



Full wwPDB X-ray Structure Validation Report ⓘ

May 25, 2020 – 05:52 pm BST

PDB ID : 5X2C
Title : Crystal structure of EGFR 696-1022 T790M/V948R in complex with SKLB(5)
Authors : Yun, C.H.
Deposited on : 2017-01-31
Resolution : 2.05 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

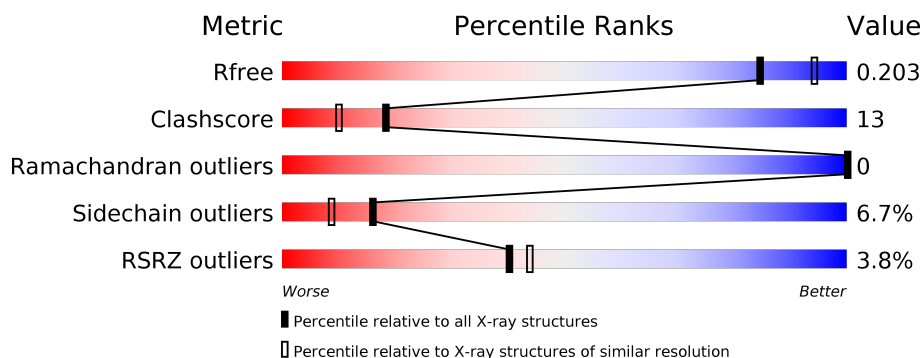
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.05 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	1692 (2.04-2.04)
Clashscore	141614	1773 (2.04-2.04)
Ramachandran outliers	138981	1752 (2.04-2.04)
Sidechain outliers	138945	1752 (2.04-2.04)
RSRZ outliers	127900	1672 (2.04-2.04)

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 $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	331	<div> <div>4%</div> <div> <div></div> <div>69%</div> <div>20%</div> <div>8%</div> </div> </div>
1	B	331	<div> <div>3%</div> <div> <div></div> <div>70%</div> <div>20%</div> <div>8%</div> </div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	EDO	A	1102	-	-	X	-
2	EDO	A	1103	-	-	X	X
2	EDO	B	1102	-	-	X	-
2	EDO	B	1104	-	-	X	-
2	EDO	B	1106	-	-	-	X

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 5597 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	304	Total	C	N	O	S	0	4	0
			2468	1581	421	445	21			
1	B	303	Total	C	N	O	S	0	8	0
			2492	1596	423	452	21			

There are 12 discrepancies between the modelled and reference sequences:

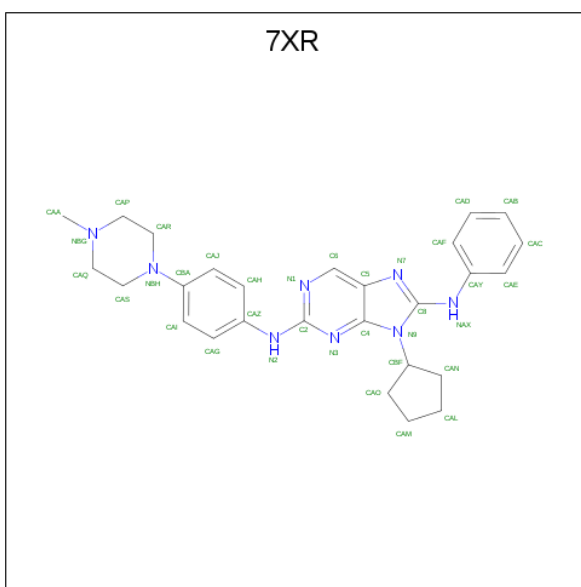
Chain	Residue	Modelled	Actual	Comment	Reference
A	692	GLY	-	expression tag	UNP P00533
A	693	SER	-	expression tag	UNP P00533
A	694	THR	-	expression tag	UNP P00533
A	695	SER	-	expression tag	UNP P00533
A	790	MET	THR	engineered mutation	UNP P00533
A	948	ARG	VAL	engineered mutation	UNP P00533
B	692	GLY	-	expression tag	UNP P00533
B	693	SER	-	expression tag	UNP P00533
B	694	THR	-	expression tag	UNP P00533
B	695	SER	-	expression tag	UNP P00533
B	790	MET	THR	engineered mutation	UNP P00533
B	948	ARG	VAL	engineered mutation	UNP P00533

- Molecule 2 is ethane-1,2-diol (three-letter code: EDO) (formula: C₂H₆O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			4	2	2		
2	A	1	Total	C	O	0	0
			4	2	2		
2	A	1	Total	C	O	0	0
			4	2	2		
2	B	1	Total	C	O	0	0
			4	2	2		
2	B	1	Total	C	O	0	0
			4	2	2		
2	B	1	Total	C	O	0	0
			4	2	2		
2	B	1	Total	C	O	0	0
			4	2	2		
2	B	1	Total	C	O	0	0
			4	2	2		

