



Full wwPDB X-ray Structure Validation Report ⓘ

Jul 24, 2024 – 10:10 pm BST

PDB ID : 8QXC
Title : Crystal structure of antibody Fab MIL-3 with PenG-Lys
Authors : Moynie, L.; Naismith, J.H.
Deposited on : 2023-10-24
Resolution : 2.30 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 : 4.02b-467
Mogul : 1.8.4, CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.37.1
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.37.1

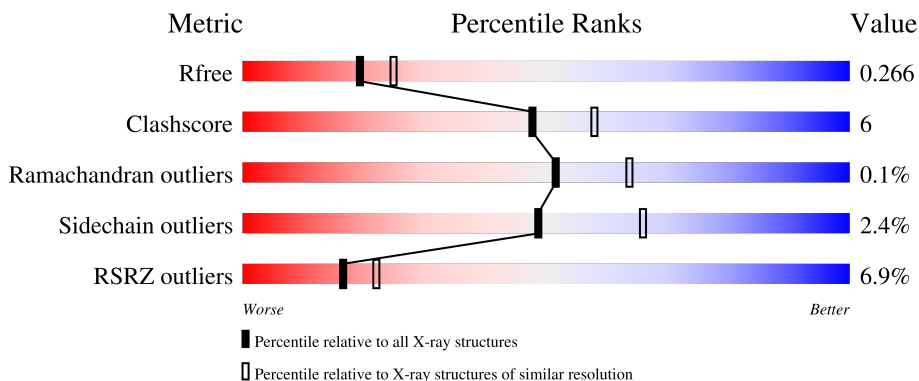
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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}	130704	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

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	264	
1	C	264	
1	H	264	
2	B	233	
2	D	233	

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Mol	Chain	Length	Quality of chain
2	L	233	 81% 10% 8%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 9890 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.

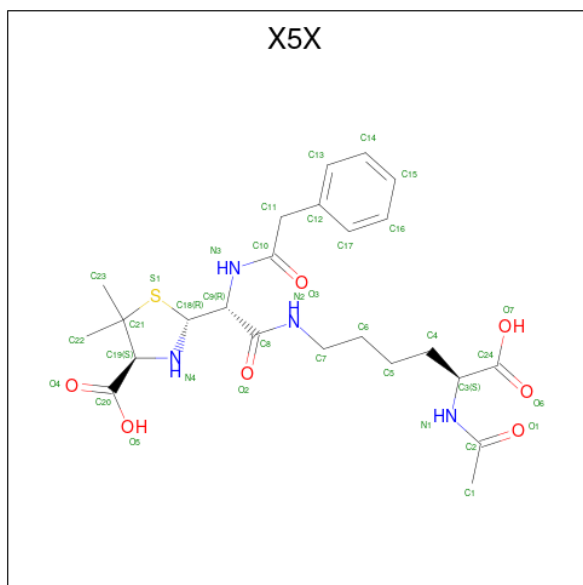
- Molecule 1 is a protein called Heavy chain of FAB MIL-3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	H	221	Total 1672	C 1054	N 284	O 325	S 9	0	0	0
1	A	219	Total 1660	C 1048	N 282	O 322	S 8	0	0	0
1	C	195	Total 1458	C 922	N 244	O 284	S 8	0	0	0

- Molecule 2 is a protein called Light chain of FAB MIL-3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	L	214	Total 1663	C 1043	N 273	O 340	S 7	0	0	0
2	B	211	Total 1644	C 1033	N 270	O 335	S 6	0	0	0
2	D	211	Total 1639	C 1030	N 270	O 333	S 6	0	0	0

- Molecule 3 is (2R,4S)-2-[(1R)-2-[[[(5S)-5-acetamido-6-oxidanyl-6-oxidanylidene-hexyl]amino]-2-oxidanylidene-1-(2-phenylethanoylamino)ethyl]-5,5-dimethyl-1,3-thiazolidine-4-carboxylic acid (three-letter code: X5X) (formula: C₂₄H₃₄N₄O₇S) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	S		
3	H	1	36	24	4	7	1	0	0
3	A	1	36	24	4	7	1	0	0

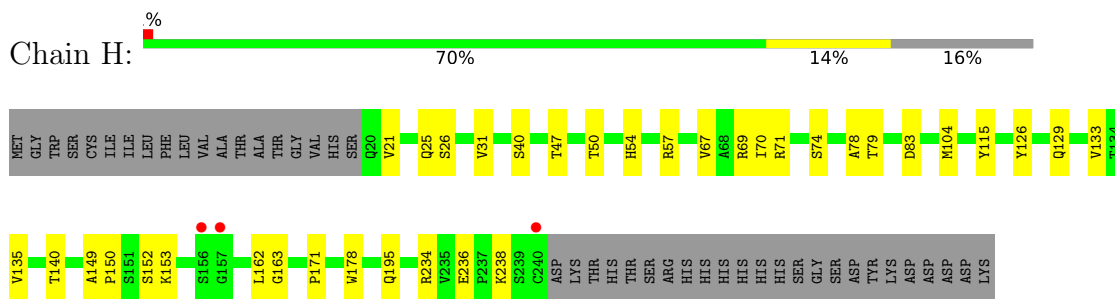
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
4	H	19	19	19	0	0
4	A	20	20	20	0	0
4	L	21	21	21	0	0
4	B	11	11	11	0	0
4	C	5	5	5	0	0
4	D	6	6	6	0	0

