Full wwPDB X-ray Structure Validation Report ⓘ

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PDB ID	:	6NOV
Title	:	A Fab derived from ixekizumab
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Deposited on	:	2019-01-16
Resolution	:	2.14 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 following versions of software and data (see references ⓘ) were used in the production of this report:

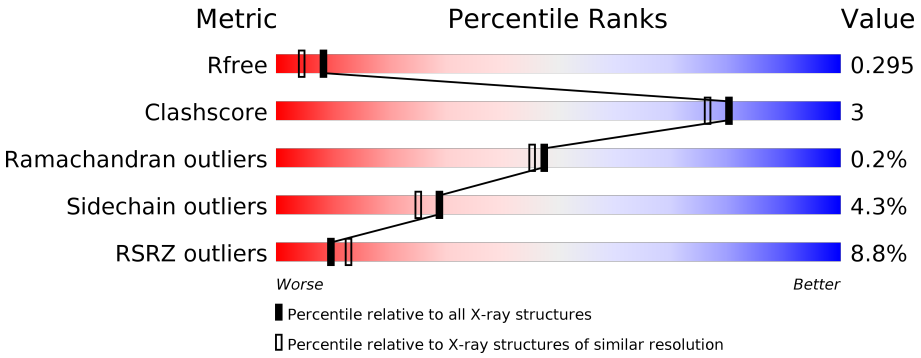
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

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 2.14 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	2523 (2.16-2.12)
Clashscore	141614	2653 (2.16-2.12)
Ramachandran outliers	138981	2618 (2.16-2.12)
Sidechain outliers	138945	2617 (2.16-2.12)
RSRZ outliers	127900	2485 (2.16-2.12)

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 on 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	A	226	15% 84% 10% 6%
1	C	226	9% 84% 10% 6%
2	B	219	3% 90% 9%
2	D	219	7% 90% 10%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 6811 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.

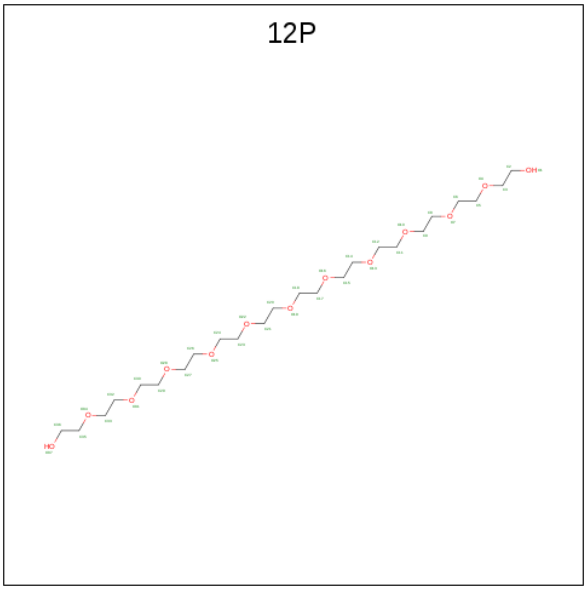
- Molecule 1 is a protein called Fab Heavy Chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	212	Total	C	N	O	S	0	0	0
			1535	977	254	297	7			
1	C	212	Total	C	N	O	S	0	0	0
			1566	993	255	311	7			

- Molecule 2 is a protein called Fab Light Chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	218	Total	C	N	O	S	0	2	0
			1678	1053	284	335	6			
2	D	219	Total	C	N	O	S	0	2	0
			1678	1055	284	332	7			

- Molecule 3 is DODECAETHYLENE GLYCOL (three-letter code: 12P) (formula: $C_{24}H_{50}O_{13}$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			30	20	10		