- Molecule 3 is 9-cyclopentyl-N2-[4-(4-methylpiperazin-1-yl)phenyl]-N8-phenyl-purine-2,8-diamine (three-letter code: 7XR) (formula: C₂₇H₃₂N₈).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C N 35 27 8	0	0
3	B	1	Total C N 35 27 8	0	0

- Molecule 4 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	B	1	Total Cl 1 1	0	0

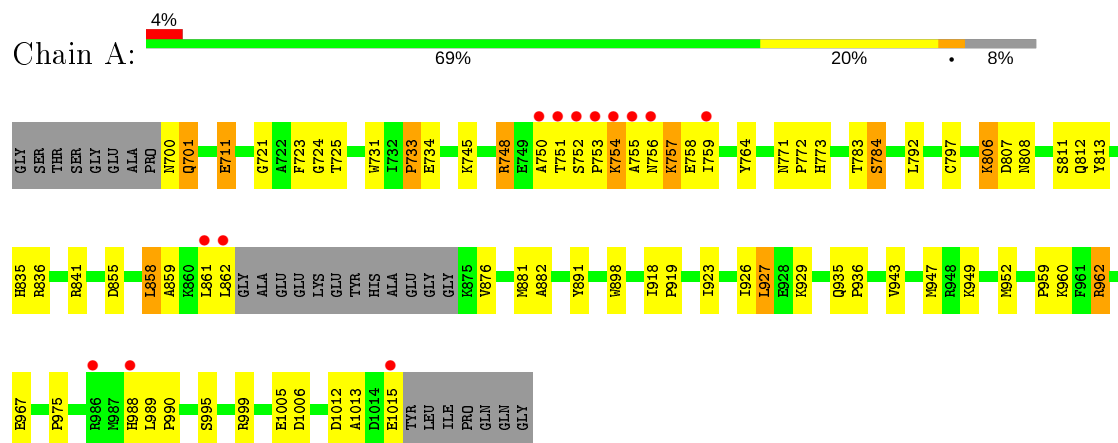
- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	263	Total O 263 263	0	0
5	B	263	Total O 263 263	0	0

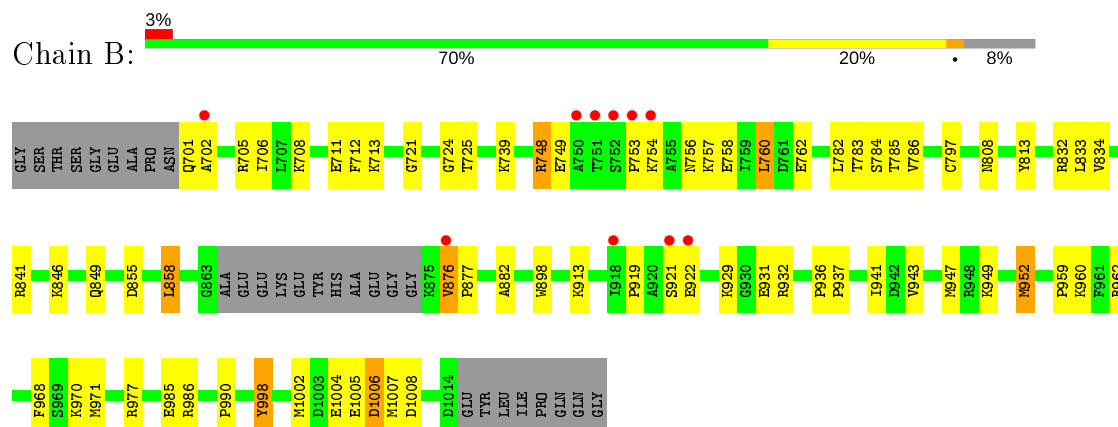
3 Residue-property plots [i](#)

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: Epidermal growth factor receptor



• Molecule 1: Epidermal growth factor receptor



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	155.76Å 72.45Å 76.16Å 90.00° 113.41° 90.00°	Depositor
Resolution (Å)	37.89 – 2.05 37.89 – 2.05	Depositor EDS
% Data completeness (in resolution range)	98.5 (37.89-2.05) 98.4 (37.89-2.05)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.19 (at 2.05Å)	Xtriage
Refinement program	PHENIX 1.8.4_1496	Depositor
R, R_{free}	0.175 , 0.202 0.176 , 0.203	Depositor DCC
R_{free} test set	985 reflections (2.04%)	wwPDB-VP
Wilson B-factor (Å ²)	27.8	Xtriage
Anisotropy	0.320	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 53.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	5597	wwPDB-VP
Average B, all atoms (Å ²)	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 55.48 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 3.1457e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹Intensities estimated from amplitudes.