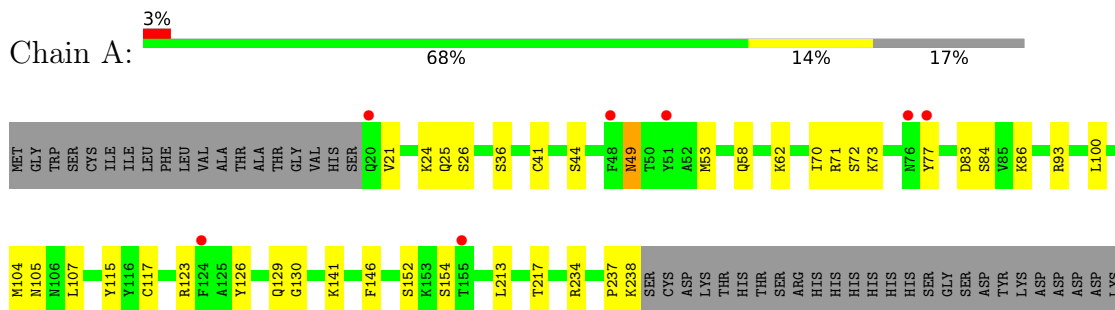
3 Residue-property plots [i](#)

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.

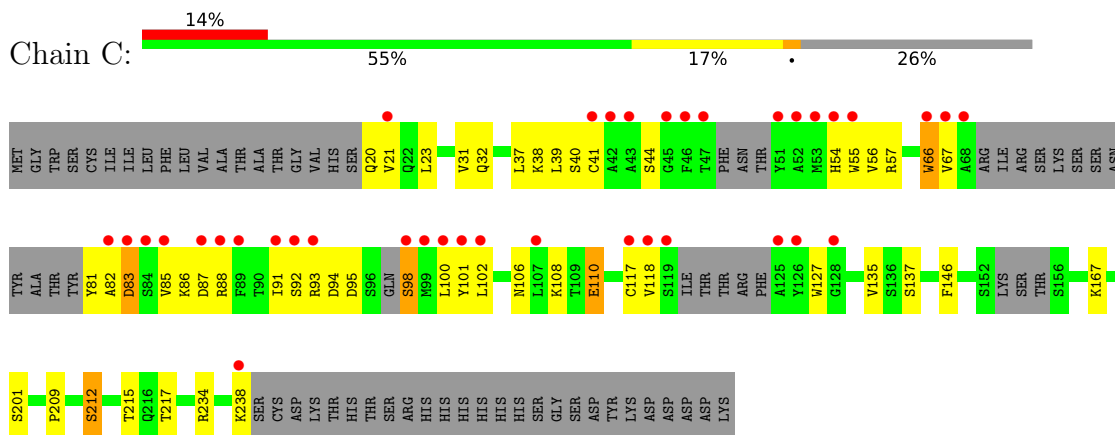
- Molecule 1: Heavy chain of FAB MIL-3




- Molecule 1: Heavy chain of FAB MIL-3

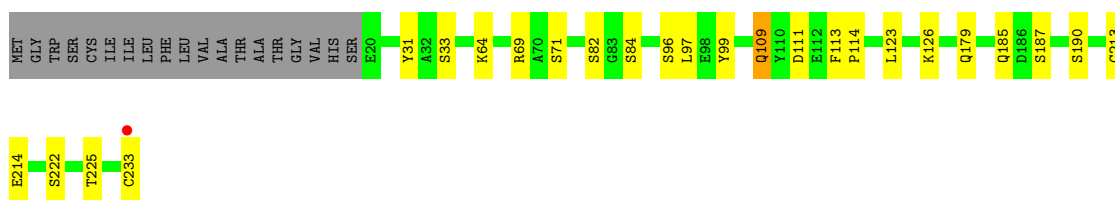


- Molecule 1: Heavy chain of FAB MIL-3




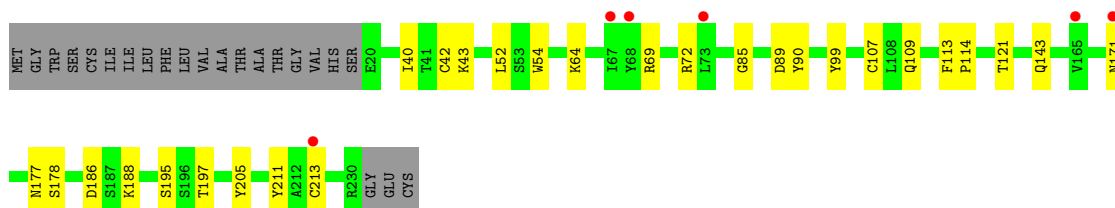
- Molecule 2: Light chain of FAB MIL-3

Chain L:  81% 10% 8%




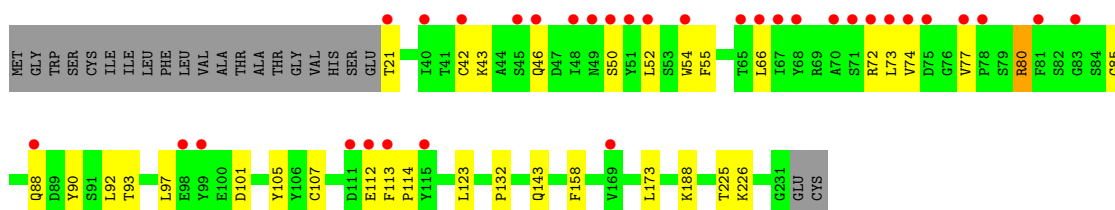
- Molecule 2: Light chain of FAB MIL-3

Chain B:  3% 79% 12% 9%



- Molecule 2: Light chain of FAB MIL-3

Chain D:  14% 76% 14% 9%



4 Data and refinement statistics i

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	81.57Å 113.24Å 82.87Å 90.00° 108.80° 90.00°	Depositor
Resolution (Å)	66.84 – 2.30 66.84 – 2.30	Depositor EDS
% Data completeness (in resolution range)	99.7 (66.84-2.30) 99.7 (66.84-2.30)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.08 (at 2.29Å)	Xtrriage
Refinement program	PHENIX 1.14_3260	Depositor
R, R_{free}	0.217 , 0.266 0.217 , 0.266	Depositor DCC
R_{free} test set	2099 reflections (3.32%)	wwPDB-VP
Wilson B-factor (Å ²)	44.2	Xtrriage
Anisotropy	0.174	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 29.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	0.005 for l,-k,h	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	9890	wwPDB-VP
Average B, all atoms (Å ²)	49.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.52% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: X5X

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	0.46	0/1699	0.65	0/2310
1	C	0.52	0/1488	0.78	3/2018 (0.1%)
1	H	0.48	0/1711	0.68	1/2326 (0.0%)
2	B	0.50	1/1680 (0.1%)	0.66	1/2277 (0.0%)
2	D	0.51	0/1675	0.80	6/2270 (0.3%)
2	L	0.47	1/1699 (0.1%)	0.63	0/2302
All	All	0.49	2/9952 (0.0%)	0.70	11/13503 (0.1%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	213	CYS	CB-SG	-7.16	1.70	1.82
2	L	213	CYS	CB-SG	-5.30	1.73	1.81

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	80	ARG	NE-CZ-NH2	9.21	124.91	120.30
2	D	80	ARG	NE-CZ-NH1	-7.18	116.71	120.30
1	C	110	GLU	OE1-CD-OE2	6.75	131.40	123.30
2	D	112	GLU	CA-CB-CG	6.60	127.91	113.40
2	B	72	ARG	NE-CZ-NH1	-6.43	117.08	120.30
2	D	80	ARG	CG-CD-NE	6.36	125.16	111.80
1	C	98	SER	N-CA-C	-6.13	94.46	111.00
1	C	83	ASP	CB-CG-OD2	-5.84	113.05	118.30
2	D	188	LYS	CA-CB-CG	5.70	125.93	113.40
2	D	188	LYS	CB-CA-C	-5.61	99.19	110.40
1	H	236	GLU	CA-CB-CG	5.27	125.00	113.40

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	1660	0	1641	24	0
1	C	1458	0	1433	34	0
1	H	1672	0	1651	19	0
2	B	1644	0	1590	13	0
2	D	1639	0	1587	20	0
2	L	1663	0	1604	12	0
3	A	36	0	0	1	0
3	H	36	0	0	0	0
4	A	20	0	0	1	0
4	B	11	0	0	0	0
4	C	5	0	0	0	0
4	D	6	0	0	0	0
4	H	19	0	0	0	0
4	L	21	0	0	0	0
All	All	9890	0	9506	118	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 6.