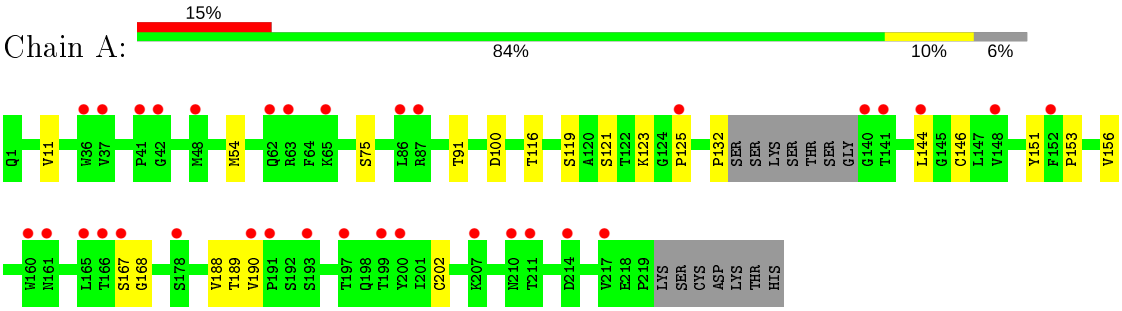
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	56	Total	O	0	0
			56	56		
4	B	75	Total	O	0	0
			75	75		
4	C	106	Total	O	0	0
			106	106		
4	D	87	Total	O	0	0
			87	87		

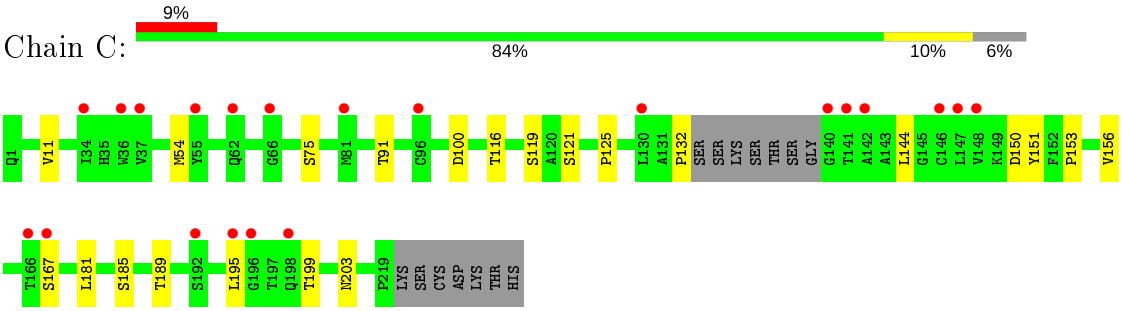
3 Residue-property plots (i)

These plots are drawn for all protein, RNA and DNA 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.

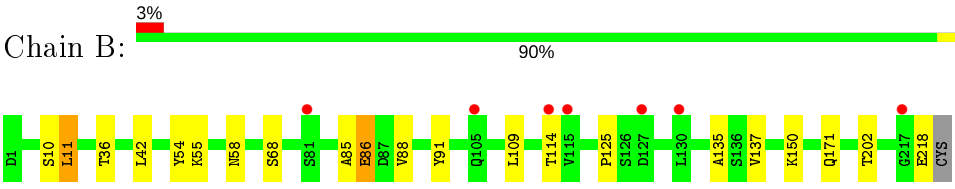
- Molecule 1: Fab Heavy Chain



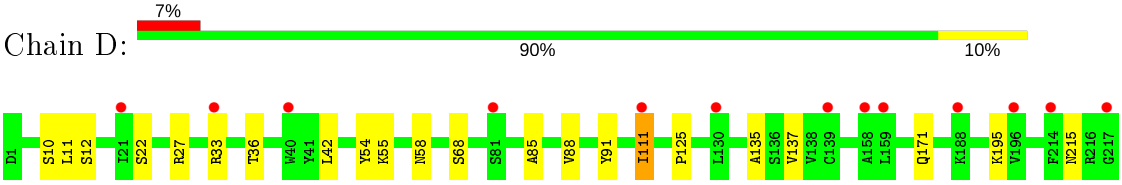
- Molecule 1: Fab Heavy Chain



- Molecule 2: Fab Light Chain



- Molecule 2: Fab Light Chain




E218
C219

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α, β, γ	118.40Å 197.50Å 44.54Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.87 – 2.14 19.87 – 2.14	Depositor EDS
% Data completeness (in resolution range)	99.2 (19.87-2.14) 99.2 (19.87-2.14)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.13	Depositor
$< I/\sigma(I) >$ [1]	2.66 (at 2.15Å)	Xtriage
Refinement program	BUSTER 2.11.7	Depositor
R, R_{free}	0.238 , 0.278 0.251 , 0.295	Depositor DCC
R_{free} test set	2822 reflections (4.85%)	wwPDB-VP
Wilson B-factor (Å^2)	32.3	Xtriage
Anisotropy	0.997	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 58.7	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	6811	wwPDB-VP
Average B, all atoms (Å^2)	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.98% 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: 12P

