WORLDWIDE PDB

PROTEIN DATA BANK

Full wwPDB X-ray Structure Validation Report (i)

Mar 18, 2024 – 10:07 AM JST

PDB ID	:	5X2K
Title	:	Crystal structure of EGFR 696-1022 T790M in complex with WZ4003
Authors	:	Zhu, S.J.; Zhao, P.; Yun, C.H.
Deposited on	:	2017-02-01
Resolution	:	3.20 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
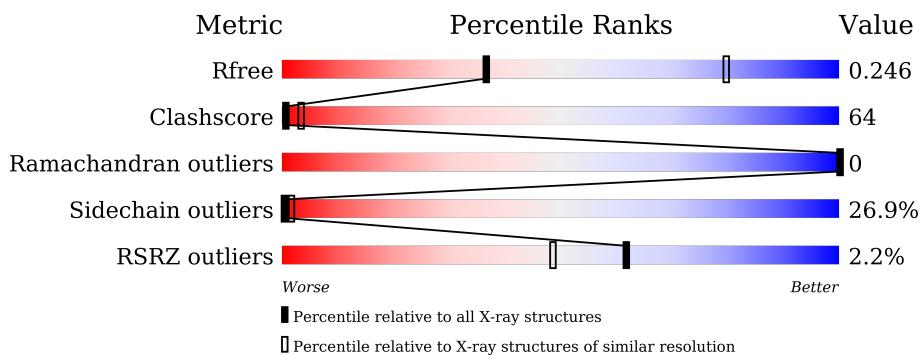
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 3.20 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	Percentile Ranks	Value
Rfree		0.246
Clashscore		64
Ramachandran outliers		0
Sidechain outliers		26.9%
RSRZ outliers		2.2%

Worse — Better

▌Percentile relative to all X-ray structures

▯Percentile relative to X-ray structures of similar resolution

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1133 (3.20-3.20)
Clashscore	141614	1253 (3.20-3.20)
Ramachandran outliers	138981	1234 (3.20-3.20)
Sidechain outliers	138945	1233 (3.20-3.20)
RSRZ outliers	127900	1095 (3.20-3.20)

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	327	2% ⬛ 32% 49% 15% •

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 2456 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.
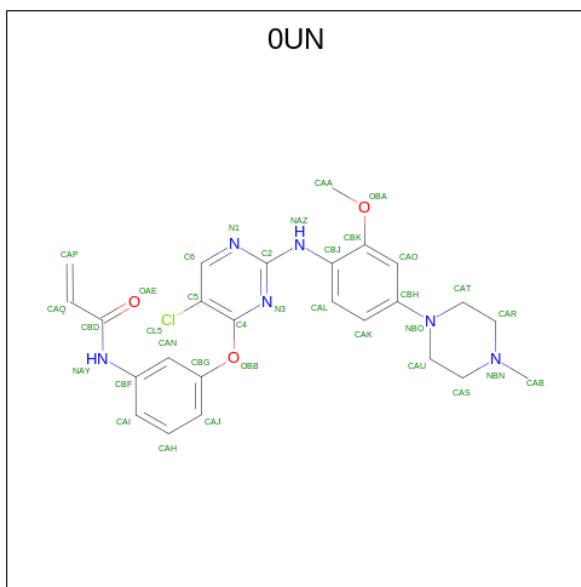
- Molecule 1 is a protein called Epidermal growth factor receptor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	314	Total 2412	C 1549	N 400	O 445	S 18	6	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	790	MET	THR	engineered mutation	UNP P00533

- Molecule 2 is N-{3-[(5-chloro-2-{[2-methoxy-4-(4-methylpiperazin-1-yl)phenyl]amino}pyrimidin-4-yl)oxy]phenyl}prop-2-enamide (three-letter code: 0UN) (formula: $C_{25}H_{27}ClN_6O_3$).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total 35	C 25	Cl 1	N 6	O 3	0	0
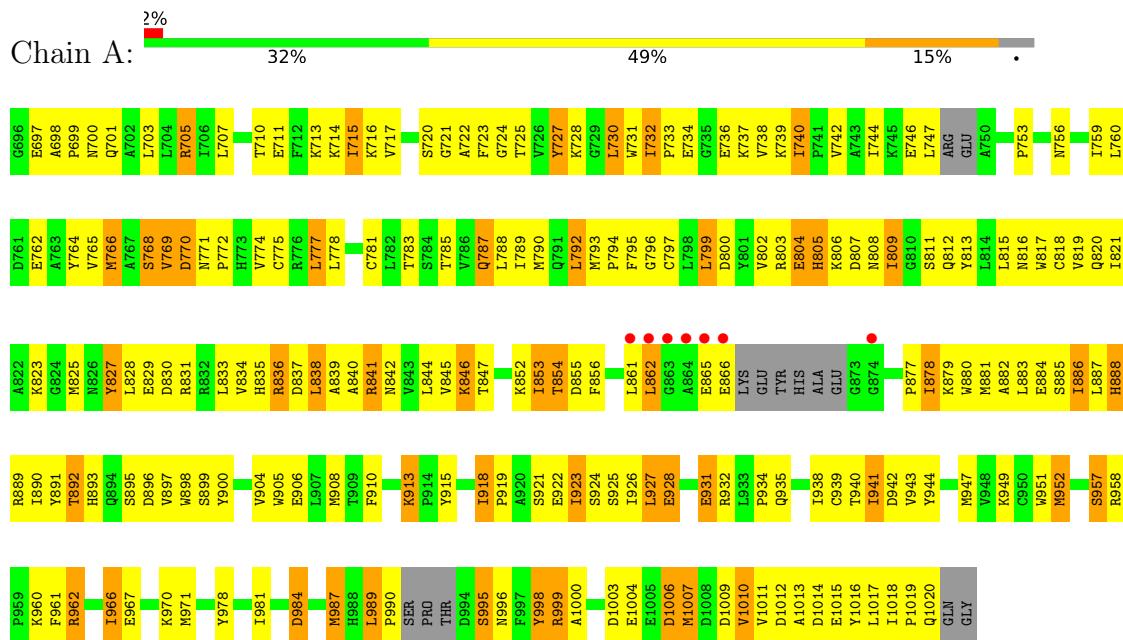
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	9	Total 9	O 9	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: Epidermal growth factor receptor