All (118) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:94:ASP:O	1:C:98:SER:N	2.04	0.90
1:C:88:ARG:NH1	1:C:106:ASN:O	2.04	0.90
1:C:83:ASP:O	1:C:86:LYS:HE2	1.75	0.86
1:C:86:LYS:HG3	1:C:87:ASP:H	1.40	0.85
1:A:217:THR:HG23	1:A:234:ARG:HE	1.45	0.81
1:A:83:ASP:HA	1:A:86:LYS:HD3	1.68	0.75
2:D:52:LEU:HD21	2:D:107:CYS:HB2	1.69	0.72
1:C:54:HIS:HB2	1:C:118:VAL:HG23	1.72	0.71
1:A:21:VAL:HG21	1:A:126:TYR:CZ	2.27	0.70
1:A:213:LEU:HD13	1:A:237:PRO:HG2	1.73	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:141:LYS:NZ	4:A:402:HOH:O	2.27	0.68
2:D:80:ARG:NH2	2:D:101:ASP:OD1	2.27	0.68
1:H:149:ALA:HB3	1:H:238:LYS:HD2	1.77	0.67
1:A:58:GLN:NE2	1:A:62:LYS:O	2.22	0.65
1:C:41:CYS:HB3	1:C:100:LEU:HD23	1.78	0.65
1:H:57:ARG:HG3	1:H:67:VAL:HG21	1.79	0.64
1:C:23:LEU:HB3	1:C:41:CYS:SG	2.37	0.63
1:C:88:ARG:HH12	1:C:108:LYS:HG3	1.62	0.63
1:C:88:ARG:NH1	1:C:108:LYS:HG3	2.13	0.62
1:C:118:VAL:HG12	1:C:127:TRP:HA	1.82	0.61
2:D:173:LEU:H	2:D:173:LEU:HD12	1.65	0.60
1:H:195:GLN:HA	2:L:179:GLN:HE22	1.67	0.58
1:H:57:ARG:HG3	1:H:67:VAL:CG2	2.34	0.58
2:L:214:GLU:HG2	2:L:225:THR:HG22	1.85	0.58
1:C:86:LYS:HG3	1:C:87:ASP:N	2.16	0.58
1:C:55:TRP:NE1	1:C:102:LEU:HB2	2.18	0.58
2:L:97:LEU:HD11	2:L:123:LEU:HD21	1.85	0.57
2:D:97:LEU:HD11	2:D:123:LEU:HD21	1.85	0.57
1:A:36:SER:OG	1:A:105:ASN:OD1	2.23	0.56
1:C:100:LEU:CD2	1:C:117:CYS:HB2	2.36	0.55
1:A:25:GLN:H	1:A:129:GLN:HE22	1.55	0.55
2:D:50:SER:HA	2:D:90:TYR:CE2	2.41	0.55
2:D:73:LEU:HD23	2:D:74:VAL:O	2.07	0.54
1:A:21:VAL:HG11	1:A:126:TYR:CG	2.44	0.53
1:A:71:ARG:O	1:A:93:ARG:NH1	2.41	0.53
1:A:41:CYS:HB3	1:A:100:LEU:HB3	1.91	0.53
1:H:47:THR:HG22	1:H:50:THR:HG23	1.91	0.52
1:C:110:GLU:H	1:C:110:GLU:CD	2.12	0.52
1:A:21:VAL:HG11	1:A:126:TYR:CD2	2.44	0.52
1:A:104:MET:HB3	1:A:107:LEU:HD21	1.92	0.51
1:C:40:SER:HA	1:C:100:LEU:O	2.09	0.51
2:D:113:PHE:CD1	2:D:114:PRO:HA	2.45	0.51
1:A:73:LYS:HG3	1:A:77:TYR:CZ	2.46	0.51
1:C:39:LEU:O	1:C:101:TYR:HA	2.10	0.51
2:L:31:TYR:HB3	2:L:126:LYS:HG3	1.92	0.51
1:C:81:TYR:OH	1:C:91:ILE:HG22	2.11	0.51
1:C:167:LYS:HA	1:C:201:SER:HB2	1.92	0.50
1:H:70:ILE:HG13	1:H:79:THR:HG22	1.93	0.50
1:A:53:MET:HB3	1:A:100:LEU:HD22	1.94	0.50
2:D:54:TRP:CZ3	2:D:107:CYS:HB3	2.46	0.49
2:B:186:ASP:OD1	2:B:188:LYS:HG2	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:57:ARG:HG3	1:C:67:VAL:CG2	2.42	0.49
2:B:178:SER:HA	2:B:197:THR:O	2.12	0.49
1:H:150:PRO:HD3	1:H:162:LEU:HB3	1.94	0.48
2:D:50:SER:HA	2:D:90:TYR:HE2	1.79	0.48
1:C:38:LYS:HA	1:C:102:LEU:O	2.13	0.48
2:L:99:TYR:OH	2:L:187:SER:HB2	2.14	0.48
2:D:132:PRO:HB3	2:D:158:PHE:HB3	1.95	0.48