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	0.49	0/1576	0.71	0/2158
1	C	0.49	0/1607	0.70	0/2198
2	B	0.52	0/1715	0.69	0/2332
2	D	0.53	0/1716	0.68	0/2336
All	All	0.51	0/6614	0.69	0/9024

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1535	0	1426	9	0
1	C	1566	0	1478	7	0
2	B	1678	0	1617	10	0
2	D	1678	0	1611	8	0
3	A	30	0	36	3	0
4	A	56	0	0	0	0
4	B	75	0	0	0	0
4	C	106	0	0	0	0
4	D	87	0	0	1	0
All	All	6811	0	6168	34	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 3.

All (34) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:100:ASP:HB2	3:A:301:12P:H241	1.65	0.79
1:A:100:ASP:HA	3:A:301:12P:H201	1.73	0.69
1:A:11:VAL:HB	1:A:153:PRO:HG3	1.79	0.64
1:C:11:VAL:HB	1:C:153:PRO:HG3	1.85	0.58
1:A:121:SER:O	1:A:123:LYS:HD2	2.06	0.56
2:B:11:LEU:HD23	2:B:109:LEU:HA	1.86	0.56
2:B:88:VAL:HG21	2:B:171:GLN:HB3	1.88	0.56
1:A:188:VAL:HG22	1:A:190:VAL:HG13	1.88	0.54
1:A:125:PRO:HB3	1:A:151:TYR:HB3	1.89	0.54
1:A:91:THR:HG23	1:A:116:THR:HA	1.90	0.53
2:D:88:VAL:HG21	2:D:171:GLN:HB3	1.90	0.53
1:C:91:THR:HG23	1:C:116:THR:HA	1.91	0.52
1:C:125:PRO:HB3	1:C:151:TYR:HB3	1.91	0.51
2:B:150:LYS:HB3	2:B:202:THR:HB	1.93	0.51
2:D:125:PRO:HG3	2:D:135:ALA:HB1	1.94	0.47
2:D:125:PRO:HD3	2:D:137:VAL:HG22	1.97	0.47
3:A:301:12P:H292	1:C:100:ASP:HB2	1.97	0.46
2:B:125:PRO:HG3	2:B:135:ALA:HB1	1.95	0.46
1:C:185:SER:HB2	4:D:319:HOH:O	2.14	0.46
2:D:195:LYS:O	2:D:215:ASN:HA	2.15	0.46
1:A:132:PRO:HG3	1:A:144:LEU:HB3	1.97	0.46
2:B:125:PRO:HD3	2:B:137:VAL:HG22	1.99	0.45
2:D:54:TYR:O	2:D:58:ASN:HB2	2.16	0.45
1:A:168:GLY:O	1:A:188:VAL:HA	2.17	0.45
1:C:132:PRO:HG3	1:C:144:LEU:HB3	1.99	0.44
2:D:85:ALA:HA	2:D:111:ILE:HD12	2.00	0.42
2:B:42:LEU:HD13	2:B:91:TYR:CZ	2.55	0.42
2:B:54:TYR:O	2:B:58:ASN:HB2	2.20	0.41
2:B:85:ALA:O	2:B:88:VAL:HG12	2.20	0.41
2:D:42:LEU:HD13	2:D:91:TYR:CZ	2.55	0.41
2:B:86:GLU:O	2:B:86:GLU:HG2	2.21	0.41
2:B:36:THR:O	2:B:55:LYS:HA	2.21	0.41
1:C:150:ASP:HB3	1:C:181:LEU:HD13	2.02	0.41
2:D:36:THR:O	2:D:55:LYS:HA	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	208/226 (92%)	200 (96%)	8 (4%)	0	100 100
1	C	208/226 (92%)	201 (97%)	5 (2%)	2 (1%)	15 8
2	B	218/219 (100%)	209 (96%)	9 (4%)	0	100 100
2	D	219/219 (100%)	211 (96%)	8 (4%)	0	100 100
All	All	853/890 (96%)	821 (96%)	30 (4%)	2 (0%)	47 45

