Full wwPDB X-ray Structure Validation Report ⓘ

Nov 21, 2023 – 06:01 AM JST

PDB ID	:	7EZC
Title	:	Adenosine A2a receptor mutant-I92N
Authors	:	Cui, M.; Zhou, Q.; Yao, D.; Zhao, S.; Song, G.
Deposited on	:	2021-06-01
Resolution	:	3.80 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:

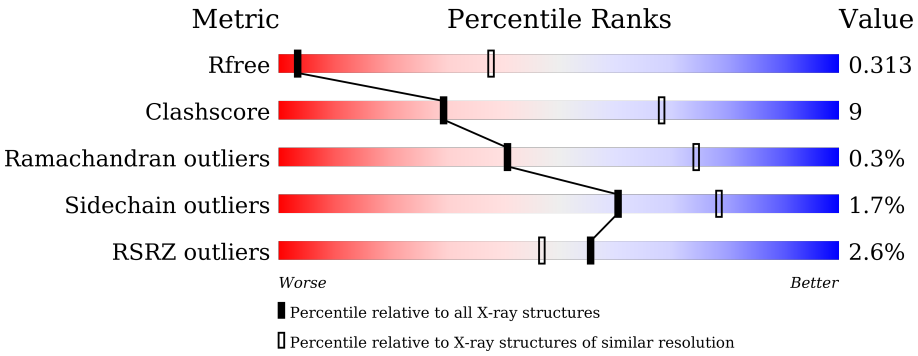
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (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 3.80 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	1212 (4.00-3.60)
Clashscore	141614	1288 (4.00-3.60)
Ramachandran outliers	138981	1243 (4.00-3.60)
Sidechain outliers	138945	1237 (4.00-3.60)
RSRZ outliers	127900	1121 (4.00-3.60)

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	A	431	3% 68% 19% 13%
1	B	431	% 68% 20% 12%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 5883 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 Adenosine receptor A2a,Soluble cytochrome b562.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	377	Total	C	N	O	S	0	0	0
			2873	1872	481	499	21			
1	B	379	Total	C	N	O	S	0	0	0
			2896	1887	484	504	21			

There are 70 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-8	ASP	-	expression tag	UNP P29274
A	-7	TYR	-	expression tag	UNP P29274
A	-6	LYS	-	expression tag	UNP P29274
A	-5	ASP	-	expression tag	UNP P29274
A	-4	ASP	-	expression tag	UNP P29274
A	-3	ASP	-	expression tag	UNP P29274
A	-2	ASP	-	expression tag	UNP P29274
A	-1	GLY	-	expression tag	UNP P29274
A	0	ALA	-	expression tag	UNP P29274
A	1	PRO	-	expression tag	UNP P29274
A	92	ASN	ILE	engineered mutation	UNP P29274
A	1007	TRP	MET	engineered mutation	UNP P0ABE7
A	1102	ILE	-	linker	UNP P0ABE7
A	1103	GLN	-	linker	UNP P0ABE7
A	1104	LYS	-	linker	UNP P0ABE7
A	1105	TYR	-	linker	UNP P0ABE7
A	1106	LEU	-	linker	UNP P0ABE7
A	309	ARG	-	expression tag	UNP P29274
A	310	GLN	-	expression tag	UNP P29274
A	311	GLN	-	expression tag	UNP P29274
A	312	GLU	-	expression tag	UNP P29274
A	313	PRO	-	expression tag	UNP P29274
A	314	PHE	-	expression tag	UNP P29274
A	315	LYS	-	expression tag	UNP P29274
A	316	ALA	-	expression tag	UNP P29274

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Chain	Residue	Modelled	Actual	Comment	Reference
A	317	HIS	-	expression tag	UNP P29274
A	318	HIS	-	expression tag	UNP P29274
A	319	HIS	-	expression tag	UNP P29274
A	320	HIS	-	expression tag	UNP P29274
A	321	HIS	-	expression tag	UNP P29274
A	322	HIS	-	expression tag	UNP P29274
A	323	HIS	-	expression tag	UNP P29274
A	324	HIS	-	expression tag	UNP P29274
A	325	HIS	-	expression tag	UNP P29274
A	326	HIS	-	expression tag	UNP P29274
B	-8	ASP	-	expression tag	UNP P29274
B	-7	TYR	-	expression tag	UNP P29274
B	-6	LYS	-	expression tag	UNP P29274
B	-5	ASP	-	expression tag	UNP P29274
B	-4	ASP	-	expression tag	UNP P29274
B	-3	ASP	-	expression tag	UNP P29274
B	-2	ASP	-	expression tag	UNP P29274
B	-1	GLY	-	expression tag	UNP P29274
B	0	ALA	-	expression tag	UNP P29274
B	1	PRO	-	expression tag	UNP P29274
B	92	ASN	ILE	engineered mutation	UNP P29274
B	1007	TRP	MET	engineered mutation	UNP P0ABE7
B	1102	ILE	-	linker	UNP P0ABE7
B	1103	GLN	-	linker	UNP P0ABE7
B	1104	LYS	-	linker	UNP P0ABE7
B	1105	TYR	-	linker	UNP P0ABE7
B	1106	LEU	-	linker	UNP P0ABE7
B	309	ARG	-	expression tag	UNP P29274
B	310	GLN	-	expression tag	UNP P29274
B	311	GLN	-	expression tag	UNP P29274
B	312	GLU	-	expression tag	UNP P29274
B	313	PRO	-	expression tag	UNP P29274
B	314	PHE	-	expression tag	UNP P29274
B	315	LYS	-	expression tag	UNP P29274
B	316	ALA	-	expression tag	UNP P29274
B	317	HIS	-	expression tag	UNP P29274
B	318	HIS	-	expression tag	UNP P29274
B	319	HIS	-	expression tag	UNP P29274
B	320	HIS	-	expression tag	UNP P29274
B	321	HIS	-	expression tag	UNP P29274
B	322	HIS	-	expression tag	UNP P29274
B	323	HIS	-	expression tag	UNP P29274