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

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: EDO, 7XR, CL

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	0.86	0/2526	0.78	0/3416
1	B	0.82	0/2555	0.77	0/3454
All	All	0.84	0/5081	0.78	0/6870

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	733	PRO	Peptide

5.2 Too-close contacts [i](#)

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	2468	0	2504	70	0
1	B	2492	0	2537	63	0
2	A	12	0	17	12	0
2	B	28	0	42	14	0
3	A	35	0	0	1	0
3	B	35	0	0	1	0
4	B	1	0	0	0	0
5	A	263	0	0	8	0
5	B	263	0	0	20	0
All	All	5597	0	5100	135	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 13.

All (135) 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:753:PRO:O	1:A:756:ASN:HB2	1.39	1.20
1:A:750:ALA:HB1	2:A:1103:EDO:H22	1.36	1.07
1:B:941:ILE:HG13	5:B:1383:HOH:O	1.52	1.06
1:B:753:PRO:O	1:B:756:ASN:HB2	1.61	1.01
1:B:712:PHE:O	1:B:713:LYS:HD3	1.66	0.93
1:A:797[B]:CYS:SG	1:A:841[B]:ARG:HA	2.11	0.90
1:B:808:ASN:HB2	5:B:1225:HOH:O	1.73	0.88
1:B:834:VAL:H	2:B:1102:EDO:C1	1.86	0.87
1:B:952[A]:MET:HE3	2:B:1104:EDO:H11	1.56	0.87
1:B:834:VAL:H	2:B:1102:EDO:H11	1.39	0.86
1:B:701:GLN:HB2	5:B:1239:HOH:O	1.75	0.85
1:A:723:PHE:CE2	1:A:745:LYS:HE2	2.12	0.85
1:B:990:PRO:O	5:B:1201:HOH:O	1.94	0.84
1:A:836:ARG:NH2	5:A:1201:HOH:O	2.10	0.83
1:B:832:ARG:HG2	5:B:1381:HOH:O	1.78	0.83
1:A:700:ASN:N	5:A:1202:HOH:O	2.13	0.82
1:B:985:GLU:OE1	5:B:1202:HOH:O	1.96	0.81
1:A:784:SER:HA	2:A:1103:EDO:H21	1.64	0.80
1:A:734:GLU:O	1:A:734:GLU:CG	2.30	0.79
1:A:751:THR:CG2	1:A:783:THR:O	2.31	0.78
1:B:970:LYS:HD3	5:B:1293:HOH:O	1.84	0.78
1:B:785:THR:O	5:B:1204:HOH:O	2.02	0.77
1:B:783:THR:HG22	5:B:1325:HOH:O	1.87	0.74
1:B:705:ARG:NH1	5:B:1206:HOH:O	2.20	0.73
1:B:708:LYS:N	1:B:711:GLU:OE2	2.19	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1007:MET:HB3	5:B:1237:HOH:O	1.89	0.71
1:A:753:PRO:O	1:A:756:ASN:CB	2.30	0.70
1:B:783:THR:CG2	5:B:1325:HOH:O	2.39	0.70
1:B:998:TYR:HE1	1:B:1002:MET:HE3	1.58	0.69
1:A:701:GLN:HG2	1:A:764:TYR:CE2	2.30	0.66
1:B:1007:MET:C	2:B:1107:EDO:H21	2.16	0.66
1:A:882:ALA:HA	1:A:898:TRP:CD2	2.32	0.64
1:A:723:PHE:CD2	1:A:724:GLY:N	2.66	0.64
1:A:723:PHE:CE2	1:A:745:LYS:CE	2.79	0.64
1:B:960:LYS:HE2	1:B:962:ARG:HH12	1.63	0.64
1:A:751:THR:HG21	5:A:1206:HOH:O	1.96	0.64
1:B:952[A]:MET:CE	2:B:1104:EDO:H11	2.28	0.63
