



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 9, 2023 – 07:07 AM EDT

PDB ID : 8D76
Title : Crystal Structure of EGFR LRTM with compound 24
Authors : Kim, J.L.
Deposited on : 2022-06-07
Resolution : 2.40 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 : 2.35.1
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) : 2.35.1

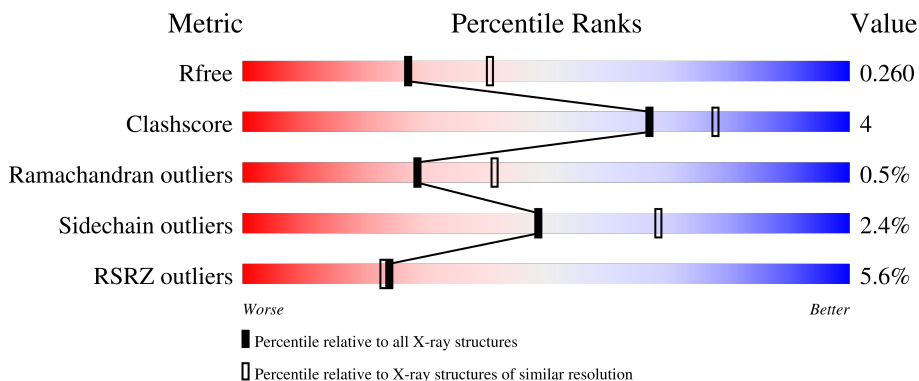
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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	3907 (2.40-2.40)
Clashscore	141614	4398 (2.40-2.40)
Ramachandran outliers	138981	4318 (2.40-2.40)
Sidechain outliers	138945	4319 (2.40-2.40)
RSRZ outliers	127900	3811 (2.40-2.40)

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 $\leq 5\%$. 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	348	 4% 80% 10% 10%
1	B	348	 6% 79% 11% 10%

2 Entry composition i

There are 4 unique types of molecules in this entry. The entry contains 5778 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
			Total	C	N	O	S			
1	A	312	2524	1619	427	458	20	0	3	0
1	B	313	2533	1624	428	460	21	0	4	0

There are 46 discrepancies between the modelled and reference sequences:

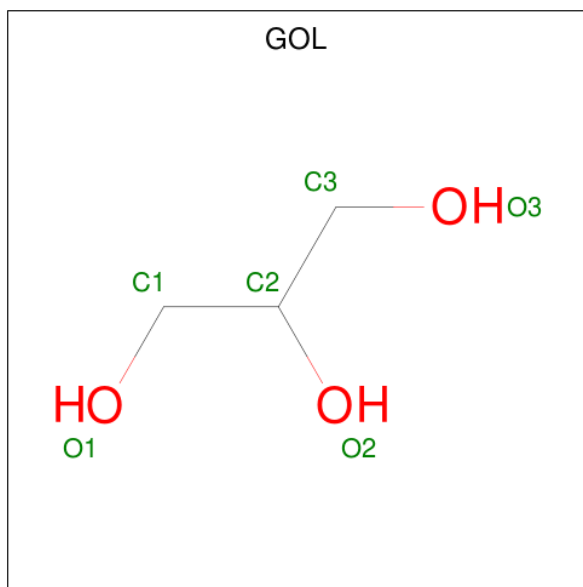
Chain	Residue	Modelled	Actual	Comment	Reference
A	675	MET	-	initiating methionine	UNP P00533
A	676	GLY	-	expression tag	UNP P00533
A	677	SER	-	expression tag	UNP P00533
A	678	SER	-	expression tag	UNP P00533
A	679	HIS	-	expression tag	UNP P00533
A	680	HIS	-	expression tag	UNP P00533
A	681	HIS	-	expression tag	UNP P00533
A	682	HIS	-	expression tag	UNP P00533
A	683	HIS	-	expression tag	UNP P00533
A	684	HIS	-	expression tag	UNP P00533
A	685	SER	-	expression tag	UNP P00533
A	686	SER	-	expression tag	UNP P00533
A	687	GLY	-	expression tag	UNP P00533
A	688	GLU	-	expression tag	UNP P00533
A	689	ASN	-	expression tag	UNP P00533
A	690	LEU	-	expression tag	UNP P00533
A	691	TYR	-	expression tag	UNP P00533
A	692	PHE	-	expression tag	UNP P00533
A	693	GLN	-	expression tag	UNP P00533
A	694	GLY	-	expression tag	UNP P00533
A	790	MET	THR	engineered mutation	UNP P00533
A	858	ARG	LEU	engineered mutation	UNP P00533
A	948	ARG	VAL	engineered mutation	UNP P00533
B	675	MET	-	initiating methionine	UNP P00533
B	676	GLY	-	expression tag	UNP P00533