4 Data and refinement statistics ⓘ

Property	Value	Source
Space group	I 2 3	Depositor
Cell constants a, b, c, α, β, γ	149.27Å 149.27Å 149.27Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	43.09 – 3.20 43.09 – 3.20	Depositor EDS
% Data completeness (in resolution range)	96.2 (43.09-3.20) 96.2 (43.09-3.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.60 (at 3.19Å)	Xtriage
Refinement program	PHENIX 1.8.4_1496	Depositor
R, R_{free}	0.226 , 0.244 0.229 , 0.246	Depositor DCC
R_{free} test set	428 reflections (4.79%)	wwPDB-VP
Wilson B-factor (Å^2)	71.6	Xtriage
Anisotropy	0.000	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.31 , 53.8	EDS
L-test for twinning[2]	$< |L| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	0.027 for -l,-k,-h	Xtriage
F_o,F_c correlation	0.91	EDS
Total number of atoms	2456	wwPDB-VP
Average B, all atoms (Å^2)	61.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.41% of the height of the origin peak. No significant pseudotranslation is detected.*

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[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: 0UN

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	0.50	0/2460	0.55	0/3335

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	2412	0	2355	306	0
2	A	35	0	27	4	0
3	A	9	0	0	0	0
All	All	2456	0	2382	310	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 64.

