Full wwPDB X-ray Structure Validation Report (i)

Nov 15, 2023 – 10:12 PM JST

PDB ID	:	6JU0
Title	:	Mouse antibody 3.3 Fab in complex with PEG
Authors	:	Lee, C.C.; Ko, T.P.; Lin, L.L.; Wang, A.H.J.
Deposited on	:	2019-04-12
Resolution	:	2.60 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 (i) 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 (i)) were used in the production of this report:

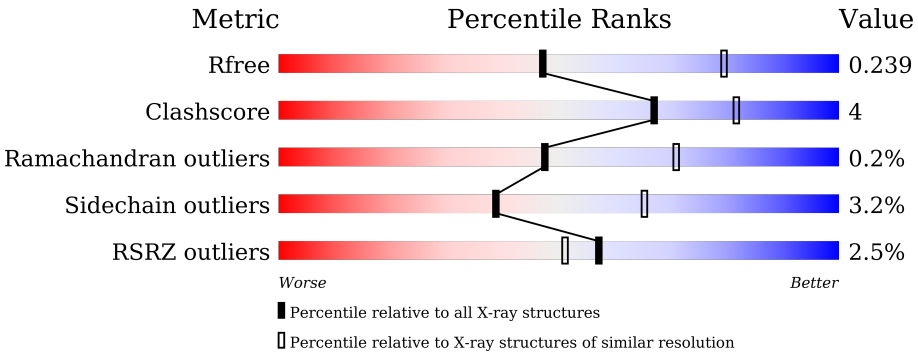
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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 2.60 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	3163 (2.60-2.60)
Clashscore	141614	3518 (2.60-2.60)
Ramachandran outliers	138981	3455 (2.60-2.60)
Sidechain outliers	138945	3455 (2.60-2.60)
RSRZ outliers	127900	3104 (2.60-2.60)

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 <=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	H	219	87% 10%
1	I	219	3% 84% 13%
1	J	219	3% 89% 7%
1	K	219	3% 88% 9%
2	L	213	2% 87% 11%
2	M	213	3% 84% 15%

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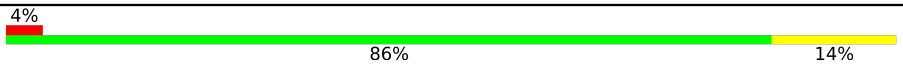
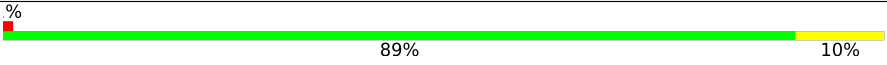
Mol	Chain	Length	Quality of chain
2	N	213	
2	O	213	

2 Entry composition (i)

There are 7 unique types of molecules in this entry. The entry contains 14026 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.

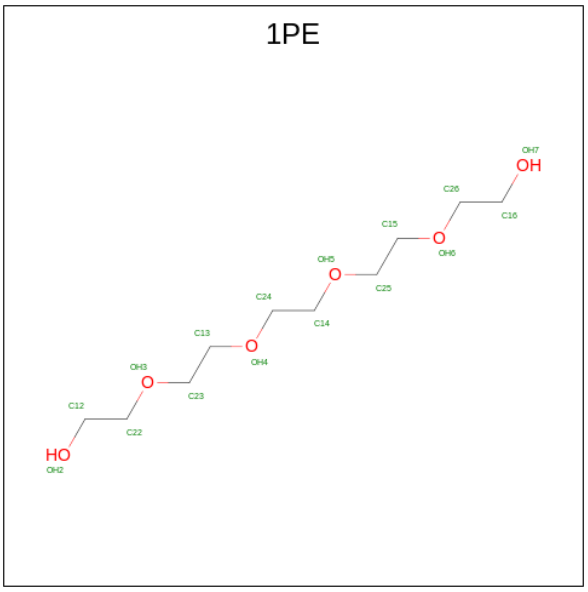
- Molecule 1 is a protein called Fab heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	H	212	Total	C	N	O	S	0	0	0
			1621	1029	264	320	8			
1	I	213	Total	C	N	O	S	0	0	0
			1629	1033	265	323	8			
1	J	212	Total	C	N	O	S	0	0	0
			1621	1029	264	320	8			
1	K	213	Total	C	N	O	S	0	0	0
			1629	1033	265	323	8			

- Molecule 2 is a protein called Fab light chain.

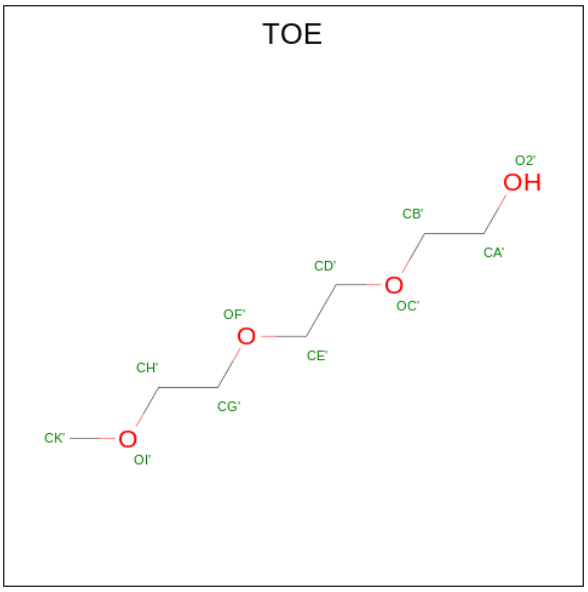
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	L	213	Total	C	N	O	S	0	0	0
			1636	1021	275	332	8			
2	M	213	Total	C	N	O	S	0	0	0
			1636	1021	275	332	8			
2	N	213	Total	C	N	O	S	0	0	0
			1636	1021	275	332	8			
2	O	213	Total	C	N	O	S	0	0	0
			1636	1021	275	332	8			

- Molecule 3 is PENTAETHYLENE GLYCOL (three-letter code: 1PE) (formula: $C_{10}H_{22}O_6$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	H	1	Total C O 32 20 12	0	1

- Molecule 4 is 2-[2-(2-METHOXY-ETHOXY)-ETHOXY]-ETHOXYL (three-letter code: TOE) (formula: $C_7H_{16}O_4$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	H	1	Total C O 11 7 4	0	0
4	I	1	Total C O 10 6 4	0	0