1:A:123:ARG:HH11	1:A:123:ARG:HG2	1.78	0.47
2:L:109:GLN:OE1	2:L:111:ASP:N	2.45	0.47
2:B:42:CYS:HB2	2:B:54:TRP:CH2	2.50	0.47
2:B:40:ILE:HG12	2:B:121:THR:HG21	1.95	0.47
1:C:238:LYS:HD3	1:C:238:LYS:HA	1.52	0.47
2:D:66:LEU:HA	2:D:77:VAL:HG21	1.97	0.47
2:D:225:THR:O	2:D:226:LYS:HD3	2.14	0.47
1:C:146:PHE:CE2	2:D:143:GLN:HG3	2.50	0.47
1:C:20:GLN:HG2	1:C:21:VAL:N	2.30	0.47
1:H:26:SER:OG	1:H:40:SER:HB2	2.16	0.46
2:B:69:ARG:HD2	2:B:69:ARG:HA	1.77	0.46
1:H:71:ARG:HD3	1:H:78:ALA:HB3	1.98	0.46
2:B:205:TYR:O	2:B:211:TYR:OH	2.31	0.46
1:C:54:HIS:CD2	1:C:66:TRP:HZ2	2.33	0.46
1:A:49:ASN:OD1	1:A:49:ASN:N	2.49	0.46
2:L:96:SER:O	2:L:96:SER:OG	2.33	0.45
2:D:21:THR:HG21	2:D:46:GLN:HG2	1.98	0.45
1:H:104:MET:HE1	1:H:133:VAL:HG21	1.97	0.45
1:H:234:ARG:CD	1:C:215:THR:HG21	2.47	0.45
2:L:214:GLU:HG2	2:L:225:THR:CG2	2.46	0.45
1:H:140:THR:HG22	1:H:171:PRO:HD3	1.99	0.45
1:A:146:PHE:CE2	2:B:143:GLN:HG3	2.52	0.45
2:B:43:LYS:HE2	2:B:89:ASP:OD1	2.17	0.45
1:C:31:VAL:O	1:C:135:VAL:HA	2.16	0.45
2:B:113:PHE:CG	2:B:114:PRO:HA	2.51	0.44
2:D:92:LEU:HD12	2:D:93:THR:H	1.82	0.44
2:L:185:GLN:NE2	2:L:190:SER:HB3	2.32	0.44
1:C:37:LEU:HD23	1:C:38:LYS:H	1.83	0.44
1:H:21:VAL:HG11	1:H:126:TYR:CG	2.53	0.44
2:D:43:LYS:HA	2:D:88:GLN:O	2.18	0.44
1:H:57:ARG:HD3	1:H:115:TYR:CZ	2.53	0.43
1:H:149:ALA:CB	1:H:238:LYS:HD2	2.48	0.43
1:A:72:SER:HB3	3:A:301:X5X:O7	2.19	0.43
2:B:177:ASN:OD1	2:B:177:ASN:N	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:209:PRO:O	1:C:212:SER:HB3	2.18	0.43
2:L:113:PHE:CG	2:L:114:PRO:HA	2.54	0.43
1:A:115:TYR:O	1:A:130:GLY:HA2	2.19	0.43
2:D:85:GLY:HA3	2:D:90:TYR:HA	2.00	0.42
1:A:25:GLN:H	1:A:129:GLN:NE2	2.17	0.42
1:H:163:GLY:HA2	1:H:178:TRP:CZ2	2.54	0.42
1:H:31:VAL:O	1:H:135:VAL:HA	2.19	0.42
1:H:25:GLN:H	1:H:129:GLN:HE22	1.67	0.42
1:H:54:HIS:CE1	1:H:69:ARG:HG3	2.55	0.42
1:C:37:LEU:HD23	1:C:38:LYS:N	2.34	0.41
2:L:69:ARG:O	2:L:71:SER:N	2.52	0.41
2:B:52:LEU:HD21	2:B:107:CYS:HB2	2.01	0.41
1:C:56:VAL:HG23	1:C:118:VAL:HG21	2.03	0.41
2:L:64:LYS:HE2	2:L:64:LYS:HB3	1.85	0.41
2:D:55:PHE:O	2:D:105:TYR:HA	2.21	0.41
1:A:70:ILE:HG12	1:A:93:ARG:HD2	2.03	0.41
1:A:100:LEU:HD23	1:A:117:CYS:HB2	2.00	0.41
2:D:73:LEU:HD21	2:D:77:VAL:O	2.20	0.41
2:B:64:LYS:HA	2:B:64:LYS:HD2	1.80	0.41
1:C:55:TRP:CE2	1:C:102:LEU:HB2	2.55	0.41
1:A:238:LYS:HD2	1:A:238:LYS:HA	1.81	0.41
1:C:32:GLN:HB3	1:C:137:SER:HA	2.03	0.41
1:C:82:ALA:HB3	1:C:85:VAL:HG22	2.03	0.41
1:C:217:THR:HG23	1:C:234:ARG:NH1	2.36	0.40
2:D:42:CYS:HB2	2:D:54:TRP:CH2	2.56	0.40
2:B:85:GLY:HA3	2:B:90:TYR:HA	2.04	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [\(i\)](#)