All (310) 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:733:PRO:HB2	1:A:736:GLU:CG	1.43	1.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:733:PRO:CB	1:A:736:GLU:HG3	1.47	1.44
1:A:775:CYS:SG	1:A:854:THR:HG22	1.66	1.35
1:A:799:LEU:HD12	1:A:799:LEU:O	1.33	1.27
1:A:919:PRO:CG	1:A:922:GLU:HG3	1.64	1.26
1:A:756:ASN:O	1:A:759:ILE:HG22	1.41	1.18
1:A:919:PRO:HG2	1:A:922:GLU:CG	1.76	1.14
1:A:720:SER:HA	1:A:725:THR:HG22	1.25	1.12
1:A:775:CYS:SG	1:A:854:THR:CG2	2.38	1.11
1:A:730:LEU:CD2	1:A:739:LYS:HB3	1.86	1.03
1:A:919:PRO:HG2	1:A:922:GLU:HG3	1.05	1.03
1:A:918:ILE:HG22	1:A:919:PRO:HD2	1.42	1.02
1:A:825:MET:SD	1:A:838:LEU:CD2	2.48	1.01
1:A:825:MET:SD	1:A:838:LEU:HD22	2.02	0.99
1:A:775:CYS:HG	1:A:854:THR:HG22	1.23	0.99
1:A:799:LEU:HD12	1:A:799:LEU:C	1.80	0.99
1:A:919:PRO:CG	1:A:922:GLU:CG	2.41	0.95
1:A:898:TRP:CE3	1:A:958:ARG:NH2	2.35	0.94
1:A:813:TYR:CE2	1:A:989:LEU:CD1	2.52	0.93
1:A:925:SER:HA	1:A:928:GLU:OE1	1.69	0.93
2:A:1101:0UN:HAI	2:A:1101:0UN:OAE	1.65	0.92
1:A:918:ILE:CG2	1:A:919:PRO:HD2	1.99	0.92
1:A:730:LEU:HD21	1:A:739:LYS:HB3	1.46	0.92
1:A:740:ILE:CD1	1:A:1016:TYR:CD2	2.53	0.91
1:A:759:ILE:CG2	1:A:760:LEU:HD12	2.00	0.91
1:A:724:GLY:HA3	1:A:746:GLU:O	1.71	0.91
1:A:771:ASN:HB3	1:A:774:VAL:HG23	1.50	0.89
1:A:834:VAL:HG12	1:A:836:ARG:HG2	1.52	0.89
1:A:813:TYR:CE2	1:A:989:LEU:HD12	2.07	0.89
1:A:740:ILE:HD11	1:A:1016:TYR:CD2	2.07	0.89
1:A:877:PRO:O	1:A:881:MET:HG3	1.74	0.88
1:A:756:ASN:O	1:A:760:LEU:HD12	1.74	0.87
1:A:898:TRP:HE3	1:A:958:ARG:NH2	1.73	0.86
1:A:898:TRP:CZ2	1:A:927:LEU:CD1	2.60	0.85
1:A:720:SER:CA	1:A:725:THR:HG22	2.07	0.84
1:A:915:TYR:O	1:A:918:ILE:HG13	1.77	0.84
2:A:1101:0UN:HAL	2:A:1101:0UN:N3	1.90	0.84
1:A:888:HIS:HB2	1:A:890:ILE:HG13	1.59	0.84
1:A:797:CYS:SG	1:A:800:ASP:OD2	2.36	0.83
1:A:730:LEU:HD23	1:A:739:LYS:HB3	1.59	0.83
1:A:919:PRO:HG3	1:A:922:GLU:HG3	1.60	0.83
1:A:1006:ASP:O	1:A:1007:MET:SD	2.37	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:771:ASN:OD1	1:A:772:PRO:HD2	1.79	0.82
1:A:725:THR:HG1	1:A:727:TYR:HE1	0.83	0.82
1:A:725:THR:OG1	1:A:727:TYR:HE1	1.62	0.82
1:A:819:VAL:O	1:A:823:LYS:HG3	1.81	0.81
1:A:940:THR:HG22	1:A:942:ASP:H	1.44	0.81
1:A:813:TYR:CE2	1:A:989:LEU:HD11	2.15	0.80
1:A:840:ALA:HB3	1:A:906:GLU:OE1	1.81	0.80
1:A:967:GLU:O	1:A:971:MET:HG3	1.82	0.79
1:A:1019:PRO:O	1:A:1020:GLN:CB	2.31	0.79
1:A:759:ILE:HG23	1:A:760:LEU:HD12	1.65	0.78
1:A:827:TYR:C	1:A:827:TYR:CD2	2.57	0.78
1:A:707:LEU:O	1:A:781:CYS:SG	2.41	0.78
1:A:996:ASN:HA	1:A:999:ARG:HG3	1.66	0.78
1:A:898:TRP:HZ2	1:A:927:LEU:CD1	1.98	0.76
1:A:804:GLU:HB3	1:A:805:HIS:ND1	2.01	0.76
2:A:1101:0UN:OAE	2:A:1101:0UN:CAI	2.32	0.76
1:A:926:ILE:HG23	1:A:931:GLU:HG2	1.68	0.75
1:A:756:ASN:O	1:A:759:ILE:CG2	2.31	0.75
1:A:772:PRO:O	1:A:852:LYS:CE	2.35	0.74
1:A:919:PRO:HG2	1:A:922:GLU:CB	2.18	0.74
1:A:892:THR:H	1:A:895:SER:HB3	1.52	0.74
1:A:898:TRP:HZ2	1:A:927:LEU:HD11	1.51	0.73
1:A:772:PRO:O	1:A:852:LYS:HE3	1.88	0.73
1:A:940:THR:HG21	1:A:942:ASP:OD1	1.88	0.73
1:A:839:ALA:CB	1:A:841:ARG:HE	2.00	0.73
1:A:840:ALA:CB	1:A:906:GLU:OE1	2.36	0.73
1:A:740:ILE:HD12	1:A:1016:TYR:CD2	2.22	0.73
1:A:762:GLU:O	1:A:766:MET:HG3	1.89	0.72
1:A:813:TYR:HE2	1:A:989:LEU:CD1	2.01	0.72
1:A:943:VAL:HG22	1:A:971:MET:HE1	1.70	0.72
1:A:724:GLY:CA	1:A:746:GLU:O	2.38	0.72
1:A:898:TRP:CZ3	1:A:958:ARG:NH2	2.56	0.72
1:A:756:ASN:C	1:A:759:ILE:HG22	2.09	0.72
1:A:846:LYS:HG3	1:A:847:THR:HG23	1.71	0.72
1:A:730:LEU:HD21	1:A:739:LYS:CB	2.19	0.71
1:A:769:VAL:CG2	1:A:769:VAL:O	2.39	0.71
1:A:716:LYS:HG2	1:A:717:VAL:N	2.06	0.71
1:A:940:THR:CG2	1:A:942:ASP:OD1	2.39	0.70
1:A:919:PRO:HG3	1:A:922:GLU:OE1	1.90	0.70
1:A:892:THR:O	1:A:895:SER:HB3	1.91	0.70
1:A:774:VAL:CG1	1:A:856:PHE:HZ	2.04	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:744:ILE:CG2	1:A:787:GLN:HG2	2.22	0.69
1:A:853:ILE:O	1:A:854:THR:HG22	1.92	0.69
1:A:834:VAL:CG1	1:A:836:ARG:HG2	2.22	0.69
1:A:812:GLN:HG3	1:A:816:ASN:ND2	2.07	0.69
1:A:838:LEU:HD12	1:A:839:ALA:N	2.07	0.69
1:A:716:LYS:CG	1:A:717:VAL:N	2.56	0.69
1:A:877:PRO:O	1:A:881:MET:CG	2.41	0.68
1:A:771:ASN:OD1	1:A:772:PRO:CD	2.39	0.68
2:A:1101:0UN:N3	2:A:1101:0UN:CAL	2.50	0.68
1:A:813:TYR:HE2	1:A:989:LEU:HD12	1.55	0.68
1:A:839:ALA:HB3	1:A:841:ARG:HE	1.56	0.68
1:A:774:VAL:HG12	1:A:856:PHE:HZ	1.59	0.68
1:A:984:ASP:HA	1:A:987:MET:SD	2.34	0.67
1:A:740:ILE:HD12	1:A:1016:TYR:HD2	1.58	0.67
1:A:775:CYS:SG	1:A:854:THR:HG21	2.35	0.67
1:A:765:VAL:CG1	1:A:833:LEU:HD21	2.25	0.67
1:A:733:PRO:HB2	1:A:736:GLU:CB	2.23	0.67
1:A:759:ILE:HG23	1:A:760:LEU:N	2.09	0.66
1:A:812:GLN:HG3	1:A:816:ASN:HD21	1.60	0.66