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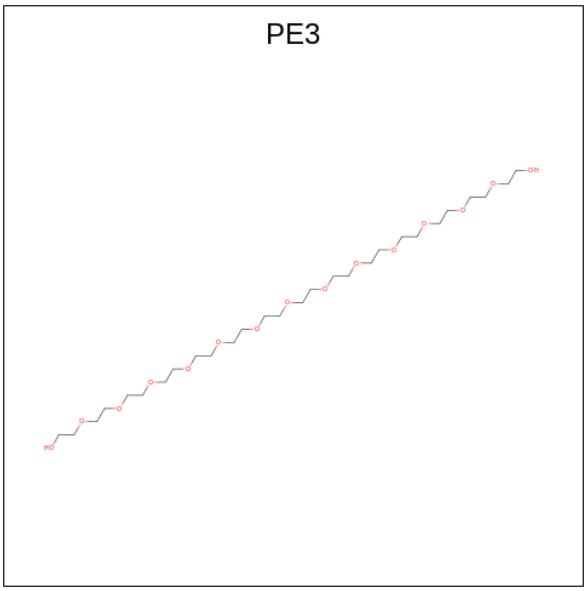
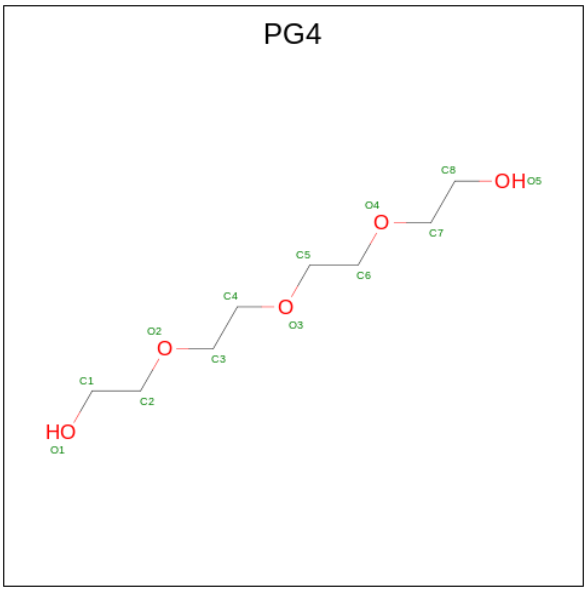
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	J	1	Total C O 11 7 4	0	0
4	K	1	Total C O 10 6 4	0	0

- Molecule 5 is 3,6,9,12,15,18,21,24,27,30,33,36,39-TRIDECAOXAHENTETRACONTANE-1,41-DIOL (three-letter code: PE3) (formula: $C_{28}H_{58}O_{15}$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	I	1	Total C O 35 23 12	0	0
5	K	1	Total C O 35 23 12	0	0

- Molecule 6 is TETRAETHYLENE GLYCOL (three-letter code: PG4) (formula: $C_8H_{18}O_5$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	K	1	Total C O 13 8 5	0	0

- Molecule 7 is water.

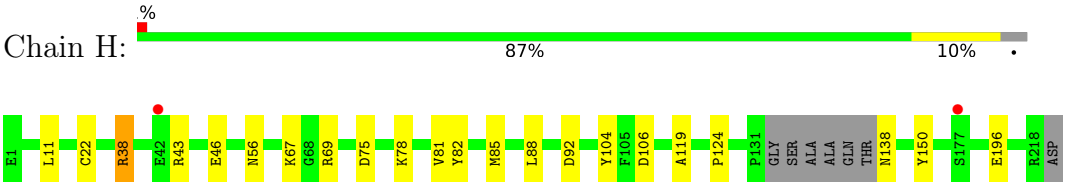
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	H	106	Total O 106 106	0	0
7	L	116	Total O 116 116	0	0
7	I	95	Total O 95 95	0	0
7	M	78	Total O 78 78	0	0
7	J	116	Total O 116 116	0	0
7	N	109	Total O 109 109	0	0
7	K	107	Total O 107 107	0	0
7	O	98	Total O 98 98	0	0

3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

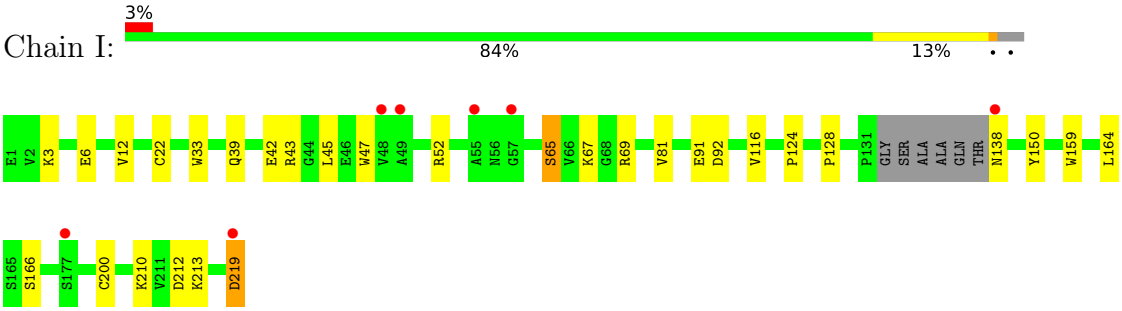
• Molecule 1: Fab heavy chain

Chain H:



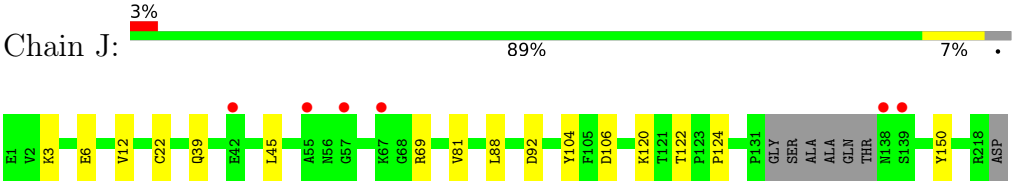
• Molecule 1: Fab heavy chain

Chain I:



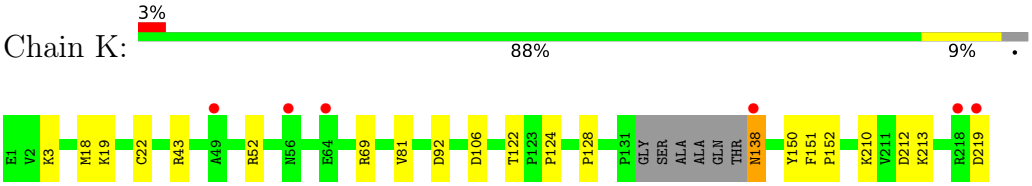
• Molecule 1: Fab heavy chain

Chain J:



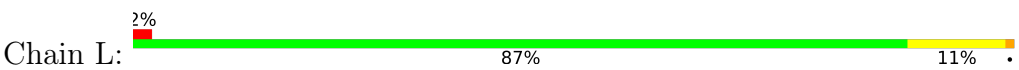
• Molecule 1: Fab heavy chain

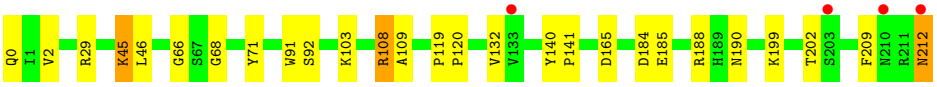
Chain K:



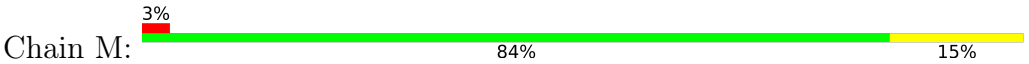
• Molecule 2: Fab light chain

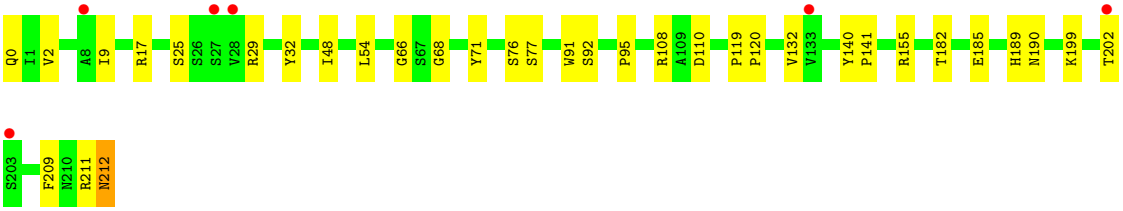
Chain L:



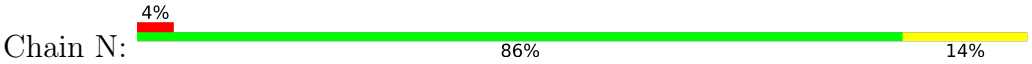


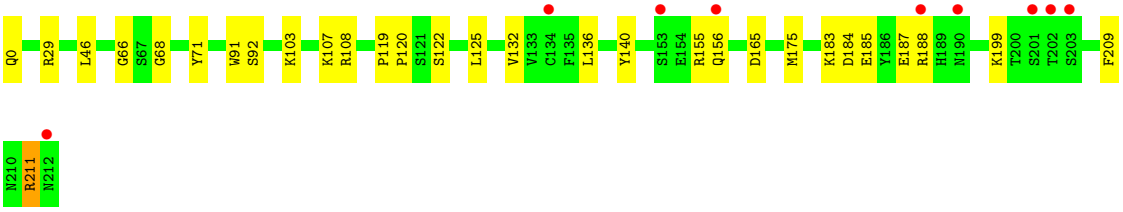
• Molecule 2: Fab light chain



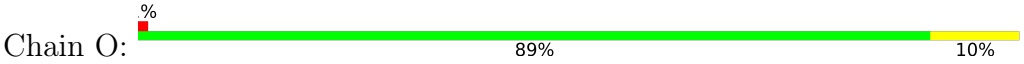


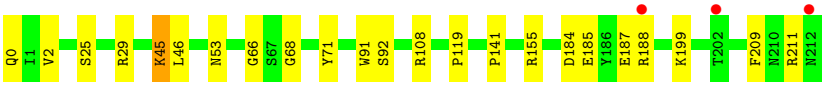
• Molecule 2: Fab light chain





• Molecule 2: Fab light chain





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	69.30Å 177.35Å 89.02Å 90.00° 91.99° 90.00°	Depositor
Resolution (Å)	24.50 – 2.60 25.02 – 2.60	Depositor EDS
% Data completeness (in resolution range)	96.8 (24.50-2.60) 92.1 (25.02-2.60)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.42 (at 2.60Å)	Xtriage
Refinement program	PHENIX (1.13_2998: ???)	Depositor
R, R_{free}	0.211 , 0.240 0.211 , 0.239	Depositor DCC
R_{free} test set	1976 reflections (3.10%)	wwPDB-VP
Wilson B-factor (Å^2)	39.8	Xtriage
Anisotropy	0.055	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.33 , 44.4	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	0.039 for h,-k,-l	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	14026	wwPDB-VP
Average B, all atoms (Å^2)	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.83% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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: TOE, PE3, PCA, 1PE, PG4

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	H	0.26	0/1664	0.51	0/2271
1	I	0.25	0/1672	0.48	0/2282
1	J	0.26	0/1664	0.50	0/2271
1	K	0.26	0/1672	0.50	0/2282
2	L	0.25	0/1670	0.48	0/2271
2	M	0.26	0/1670	0.50	0/2271
2	N	0.26	0/1670	0.48	0/2271
2	O	0.27	0/1670	0.49	0/2271
All	All	0.26	0/13352	0.49	0/18190