1:A:772:PRO:HD2	2:A:1102:EDO:H21	1.80	0.63
1:A:723:PHE:CD2	1:A:745:LYS:HE2	2.33	0.62
1:B:913:LYS:NZ	5:B:1208:HOH:O	2.26	0.62
1:A:721:GLY:HA3	1:A:723:PHE:CZ	2.34	0.62
1:A:806:LYS:HD3	1:A:807:ASP:OD2	2.00	0.62
1:B:998:TYR:CE1	1:B:1002:MET:HE3	2.35	0.61
1:B:833:LEU:HA	2:B:1102:EDO:H11	1.82	0.60
1:A:723:PHE:HD2	1:A:724:GLY:N	1.99	0.60
1:B:760:LEU:HD13	1:B:782:LEU:HD11	1.83	0.59
1:B:797[B]:CYS:SG	1:B:841[B]:ARG:HA	2.43	0.59
2:B:1103:EDO:H22	5:B:1380:HOH:O	2.02	0.58
1:A:759:ILE:HG23	1:A:861:LEU:HD21	1.86	0.57
1:A:723:PHE:CE2	1:A:745:LYS:NZ	2.72	0.57
1:A:792:LEU:HD21	2:A:1101:EDO:H22	1.86	0.57
1:B:721:GLY:O	1:B:748:ARG:NH2	2.38	0.57
1:A:771:ASN:HD21	2:A:1102:EDO:C1	2.18	0.56
1:B:968:PHE:CD1	1:B:971:MET:CE	2.88	0.56
1:A:723:PHE:CD2	1:A:745:LYS:CE	2.89	0.56
1:A:949:LYS:HE3	1:A:952:MET:CE	2.35	0.56
1:B:1008:ASP:OD1	2:B:1107:EDO:H22	2.06	0.55
1:A:949:LYS:HE2	1:A:959:PRO:HG3	1.88	0.55
1:B:724:GLY:HA2	1:B:748:ARG:HD3	1.89	0.55
1:A:811:SER:OG	1:A:975:PRO:HB2	2.06	0.55
1:B:949:LYS:HG2	1:B:959:PRO:HD3	1.87	0.55
1:A:943:VAL:HG12	1:A:947:MET:CE	2.37	0.54
1:B:849:GLN:NE2	5:B:1214:HOH:O	2.36	0.54
1:A:725:THR:OG1	1:B:832:ARG:NH2	2.40	0.54
1:A:949:LYS:NZ	5:A:1209:HOH:O	2.36	0.54
1:A:731:TRP:CZ2	1:A:733:PRO:HB3	2.43	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:711:GLU:OE1	5:A:1203:HOH:O	2.19	0.53
1:A:723:PHE:O	1:A:748:ARG:HG2	2.08	0.53
1:B:882:ALA:HA	1:B:898:TRP:CD2	2.43	0.53
1:A:771:ASN:HD21	2:A:1102:EDO:H12	1.74	0.53
1:A:995:SER:O	1:A:999:ARG:HG2	2.08	0.52
1:A:835:HIS:O	1:A:836:ARG:HB2	2.09	0.51
1:B:834:VAL:N	2:B:1102:EDO:H11	2.16	0.51
1:B:968:PHE:CD1	1:B:971:MET:HE3	2.45	0.51
1:A:943:VAL:HG12	1:A:947:MET:HE2	1.92	0.51
1:B:724:GLY:HA2	1:B:748:ARG:CD	2.41	0.51
1:A:858:LEU:HA	1:A:861:LEU:HB3	1.92	0.51
1:B:711:GLU:HG2	5:B:1310:HOH:O	2.10	0.51
1:A:812:GLN:NE2	1:A:989:LEU:HD12	2.25	0.51
1:A:813:TYR:OH	1:A:990:PRO:HD3	2.11	0.51
1:B:846:LYS:NZ	1:B:1005:GLU:HG2	2.26	0.50
1:A:757:LYS:O	1:A:757:LYS:HD2	2.12	0.50
3:B:1108:7XR:N3	3:B:1108:7XR:CAG	2.74	0.50
1:A:753:PRO:C	1:A:756:ASN:HB2	2.22	0.50
1:A:862:LEU:HD12	1:A:862:LEU:C	2.32	0.50
3:A:1104:7XR:CAG	3:A:1104:7XR:N3	2.76	0.49
1:B:1004:GLU:HG3	5:B:1312:HOH:O	2.13	0.49
1:B:813:TYR:OH	1:B:990:PRO:HD3	2.12	0.49
1:A:771:ASN:HD21	2:A:1102:EDO:C2	2.26	0.49
1:B:834:VAL:H	2:B:1102:EDO:H12	1.72	0.48
1:A:1013:ALA:HB1	1:A:1015:GLU:O	2.14	0.48