1:A:898:TRP:HE3	1:A:958:ARG:CZ	2.09	0.66
1:A:759:ILE:HG22	1:A:760:LEU:HD12	1.77	0.66
1:A:1006:ASP:OD2	1:A:1006:ASP:C	2.33	0.66
1:A:733:PRO:HB2	1:A:736:GLU:HG3	0.69	0.65
1:A:835:HIS:CE1	1:A:837:ASP:O	2.49	0.65
1:A:796:GLY:O	1:A:845:VAL:HG23	1.96	0.65
1:A:878:ILE:HG22	1:A:886:ILE:HD13	1.79	0.64
1:A:766:MET:HE2	1:A:777:LEU:HB2	1.79	0.64
1:A:1006:ASP:C	1:A:1007:MET:SD	2.76	0.64
1:A:943:VAL:CG2	1:A:971:MET:HE1	2.27	0.64
1:A:885:SER:HA	1:A:890:ILE:H	1.62	0.63
1:A:1000:ALA:O	1:A:1004:GLU:N	2.30	0.63
1:A:817:TRP:O	1:A:821:ILE:HG13	1.98	0.63
1:A:775:CYS:HG	1:A:854:THR:CG2	2.03	0.63
1:A:846:LYS:CG	1:A:847:THR:HG23	2.29	0.63
1:A:804:GLU:HB3	1:A:805:HIS:CE1	2.34	0.62
1:A:898:TRP:CZ2	1:A:927:LEU:HD11	2.30	0.62
1:A:998:TYR:C	1:A:998:TYR:CD2	2.72	0.62
1:A:756:ASN:O	1:A:760:LEU:CD1	2.46	0.61
1:A:940:THR:HB	1:A:978:TYR:O	2.00	0.61
1:A:725:THR:OG1	1:A:727:TYR:CE1	2.42	0.61
1:A:771:ASN:OD1	1:A:772:PRO:N	2.34	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:846:LYS:NZ	1:A:1014:ASP:OD2	2.33	0.61
1:A:884:GLU:HG2	1:A:885:SER:N	2.16	0.61
1:A:989:LEU:O	1:A:990:PRO:C	2.38	0.61
1:A:740:ILE:HD11	1:A:1016:TYR:CG	2.36	0.60
1:A:880:TRP:NE1	1:A:906:GLU:OE2	2.34	0.60
1:A:836:ARG:HD2	1:A:891:TYR:CD2	2.36	0.60
1:A:772:PRO:O	1:A:852:LYS:HE2	2.01	0.60
1:A:834:VAL:HG12	1:A:836:ARG:CG	2.29	0.59
1:A:829:GLU:HA	1:A:893:HIS:CD2	2.36	0.59
1:A:866:GLU:O	1:A:866:GLU:HG3	2.02	0.59
1:A:770:ASP:C	1:A:770:ASP:OD1	2.41	0.59
1:A:785:THR:HG23	1:A:785:THR:O	2.01	0.59
1:A:813:TYR:CD2	1:A:989:LEU:HD11	2.37	0.58
1:A:835:HIS:O	1:A:836:ARG:HB2	2.03	0.58
1:A:827:TYR:C	1:A:827:TYR:HD2	2.07	0.58
1:A:940:THR:CG2	1:A:941:ILE:N	2.66	0.58
1:A:940:THR:HG22	1:A:941:ILE:N	2.18	0.58
1:A:711:GLU:HG2	1:A:732:ILE:O	2.03	0.58
1:A:765:VAL:O	1:A:769:VAL:HG13	2.04	0.58
1:A:1003:ASP:C	1:A:1004:GLU:CG	2.70	0.58
1:A:774:VAL:HG12	1:A:856:PHE:CZ	2.39	0.58
1:A:898:TRP:CZ2	1:A:927:LEU:HD13	2.39	0.57
1:A:721:GLY:O	1:A:722:ALA:HB3	2.03	0.57
1:A:759:ILE:CG2	1:A:760:LEU:N	2.67	0.57
1:A:989:LEU:CB	1:A:990:PRO:HD2	2.34	0.57
1:A:766:MET:CE	1:A:790:MET:CE	2.83	0.57
1:A:845:VAL:HG12	1:A:847:THR:O	2.05	0.57
1:A:926:ILE:CG2	1:A:931:GLU:HG2	2.35	0.57
1:A:888:HIS:CB	1:A:890:ILE:HG13	2.33	0.57
1:A:774:VAL:CG1	1:A:856:PHE:CZ	2.88	0.56
1:A:797:CYS:SG	1:A:800:ASP:CG	2.84	0.56
1:A:919:PRO:HG3	1:A:922:GLU:CG	2.27	0.56
1:A:771:ASN:HB3	1:A:774:VAL:CG2	2.29	0.56
1:A:853:ILE:C	1:A:854:THR:CG2	2.74	0.55
1:A:919:PRO:HG2	1:A:922:GLU:HB2	1.88	0.55
1:A:883:LEU:HA	1:A:886:ILE:HG13	1.89	0.55
1:A:931:GLU:HG3	1:A:932:ARG:N	2.21	0.55
1:A:756:ASN:HA	1:A:759:ILE:HG22	1.88	0.55
1:A:723:PHE:O	1:A:747:LEU:C	2.45	0.55
1:A:727:TYR:CD1	1:A:727:TYR:N	2.75	0.55
1:A:923:ILE:HG22	1:A:924:SER:N	2.22	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:952:MET:O	1:A:958:ARG:NH2	2.39	0.55
1:A:793:MET:CE	1:A:852:LYS:HD2	2.37	0.55
1:A:827:TYR:HD2	1:A:828:LEU:N	2.05	0.55
1:A:736:GLU:OE2	1:A:736:GLU:HA	2.07	0.54
1:A:1003:ASP:O	1:A:1004:GLU:CG	2.55	0.54
1:A:846:LYS:HG3	1:A:847:THR:CG2	2.37	0.54
1:A:915:TYR:C	1:A:918:ILE:HG13	2.28	0.54
1:A:778:LEU:HB2	1:A:789:ILE:HG22	1.89	0.54
1:A:769:VAL:O	1:A:769:VAL:HG22	2.07	0.53
1:A:766:MET:HE1	1:A:790:MET:CE	2.38	0.53
1:A:713:LYS:CG	1:A:713:LYS:O	2.56	0.53
1:A:764:TYR:CD1	1:A:764:TYR:C	2.82	0.53
1:A:837:ASP:O	1:A:842:ASN:ND2	2.41	0.53
1:A:1012:ASP:CG	1:A:1013:ALA:N	2.61	0.53
1:A:733:PRO:CB	1:A:736:GLU:CG	2.34	0.53
1:A:744:ILE:HG23	1:A:787:GLN:HG2	1.91	0.53
1:A:792:LEU:O	1:A:794:PRO:HD3	2.08	0.53
1:A:931:GLU:C	1:A:932:ARG:HG2	2.29	0.53
1:A:949:LYS:O	1:A:952:MET:HG3	2.08	0.53
1:A:885:SER:O	1:A:889:ARG:N	2.42	0.52
1:A:891:TYR:CD1	1:A:891:TYR:N	2.77	0.52
1:A:727:TYR:N	1:A:727:TYR:HD1	2.07	0.52
1:A:809:ILE:HG22	1:A:809:ILE:O	2.08	0.52
1:A:862:LEU:O	1:A:862:LEU:HD22	2.10	0.52
1:A:766:MET:SD	1:A:790:MET:HE3	2.50	0.52
1:A:756:ASN:HA	1:A:759:ILE:CG2	2.41	0.51
1:A:793:MET:HE1	1:A:852:LYS:HD2	1.92	0.51
1:A:799:LEU:O	1:A:803:ARG:HG3	2.09	0.51
1:A:769:VAL:O	1:A:769:VAL:HG23	2.10	0.51
1:A:898:TRP:CH2	1:A:927:LEU:HD13	2.46	0.51
1:A:838:LEU:HD12	1:A:839:ALA:H	1.75	0.51
1:A:732:ILE:HG23	1:A:738:VAL:O	2.10	0.51
1:A:918:ILE:CG2	1:A:919:PRO:CD	2.82	0.51
1:A:793:MET:HE1	1:A:852:LYS:CD	2.41	0.51
1:A:812:GLN:O	1:A:816:ASN:ND2	2.43	0.51
1:A:815:LEU:O	1:A:819:VAL:HG23	2.10	0.51
1:A:853:ILE:HG22	1:A:854:THR:N	2.26	0.51
1:A:898:TRP:CH2	1:A:927:LEU:CD1	2.93	0.51
1:A:740:ILE:CD1	1:A:1016:TYR:CG	2.93	0.50
1:A:998:TYR:CD2	1:A:998:TYR:O	2.64	0.50
1:A:756:ASN:CA	1:A:759:ILE:HG22	2.40	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:825:MET:SD	1:A:838:LEU:HD21	2.45	0.50
1:A:795:PHE:HB2	1:A:845:VAL:HB	1.94	0.50