5.3.1 Protein backbone [\(i\)](#)

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	217/264 (82%)	208 (96%)	9 (4%)	0	100	100
1	C	183/264 (69%)	177 (97%)	6 (3%)	0	100	100
1	H	219/264 (83%)	210 (96%)	8 (4%)	1 (0%)	29	35
2	B	209/233 (90%)	206 (99%)	3 (1%)	0	100	100
2	D	209/233 (90%)	204 (98%)	5 (2%)	0	100	100
2	L	212/233 (91%)	208 (98%)	4 (2%)	0	100	100
All	All	1249/1491 (84%)	1213 (97%)	35 (3%)	1 (0%)	51	64

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	H	152	SER

5.3.2 Protein sidechains [i](#)

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	187/227 (82%)	180 (96%)	7 (4%)	34	48
1	C	164/227 (72%)	158 (96%)	6 (4%)	34	48
1	H	189/227 (83%)	186 (98%)	3 (2%)	62	78
2	B	188/205 (92%)	184 (98%)	4 (2%)	53	70
2	D	187/205 (91%)	186 (100%)	1 (0%)	88	95
2	L	190/205 (93%)	184 (97%)	6 (3%)	39	54
All	All	1105/1296 (85%)	1078 (98%)	27 (2%)	49	66

All (27) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	H	74	SER
1	H	83	ASP
1	H	153	LYS
1	A	24	LYS

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Mol	Chain	Res	Type
1	A	26	SER
1	A	44	SER
1	A	49	ASN
1	A	84	SER
1	A	152	SER
1	A	154	SER
2	L	33	SER
2	L	82	SER
2	L	84	SER
2	L	109	GLN
2	L	222	SER
2	L	233	CYS
2	B	99	TYR
2	B	109	GLN
2	B	171	ASN
2	B	195	SER
1	C	44	SER
1	C	66	TRP
1	C	92	SER
1	C	93	ARG
1	C	95	ASP
1	C	212	SER
2	D	72	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	129	GLN
1	A	223	ASN
1	C	32	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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

2 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
3	X5X	A	301	-	33,37,37	0.76	1 (3%)	42,51,51	1.00	3 (7%)
3	X5X	H	301	-	33,37,37	0.77	1 (3%)	42,51,51	1.09	3 (7%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	X5X	A	301	-	-	9/32/51/51	0/2/2/2
3	X5X	H	301	-	-	4/32/51/51	0/2/2/2

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	H	301	X5X	C21-S1	-2.63	1.80	1.85
3	A	301	X5X	C21-S1	-2.50	1.80	1.85

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	H	301	X5X	C18-C9-N3	4.57	120.05	110.02
3	A	301	X5X	C18-C9-N3	4.04	118.87	110.02
3	H	301	X5X	C7-N2-C8	2.92	127.79	122.59
3	A	301	X5X	C19-C21-S1	-2.59	98.67	103.81

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	301	X5X	C9-N3-C10	-2.54	116.97	121.83
3	H	301	X5X	C4-C3-N1	2.04	115.00	110.88

There are no chirality outliers.