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	H	1621	0	1574	12	0
1	I	1629	0	1578	18	0
1	J	1621	0	1574	8	0
1	K	1629	0	1578	14	0
2	L	1636	0	1560	14	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	M	1636	0	1560	16	0
2	N	1636	0	1560	15	0
2	O	1636	0	1560	10	0
3	H	32	0	44	1	0
4	H	11	0	16	0	0
4	I	10	0	13	3	0
4	J	11	0	16	0	0
4	K	10	0	13	3	0
5	I	35	0	45	2	0
5	K	35	0	45	1	0
6	K	13	0	18	1	0
7	H	106	0	0	0	0
7	I	95	0	0	0	0
7	J	116	0	0	0	0
7	K	107	0	0	1	0
7	L	116	0	0	1	0
7	M	78	0	0	0	0
7	N	109	0	0	1	0
7	O	98	0	0	2	0
All	All	14026	0	12754	100	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 (100) 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:K:52:ARG:HH22	4:K:302:TOE:H5	1.48	0.78
2:L:190:ASN:ND2	2:L:212:ASN:OD1	2.18	0.77
1:J:69:ARG:NH2	1:J:92:ASP:OD2	2.20	0.74
1:H:43:ARG:NE	1:H:46:GLU:OE2	2.18	0.72
1:K:69:ARG:NH2	1:K:92:ASP:OD2	2.23	0.71
1:I:219:ASP:N	1:I:219:ASP:OD1	2.25	0.69
2:N:187:GLU:O	2:N:211:ARG:NH1	2.26	0.65
1:H:38:ARG:HG2	1:H:46:GLU:HB2	1.77	0.65
1:I:69:ARG:NH2	1:I:92:ASP:OD2	2.33	0.62
2:M:190:ASN:ND2	2:M:212:ASN:OD1	2.33	0.60
2:O:184:ASP:O	2:O:188:ARG:HG3	2.03	0.59
1:I:65:SER:O	1:I:69:ARG:NH1	2.37	0.57
1:I:212:ASP:HB2	1:K:210:LYS:HB3	1.87	0.56
1:K:124:PRO:HB3	1:K:150:TYR:HB3	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L:199:LYS:NZ	7:L:301:HOH:O	2.38	0.56
1:J:106:ASP:OD1	2:N:46:LEU:HB2	2.06	0.55
2:N:199:LYS:NZ	7:N:302:HOH:O	2.39	0.55
1:H:69:ARG:NH2	1:H:92:ASP:OD2	2.39	0.55
2:L:212:ASN:OD1	2:L:212:ASN:N	2.39	0.55
1:K:52:ARG:NH2	4:K:302:TOE:H5	2.19	0.54
2:O:2:VAL:HG22	2:O:25:SER:HB3	1.89	0.53
2:M:2:VAL:HG22	2:M:25:SER:HB3	1.91	0.53
2:O:45:LYS:NZ	7:O:302:HOH:O	2.32	0.53
1:K:19:LYS:NZ	6:K:303:PG4:O4	2.42	0.53
1:I:43:ARG:HH21	1:I:91:GLU:HB2	1.74	0.53
2:N:211:ARG:HH21	2:N:211:ARG:HB3	1.74	0.52
2:O:187:GLU:OE2	2:O:211:ARG:NH2	2.43	0.52
2:N:120:PRO:HD3	2:N:132:VAL:HG22	1.93	0.51
1:H:22:CYS:HB3	1:H:81:VAL:HG12	1.91	0.51
1:I:22:CYS:HB3	1:I:81:VAL:HG12	1.95	0.49
2:M:189:HIS:O	2:M:211:ARG:HD3	2.12	0.49
2:N:119:PRO:HB3	2:N:209:PHE:CE2	2.48	0.48
2:L:45:LYS:HD3	2:L:46:LEU:N	2.29	0.48
1:K:22:CYS:HB3	1:K:81:VAL:HG12	1.95	0.48
2:M:120:PRO:HD3	2:M:132:VAL:HG22	1.95	0.47
1:I:128:PRO:HD3	1:I:213:LYS:HE2	1.96	0.47
1:H:124:PRO:HB3	1:H:150:TYR:HB3	1.97	0.47
2:O:29:ARG:HD3	2:O:92:SER:OG	2.14	0.47
2:L:199:LYS:O	2:L:199:LYS:HG2	2.16	0.46
1:I:47:TRP:HZ3	2:M:95:PRO:HB3	1.79	0.46
2:N:103:LYS:HE2	2:N:165:ASP:OD1	2.16	0.46
1:I:159:TRP:HB3	1:I:164:LEU:HD23	1.97	0.46
2:M:110:ASP:OD2	2:M:199:LYS:HE2	2.16	0.46
2:O:53:ASN:ND2	7:O:304:HOH:O	2.48	0.46
1:I:124:PRO:HB3	1:I:150:TYR:HB3	1.97	0.46
2:M:29:ARG:HD3	2:M:92:SER:OG	2.15	0.46
1:H:75:ASP:OD2	1:H:78:LYS:HD2	2.16	0.46
1:I:210:LYS:HB3	1:K:212:ASP:HB2	1.97	0.46
2:N:107:LYS:HA	2:N:140:TYR:OH	2.16	0.46
1:I:52:ARG:HH22	4:I:302:TOE:H8	1.81	0.46
1:H:82:TYR:CE1	3:H:301[B]:1PE:H262	2.51	0.46
2:N:184:ASP:O	2:N:188:ARG:HG3	2.16	0.46
1:J:22:CYS:HB3	1:J:81:VAL:HG12	1.98	0.45
1:K:52:ARG:HH22	4:K:302:TOE:H9	1.81	0.45
4:I:302:TOE:H11	2:M:32:TYR:CZ	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:M:182:THR:OG1	2:M:185:GLU:HG3	2.16	0.45
2:L:29:ARG:HD3	2:L:92:SER:OG	2.17	0.45
2:N:29:ARG:HD3	2:N:92:SER:OG	2.16	0.45
1:I:39:GLN:HB2	1:I:45:LEU:HD23	1.98	0.45
2:M:48:ILE:HG12	2:M:54:LEU:HD23	1.99	0.44
2:O:66:GLY:HA3	2:O:71:TYR:HA	1.97	0.44
2:O:119:PRO:HB3	2:O:209:PHE:CE2	2.52	0.44
2:L:120:PRO:HD3	2:L:132:VAL:HG22	2.00	0.44
1:J:124:PRO:HB3	1:J:150:TYR:HB3	1.99	0.44
2:N:136:LEU:HD22	2:N:175:MET:CE	2.47	0.44
1:K:138:ASN:N	1:K:138:ASN:HD22	2.15	0.44
1:H:11:LEU:HD21	1:H:119:ALA:O	2.18	0.44
2:L:119:PRO:HB3	2:L:209:PHE:CE2	2.53	0.44
1:H:106:ASP:OD1	2:L:46:LEU:HB2	2.17	0.43
1:K:106:ASP:OD1	2:O:46:LEU:HB2	2.17	0.43
1:J:12:VAL:HG11	1:J:88:LEU:HD13	2.00	0.43
2:L:66:GLY:HA3	2:L:71:TYR:HA	1.99	0.43
2:N:122:SER:HA	2:N:125:LEU:HD12	1.99	0.43
1:J:3:LYS:HD2	1:J:3:LYS:HA	1.84	0.43
2:N:211:ARG:HB3	2:N:211:ARG:NH2	2.34	0.43
1:K:18:MET:HE2	7:K:442:HOH:O	2.18	0.42
2:N:66:GLY:HA3	2:N:71:TYR:HA	1.99	0.42
2:N:187:GLU:HA	2:N:211:ARG:HE	1.84	0.42
1:H:22:CYS:HB3	1:H:81:VAL:CG1	2.49	0.42
1:I:47:TRP:CZ3	2:M:95:PRO:HB3	2.54	0.42
2:M:155:ARG:HD2	2:M:155:ARG:HA	1.91	0.42
1:J:104:TYR:CZ	5:K:301:PE3:H392	2.54	0.42
2:M:119:PRO:HB3	2:M:209:PHE:CE2	2.53	0.42
1:I:42:GLU:N	1:I:42:GLU:OE2	2.53	0.42
4:I:302:TOE:H11	2:M:32:TYR:CE1	2.54	0.42
2:O:141:PRO:HD2	2:O:199:LYS:HG2	2.01	0.42
2:L:184:ASP:O	2:L:188:ARG:HG3	2.19	0.42
2:M:66:GLY:HA3	2:M:71:TYR:HA	2.02	0.41
1:I:33:TRP:CE2	5:I:301:PE3:H201	2.55	0.41
1:H:104:TYR:CZ	5:I:301:PE3:H392	2.55	0.41
1:K:128:PRO:HD3	1:K:213:LYS:HE2	2.03	0.41
2:L:108:ARG:HD3	2:L:109:ALA:O	2.20	0.41
2:M:140:TYR:CD1	2:M:141:PRO:HA	2.56	0.41
2:L:103:LYS:HE2	2:L:165:ASP:OD1	2.21	0.41
1:I:12:VAL:O	1:I:116:VAL:HA	2.21	0.41
1:J:39:GLN:HB2	1:J:45:LEU:HD23	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:85:MET:HB3	1:H:88:LEU:HD21	2.03	0.41
1:I:159:TRP:CZ3	1:I:200:CYS:HB3	2.56	0.40
1:K:151:PHE:HA	1:K:152:PRO:HA	1.91	0.40
2:L:140:TYR:CG	2:L:141:PRO:HA	2.57	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	H	208/219 (95%)	204 (98%)	4 (2%)	0	100	100
1	I	209/219 (95%)	206 (99%)	3 (1%)	0	100	100
1	J	208/219 (95%)	204 (98%)	4 (2%)	0	100	100
1	K	209/219 (95%)	205 (98%)	4 (2%)	0	100	100
2	L	211/213 (99%)	207 (98%)	3 (1%)	1 (0%)	29	52
2	M	211/213 (99%)	206 (98%)	4 (2%)	1 (0%)	29	52
2	N	211/213 (99%)	207 (98%)	3 (1%)	1 (0%)	29	52
2	O	211/213 (99%)	207 (98%)	3 (1%)	1 (0%)	29	52
All	All	1678/1728 (97%)	1646 (98%)	28 (2%)	4 (0%)	47	71