1:A:839:ALA:CB	1:A:841:ARG:NE	2.72	0.50
1:A:880:TRP:CZ2	1:A:906:GLU:OE2	2.65	0.50
1:A:918:ILE:HG22	1:A:919:PRO:CD	2.30	0.50
1:A:898:TRP:CD1	1:A:898:TRP:C	2.86	0.49
1:A:971:MET:HA	1:A:978:TYR:CE2	2.48	0.49
1:A:785:THR:O	1:A:785:THR:CG2	2.61	0.49
1:A:904:VAL:O	1:A:908:MET:HG2	2.13	0.49
1:A:753:PRO:HA	1:A:756:ASN:OD1	2.13	0.48
1:A:935:GLN:HB2	1:A:944:TYR:CD2	2.48	0.48
1:A:1006:ASP:O	1:A:1006:ASP:OD2	2.31	0.48
1:A:728:LYS:CD	1:A:1003:ASP:OD1	2.62	0.48
1:A:835:HIS:HE1	1:A:837:ASP:O	1.96	0.48
1:A:932:ARG:NH2	1:A:951:TRP:O	2.47	0.48
1:A:723:PHE:CG	1:A:724:GLY:N	2.82	0.48
1:A:839:ALA:HB2	1:A:841:ARG:HH11	1.77	0.48
1:A:838:LEU:HB3	1:A:899:SER:HB3	1.96	0.48
1:A:989:LEU:HB3	1:A:990:PRO:HD2	1.96	0.47
1:A:1010:VAL:O	1:A:1010:VAL:CG1	2.62	0.47
1:A:737:LYS:O	1:A:737:LYS:HG3	2.14	0.47
1:A:981:ILE:HB	1:A:984:ASP:OD1	2.14	0.47
1:A:766:MET:CE	1:A:790:MET:HE3	2.45	0.47
1:A:715:ILE:HG22	1:A:716:LYS:N	2.29	0.47
1:A:793:MET:CE	1:A:852:LYS:CD	2.92	0.47
1:A:812:GLN:CG	1:A:816:ASN:HD21	2.28	0.47
1:A:984:ASP:OD1	1:A:984:ASP:N	2.46	0.47
1:A:733:PRO:CG	1:A:736:GLU:HG3	2.35	0.46
1:A:840:ALA:HB2	1:A:906:GLU:OE1	2.14	0.46
1:A:962:ARG:O	1:A:966:ILE:HG13	2.15	0.46
1:A:913:LYS:H	1:A:913:LYS:HG2	1.37	0.46
1:A:812:GLN:CG	1:A:816:ASN:ND2	2.78	0.46
1:A:908:MET:HG3	1:A:947:MET:HE1	1.98	0.46
1:A:981:ILE:O	1:A:984:ASP:OD1	2.33	0.46
1:A:766:MET:HB3	1:A:766:MET:HE3	1.39	0.45
1:A:915:TYR:O	1:A:918:ILE:CG1	2.55	0.45
1:A:802:VAL:CG1	1:A:910:PHE:HA	2.46	0.45
1:A:897:VAL:O	1:A:900:TYR:HB3	2.16	0.45
1:A:1017:LEU:O	1:A:1018:ILE:C	2.54	0.45
1:A:882:ALA:O	1:A:886:ILE:CG1	2.64	0.45
1:A:802:VAL:HG11	1:A:910:PHE:HA	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:865:GLU:O	1:A:866:GLU:HB2	2.16	0.45
1:A:882:ALA:O	1:A:886:ILE:HG12	2.17	0.45
1:A:890:ILE:C	1:A:891:TYR:CD1	2.90	0.45
1:A:828:LEU:HD11	1:A:856:PHE:HE1	1.82	0.45
1:A:918:ILE:HG23	1:A:919:PRO:HD2	1.91	0.45
1:A:770:ASP:O	1:A:827:TYR:CE1	2.70	0.45
1:A:879:LYS:HE2	1:A:915:TYR:HB2	1.98	0.44
1:A:940:THR:CB	1:A:978:TYR:O	2.64	0.44
1:A:995:SER:O	1:A:999:ARG:HG2	2.18	0.44
1:A:765:VAL:O	1:A:768:SER:OG	2.35	0.44
1:A:807:ASP:O	1:A:987:MET:CE	2.65	0.44
1:A:887:LEU:N	1:A:887:LEU:HD23	2.31	0.44
1:A:905:TRP:CZ2	1:A:934:PRO:HD2	2.52	0.44
1:A:1011:VAL:CG1	1:A:1012:ASP:N	2.81	0.44
1:A:771:ASN:HB2	1:A:827:TYR:CE1	2.53	0.44
1:A:829:GLU:HA	1:A:893:HIS:NE2	2.33	0.44
1:A:884:GLU:HG2	1:A:885:SER:H	1.82	0.44
1:A:730:LEU:HD11	1:A:1007:MET:HE3	2.00	0.43
1:A:795:PHE:CD1	1:A:795:PHE:N	2.85	0.43
1:A:1012:ASP:CG	1:A:1013:ALA:H	2.21	0.43
1:A:716:LYS:CG	1:A:717:VAL:H	2.27	0.43
1:A:700:ASN:HD21	1:A:768:SER:HB3	1.82	0.43
1:A:898:TRP:CD1	1:A:898:TRP:O	2.72	0.43
1:A:766:MET:CE	1:A:790:MET:HE2	2.48	0.43
1:A:925:SER:CA	1:A:928:GLU:OE1	2.54	0.43
1:A:967:GLU:O	1:A:971:MET:CG	2.62	0.43
1:A:805:HIS:ND1	1:A:805:HIS:N	2.66	0.43
1:A:1010:VAL:O	1:A:1010:VAL:HG13	2.19	0.43
1:A:1011:VAL:HG12	1:A:1012:ASP:O	2.19	0.43
1:A:759:ILE:HG23	1:A:760:LEU:CD1	2.43	0.43
1:A:1000:ALA:O	1:A:1004:GLU:CA	2.67	0.43
1:A:698:ALA:HB1	1:A:699:PRO:HD2	2.00	0.42
1:A:940:THR:HG22	1:A:942:ASP:N	2.23	0.42
1:A:705:ARG:HG2	1:A:707:LEU:HD21	2.00	0.42
1:A:966:ILE:O	1:A:970:LYS:HG3	2.18	0.42
1:A:841:ARG:HG2	1:A:842:ASN:N	2.33	0.42
1:A:1000:ALA:O	1:A:1004:GLU:HA	2.18	0.42
1:A:737:LYS:O	1:A:737:LYS:CG	2.66	0.42
1:A:759:ILE:CG2	1:A:760:LEU:H	2.32	0.42
1:A:999:ARG:HE	1:A:999:ARG:HB3	1.51	0.42
1:A:935:GLN:NE2	1:A:939:CYS:O	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:952:MET:HE3	1:A:957:SER:HB3	2.02	0.42
1:A:716:LYS:HG3	1:A:717:VAL:H	1.85	0.42
1:A:827:TYR:O	1:A:830:ASP:HB2	2.19	0.42
1:A:880:TRP:CE2	1:A:906:GLU:OE2	2.73	0.42
1:A:733:PRO:HB2	1:A:736:GLU:HG2	1.74	0.41
1:A:742:VAL:HG11	1:A:778:LEU:HD12	2.01	0.41
1:A:818:CYS:SG	1:A:904:VAL:HG22	2.61	0.41
1:A:893:HIS:O	1:A:896:ASP:HB2	2.21	0.41
1:A:797:CYS:HA	1:A:844:LEU:HD23	2.01	0.41
1:A:989:LEU:CB	1:A:990:PRO:CD	2.97	0.41
1:A:789:ILE:HD12	1:A:789:ILE:N	2.35	0.41
1:A:771:ASN:ND2	1:A:827:TYR:CD1	2.80	0.41
1:A:960:LYS:HE3	1:A:960:LYS:HB3	1.86	0.41
1:A:707:LEU:HD22	1:A:731:TRP:CZ2	2.56	0.41
1:A:940:THR:HG22	1:A:942:ASP:OD1	2.17	0.41
1:A:730:LEU:HD11	1:A:1007:MET:CE	2.51	0.41
1:A:825:MET:HE2	1:A:961:PHE:CZ	2.57	0.40
1:A:816:ASN:O	1:A:820:GLN:HG3	2.22	0.40
1:A:952:MET:CE	1:A:957:SER:HB3	2.51	0.40
1:A:720:SER:CB	1:A:725:THR:HG22	2.52	0.40
1:A:721:GLY:O	1:A:722:ALA:CB	2.68	0.40
1:A:926:ILE:HG22	1:A:927:LEU:HD23	2.03	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	306/327 (94%)	298 (97%)	8 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	249/287 (87%)	182 (73%)	67 (27%)	0	2

