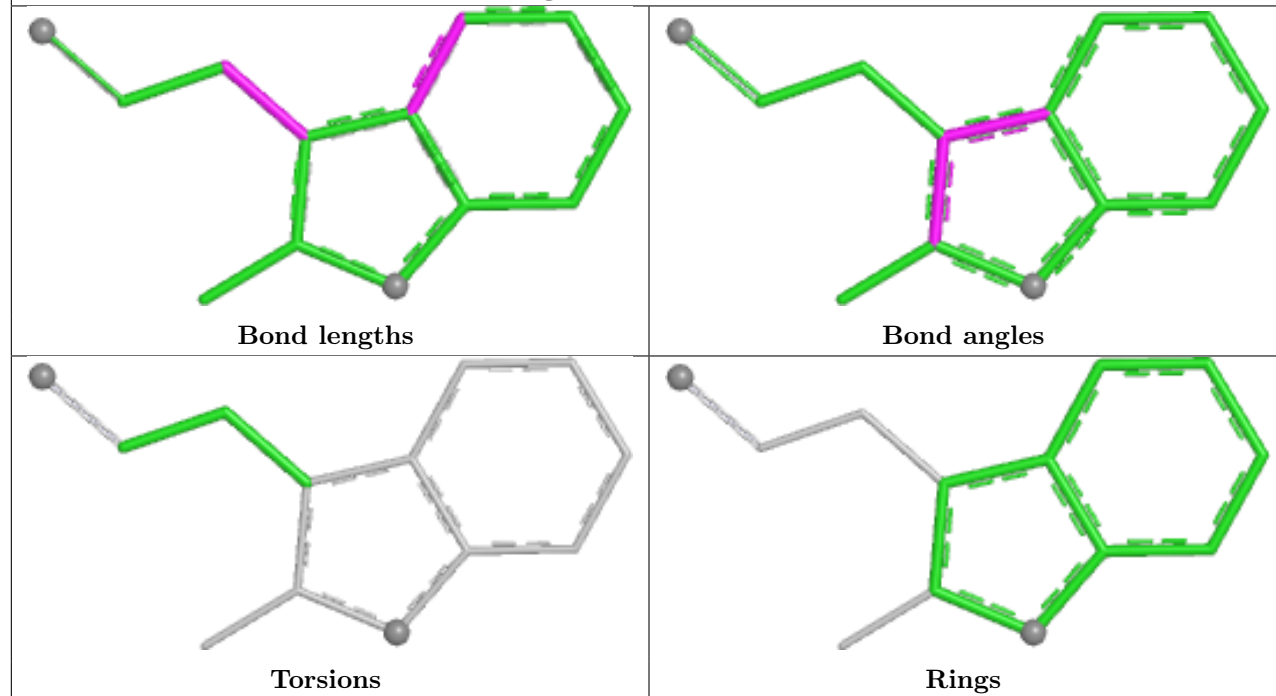
Ligand F66 G 401



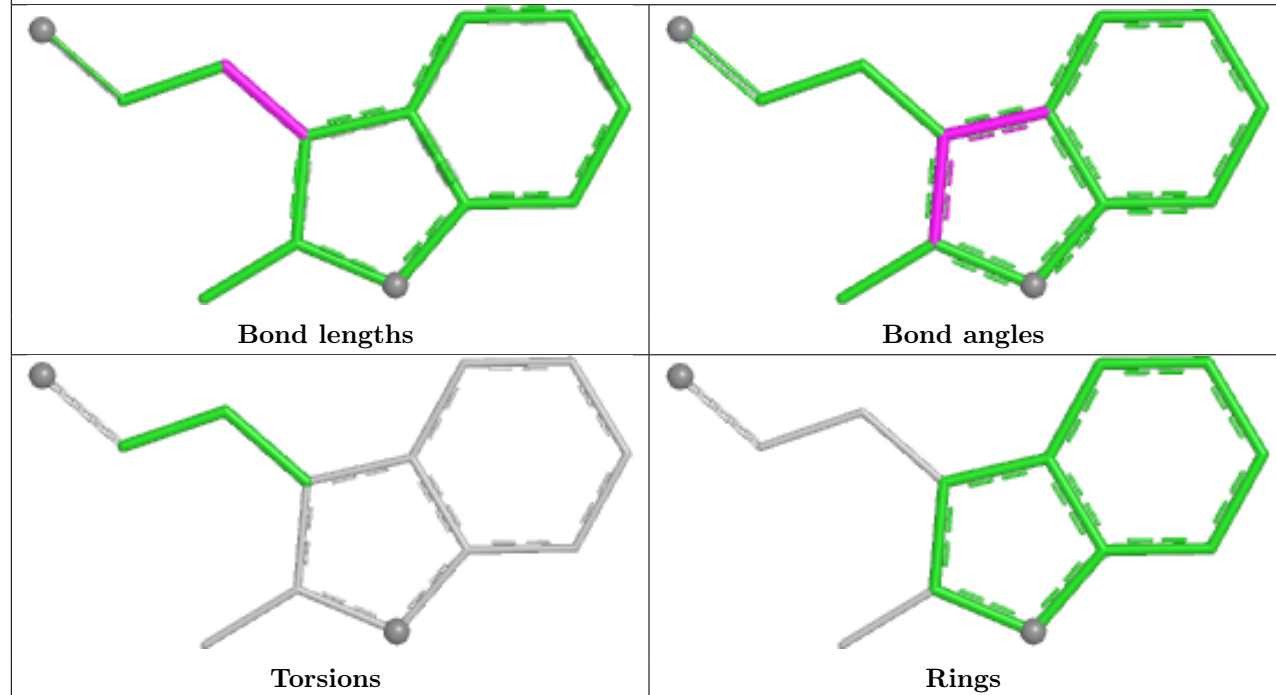
Ligand F66 D 401

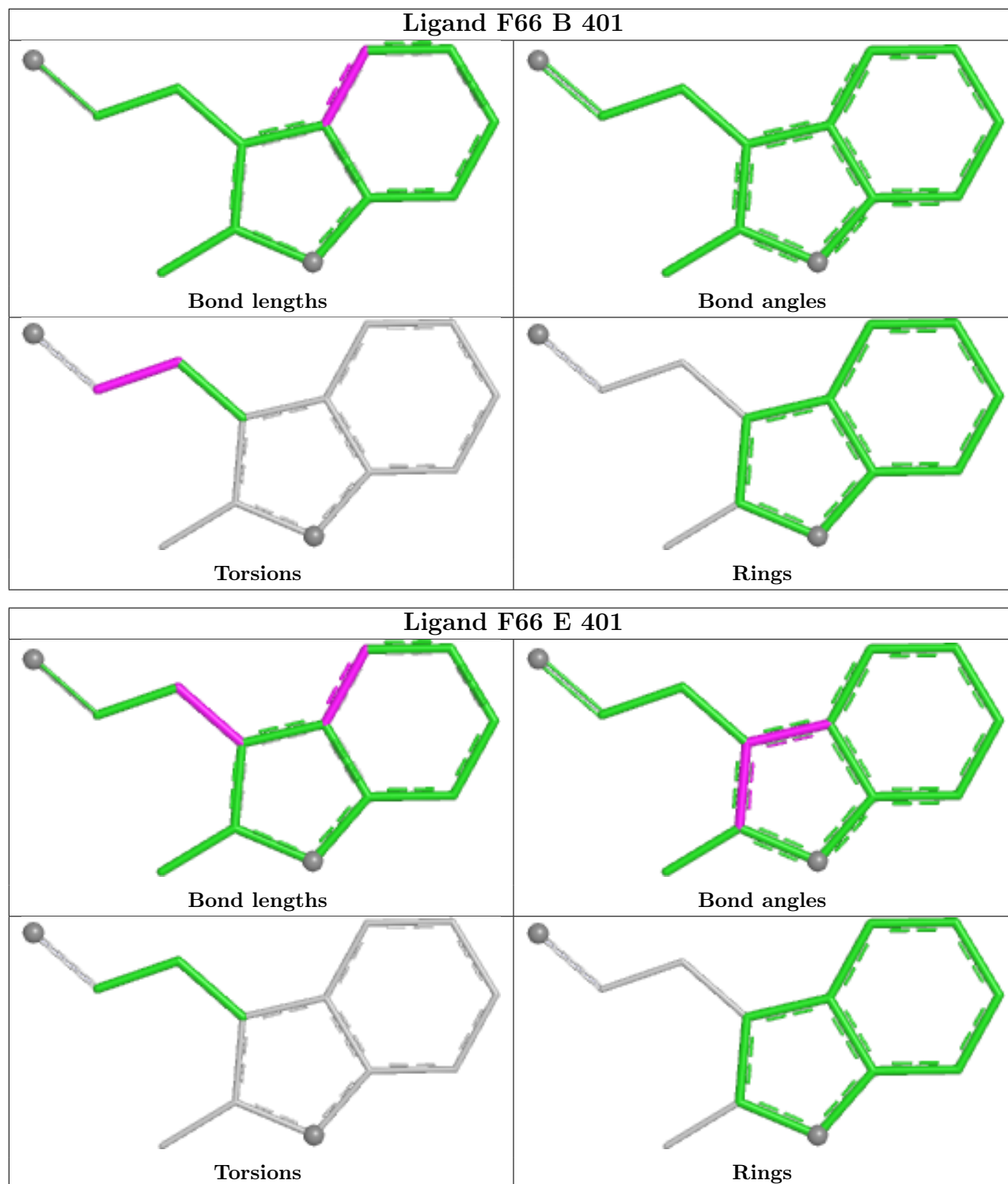


Ligand F66 C 401



Ligand F66 H 401





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	303/318 (95%)	-0.36	3 (0%) 79 77	21, 38, 70, 89	1 (0%)
1	B	302/318 (94%)	-0.23	9 (2%) 52 48	19, 39, 74, 132	2 (0%)
1	C	302/318 (94%)	-0.25	2 (0%) 84 82	26, 42, 72, 91	1 (0%)
1	D	302/318 (94%)	-0.28	5 (1%) 69 66	20, 38, 69, 121	2 (0%)
1	E	302/318 (94%)	0.05	3 (0%) 79 77	26, 55, 88, 121	1 (0%)