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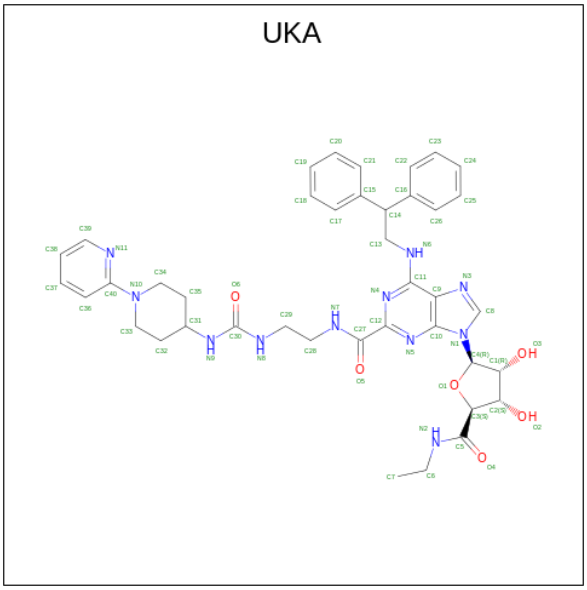
Chain	Residue	Modelled	Actual	Comment	Reference
B	324	HIS	-	expression tag	UNP P29274
B	325	HIS	-	expression tag	UNP P29274
B	326	HIS	-	expression tag	UNP P29274

- Molecule 2 is 6-(2,2-diphenylethylamino)-9-[(2R,3R,4S,5S)-5-(ethylcarbamoyl)-3,4-dihydroxy-oxolan-2-yl]-N-[2-[(1-pyridin-2-ylpiperidin-4-yl)carbamoylamino]ethyl]purine-2-carboxamide (three-letter code: UKA) (formula: $C_{40}H_{47}N_{11}O_6$).



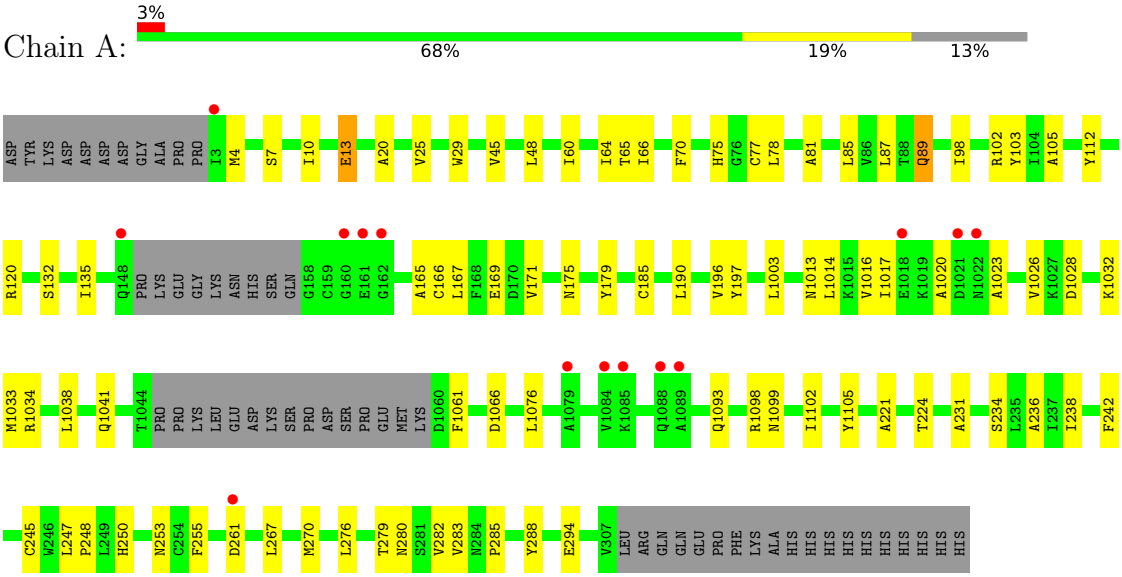
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			57	40	11	6		
2	B	1	Total	C	N	O	0	0
			57	40	11	6		

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.