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	199	THR
1	C	195	LEU

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	158/193 (82%)	150 (95%)	8 (5%)	24 19
1	C	170/193 (88%)	162 (95%)	8 (5%)	26 21
2	B	190/196 (97%)	184 (97%)	6 (3%)	39 37
2	D	189/196 (96%)	181 (96%)	8 (4%)	30 26
All	All	707/778 (91%)	677 (96%)	30 (4%)	29 26

All (30) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	54	MET
1	A	75	SER
1	A	119	SER
1	A	146	CYS
1	A	156	VAL
1	A	167	SER
1	A	189	THR
1	A	202	CYS
2	B	10	SER
2	B	11	LEU
2	B	68	SER
2	B	86	GLU
2	B	114	THR
2	B	218	GLU
1	C	54	MET
1	C	75	SER
1	C	119	SER
1	C	121	SER
1	C	156	VAL
1	C	167	SER
1	C	189	THR
1	C	203	ASN
2	D	10	SER
2	D	11	LEU
2	D	12	SER
2	D	22	SER
2	D	27	ARG
2	D	33	ARG
2	D	68	SER
2	D	111	ILE

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

Mol	Chain	Res	Type
2	B	143	ASN
2	D	143	ASN

5.3.3 RNA

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 carbohydrates in this entry.

5.6 Ligand geometry (i)

1 ligand is 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	12P	A	301	-	29,29,36	0.20	0	28,28,35	0.28	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
3	12P	A	301	-	-	17/27/27/34	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (17) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	301	12P	O22-C23-C24-O25
3	A	301	12P	O25-C26-C27-O28
3	A	301	12P	O28-C29-C30-O31
3	A	301	12P	O13-C14-C15-O16

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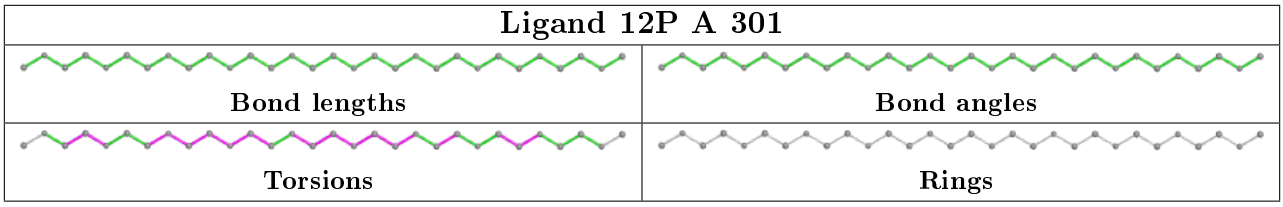
Mol	Chain	Res	Type	Atoms
3	A	301	12P	C20-C21-O22-C23
3	A	301	12P	C15-C14-O13-C12
3	A	301	12P	C23-C24-O25-C26
3	A	301	12P	C24-C23-O22-C21
3	A	301	12P	C21-C20-O19-C18
3	A	301	12P	C18-C17-O16-C15
3	A	301	12P	C29-C30-O31-C32
3	A	301	12P	C8-C9-O10-C11
3	A	301	12P	C14-C15-O16-C17
3	A	301	12P	C11-C12-O13-C14
3	A	301	12P	O19-C20-C21-O22
3	A	301	12P	O16-C17-C18-O19
3	A	301	12P	O7-C8-C9-O10

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	301	12P	3	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

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, 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	A	212/226 (93%)	0.75	33 (15%) 2 2	21, 47, 85, 97	0
1	C	212/226 (93%)	0.55	21 (9%) 7 10	23, 42, 74, 97	0
2	B	218/219 (99%)	0.44	7 (3%) 47 55	20, 41, 60, 85	0
2	D	219/219 (100%)	0.50	15 (6%) 17 22	21, 41, 60, 105	0
All	All	861/890 (96%)	0.56	76 (8%) 10 13	20, 42, 76, 105	0

All (76) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	219	CYS	8.3
1	C	140	GLY	7.3
2	D	159	LEU	4.5
1	A	42	GLY	4.2
2	B	115	VAL	4.2
1	C	195	LEU	3.9
1	A	167	SER	3.9
2	D	218	GLU	3.6
1	A	140	GLY	3.5
1	C	141	THR	3.5
2	D	188	LYS	3.5
1	C	34	ILE	3.5
1	A	190	VAL	3.5
1	C	147	LEU	3.4
1	C	36	TRP	3.4
1	A	200	TYR	3.3
1	A	160	TRP	3.3
1	C	166	THR	3.2
1	A	48	MET	3.2
2	D	217	GLY	3.2
1	A	36	TRP	3.2