1	F	304/318 (95%)	-0.02	6 (1%) 65 61	21, 54, 93, 117	1 (0%)
1	G	307/318 (96%)	0.01	3 (0%) 79 77	32, 58, 88, 117	0
1	H	304/318 (95%)	-0.10	3 (0%) 79 77	26, 51, 82, 93	0
All	All	2426/2544 (95%)	-0.15	34 (1%) 73 71	19, 46, 84, 132	8 (0%)

All (34) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	277	HIS	3.8
1	B	272	LEU	3.6
1	D	277	HIS	3.4
1	D	276	MET	3.3
1	E	71	ASN	3.0
1	H	210	GLY	2.9
1	A	70	PRO	2.8
1	B	280	VAL	2.8
1	H	30	ILE	2.8
1	E	70	PRO	2.7
1	B	279	ARG	2.6
1	C	210	GLY	2.6
1	E	69	GLY	2.6
1	F	70	PRO	2.6
1	B	276	MET	2.5
1	F	334	ASP	2.5

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Mol	Chain	Res	Type	RSRZ
1	G	70	PRO	2.5
1	B	274	GLY	2.5
1	B	275	ASN	2.5
1	F	275	ASN	2.4
1	B	281	ASP	2.4
1	B	282	PRO	2.4
1	C	70	PRO	2.3
1	G	85	ASN	2.2
1	D	278	GLY	2.2
1	F	324	PHE	2.2
1	G	29	PRO	2.2
1	F	276	MET	2.2
1	A	72	SER	2.2
1	D	70	PRO	2.1
1	F	274	GLY	2.1
1	A	109	TYR	2.1
1	H	70	PRO	2.0
1	D	71	ASN	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	PEG	H	402	7/7	0.68	0.14	70,85,96,96	0
3	PEG	D	403	7/7	0.75	0.15	63,71,77,79	0
2	F66	B	401	13/13	0.76	0.26	74,81,85,86	0
3	PEG	B	402	7/7	0.78	0.11	64,67,70,73	0
3	PEG	D	402	7/7	0.78	0.20	48,57,65,66	0