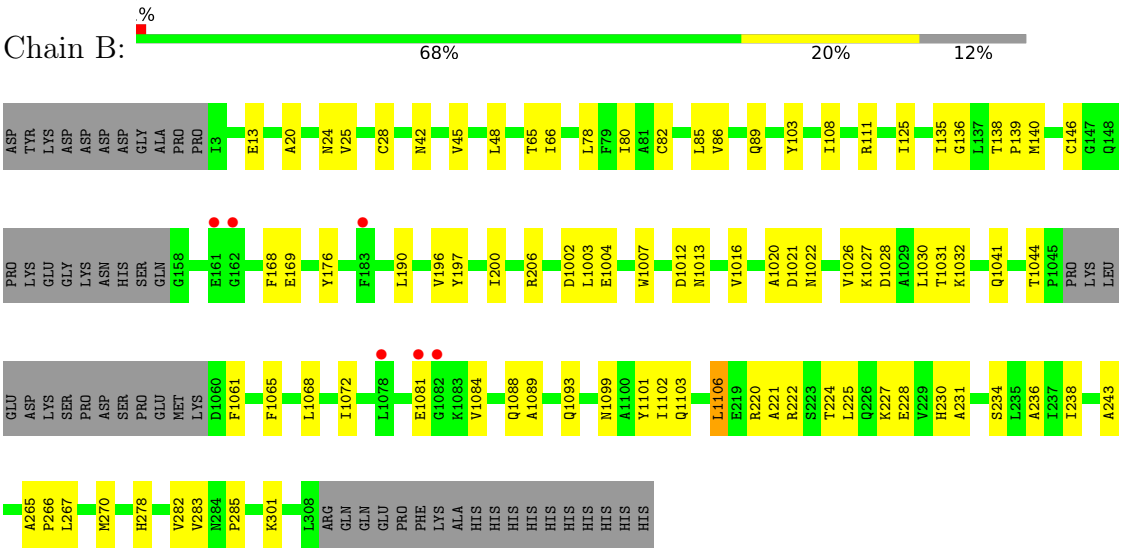
• Molecule 1: Adenosine receptor A2a,Soluble cytochrome b562

Chain A:



• Molecule 1: Adenosine receptor A2a,Soluble cytochrome b562

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	71.23Å 175.73Å 112.71Å 90.00° 91.22° 90.00°	Depositor
Resolution (Å)	47.43 – 3.80 47.43 – 3.80	Depositor EDS
% Data completeness (in resolution range)	99.6 (47.43-3.80) 91.4 (47.43-3.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.02 (at 3.77Å)	Xtriage
Refinement program	PHENIX 1.10.1_2155	Depositor
R, R_{free}	0.288 , 0.313 0.288 , 0.313	Depositor DCC
R_{free} test set	692 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å^2)	93.6	Xtriage
Anisotropy	0.830	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.27 , 52.8	EDS
L-test for twinning[2]	$< \|L\| > = 0.47$, $< L^2 > = 0.30$	Xtriage
Estimated twinning fraction	0.044 for h,-k,-l	Xtriage
F_o,F_c correlation	0.89	EDS
Total number of atoms	5883	wwPDB-VP
Average B, all atoms (Å^2)	124.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.08% 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: UKA

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	0.26	0/2933	0.40	0/4004
1	B	0.25	0/2957	0.41	1/4036 (0.0%)
All	All	0.25	0/5890	0.40	1/8040 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	1106	LEU	CB-CG-CD2	-6.22	100.43	111.00

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	2873	0	2859	54	1
1	B	2896	0	2890	57	1
2	A	57	0	46	3	0
2	B	57	0	46	3	0
All	All	5883	0	5841	111	1

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 9.