All (13) torsion outliers are listed below:

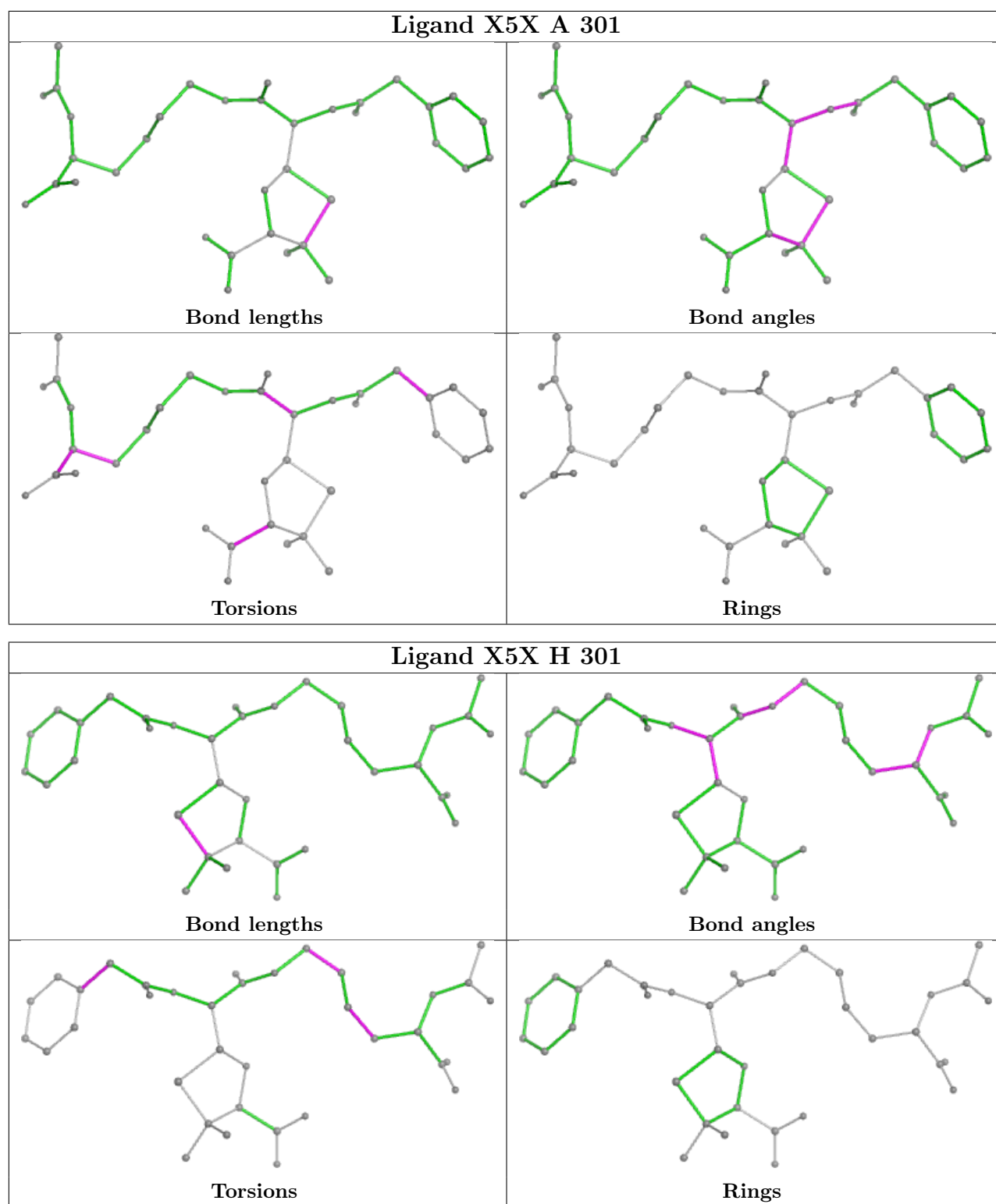
Mol	Chain	Res	Type	Atoms
3	A	301	X5X	N1-C3-C4-C5
3	A	301	X5X	C24-C3-C4-C5
3	H	301	X5X	C5-C6-C7-N2
3	A	301	X5X	O6-C24-C3-N1
3	A	301	X5X	O7-C24-C3-N1
3	H	301	X5X	C3-C4-C5-C6
3	H	301	X5X	C10-C11-C12-C13
3	A	301	X5X	N4-C19-C20-O4
3	A	301	X5X	N4-C19-C20-O5
3	H	301	X5X	C10-C11-C12-C17
3	A	301	X5X	C10-C11-C12-C13
3	A	301	X5X	N2-C8-C9-C18
3	A	301	X5X	C10-C11-C12-C17

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	301	X5X	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