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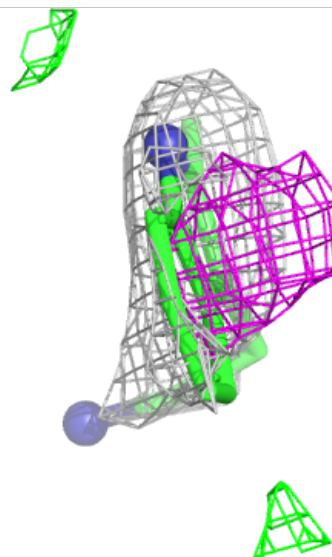
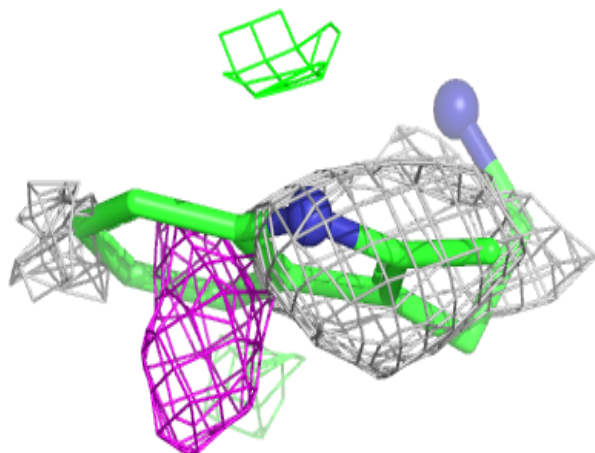
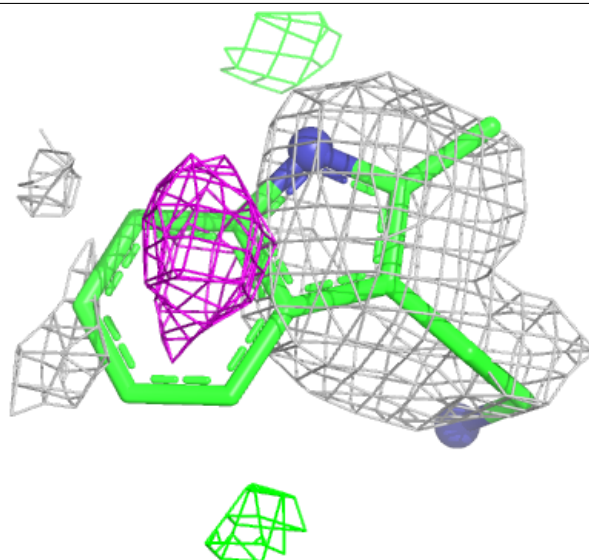
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	F66	D	401	13/13	0.79	0.25	72,80,90,92	0
3	PEG	E	402	7/7	0.80	0.14	58,63,65,69	0
2	F66	C	401	13/13	0.80	0.23	69,79,80,81	0
2	F66	A	401	13/13	0.81	0.25	78,83,92,92	0
3	PEG	F	402	7/7	0.82	0.15	58,67,71,76	0
2	F66	G	401	13/13	0.83	0.21	84,87,93,94	0
2	F66	E	401	13/13	0.84	0.24	76,83,93,94	0
2	F66	H	401	13/13	0.84	0.17	70,75,79,79	0
2	F66	F	401	13/13	0.86	0.25	109,115,122,125	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.