All (111) 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:B:1016:VAL:O	1:B:1020:ALA:N	2.15	0.78
1:B:78:LEU:HD22	1:B:140:MET:HG2	1.72	0.70
1:A:103:TYR:HB2	1:A:196:VAL:HG13	1.72	0.70
1:A:1016:VAL:O	1:A:1020:ALA:N	2.25	0.70
1:A:120:ARG:HH12	1:B:146:CYS:H	1.42	0.66
1:B:1016:VAL:HG12	1:B:1020:ALA:HB2	1.78	0.66
1:B:282:VAL:HG23	1:B:283:VAL:HG13	1.81	0.62
1:A:48:LEU:HG	1:A:285:PRO:HG3	1.81	0.62
1:A:66:ILE:HD11	1:A:81:ALA:HA	1.83	0.60
1:A:10:ILE:HG23	1:A:64:ILE:HD13	1.83	0.60
1:A:250:HIS:HA	1:A:253:ASN:HB2	1.83	0.59
1:B:224:THR:OG1	1:B:228:GLU:OE1	2.20	0.59
1:B:1012:ASP:O	1:B:1016:VAL:HG23	2.03	0.58
1:A:1093:GLN:HG2	1:A:1098:ARG:HD2	1.87	0.57
1:B:1041:GLN:HA	1:B:1044:THR:HG22	1.86	0.57
1:B:1007:TRP:CZ3	1:B:1106:LEU:HD21	2.40	0.57
1:A:1093:GLN:HA	1:A:1098:ARG:HB2	1.86	0.57
1:B:1026:VAL:O	1:B:1030:LEU:HG	2.05	0.57
1:A:282:VAL:HG23	1:A:283:VAL:HG13	1.87	0.56
1:B:13:GLU:OE2	1:B:278:HIS:ND1	2.36	0.56
1:A:169:GLU:OE2	2:A:1200:UKA:N9	2.38	0.56
1:A:120:ARG:NH1	1:B:146:CYS:H	2.05	0.55
1:A:248:PRO:HG2	1:A:276:LEU:HD23	1.88	0.55
1:A:1041:GLN:NE2	1:A:1066:ASP:OD1	2.40	0.55
1:A:238:ILE:HD11	1:A:288:TYR:HB2	1.88	0.55
1:B:1081:GLU:OE2	1:B:1081:GLU:HA	2.07	0.54
1:B:1007:TRP:CH2	1:B:1106:LEU:HD21	2.41	0.54
1:B:1061:PHE:CZ	1:B:220:ARG:HB2	2.42	0.54
2:B:1200:UKA:O4	2:B:1200:UKA:H8	2.07	0.54
1:B:135:ILE:O	1:B:176:TYR:OH	2.27	0.53
1:B:103:TYR:HB2	1:B:196:VAL:HG13	1.89	0.53
1:B:48:LEU:HG	1:B:285:PRO:HG3	1.91	0.53
1:B:1021:ASP:OD1	1:B:1022:ASN:N	2.41	0.52
1:A:89:GLN:HG2	1:A:132:SER:HA	1.91	0.52
1:B:1007:TRP:CZ3	1:B:1106:LEU:HD11	2.45	0.52
1:A:13:GLU:HB3	1:A:64:ILE:HD11	1.93	0.51
1:B:103:TYR:HA	1:B:200:ILE:HD11	1.93	0.51
1:B:231:ALA:HA	1:B:234:SER:HB2	1.91	0.51
1:A:1061:PHE:CE1	1:A:1105:TYR:HD2	2.29	0.51
1:B:85:LEU:O	1:B:89:GLN:NE2	2.44	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1084:VAL:O	1:B:1088:GLN:HG3	2.11	0.50
1:A:85:LEU:O	1:A:89:GLN:HB2	2.11	0.49
1:A:66:ILE:O	1:A:167:LEU:HA	2.12	0.49
1:A:77:CYS:HB3	1:A:171:VAL:HG11	1.94	0.49
1:A:45:VAL:HA	1:A:98:ILE:HD11	1.95	0.49
1:A:270:MET:O	2:A:1200:UKA:H25	2.13	0.49
1:B:25:VAL:HA	1:B:28:CYS:HB2	1.94	0.49
1:A:1099:ASN:HB3	1:A:1102:ILE:HG22	1.95	0.49
1:A:1014:LEU:HD12	1:A:1017:ILE:HB	1.95	0.49
1:A:245:CYS:SG	1:A:280:ASN:HB2	2.52	0.48
1:B:234:SER:O	1:B:238:ILE:HG12	2.13	0.48
1:A:75:HIS:HA	1:A:78:LEU:HB2	1.95	0.48
1:A:1013:ASN:O	1:A:1016:VAL:HB	2.14	0.48
1:B:108:ILE:HG22	1:B:111:ARG:HB2	1.95	0.48
1:B:190:LEU:HD11	1:B:243:ALA:HB2	1.95	0.48
1:B:220:ARG:O	1:B:224:THR:HG22	2.14	0.48
1:B:138:THR:HB	1:B:139:PRO:HD3	1.96	0.48
1:A:165:ALA:O	1:A:167:LEU:N	2.44	0.48
1:B:1089:ALA:O	1:B:1093:GLN:HG2	2.14	0.47
1:B:169:GLU:OE1	1:B:169:GLU:N	2.40	0.47
1:A:1013:ASN:ND2	1:A:1032:LYS:HB2	2.30	0.47
1:B:86:VAL:HG22	1:B:136:GLY:HA3	1.96	0.47
1:A:4:MET:HB2	1:A:7:SER:HB2	1.98	0.46
1:B:20:ALA:O	1:B:24:ASN:ND2	2.49	0.46
1:B:65:THR:HG21	1:B:80:ILE:HD13	1.98	0.45
1:B:169:GLU:HB3	2:B:1200:UKA:H21	1.97	0.45
1:A:247:LEU:HD23	1:A:247:LEU:HA	1.84	0.45
1:A:65:THR:HG22	1:A:70:PHE:CE1	2.51	0.45
2:A:1200:UKA:H8	2:A:1200:UKA:O4	2.16	0.45
1:B:1002:ASP:OD1	1:B:1003:LEU:N	2.49	0.45
1:B:1028:ASP:O	1:B:1032:LYS:HG3	2.16	0.45
1:A:1020:ALA:HB1	1:A:1026:VAL:HG12	1.98	0.45
1:B:197:TYR:CE2	1:B:236:ALA:HB2	2.52	0.45
1:A:1017:ILE:HA	1:A:1020:ALA:HB2	1.97	0.44
1:B:1102:ILE:O	1:B:1106:LEU:HD13	2.16	0.44
1:A:87:LEU:HD23	1:A:87:LEU:HA	1.83	0.44
1:A:1013:ASN:HD22	1:A:1033:MET:HG3	1.83	0.44
1:A:1003:LEU:HD13	1:A:1105:TYR:OH	2.18	0.44
1:B:78:LEU:HD21	1:B:139:PRO:HB2	2.01	0.43
1:B:1099:ASN:O	1:B:1103:GLN:HG3	2.18	0.43
1:A:197:TYR:CE2	1:A:236:ALA:HB2	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:301:LYS:HB2	1:B:301:LYS:HE3	1.72	0.42
1:B:221:ALA:O	1:B:225:LEU:HD13	2.19	0.42
1:A:25:VAL:O	1:A:29:TRP:N	2.49	0.42
1:A:221:ALA:HA	1:A:224:THR:HG22	2.02	0.42
1:B:1041:GLN:OE1	1:B:1065:PHE:HB3	2.19	0.42
1:B:1027:LYS:O	1:B:1031:THR:HG23	2.19	0.42
1:B:82:CYS:O	1:B:86:VAL:HG23	2.20	0.42
1:B:42:ASN:HA	1:B:45:VAL:HG23	2.01	0.42
1:A:175:ASN:O	1:A:179:TYR:HB2	2.19	0.42
1:A:1034:ARG:O	1:A:1038:LEU:HG	2.19	0.42
1:A:190:LEU:HD13	1:A:242:PHE:HD2	1.85	0.41
1:A:20:ALA:HB2	1:A:282:VAL:HG12	2.02	0.41
1:A:279:THR:O	1:A:283:VAL:HG22	2.20	0.41
1:A:105:ALA:HB2	1:A:112:TYR:CE1	2.56	0.41
1:A:231:ALA:HA	1:A:234:SER:HB2	2.03	0.41
1:B:125:ILE:HD13	1:B:125:ILE:HA	1.91	0.41
1:B:66:ILE:HG21	1:B:168:PHE:HB2	2.03	0.41
1:B:227:LYS:O	1:B:230:HIS:HB3	2.21	0.41
1:A:135:ILE:HD13	1:A:185:CYS:SG	2.61	0.41
1:A:1028:ASP:OD1	1:A:1028:ASP:N	2.54	0.41
1:B:1068:LEU:O	1:B:1072:ILE:HG13	2.21	0.41
1:A:1003:LEU:HD11	1:A:1105:TYR:HE1	1.86	0.40
1:A:1017:ILE:HA	1:A:1020:ALA:CB	2.51	0.40
1:B:270:MET:O	2:B:1200:UKA:H25	2.21	0.40
1:A:1076:LEU:HD12	1:A:1076:LEU:HA	1.89	0.40
1:B:1099:ASN:OD1	1:B:1101:TYR:N	2.50	0.40
1:B:266:PRO:O	1:B:270:MET:HG3	2.20	0.40
1:A:13:GLU:HG3	1:A:60:ILE:HG23	2.03	0.40
1:B:1106:LEU:O	1:B:222:ARG:N	2.45	0.40
1:B:265:ALA:HB3	1:B:270:MET:HG2	2.03	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1098:ARG:NH1	1:B:1004:GLU:OE2[3_455]	2.15	0.05