All (67) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	697	GLU
1	A	701	GLN
1	A	703	LEU
1	A	705	ARG
1	A	710	THR
1	A	714	LYS
1	A	715	ILE
1	A	727	TYR
1	A	730	LEU
1	A	732	ILE
1	A	734	GLU
1	A	740	ILE
1	A	766	MET
1	A	768	SER
1	A	769	VAL
1	A	770	ASP
1	A	777	LEU
1	A	783	THR
1	A	787	GLN
1	A	788	LEU
1	A	792	LEU
1	A	799	LEU
1	A	804	GLU
1	A	805	HIS
1	A	806	LYS
1	A	808	ASN
1	A	809	ILE
1	A	811	SER
1	A	827	TYR
1	A	831	ARG

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Mol	Chain	Res	Type
1	A	836	ARG
1	A	838	LEU
1	A	841	ARG
1	A	846	LYS
1	A	853	ILE
1	A	854	THR
1	A	855	ASP
1	A	861	LEU
1	A	862	LEU
1	A	878	ILE
1	A	886	ILE
1	A	888	HIS
1	A	892	THR
1	A	913	LYS
1	A	918	ILE
1	A	921	SER
1	A	923	ILE
1	A	927	LEU
1	A	928	GLU
1	A	931	GLU
1	A	938	ILE
1	A	941	ILE
1	A	952	MET
1	A	957	SER
1	A	962	ARG
1	A	966	ILE
1	A	984	ASP
1	A	987	MET
1	A	989	LEU
1	A	995	SER
1	A	998	TYR
1	A	999	ARG
1	A	1006	ASP
1	A	1007	MET
1	A	1009	ASP
1	A	1010	VAL
1	A	1015	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	787	GLN