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

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data [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	219/264 (82%)	0.42	7 (3%) 47 54	30, 48, 75, 89	0
1	C	195/264 (73%)	1.10	38 (19%) 1 1	33, 53, 93, 99	0
1	H	221/264 (83%)	0.34	3 (1%) 75 80	31, 40, 60, 96	0
2	B	211/233 (90%)	0.36	6 (2%) 53 60	30, 48, 61, 69	0
2	D	211/233 (90%)	0.90	33 (15%) 2 2	33, 56, 84, 92	0
2	L	214/233 (91%)	0.16	1 (0%) 91 94	28, 42, 53, 81	0
All	All	1271/1491 (85%)	0.54	88 (6%) 16 22	28, 46, 80, 99	0

All (88) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	46	PHE	8.4
2	D	67	ILE	7.4
2	D	73	LEU	6.7
1	C	53	MET	6.0
1	C	54	HIS	5.9
1	C	42	ALA	5.8
1	C	126	TYR	5.6
1	C	43	ALA	5.3
2	D	66	LEU	5.2
1	C	89	PHE	5.1
1	C	51	TYR	5.0
1	C	52	ALA	4.9
1	C	91	ILE	4.8
1	C	45	GLY	4.8
1	C	84	SER	4.7
2	D	51	TYR	4.7
1	C	100	LEU	4.6
2	D	81	PHE	4.5
1	C	119	SER	4.4

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Mol	Chain	Res	Type	RSRZ
2	D	113	PHE	4.4
1	C	93	ARG	4.3
1	C	83	ASP	4.3
1	C	125	ALA	4.2
1	C	238	LYS	4.1
2	D	70	ALA	4.1
1	C	118	VAL	4.0
1	C	41	CYS	4.0
1	C	82	ALA	4.0
2	D	112	GLU	3.9
1	C	47	THR	3.8
2	D	21	THR	3.7
1	A	76	ASN	3.6
1	C	68	ALA	3.6
2	D	52	LEU	3.5
1	H	157	GLY	3.4
2	D	115	TYR	3.4
1	A	20	GLN	3.3
2	D	68	TYR	3.3
2	B	73	LEU	3.3
1	C	117	CYS	3.3
1	H	156	SER	3.2
2	L	233	CYS	3.2
2	D	72	ARG	3.2
2	D	77	VAL	3.1
2	D	48	ILE	3.1
2	D	74	VAL	3.1
1	C	102	LEU	3.1
1	C	66	TRP	3.0
1	C	55	TRP	3.0
1	C	101	TYR	2.9
1	C	88	ARG	2.9
2	D	42	CYS	2.8
2	D	78	PRO	2.8
1	C	92	SER	2.6
1	C	98	SER	2.6
1	H	240	CYS	2.6
1	A	51	TYR	2.5
1	C	107	LEU	2.5
1	C	85	VAL	2.5
2	B	67	ILE	2.4
2	D	45	SER	2.4

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Mol	Chain	Res	Type	RSRZ
1	C	67	VAL	2.3
2	B	68	TYR	2.3
2	D	88	GLN	2.3
1	C	128	GLY	2.3
2	D	54	TRP	2.3
1	A	48	PHE	2.3
2	D	99	TYR	2.3
2	D	50	SER	2.3
2	D	71	SER	2.3
1	A	155	THR	2.2
2	D	49	ASN	2.2
2	D	98	GLU	2.2
1	C	21	VAL	2.2
1	C	87	ASP	2.2
1	A	77	TYR	2.2
2	D	111	ASP	2.1
2	D	65	THR	2.1
2	B	165	VAL	2.1
2	D	83	GLY	2.1
2	B	171	ASN	2.1
2	D	46	GLN	2.1
2	D	40	ILE	2.0
2	D	169	VAL	2.0
1	A	124	PHE	2.0
2	B	213	CYS	2.0
1	C	99	MET	2.0
2	D	75	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 monosaccharides in this entry.

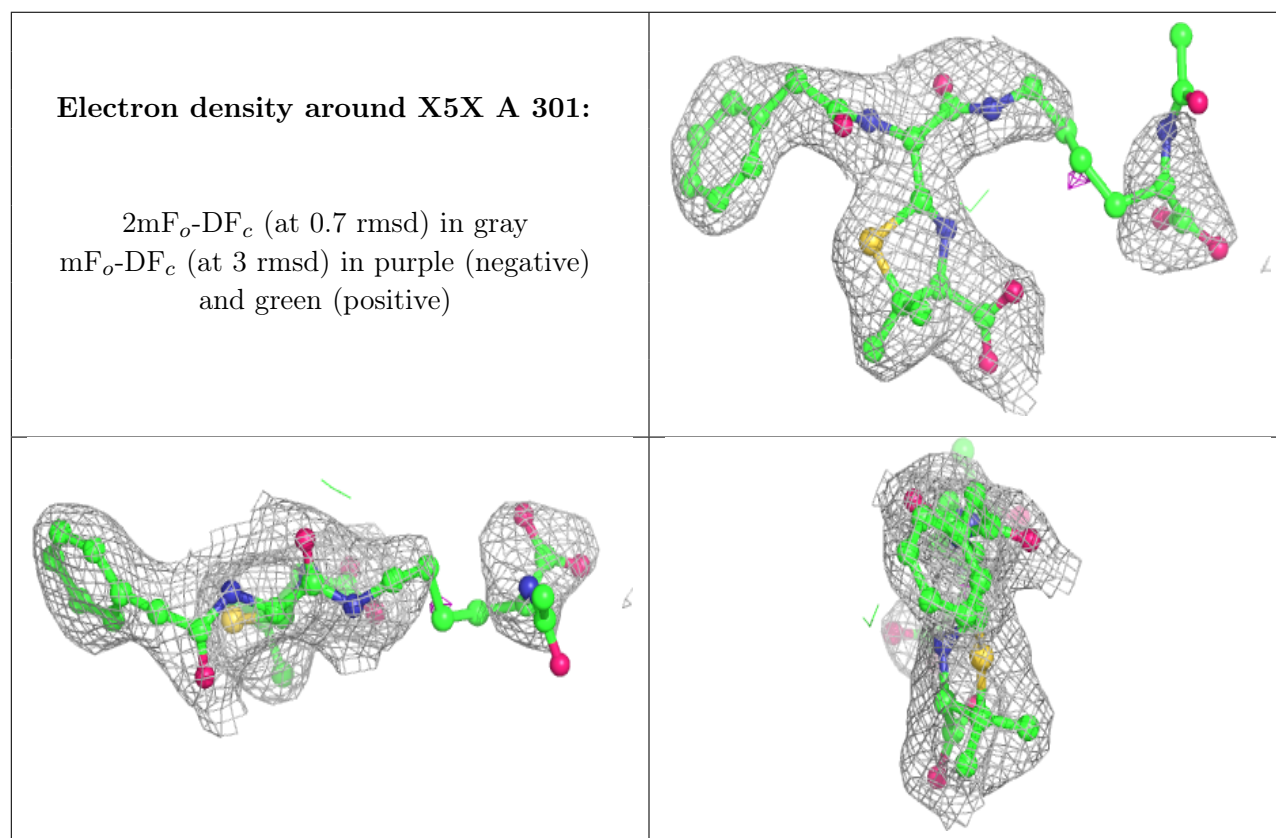
6.4 Ligands [i](#)