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	L	68	GLY
2	M	68	GLY
2	N	68	GLY
2	O	68	GLY

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	H	184/188 (98%)	179 (97%)	5 (3%)	44	71
1	I	185/188 (98%)	178 (96%)	7 (4%)	33	59
1	J	184/188 (98%)	181 (98%)	3 (2%)	62	82
1	K	185/188 (98%)	180 (97%)	5 (3%)	44	71
2	L	186/186 (100%)	179 (96%)	7 (4%)	33	59
2	M	186/186 (100%)	178 (96%)	8 (4%)	29	54
2	N	186/186 (100%)	179 (96%)	7 (4%)	33	59
2	O	186/186 (100%)	181 (97%)	5 (3%)	44	71
All	All	1482/1496 (99%)	1435 (97%)	47 (3%)	39	65

All (47) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	H	38	ARG
1	H	56	ASN
1	H	67	LYS
1	H	138	ASN
1	H	196	GLU
2	L	2	VAL
2	L	45	LYS
2	L	91	TRP
2	L	108	ARG
2	L	185	GLU
2	L	202	THR
2	L	212	ASN
1	I	3	LYS
1	I	6	GLU
1	I	65	SER
1	I	67	LYS
1	I	138	ASN
1	I	166	SER
1	I	219	ASP

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Mol	Chain	Res	Type
2	M	9	ILE
2	M	17	ARG
2	M	76	SER
2	M	77	SER
2	M	91	TRP
2	M	108	ARG
2	M	202	THR
2	M	212	ASN
1	J	6	GLU
1	J	120	LYS
1	J	122	THR
2	N	91	TRP
2	N	108	ARG
2	N	155	ARG
2	N	156	GLN
2	N	183	LYS
2	N	185	GLU
2	N	211	ARG
1	K	3	LYS
1	K	43	ARG
1	K	122	THR
1	K	138	ASN
1	K	219	ASP
2	O	45	LYS
2	O	91	TRP
2	O	108	ARG
2	O	155	ARG
2	O	185	GLU

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

Mol	Chain	Res	Type
1	H	56	ASN
2	N	156	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)

4 non-standard protein/DNA/RNA residues 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	PCA	O	0	2	7,8,9	1.79	1 (14%)	9,10,12	2.21	5 (55%)
2	PCA	N	0	2	7,8,9	1.80	1 (14%)	9,10,12	2.14	5 (55%)
2	PCA	M	0	2	7,8,9	1.81	1 (14%)	9,10,12	2.24	5 (55%)
2	PCA	L	0	2	7,8,9	1.80	1 (14%)	9,10,12	2.21	5 (55%)