1:A:751:THR:O	1:A:751:THR:HG23	2.13	0.48
1:A:759:ILE:HA	1:A:861:LEU:HD11	1.94	0.48
1:B:977[B]:ARG:CZ	5:B:1223:HOH:O	2.61	0.47
1:A:751:THR:HG22	1:A:783:THR:O	2.11	0.47
1:B:977[B]:ARG:NH1	5:B:1223:HOH:O	2.48	0.47
1:A:701:GLN:HG2	1:A:764:TYR:CZ	2.49	0.47
1:B:986:ARG:NH1	5:B:1221:HOH:O	2.47	0.47
1:A:988:HIS:CE1	5:A:1384:HOH:O	2.68	0.46
1:B:985:GLU:OE2	2:B:1106:EDO:C1	2.63	0.46
1:A:962[B]:ARG:HH11	1:A:962[B]:ARG:HG2	1.80	0.46
1:B:876:VAL:HG23	1:B:877:PRO:HD2	1.98	0.46
1:A:771:ASN:HD21	2:A:1102:EDO:H21	1.80	0.45
1:B:952[A]:MET:HE3	2:B:1104:EDO:C1	2.39	0.45
1:B:1006:ASP:OD2	1:B:1006:ASP:N	2.38	0.45
1:A:751:THR:O	2:A:1103:EDO:O2	2.34	0.45
1:A:771:ASN:ND2	2:A:1102:EDO:H21	2.32	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:967:GLU:OE2	5:A:1204:HOH:O	2.21	0.45
1:A:967:GLU:HG2	5:A:1431:HOH:O	2.16	0.44
1:A:949:LYS:HE2	1:A:949:LYS:HB3	1.54	0.44
1:A:773:HIS:HD2	2:A:1102:EDO:H22	1.81	0.44
1:B:932:ARG:NE	2:B:1104:EDO:H22	2.32	0.44
1:A:876:VAL:HG12	1:A:881:MET:SD	2.58	0.44
1:B:968:PHE:CE1	1:B:971:MET:HE1	2.53	0.44
1:B:858[B]:LEU:HA	1:B:858[B]:LEU:HD23	1.49	0.44
1:A:836:ARG:HG2	1:A:891:TYR:CD2	2.52	0.43
1:A:935:GLN:HA	1:A:936:PRO:HD3	1.87	0.43
1:B:929:LYS:HD2	1:B:931:GLU:OE2	2.19	0.43
1:B:701:GLN:HB2	1:B:702:ALA:H	1.59	0.43
1:A:751:THR:HG23	1:A:783:THR:O	2.19	0.42
1:A:858:LEU:HD12	1:A:859:ALA:N	2.34	0.42
1:B:833:LEU:CA	2:B:1102:EDO:H11	2.49	0.42
1:A:754:LYS:HE2	1:A:754:LYS:HB3	1.50	0.42
1:A:923:ILE:HG22	1:A:927:LEU:HD22	2.01	0.42
1:A:755:ALA:O	1:A:759:ILE:HG12	2.20	0.42
1:A:784:SER:HA	2:A:1103:EDO:C2	2.42	0.42
1:B:949:LYS:O	1:B:952[B]:MET:HG2	2.19	0.41
1:B:943:VAL:HG12	1:B:947:MET:CE	2.50	0.41
1:A:918:ILE:HA	1:A:919:PRO:HD3	1.90	0.41
1:B:919:PRO:HD2	1:B:922[B]:GLU:OE1	2.20	0.40
1:B:762[B]:GLU:HG3	1:B:762[B]:GLU:O	2.21	0.40
1:B:998:TYR:CE1	1:B:1002:MET:CE	3.04	0.40
1:A:960:LYS:HE3	1:A:962[A]:ARG:HH12	1.86	0.40
1:B:758:GLU:O	1:B:762[A]:GLU:HG3	2.22	0.40
1:B:936:PRO:HA	1:B:937:PRO:HD3	1.95	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	304/331 (92%)	298 (98%)	6 (2%)	0	100	100
1	B	308/331 (93%)	303 (98%)	5 (2%)	0	100	100
All	All	612/662 (92%)	601 (98%)	11 (2%)	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	273/290 (94%)	253 (93%)	20 (7%)	14	6
1	B	277/290 (96%)	258 (93%)	19 (7%)	15	8
All	All	550/580 (95%)	511 (93%)	39 (7%)	16	7