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	371/431 (86%)	340 (92%)	29 (8%)	2 (0%)	29 66
1	B	373/431 (86%)	342 (92%)	31 (8%)	0	100 100
All	All	744/862 (86%)	682 (92%)	60 (8%)	2 (0%)	41 74

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1023	ALA
1	A	166	CYS

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	294/360 (82%)	287 (98%)	7 (2%)	49 71
1	B	298/360 (83%)	295 (99%)	3 (1%)	76 86
All	All	592/720 (82%)	582 (98%)	10 (2%)	60 78

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	13	GLU
1	A	89	GLN
1	A	102	ARG
1	A	255	PHE

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Mol	Chain	Res	Type
1	A	261	ASP
1	A	267	LEU
1	A	294	GLU
1	B	206	ARG
1	B	1013	ASN
1	B	267	LEU

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

Mol	Chain	Res	Type
1	A	1103	GLN
1	B	1006	ASN

5.3.3 RNA

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains

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

5.5 Carbohydrates

There are no monosaccharides in this entry.

5.6 Ligand geometry

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	$\#\|Z\| > 2$
2	UKA	B	1200	-	59,63,63	3.60	19 (32%)	71,87,87	3.90	17 (23%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
2	UKA	A	1200	-	59,63,63	3.55	17 (28%)	71,87,87	3.99	16 (22%)

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	UKA	B	1200	-	-	8/37/69/69	0/7/7/7
2	UKA	A	1200	-	-	7/37/69/69	0/7/7/7

All (36) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1200	UKA	O1-C4	14.76	1.61	1.41
2	A	1200	UKA	O1-C4	14.64	1.61	1.41
2	B	1200	UKA	C1-C4	-11.77	1.35	1.53
2	A	1200	UKA	C1-C4	-11.73	1.36	1.53
2	A	1200	UKA	O1-C3	-8.82	1.31	1.43
2	B	1200	UKA	O1-C3	-8.79	1.31	1.43
2	B	1200	UKA	C11-N6	7.65	1.48	1.34
2	A	1200	UKA	C11-N6	7.45	1.48	1.34
2	B	1200	UKA	C5-N2	6.48	1.47	1.33
2	A	1200	UKA	C5-N2	6.34	1.47	1.33
2	B	1200	UKA	C27-N7	6.31	1.47	1.33
2	B	1200	UKA	C30-N8	6.07	1.47	1.35
2	A	1200	UKA	C27-N7	6.05	1.47	1.33
2	A	1200	UKA	C30-N8	6.04	1.47	1.35
2	A	1200	UKA	C30-N9	5.65	1.47	1.35
2	B	1200	UKA	C30-N9	5.65	1.47	1.35
2	B	1200	UKA	C40-N10	5.08	1.47	1.37
2	A	1200	UKA	C40-N10	4.96	1.47	1.37
2	A	1200	UKA	C2-C3	3.60	1.58	1.53
2	B	1200	UKA	C2-C3	3.39	1.58	1.53
2	B	1200	UKA	O2-C2	-3.02	1.35	1.43
2	A	1200	UKA	O2-C2	-2.89	1.36	1.43
2	A	1200	UKA	C34-N10	2.86	1.51	1.46
2	B	1200	UKA	C34-N10	2.79	1.51	1.46
2	B	1200	UKA	C33-N10	2.57	1.50	1.46
2	A	1200	UKA	O3-C1	2.55	1.49	1.43
2	B	1200	UKA	O3-C1	2.52	1.48	1.43
2	A	1200	UKA	C33-N10	2.41	1.50	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1200	UKA	C9-C10	-2.37	1.34	1.40
2	B	1200	UKA	C12-C27	2.33	1.55	1.53
2	B	1200	UKA	C9-C10	-2.32	1.34	1.40
2	B	1200	UKA	C31-N9	2.14	1.51	1.46
2	B	1200	UKA	C12-N5	2.07	1.36	1.34
2	A	1200	UKA	C31-N9	2.06	1.51	1.46
2	B	1200	UKA	O4-C5	-2.03	1.19	1.23
2	A	1200	UKA	O4-C5	-2.03	1.19	1.23