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	PCA	O	0	2	-	0/0/11/13	0/1/1/1
2	PCA	N	0	2	-	0/0/11/13	0/1/1/1
2	PCA	M	0	2	-	0/0/11/13	0/1/1/1
2	PCA	L	0	2	-	0/0/11/13	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	M	0	PCA	CD-N	4.66	1.46	1.34
2	L	0	PCA	CD-N	4.65	1.46	1.34
2	N	0	PCA	CD-N	4.64	1.46	1.34
2	O	0	PCA	CD-N	4.61	1.46	1.34

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	M	0	PCA	OE-CD-CG	-3.20	121.18	126.76
2	L	0	PCA	OE-CD-CG	-3.16	121.25	126.76
2	M	0	PCA	CB-CA-C	-3.16	108.36	112.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	N	0	PCA	OE-CD-CG	-3.15	121.27	126.76
2	O	0	PCA	OE-CD-CG	-3.09	121.37	126.76
2	O	0	PCA	CA-N-CD	-2.92	103.58	113.58
2	L	0	PCA	CA-N-CD	-2.87	103.74	113.58
2	O	0	PCA	CB-CA-N	2.82	111.40	103.30
2	M	0	PCA	CA-N-CD	-2.82	103.92	113.58
2	N	0	PCA	CA-N-CD	-2.77	104.09	113.58
2	L	0	PCA	CB-CA-C	-2.77	108.90	112.70
2	N	0	PCA	CB-CA-C	-2.73	108.94	112.70
2	L	0	PCA	CB-CA-N	2.72	111.12	103.30
2	M	0	PCA	CB-CA-N	2.63	110.85	103.30
2	O	0	PCA	CB-CA-C	-2.60	109.12	112.70
2	N	0	PCA	CB-CA-N	2.59	110.73	103.30
2	O	0	PCA	CG-CD-N	2.54	114.97	108.39
2	L	0	PCA	CG-CD-N	2.53	114.94	108.39
2	M	0	PCA	CG-CD-N	2.50	114.87	108.39
2	N	0	PCA	CG-CD-N	2.46	114.77	108.39

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

9 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	$\#\|Z\|>2$
4	TOE	H	302	-	10,10,10	0.51	0	9,9,9	0.47	0
5	PE3	K	301	-	34,34,42	0.11	0	33,33,41	0.18	0
3	1PE	H	301[A]	-	15,15,15	0.54	0	14,14,14	0.49	0
3	1PE	H	301[B]	-	15,15,15	0.54	0	14,14,14	0.53	0
4	TOE	I	302	-	9,9,10	0.52	0	8,8,9	0.59	0
6	PG4	K	303	-	12,12,12	0.52	0	11,11,11	0.40	0
4	TOE	K	302	-	9,9,10	0.52	0	8,8,9	0.42	0
5	PE3	I	301	-	34,34,42	0.12	0	33,33,41	0.18	0
4	TOE	J	301	-	10,10,10	0.51	0	9,9,9	0.45	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	TOE	H	302	-	-	2/8/8/8	-
5	PE3	K	301	-	-	4/32/32/40	-
3	1PE	H	301[A]	-	-	0/13/13/13	-
3	1PE	H	301[B]	-	-	0/13/13/13	-
4	TOE	I	302	-	-	3/7/7/8	-
6	PG4	K	303	-	-	1/10/10/10	-
4	TOE	K	302	-	-	4/7/7/8	-
5	PE3	I	301	-	-	5/32/32/40	-
4	TOE	J	301	-	-	5/8/8/8	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (24) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	J	301	TOE	OF'-CG'-CH'-OI'
4	H	302	TOE	OF'-CG'-CH'-OI'
4	J	301	TOE	O2'-CA'-CB'-OC'
4	I	302	TOE	OC'-CD'-CE'-OF'
4	K	302	TOE	OC'-CD'-CE'-OF'
5	I	301	PE3	C12-C11-O10-C9
4	J	301	TOE	OC'-CD'-CE'-OF'

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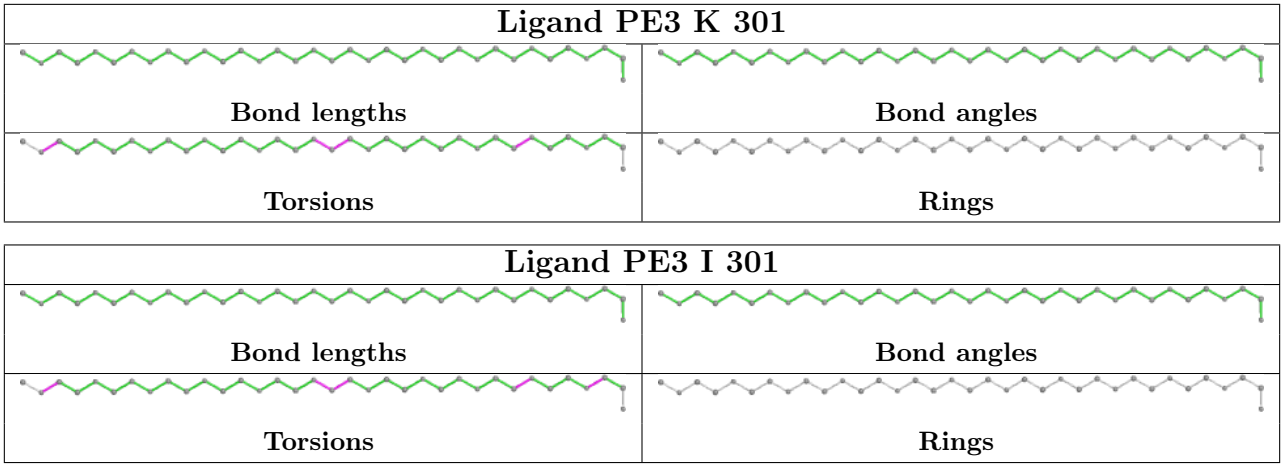
Mol	Chain	Res	Type	Atoms
5	I	301	PE3	C42-C41-O40-C39
4	J	301	TOE	CA'-CB'-OC'-CD'
4	K	302	TOE	CH'-CG'-OF'-CE'
4	I	302	TOE	CD'-CE'-OF'-CG'
4	J	301	TOE	CH'-CG'-OF'-CE'
4	K	302	TOE	CD'-CE'-OF'-CG'
5	I	301	PE3	C35-C36-O37-C38
6	K	303	PG4	O1-C1-C2-O2
4	I	302	TOE	CH'-CG'-OF'-CE'
5	K	301	PE3	C35-C36-O37-C38
5	I	301	PE3	C27-C26-O25-C24
4	H	302	TOE	OC'-CD'-CE'-OF'
4	K	302	TOE	O2'-CA'-CB'-OC'
5	K	301	PE3	C27-C26-O25-C24
5	K	301	PE3	C12-C11-O10-C9
5	K	301	PE3	O25-C26-C27-O28
5	I	301	PE3	O25-C26-C27-O28

There are no ring outliers.