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Chain	Residue	Modelled	Actual	Comment	Reference
B	677	SER	-	expression tag	UNP P00533
B	678	SER	-	expression tag	UNP P00533
B	679	HIS	-	expression tag	UNP P00533
B	680	HIS	-	expression tag	UNP P00533
B	681	HIS	-	expression tag	UNP P00533
B	682	HIS	-	expression tag	UNP P00533
B	683	HIS	-	expression tag	UNP P00533
B	684	HIS	-	expression tag	UNP P00533
B	685	SER	-	expression tag	UNP P00533
B	686	SER	-	expression tag	UNP P00533
B	687	GLY	-	expression tag	UNP P00533
B	688	GLU	-	expression tag	UNP P00533
B	689	ASN	-	expression tag	UNP P00533
B	690	LEU	-	expression tag	UNP P00533
B	691	TYR	-	expression tag	UNP P00533
B	692	PHE	-	expression tag	UNP P00533
B	693	GLN	-	expression tag	UNP P00533
B	694	GLY	-	expression tag	UNP P00533
B	790	MET	THR	engineered mutation	UNP P00533
B	858	ARG	LEU	engineered mutation	UNP P00533
B	948	ARG	VAL	engineered mutation	UNP P00533

- Molecule 2 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



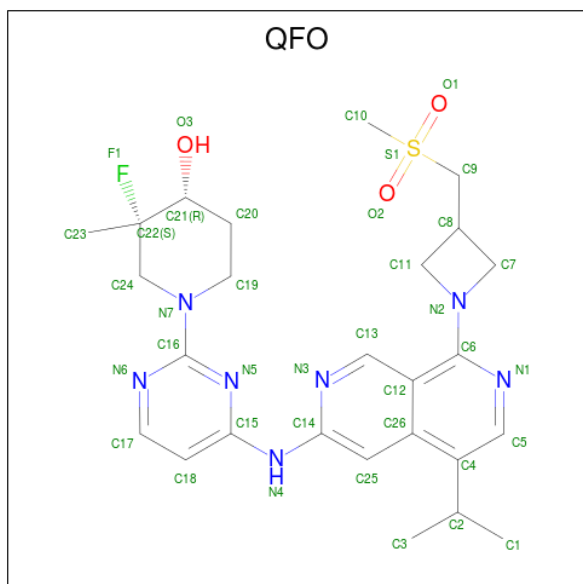
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			6	3	3		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			6	3	3		
2	A	1	Total	C	O	0	0
			6	3	3		
2	A	1	Total	C	O	0	0
			6	3	3		
2	B	1	Total	C	O	0	0
			6	3	3		
2	B	1	Total	C	O	0	0
			6	3	3		

- Molecule 3 is (3S,4R)-3-fluoro-1-(4-{[8-{3-[(methanesulfonyl)methyl]azetidin-1-yl}-5-(propan-2-yl)-2,7-naphthyridin-3-yl]amino}pyrimidin-2-yl)-3-methylpiperidin-4-ol (three-letter code: QFO) (formula: C₂₆H₃₄FN₇O₃S) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	
3	A	1	Total	C	F	N	O	S	0	0
			38	26	1	7	3	1		
3	B	1	Total	C	F	N	O	S	0	0
			38	26	1	7	3	1		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	309	Total	O	0	0
			309	309		

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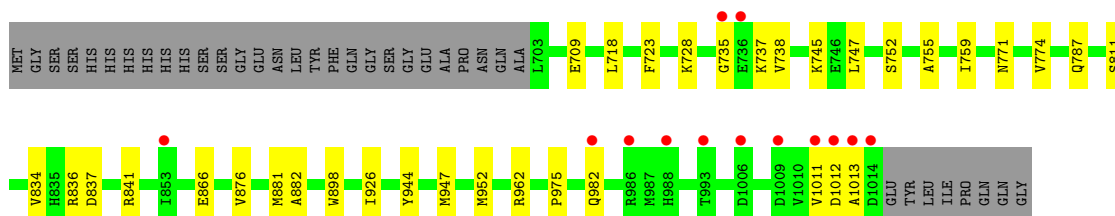
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	300	Total 300	O 300	0	0

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.