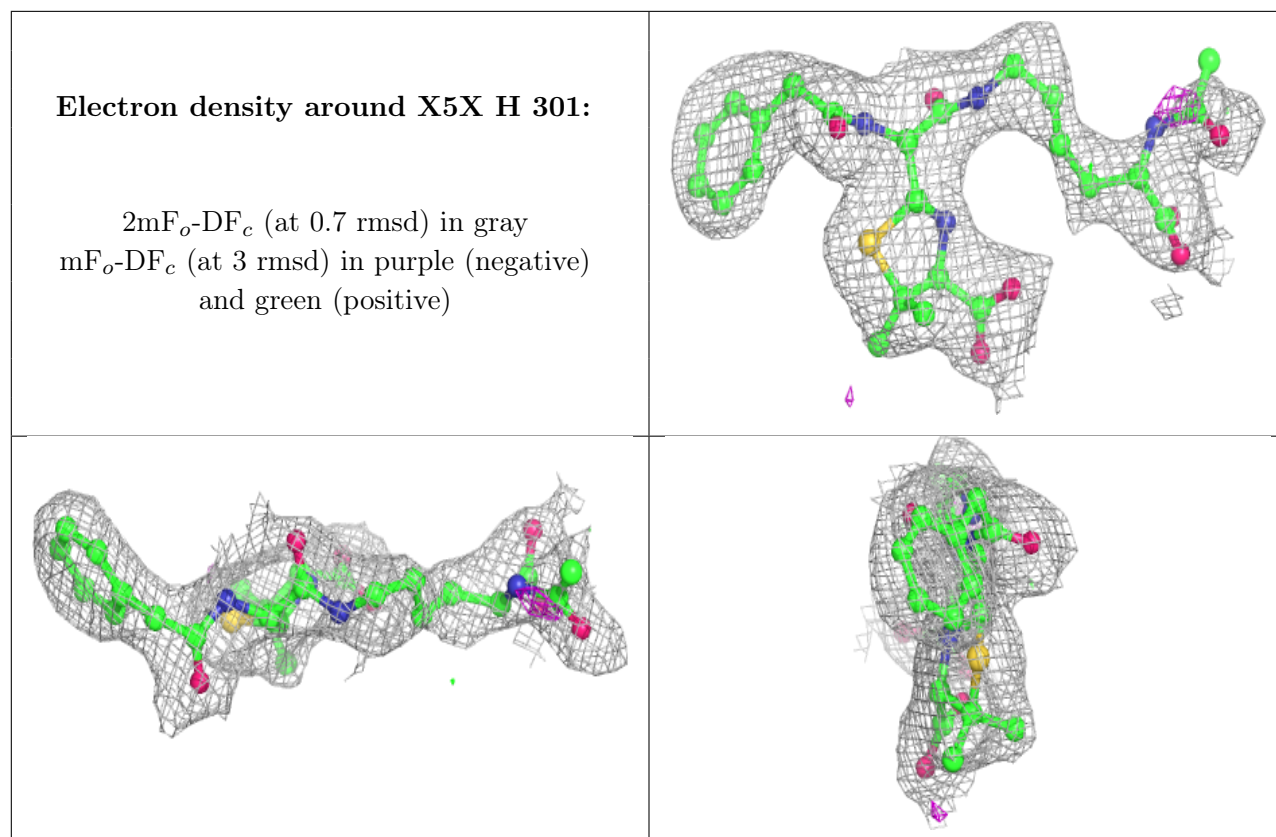
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum,

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	X5X	A	301	36/36	0.90	0.21	47,58,88,91	0
3	X5X	H	301	36/36	0.93	0.19	36,45,63,67	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.





6.5 Other polymers [i](#)

There are no such residues in this entry.