6 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	K	301	PE3	1	0
3	H	301[B]	1PE	1	0
4	I	302	TOE	3	0
6	K	303	PG4	1	0
4	K	302	TOE	3	0
5	I	301	PE3	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 then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95^{th} 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	H	212/219 (96%)	-0.17	2 (0%)	84	82	28, 39, 58, 84	0
1	I	213/219 (97%)	0.03	7 (3%)	46	39	28, 44, 68, 88	0
1	J	212/219 (96%)	-0.20	6 (2%)	53	46	26, 40, 60, 91	0
1	K	213/219 (97%)	-0.16	6 (2%)	53	46	25, 40, 62, 81	0
2	L	212/213 (99%)	-0.13	4 (1%)	66	62	29, 41, 62, 75	0
2	M	212/213 (99%)	0.31	6 (2%)	53	46	33, 53, 67, 76	0
2	N	212/213 (99%)	0.06	9 (4%)	36	29	30, 46, 72, 89	0
2	O	212/213 (99%)	-0.08	3 (1%)	75	71	28, 43, 62, 80	0
All	All	1698/1728 (98%)	-0.04	43 (2%)	57	51	25, 43, 66, 91	0

All (43) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	I	219	ASP	5.6
1	J	138	ASN	4.8
2	O	188	ARG	3.7
1	H	42	GLU	3.5
1	K	138	ASN	3.4
2	L	212	ASN	3.3
1	I	55	ALA	3.2
2	N	203	SER	3.2
2	M	27	SER	3.1
2	O	212	ASN	3.1
1	I	138	ASN	2.9
1	K	219	ASP	2.9
1	I	48	VAL	2.7
2	N	156	GLN	2.7
2	M	203	SER	2.7
1	K	56	ASN	2.7

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Mol	Chain	Res	Type	RSRZ
2	L	133	VAL	2.7
2	M	28	VAL	2.7
1	I	177	SER	2.6
2	M	202	THR	2.6
1	J	55	ALA	2.5
1	J	57	GLY	2.5
1	H	177	SER	2.4
1	K	49	ALA	2.4
2	N	212	ASN	2.3
2	N	188	ARG	2.3
2	L	210	ASN	2.3
2	N	153	SER	2.2
2	N	202	THR	2.2
2	M	133	VAL	2.2
1	J	67	LYS	2.1
1	I	57	GLY	2.1
2	M	8	ALA	2.1
1	J	139	SER	2.1
1	J	42	GLU	2.1
2	N	134	CYS	2.1
2	L	203	SER	2.1
2	O	202	THR	2.0
1	I	49	ALA	2.0
2	N	190	ASN	2.0
2	N	201	SER	2.0
1	K	64	GLU	2.0
1	K	218	ARG	2.0

6.2 Non-standard residues in protein, DNA, RNA chains (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, 95^{th} 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
2	PCA	M	0	8/9	0.82	0.22	69,73,86,91	0
2	PCA	N	0	8/9	0.84	0.32	62,69,80,84	0
2	PCA	L	0	8/9	0.93	0.27	51,57,64,75	0
2	PCA	O	0	8/9	0.94	0.27	56,59,66,72	0