All (33) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	1200	UKA	N11-C40-N10	-20.84	85.55	116.79
2	B	1200	UKA	N11-C40-N10	-20.35	86.28	116.79
2	A	1200	UKA	C36-C40-N10	15.33	149.24	121.70
2	B	1200	UKA	C36-C40-N10	15.02	148.69	121.70
2	A	1200	UKA	C27-C12-N4	12.93	133.43	117.28
2	B	1200	UKA	C27-C12-N4	12.22	132.55	117.28
2	A	1200	UKA	C27-C12-N5	-9.03	106.00	117.28
2	B	1200	UKA	C27-C12-N5	-8.06	107.22	117.28
2	B	1200	UKA	C33-N10-C40	-4.89	109.04	120.39
2	A	1200	UKA	C33-N10-C40	-4.85	109.13	120.39
2	B	1200	UKA	C3-C5-N2	4.43	120.97	115.47
2	A	1200	UKA	C34-N10-C40	-4.37	110.24	120.39
2	B	1200	UKA	C22-C16-C14	-4.10	109.65	120.81
2	B	1200	UKA	N5-C12-N4	-4.08	120.23	126.24
2	A	1200	UKA	C22-C16-C14	-4.08	109.72	120.81
2	B	1200	UKA	C12-N5-C10	3.91	119.95	115.08
2	B	1200	UKA	C34-N10-C40	-3.90	111.33	120.39
2	A	1200	UKA	N5-C12-N4	-3.86	120.57	126.24
2	A	1200	UKA	C3-C5-N2	3.83	120.22	115.47
2	B	1200	UKA	C12-C27-N7	3.71	119.29	115.60
2	A	1200	UKA	C12-N5-C10	3.69	119.68	115.08
2	A	1200	UKA	C12-C27-N7	3.67	119.25	115.60
2	B	1200	UKA	C2-C1-C4	3.59	106.38	100.98
2	B	1200	UKA	C26-C16-C14	3.52	130.38	120.81
2	B	1200	UKA	C1-C2-C3	3.51	105.73	101.64
2	A	1200	UKA	C26-C16-C14	3.47	130.24	120.81
2	A	1200	UKA	C2-C1-C4	3.03	105.55	100.98
2	A	1200	UKA	C1-C2-C3	2.98	105.11	101.64
2	B	1200	UKA	C33-C32-C31	2.48	114.85	110.50
2	B	1200	UKA	C38-C39-N11	-2.25	119.75	123.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	1200	UKA	C38-C39-N11	-2.20	119.83	123.43
2	B	1200	UKA	C11-N4-C12	2.19	120.19	116.06
2	A	1200	UKA	C11-N4-C12	2.12	120.06	116.06

There are no chirality outliers.

All (15) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1200	UKA	N11-C40-N10-C34
2	A	1200	UKA	C36-C40-N10-C34
2	A	1200	UKA	N6-C13-C14-C16
2	B	1200	UKA	O1-C3-C5-O4
2	B	1200	UKA	N11-C40-N10-C34
2	B	1200	UKA	C36-C40-N10-C34
2	B	1200	UKA	N5-C12-C27-N7
2	B	1200	UKA	N6-C13-C14-C16
2	A	1200	UKA	O1-C3-C5-N2
2	B	1200	UKA	O1-C3-C5-N2
2	B	1200	UKA	C14-C13-N6-C11
2	A	1200	UKA	N5-C12-C27-N7
2	A	1200	UKA	O1-C3-C5-O4
2	A	1200	UKA	C14-C13-N6-C11
2	B	1200	UKA	N6-C13-C14-C15

There are no ring outliers.