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Mol	Chain	Res	Type
1	A	816	ASN
1	A	850	HIS
1	A	893	HIS

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 ⓘ

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	$\#|Z| > 2$
2	0UN	A	1101	-	37,38,38	1.49	6 (16%)	48,52,52	2.70	13 (27%)

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	0UN	A	1101	-	-	2/20/30/30	0/4/4/4

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1101	0UN	CAP-CAQ	4.55	1.52	1.30
2	A	1101	0UN	CBF-NAY	-4.54	1.32	1.41
2	A	1101	0UN	CBJ-NAZ	-2.87	1.31	1.39
2	A	1101	0UN	CAQ-CBD	2.40	1.52	1.48
2	A	1101	0UN	OBB-CBG	-2.11	1.35	1.39
2	A	1101	0UN	C2-NAZ	-2.10	1.32	1.36

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1101	0UN	CAP-CAQ-CBD	-10.30	110.49	122.27
2	A	1101	0UN	CBF-NAY-CBD	-7.08	117.56	128.26
2	A	1101	0UN	CAA-OBA-CBK	-5.56	109.13	117.53
2	A	1101	0UN	CAU-NBO-CAT	5.34	123.31	111.52
2	A	1101	0UN	C5-C6-N1	-5.25	118.33	122.84
2	A	1101	0UN	N1-C2-N3	-5.16	121.66	126.55
2	A	1101	0UN	C6-N1-C2	3.62	121.35	115.88
2	A	1101	0UN	OBA-CBK-CBJ	3.21	118.73	114.80
2	A	1101	0UN	CBJ-NAZ-C2	-2.66	121.59	129.60
2	A	1101	0UN	CBG-OBB-C4	-2.41	113.39	118.16
2	A	1101	0UN	OBB-C4-N3	2.33	123.26	119.58
2	A	1101	0UN	CAQ-CBD-NAY	2.22	115.30	113.84
2	A	1101	0UN	C2-N3-C4	2.16	119.05	115.18

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1101	0UN	CAP-CAQ-CBD-NAY
2	A	1101	0UN	CAP-CAQ-CBD-OAE
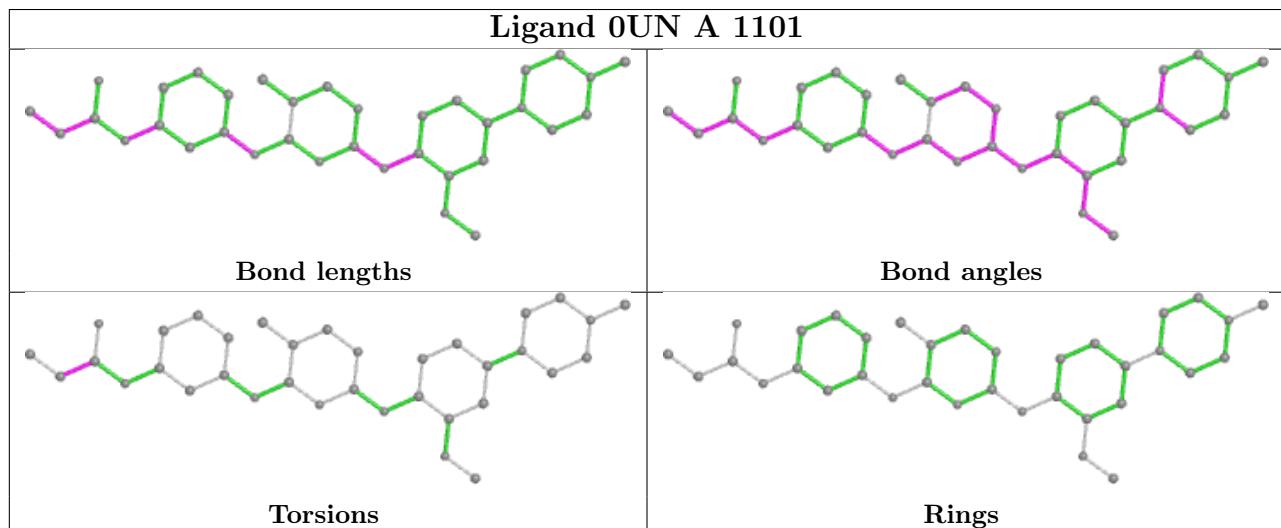
There are no ring outliers.