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

6.4 Ligands (i)

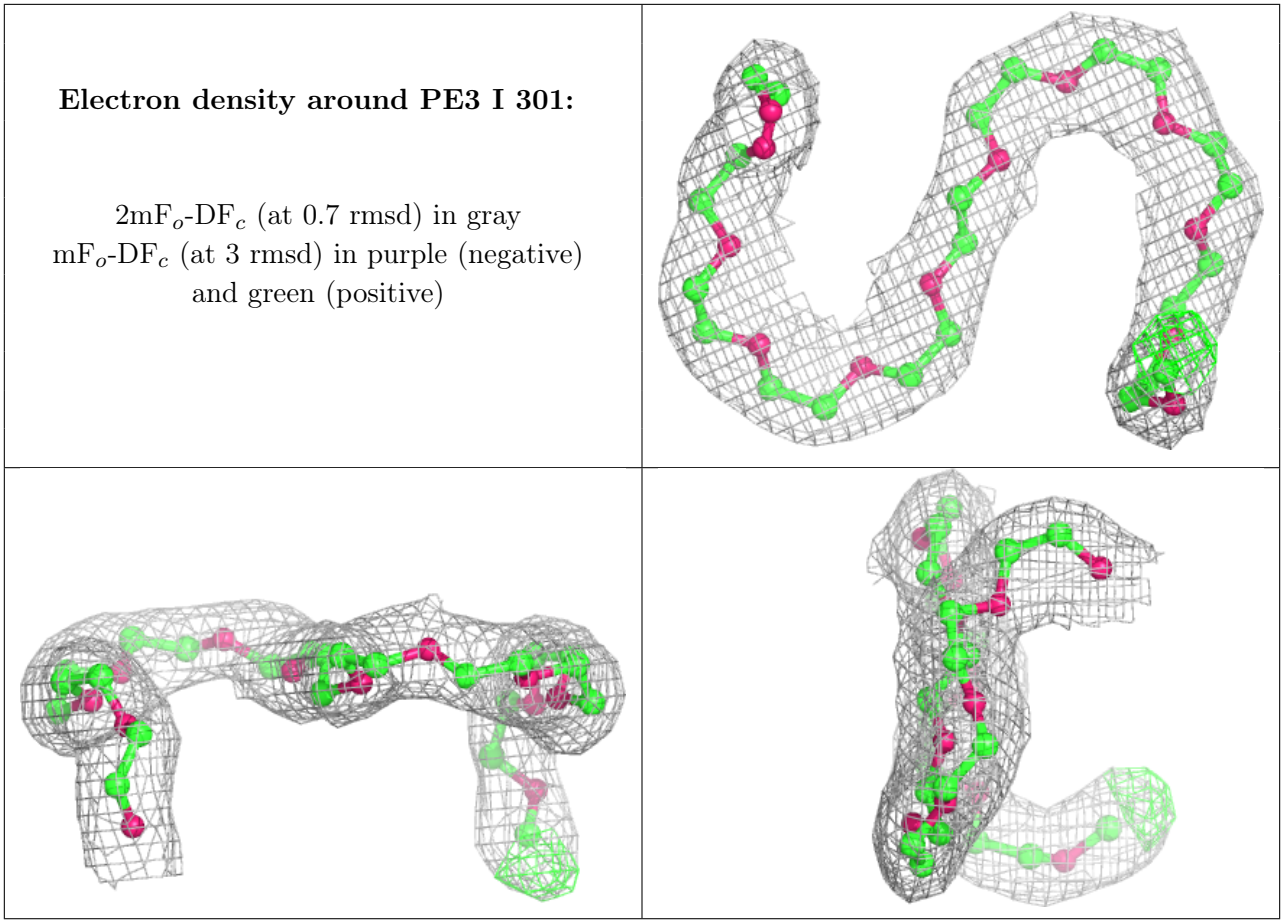
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' 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
4	TOE	K	302	10/11	0.85	0.20	52,60,66,72	0
3	1PE	H	301[B]	16/16	0.88	0.22	58,64,69,77	16
4	TOE	H	302	11/11	0.88	0.18	43,52,57,60	0
3	1PE	H	301[A]	16/16	0.88	0.22	58,64,66,81	16
6	PG4	K	303	13/13	0.89	0.34	55,61,71,75	0
4	TOE	I	302	10/11	0.91	0.22	54,58,62,62	0
4	TOE	J	301	11/11	0.91	0.16	50,54,58,59	0
5	PE3	I	301	35/43	0.92	0.14	31,43,55,61	0
5	PE3	K	301	35/43	0.93	0.15	35,41,57,69	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.

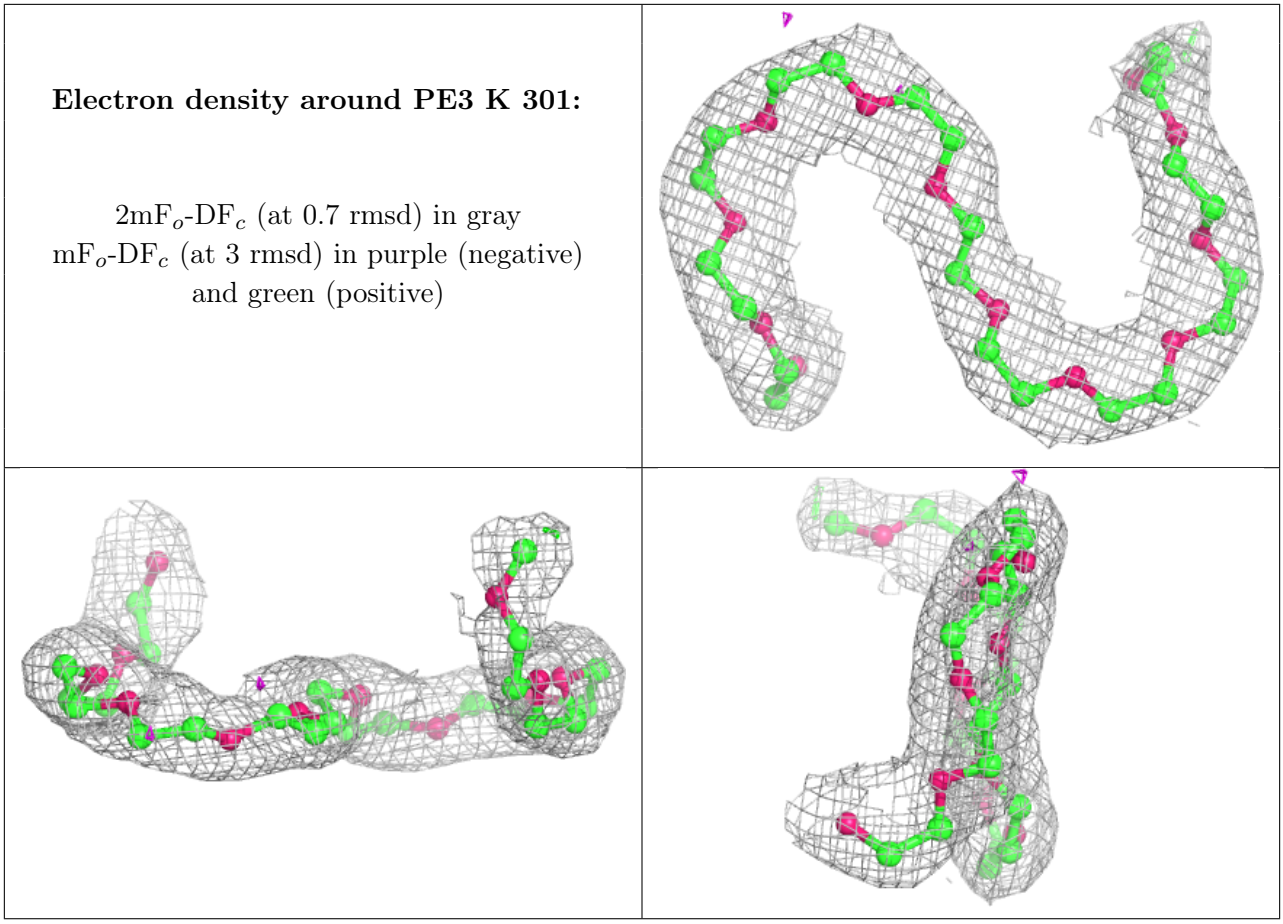
Electron density around PE3 I 301:

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



Electron density around PE3 K 301:

$2mF_o$-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.