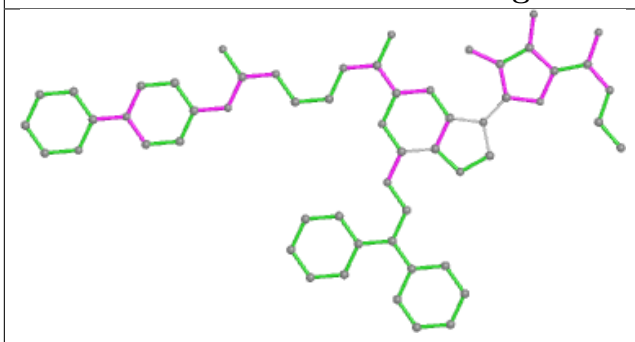
2 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	1200	UKA	3	0
2	A	1200	UKA	3	0

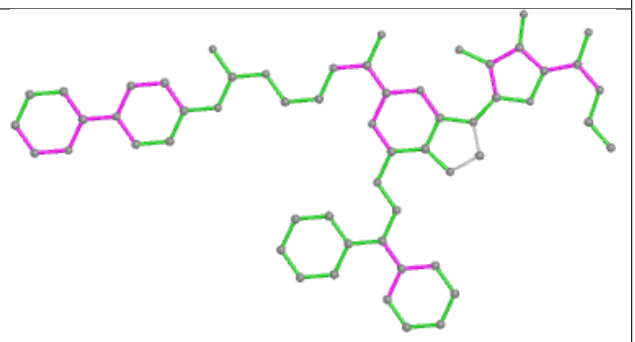
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.

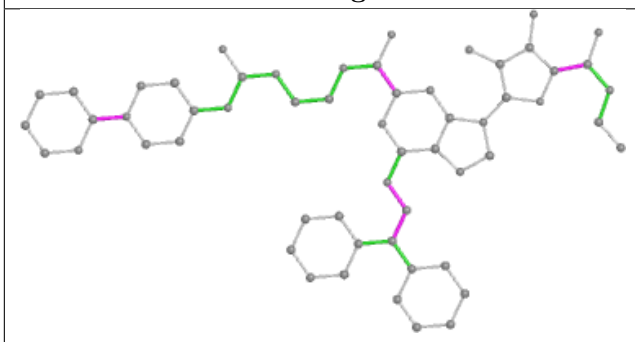
Ligand UKA B 1200



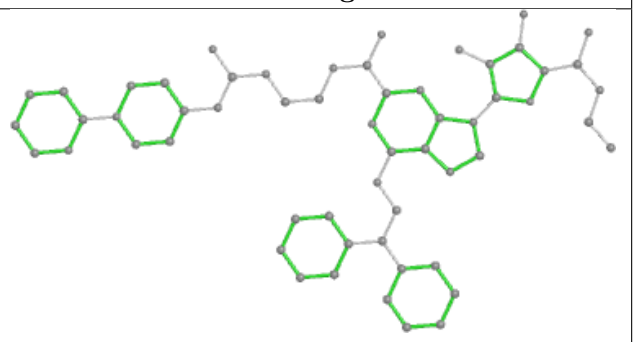
Bond lengths



Bond angles

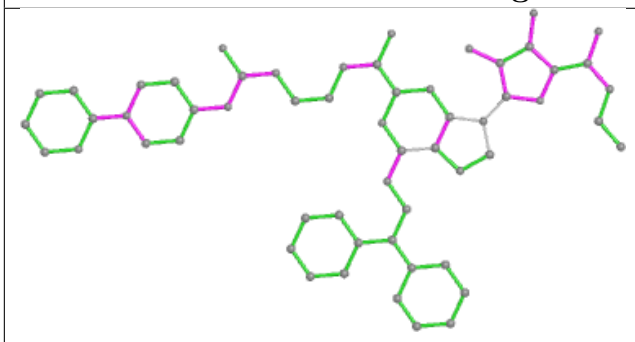


Torsions

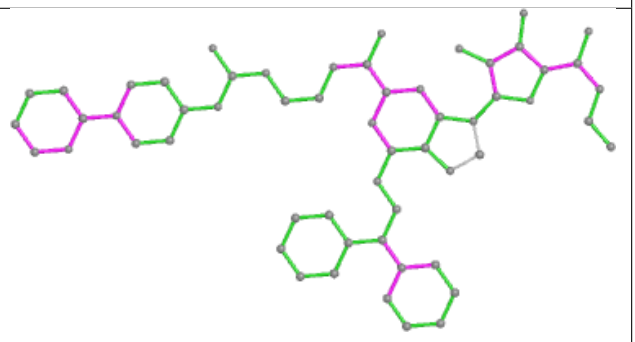


Rings

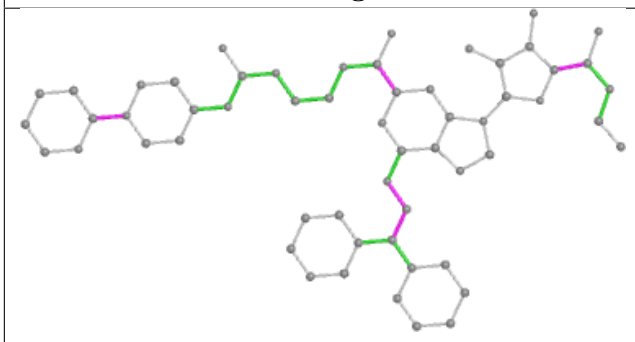
Ligand UKA A 1200



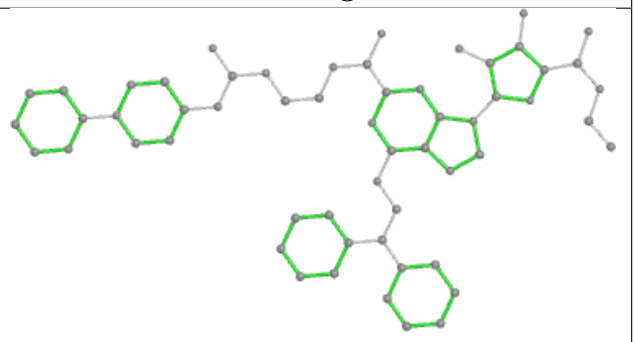
Bond lengths



Bond angles



Torsions



Rings

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	A	377/431 (87%)	-0.08	14 (3%) 41 34	69, 115, 161, 206	0
1	B	379/431 (87%)	-0.11	6 (1%) 72 64	81, 128, 194, 262	0
All	All	756/862 (87%)	-0.09	20 (2%) 56 47	69, 121, 181, 262	0