1 monomer is involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1101	0UN	4	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 0UN A 1101

Bond lengths — Bond angles — Torsions — Rings

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, 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	314/327 (96%)	-0.15	7 (2%)	62	48	30, 57, 106, 130	8 (2%)

All (7) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	863	GLY	4.8
1	A	864	ALA	4.2
1	A	874	GLY	3.5
1	A	865	GLU	3.3
1	A	866	GLU	2.7
1	A	861	LEU	2.6
1	A	862	LEU	2.5

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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

6.3 Carbohydrates ⓘ
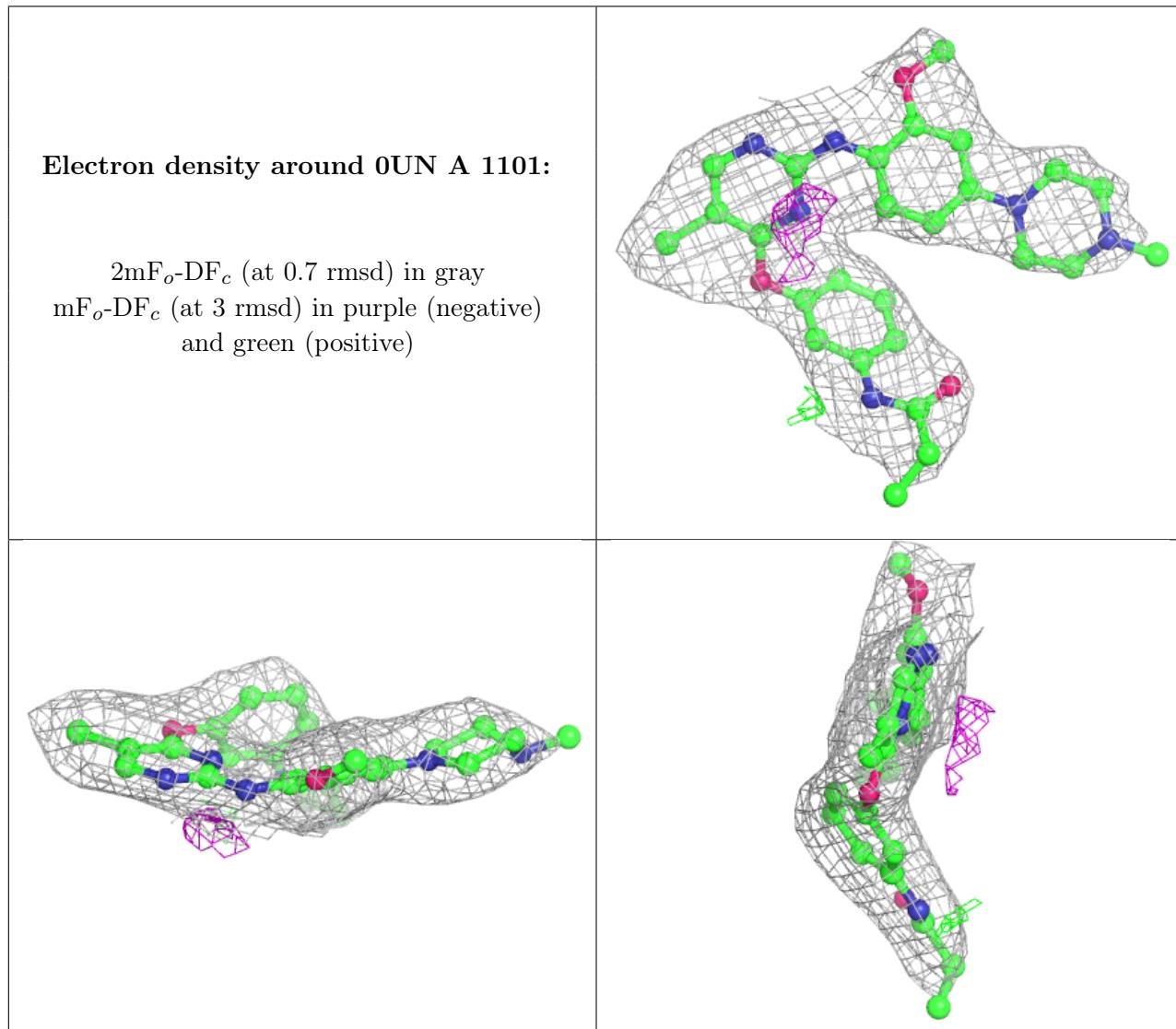
There are no monosaccharides in this entry.

6.4 Ligands ⓘ

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
2	0UN	A	1101	35/35	0.93	0.22	46,60,74,81	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 0UN A 1101:

$2mF_o$-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.