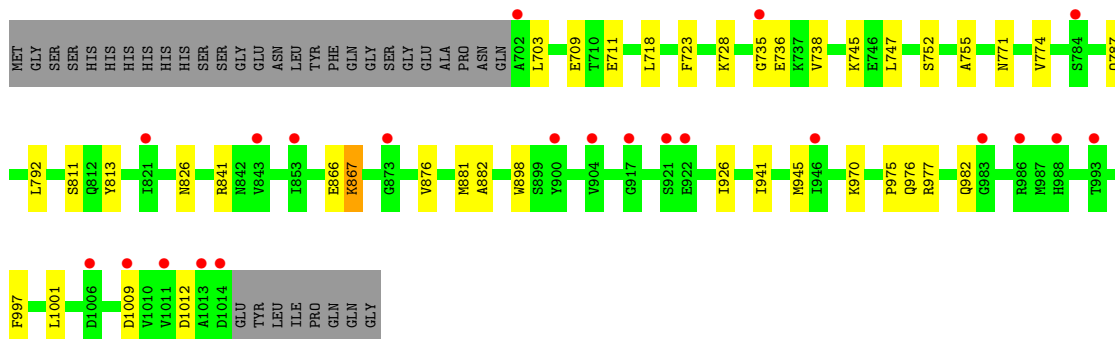
- Molecule 1: Epidermal growth factor receptor

Chain A: 



- Molecule 1: Epidermal growth factor receptor

Chain B: 



4 Data and refinement statistics i

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	41.53Å 50.32Å 85.88Å 104.19° 101.73° 90.12°	Depositor
Resolution (Å)	30.00 – 2.40 29.84 – 2.40	Depositor EDS
% Data completeness (in resolution range)	97.9 (30.00-2.40) 97.9 (29.84-2.40)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.50 (at 2.39Å)	Xtrriage
Refinement program	REFMAC 5.8.0232	Depositor
R, R_{free}	0.156 , 0.260 0.169 , 0.260	Depositor DCC
R_{free} test set	1260 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	43.0	Xtrriage
Anisotropy	0.131	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 55.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.35$	Xtrriage
Estimated twinning fraction	0.107 for h,-k,-h-l	Xtrriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	5778	wwPDB-VP
Average B, all atoms (Å ²)	65.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.01% of the height of the origin peak. No significant pseudotranslation is detected.*

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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: QFO, GOL

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	0.64	0/2588	0.77	0/3498
1	B	0.65	0/2600	0.76	0/3514
All	All	0.65	0/5188	0.76	0/7012

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	2524	0	2569	17	0
1	B	2533	0	2579	23	0
2	A	24	0	32	2	0
2	B	12	0	16	0	0
3	A	38	0	0	0	0
3	B	38	0	0	1	0
4	A	309	0	0	4	0
4	B	300	0	0	11	0
All	All	5778	0	5196	40	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 4.

All (40) 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:711:GLU:OE2	4:B:1601:HOH:O	2.14	0.66
1:B:1009:ASP:OD1	4:B:1602:HOH:O	2.15	0.64
1:A:866:GLU:HG2	4:A:1716:HOH:O	1.99	0.62
1:B:941:ILE:O	1:B:945[B]:MET:HG2	2.02	0.60
1:B:771:ASN:HB3	1:B:774:VAL:HG22	1.85	0.57
1:B:982:GLN:HG3	4:B:1841:HOH:O	2.05	0.57
1:A:771:ASN:HB3	1:A:774:VAL:HG22	1.88	0.55
1:A:811:SER:OG	1:A:975:PRO:HB2	2.10	0.52
1:B:709:GLU:HG3	1:B:787:GLN:HE22	1.75	0.52
1:B:882:ALA:HA	1:B:898:TRP:CD2	2.46	0.51
1:B:811:SER:OG	1:B:975:PRO:HB2	2.11	0.51
1:B:866:GLU:HG3	4:B:1654:HOH:O	2.10	0.51
1:A:882:ALA:HA	1:A:898:TRP:CD2	2.46	0.51
1:A:709:GLU:HG3	1:A:787:GLN:HE22	1.76	0.50
1:B:977:ARG:NE	4:B:1621:HOH:O	2.45	0.50
1:A:841:ARG:NH1	4:A:1601:HOH:O	2.45	0.49
1:A:876:VAL:HB	1:A:881:MET:SD	2.52	0.49
1:B:977:ARG:CZ	4:B:1621:HOH:O	2.61	0.48
1:B:723:PHE:HB2	1:B:745:LYS:HE3	1.95	0.48
1:B:876:VAL:HB	1:B:881:MET:SD	2.54	0.48
1:B:747:LEU:HD11	1:B:755:ALA:HB1	1.95	0.47
1:A:747:LEU:HD11	1:A:755:ALA:HB1	1.95	0.47
1:B:792:LEU:HD21	3:B:1503:QFO:C10	2.45	0.46
1:B:976:GLN:HG3	4:B:1718:HOH:O	2.14	0.46
1:B:841:ARG:NH1	4:B:1605:HOH:O	2.48	0.46
1:A:759:ILE:HB	2:A:1502:GOL:C3	2.46	0.46
1:B:826:ASN:ND2	4:B:1627:HOH:O	2.48	0.45
1:A:723:PHE:HB2	1:A:745:LYS:HE3	1.98	0.45
1:B:813:TYR:HD1	4:B:1787:HOH:O	1.99	0.45
1:A:752:SER:HB3	1:A:755:ALA:HB3	1.99	0.44
1:B:718:LEU:HD11	1:B:728:LYS:HB2	2.01	0.43
1:B:752:SER:HB3	1:B:755:ALA:HB3	1.99	0.43
1:A:718:LEU:HD11	1:A:728:LYS:HB2	2.01	0.42
1:A:962:ARG:NH2	4:A:1633:HOH:O	2.52	0.42
1:A:834[A]:VAL:HG12	1:A:836:ARG:HG2	2.01	0.42
1:B:867:LYS:HE2	4:B:1762:HOH:O	2.19	0.42
1:A:952[B]:MET:SD	2:A:1501:GOL:H2	2.61	0.41
1:A:837:ASP:OD1	4:A:1601:HOH:O	2.22	0.41
1:A:944:TYR:HA	1:A:947:MET:HE2	2.04	0.40
1:B:997:PHE:CE2	1:B:1001:LEU:HD12	2.57	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	313/348 (90%)	303 (97%)	8 (3%)	2 (1%)	25	36
1	B	315/348 (90%)	305 (97%)	9 (3%)	1 (0%)	41	55
All	All	628/696 (90%)	608 (97%)	17 (3%)	3 (0%)	29	41