All (39) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	701	GLN
1	A	711	GLU
1	A	748	ARG
1	A	752	SER
1	A	754	LYS
1	A	757	LYS
1	A	758	GLU
1	A	784	SER
1	A	806	LYS
1	A	808	ASN
1	A	855	ASP
1	A	858	LEU
1	A	926	ILE
1	A	927	LEU
1	A	929	LYS
1	A	962[A]	ARG
1	A	962[B]	ARG
1	A	1005	GLU

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Mol	Chain	Res	Type
1	A	1006	ASP
1	A	1012	ASP
1	B	706	ILE
1	B	725	THR
1	B	739	LYS
1	B	748	ARG
1	B	749	GLU
1	B	754	LYS
1	B	757	LYS
1	B	760	LEU
1	B	784	SER
1	B	786	VAL
1	B	855	ASP
1	B	858[A]	LEU
1	B	858[B]	LEU
1	B	876	VAL
1	B	921	SER
1	B	952[A]	MET
1	B	952[B]	MET
1	B	998	TYR
1	B	1006	ASP

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

Mol	Chain	Res	Type
1	A	771	ASN
1	A	773	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry

Of 13 ligands modelled in this entry, 1 is monoatomic - leaving 12 for Mogul analysis.

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	EDO	B	1106	-	3,3,3	0.38	0	2,2,2	0.21	0
3	7XR	B	1108	-	35,40,40	1.24	3 (8%)	46,56,56	1.94	8 (17%)
2	EDO	A	1103	-	3,3,3	0.34	0	2,2,2	0.43	0
2	EDO	B	1103	-	3,3,3	0.45	0	2,2,2	0.33	0
2	EDO	A	1102	-	3,3,3	0.81	0	2,2,2	0.82	0
2	EDO	B	1107	-	3,3,3	0.37	0	2,2,2	0.35	0
3	7XR	A	1104	-	35,40,40	1.10	4 (11%)	46,56,56	1.97	10 (21%)
2	EDO	B	1101	-	3,3,3	0.29	0	2,2,2	0.34	0
2	EDO	B	1104	-	3,3,3	0.45	0	2,2,2	0.57	0
2	EDO	A	1101	-	3,3,3	0.33	0	2,2,2	0.29	0
2	EDO	B	1105	-	3,3,3	0.35	0	2,2,2	0.36	0
2	EDO	B	1102	-	3,3,3	0.28	0	2,2,2	0.49	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
2	EDO	B	1106	-	-	0/1/1/1	-
3	7XR	B	1108	-	-	0/10/33/33	0/6/6/6
2	EDO	A	1103	-	-	1/1/1/1	-
2	EDO	B	1103	-	-	0/1/1/1	-
2	EDO	A	1102	-	-	0/1/1/1	-
2	EDO	B	1107	-	-	1/1/1/1	-
3	7XR	A	1104	-	-	0/10/33/33	0/6/6/6
2	EDO	B	1101	-	-	1/1/1/1	-
2	EDO	B	1104	-	-	1/1/1/1	-
2	EDO	A	1101	-	-	0/1/1/1	-
2	EDO	B	1105	-	-	1/1/1/1	-
2	EDO	B	1102	-	-	1/1/1/1	-

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	1108	7XR	CAY-NAX	-4.26	1.31	1.40
3	A	1104	7XR	CAZ-N2	-3.70	1.32	1.40
3	A	1104	7XR	CAY-NAX	-3.38	1.33	1.40
3	B	1108	7XR	CAZ-N2	-3.36	1.33	1.40
3	B	1108	7XR	C5-N7	-2.53	1.30	1.38
3	A	1104	7XR	C2-N2	-2.25	1.31	1.36
3	A	1104	7XR	C5-N7	-2.03	1.32	1.38

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1104	7XR	N1-C2-N3	-6.77	119.98	126.52
3	B	1108	7XR	N1-C2-N3	-6.32	120.42	126.52
3	B	1108	7XR	CAN-CBF-N9	-5.81	108.40	114.19
3	A	1104	7XR	CAN-CBF-N9	-5.39	108.82	114.19
3	B	1108	7XR	C6-N1-C2	4.69	122.83	115.88
3	A	1104	7XR	CAS-NBH-CAR	4.64	121.76	111.52
3	A	1104	7XR	C6-N1-C2	4.24	122.17	115.88
3	A	1104	7XR	C2-N3-C4	4.17	120.01	115.28
3	B	1108	7XR	CAS-NBH-CAR	3.76	119.82	111.52
3	B	1108	7XR	CAA-NBG-CAP	-3.71	105.11	110.66
3	B	1108	7XR	C2-N3-C4	3.56	119.31	115.28
3	B	1108	7XR	CAA-NBG-CAQ	-3.20	105.87	110.66
3	A	1104	7XR	CAA-NBG-CAQ	-2.85	106.39	110.66
3	B	1108	7XR	CAO-CBF-N9	-2.46	111.73	114.19
3	A	1104	7XR	CAQ-NBG-CAP	-2.18	106.47	109.52
3	A	1104	7XR	CAO-CBF-N9	-2.14	112.05	114.19
3	A	1104	7XR	CAQ-CAS-NBH	2.11	114.80	110.70
3	A	1104	7XR	N2-C2-N3	2.05	123.89	116.92

There are no chirality outliers.

All (6) torsion outliers are listed below:

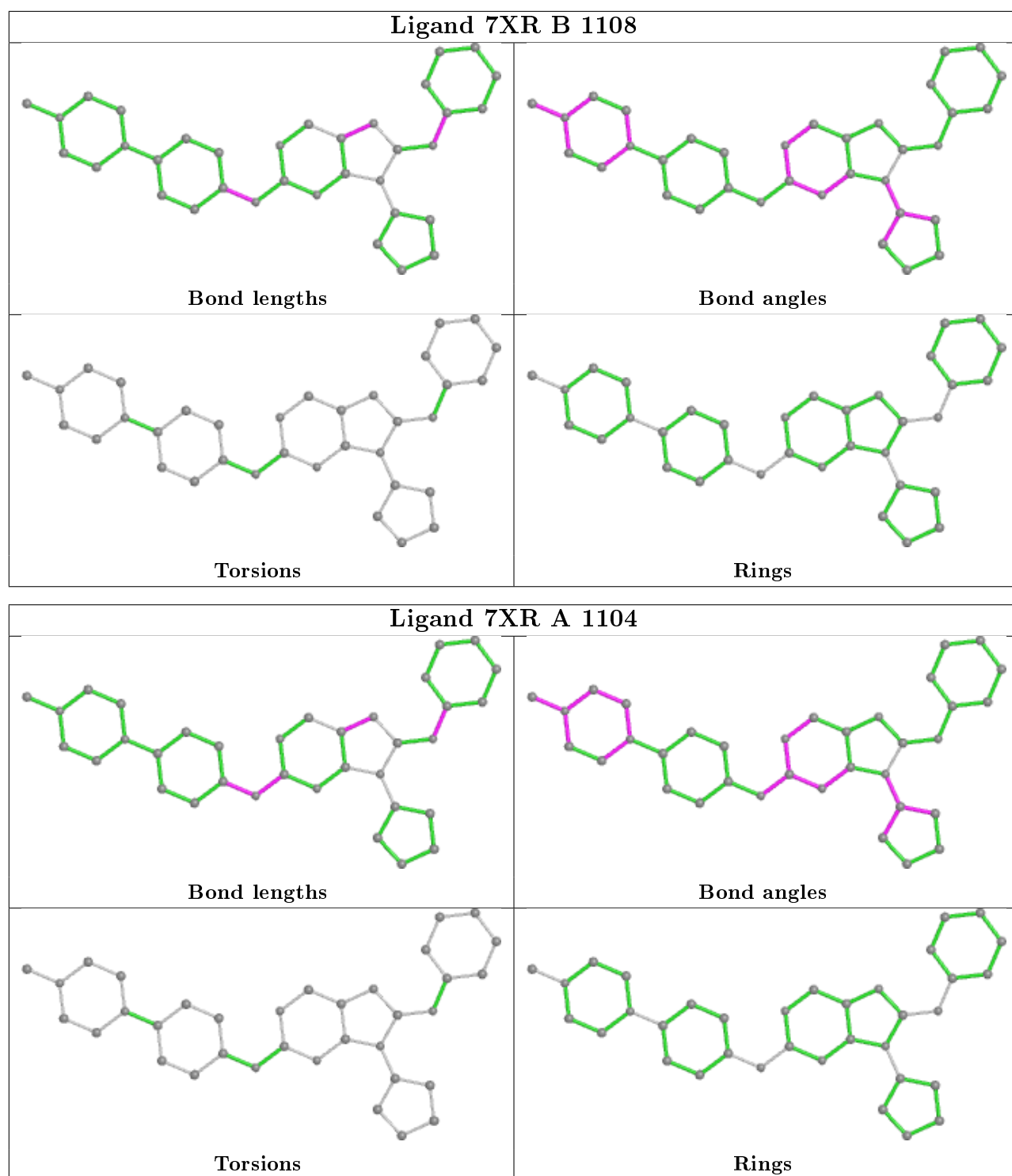
Mol	Chain	Res	Type	Atoms
2	A	1103	EDO	O1-C1-C2-O2
2	B	1101	EDO	O1-C1-C2-O2
2	B	1107	EDO	O1-C1-C2-O2
2	B	1105	EDO	O1-C1-C2-O2
2	B	1102	EDO	O1-C1-C2-O2
2	B	1104	EDO	O1-C1-C2-O2

There are no ring outliers.

10 monomers are involved in 28 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	1106	EDO	1	0
3	B	1108	7XR	1	0
2	A	1103	EDO	4	0
2	B	1103	EDO	1	0
2	A	1102	EDO	7	0
2	B	1107	EDO	2	0
3	A	1104	7XR	1	0
2	B	1104	EDO	4	0
2	A	1101	EDO	1	0
2	B	1102	EDO	6	0

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



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data

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	304/331 (91%)	-0.11	13 (4%) 35 38	17, 29, 66, 94	0
1	B	303/331 (91%)	-0.04	10 (3%) 46 50	15, 30, 60, 103	0
All	All	607/662 (91%)	-0.08	23 (3%) 40 44	15, 30, 62, 103	0

All (23) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	753	PRO	7.3
1	B	750	ALA	7.2
1	B	751	THR	6.6
1	A	861	LEU	6.5
1	B	752	SER	6.1
1	A	752	SER	5.5
1	B	754	LYS	5.2
1	B	753	PRO	5.1
1	A	750	ALA	4.9
1	A	1015	GLU	3.7
1	A	754	LYS	3.7
1	A	751	THR	3.5
1	B	876	VAL	3.1
1	A	756	ASN	3.0
1	A	862	LEU	3.0
1	A	755	ALA	2.6
1	A	759	ILE	2.5
1	A	988	HIS	2.5
1	B	702	ALA	2.5
1	B	918	ILE	2.1
1	B	921	SER	2.1
1	B	922[A]	GLU	2.0
1	A	986	ARG	2.0

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 carbohydrates in this entry.