All (20) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	1082	GLY	7.7
1	B	1081	GLU	7.2
1	A	1022	ASN	5.4
1	A	1088	GLN	5.0
1	A	1021	ASP	4.5
1	B	1078	LEU	3.7
1	A	261	ASP	3.6
1	A	1084	VAL	3.2
1	A	3	ILE	3.2
1	A	1018	GLU	3.2
1	B	162	GLY	3.0
1	A	1085	LYS	2.9
1	A	1089	ALA	2.3
1	B	161	GLU	2.2
1	A	161	GLU	2.2
1	A	148	GLN	2.1
1	B	183	PHE	2.1
1	A	162	GLY	2.1
1	A	160	GLY	2.1
1	A	1079	ALA	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)

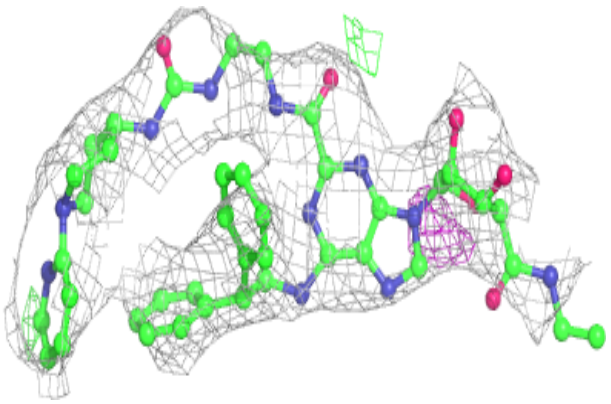
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9'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

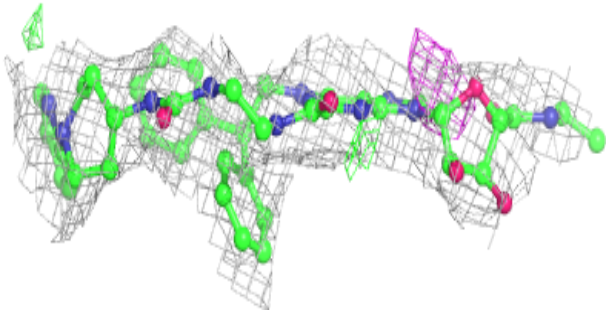
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	UKA	B	1200	57/57	0.85	0.35	113,118,142,143	0
2	UKA	A	1200	57/57	0.91	0.24	94,97,121,122	0

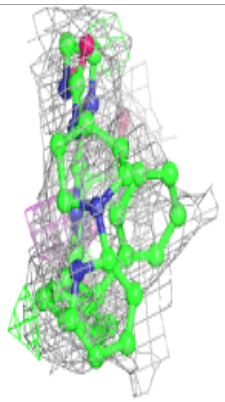
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around UKA B 1200:

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

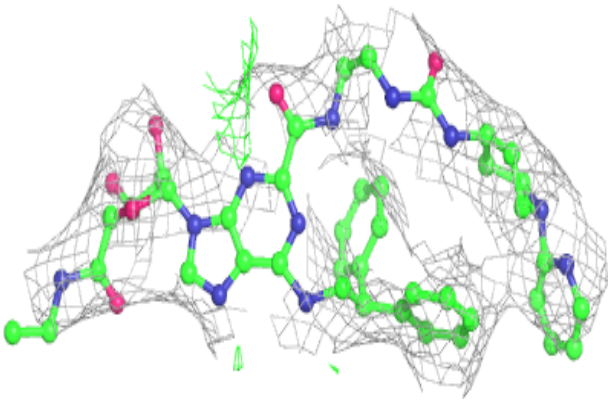


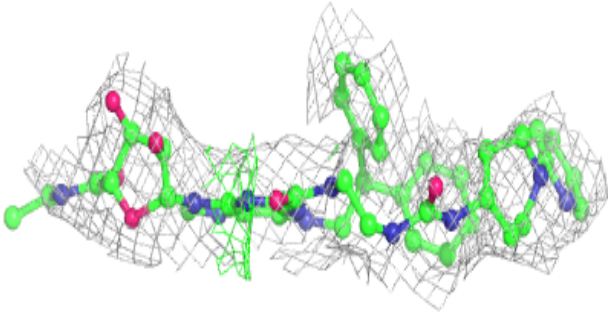


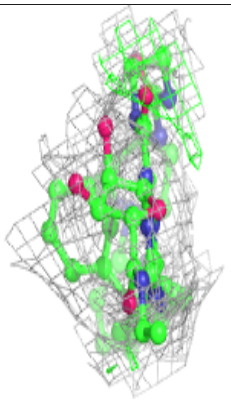


Electron density around UKA A 1200:

$2mF_o$-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.