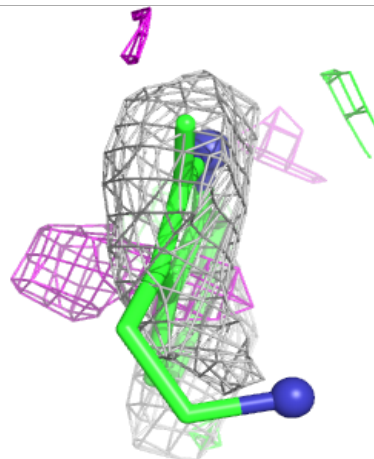
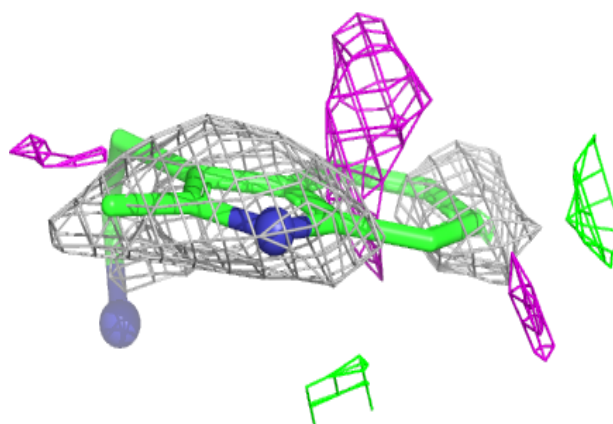
Electron density around F66 B 401:

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



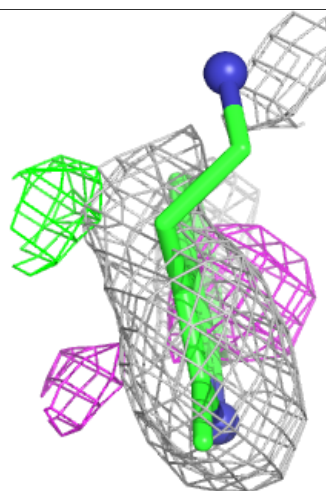
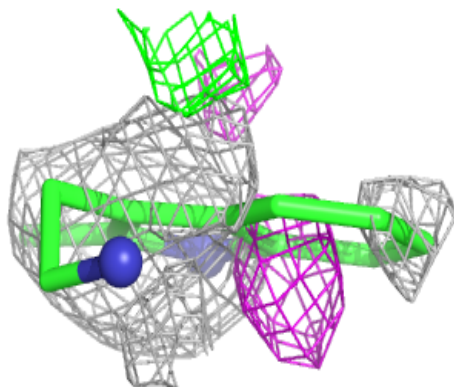
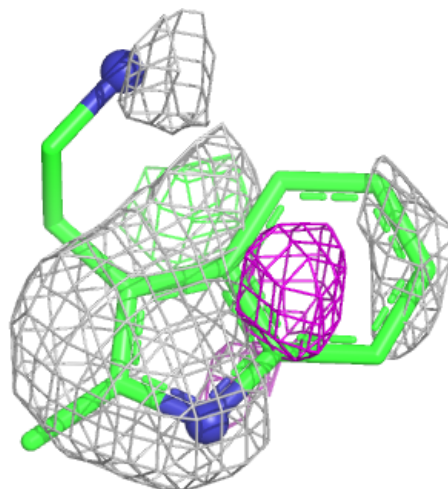
Electron density around F66 D 401:

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



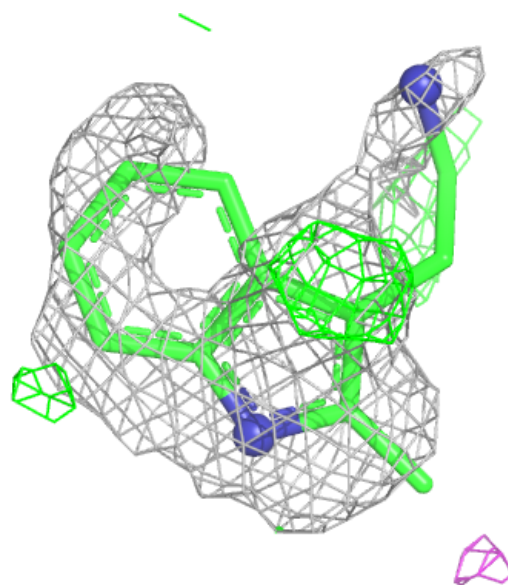
Electron density around F66 C 401:

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



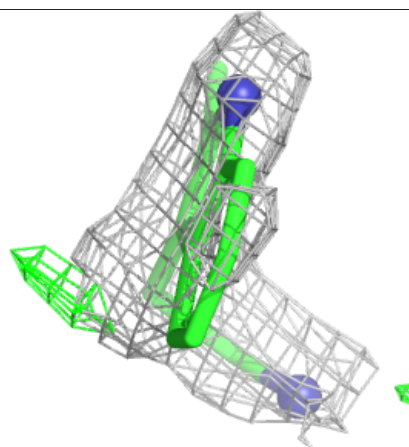
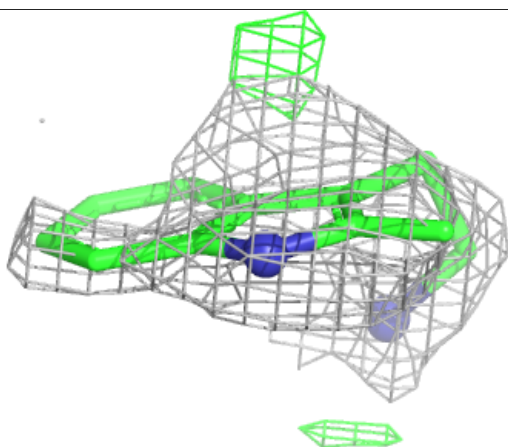
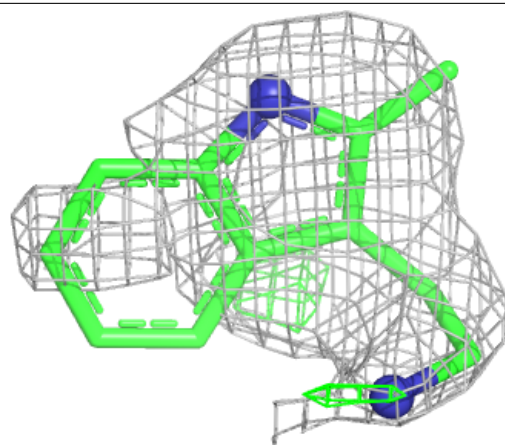
Electron density around F66 A 401:

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



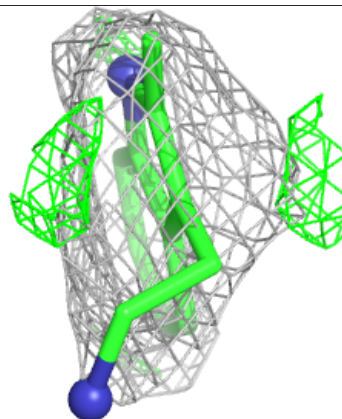
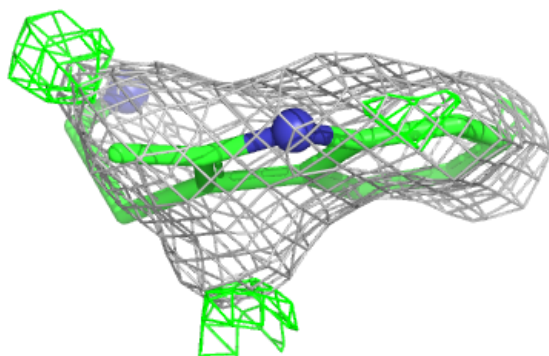
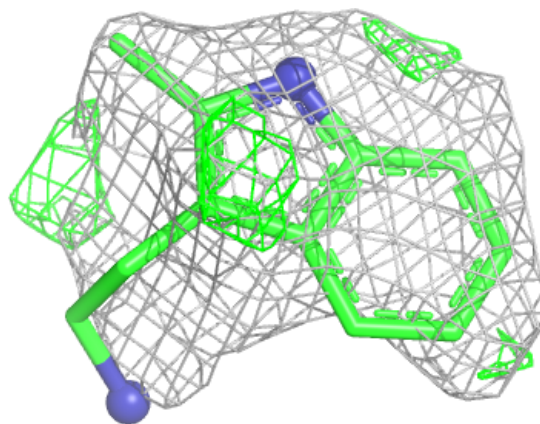
Electron density around F66 G 401:

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



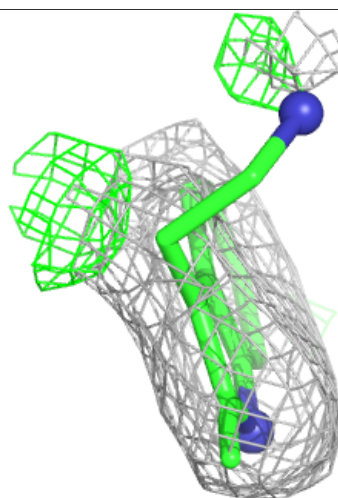
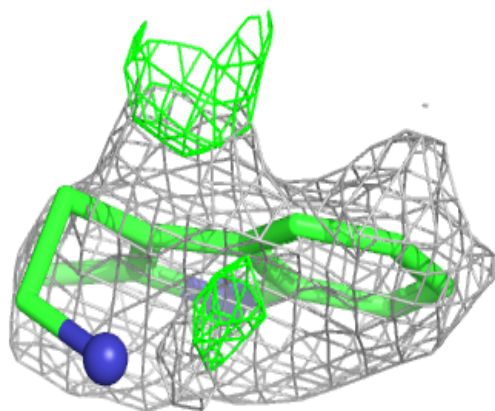
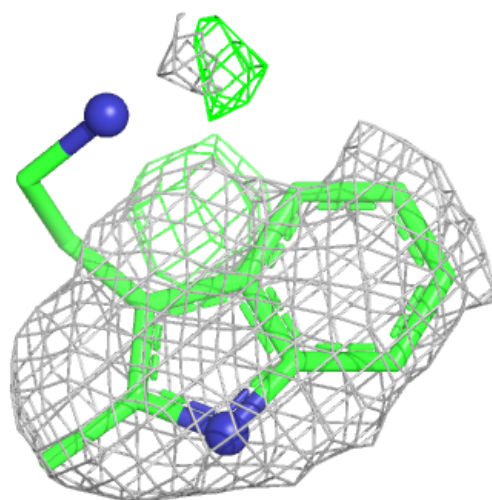
Electron density around F66 E 401:

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



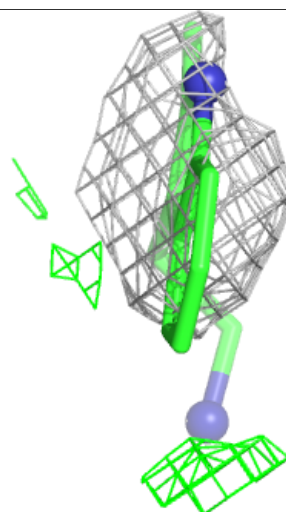
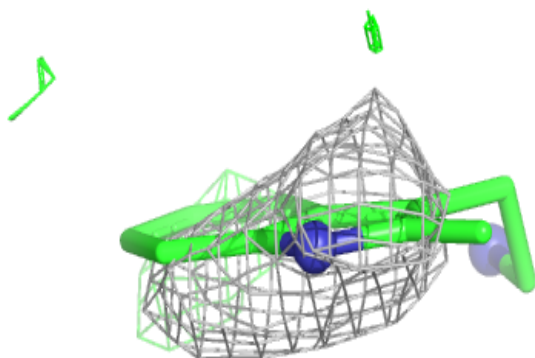
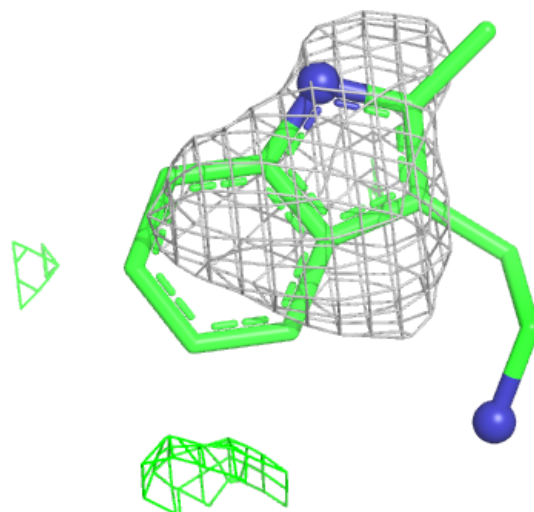
Electron density around F66 H 401:

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



Electron density around F66 F 401:

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



6.5 Other polymers [i](#)

There are no such residues in this entry.