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Mol	Chain	Res	Type	RSRZ
1	A	197	THR	3.1
1	A	214	ASP	3.1
2	B	127	ASP	3.1
2	D	196	VAL	3.1
2	B	217	GLY	3.1
1	A	37	VAL	3.1
1	C	148	VAL	3.0
1	A	141	THR	3.0
2	B	114	THR	2.9
1	C	146	CYS	2.9
1	C	66	GLY	2.8
2	B	130	LEU	2.8
1	C	192	SER	2.8
1	C	130	LEU	2.8
1	C	196	GLY	2.8
1	A	207	LYS	2.7
1	A	166	THR	2.7
2	B	81	SER	2.7
1	A	86	LEU	2.6
1	A	63	ARG	2.6
1	C	96	CYS	2.6
1	A	41	PRO	2.6
2	D	33	ARG	2.5
1	A	193	SER	2.5
2	D	158	ALA	2.5
1	A	191	PRO	2.5
1	A	125	PRO	2.4
2	B	105	GLN	2.4
2	D	81	SER	2.4
1	A	62	GLN	2.4
1	A	210	ASN	2.4
2	D	214	PHE	2.4
1	A	165	LEU	2.4
1	C	55	TYR	2.4
2	D	111	ILE	2.3
1	A	144	LEU	2.3
1	A	152	PHE	2.3
1	C	62	GLN	2.3
2	D	130	LEU	2.2
1	A	211	THR	2.2
1	C	142	ALA	2.2
1	A	161	ASN	2.2

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Mol	Chain	Res	Type	RSRZ
2	D	21	ILE	2.2
1	A	199	THR	2.2
1	C	198	GLN	2.2
1	A	65	LYS	2.1
1	C	81	MET	2.1
1	C	167	SER	2.1
1	A	178	SER	2.1
2	D	139	CYS	2.1
1	A	148	VAL	2.0
1	A	217	VAL	2.0
2	D	40	TRP	2.0
1	A	87	ARG	2.0
1	C	37	VAL	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 carbohydrates in this entry.

6.4 Ligands (i)

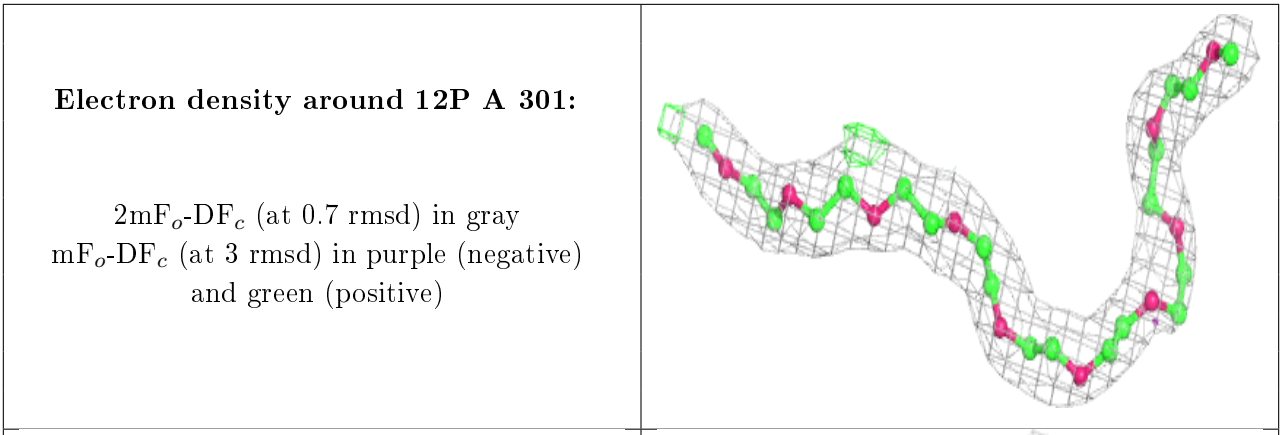
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' 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
3	12P	A	301	30/37	0.74	0.22	33,40,58,60	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 12P A 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

There are no such residues in this entry.