6.4 Ligands ⓘ

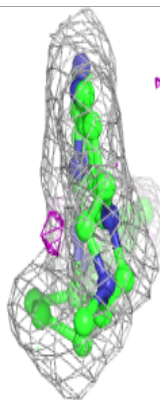
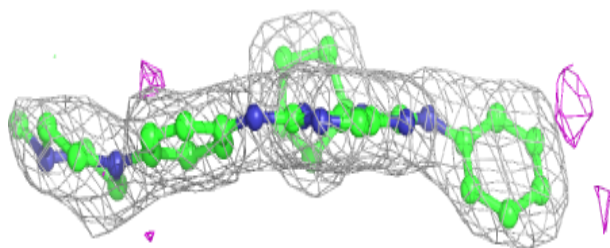
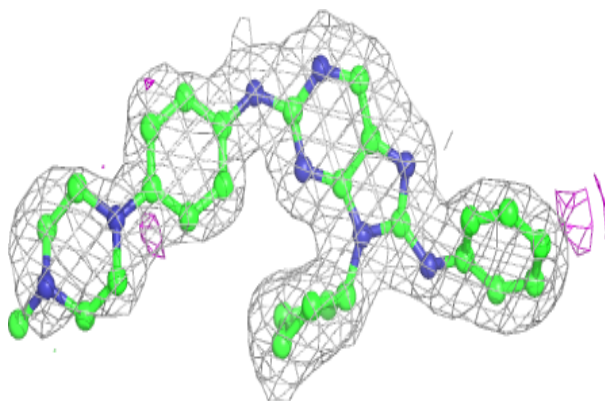
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
4	CL	B	1109	1/1	0.57	0.07	81,81,81,81	1
2	EDO	B	1106	4/4	0.76	0.47	55,55,55,57	0
2	EDO	B	1107	4/4	0.79	0.19	59,60,60,68	0
2	EDO	A	1103	4/4	0.80	0.53	76,80,81,82	0
2	EDO	B	1103	4/4	0.81	0.21	37,46,51,54	0
2	EDO	B	1101	4/4	0.92	0.07	42,46,46,55	0
2	EDO	B	1102	4/4	0.92	0.24	26,38,47,55	0
2	EDO	A	1101	4/4	0.93	0.14	40,42,47,58	0
2	EDO	B	1105	4/4	0.94	0.15	37,39,47,55	0
3	7XR	B	1108	35/35	0.94	0.13	22,30,61,65	0
2	EDO	A	1102	4/4	0.96	0.22	26,37,50,57	0
2	EDO	B	1104	4/4	0.96	0.15	28,31,33,44	0
3	7XR	A	1104	35/35	0.96	0.13	17,28,52,56	0

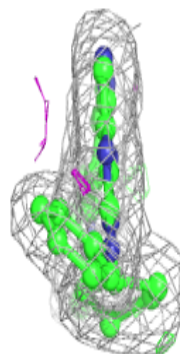
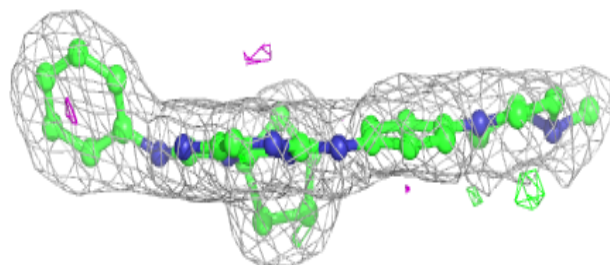
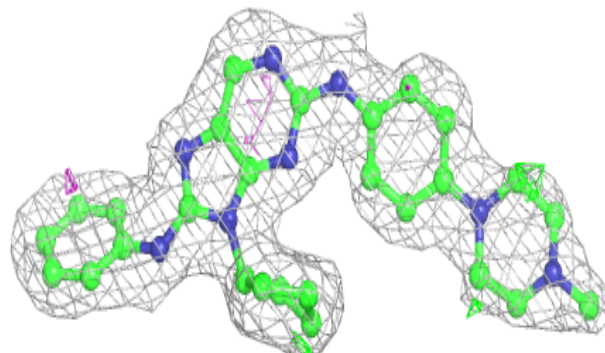
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around 7XR B 1108:

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

**Electron density around 7XR A 1104:**

$2mF_o-DF_c$ (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.