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	735	GLY
1	B	735	GLY
1	A	1013	ALA

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	279/305 (92%)	273 (98%)	6 (2%)	52	71
1	B	280/305 (92%)	273 (98%)	7 (2%)	47	67
All	All	559/610 (92%)	546 (98%)	13 (2%)	49	70

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	737	LYS
1	A	738	VAL
1	A	926	ILE
1	A	982	GLN
1	A	1011	VAL
1	A	1012	ASP
1	B	703	LEU
1	B	736	GLU
1	B	738	VAL
1	B	867	LYS
1	B	926	ILE
1	B	970	LYS
1	B	1012	ASP

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	893	HIS
1	A	976	GLN
1	B	893	HIS
1	B	976	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

8 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	GOL	A	1502	-	5,5,5	0.12	0	5,5,5	0.46	0
2	GOL	A	1503	-	5,5,5	0.12	0	5,5,5	0.32	0
3	QFO	A	1504	-	38,42,42	0.92	1 (2%)	47,64,64	1.43	4 (8%)
2	GOL	B	1501	-	5,5,5	0.16	0	5,5,5	0.49	0
3	QFO	B	1503	-	38,42,42	0.88	1 (2%)	47,64,64	1.36	4 (8%)
2	GOL	A	1505	-	5,5,5	0.09	0	5,5,5	0.28	0
2	GOL	B	1502	-	5,5,5	0.12	0	5,5,5	0.30	0
2	GOL	A	1501	-	5,5,5	0.14	0	5,5,5	0.46	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	GOL	A	1502	-	-	2/4/4/4	-
2	GOL	A	1503	-	-	3/4/4/4	-
3	QFO	A	1504	-	-	0/15/45/45	0/5/5/5
2	GOL	B	1501	-	-	2/4/4/4	-
3	QFO	B	1503	-	-	0/15/45/45	0/5/5/5
2	GOL	A	1505	-	-	0/4/4/4	-
2	GOL	B	1502	-	-	2/4/4/4	-
2	GOL	A	1501	-	-	4/4/4/4	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1504	QFO	C7-C8	2.88	1.58	1.54
3	B	1503	QFO	C7-C8	2.68	1.58	1.54

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1504	QFO	C20-C21-C22	-4.69	109.64	112.93
3	B	1503	QFO	F1-C22-C21	4.07	108.14	103.01

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1504	QFO	F1-C22-C21	3.92	107.94	103.01
3	B	1503	QFO	C20-C21-C22	-3.82	110.25	112.93
3	A	1504	QFO	C4-C26-C12	-2.62	117.88	119.75
3	B	1503	QFO	C23-C22-C21	2.50	112.54	108.71
3	A	1504	QFO	C13-N3-C14	2.41	120.25	117.81
3	B	1503	QFO	C4-C26-C12	-2.27	118.12	119.75

There are no chirality outliers.

All (13) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	1501	GOL	O1-C1-C2-C3
2	A	1501	GOL	O1-C1-C2-C3
2	A	1502	GOL	C1-C2-C3-O3
2	A	1503	GOL	O1-C1-C2-C3
2	A	1503	GOL	C1-C2-C3-O3
2	B	1502	GOL	C1-C2-C3-O3
2	B	1501	GOL	O1-C1-C2-O2
2	B	1502	GOL	O2-C2-C3-O3
2	A	1501	GOL	O2-C2-C3-O3
2	A	1501	GOL	O1-C1-C2-O2
2	A	1502	GOL	O2-C2-C3-O3
2	A	1501	GOL	C1-C2-C3-O3
2	A	1503	GOL	O1-C1-C2-O2

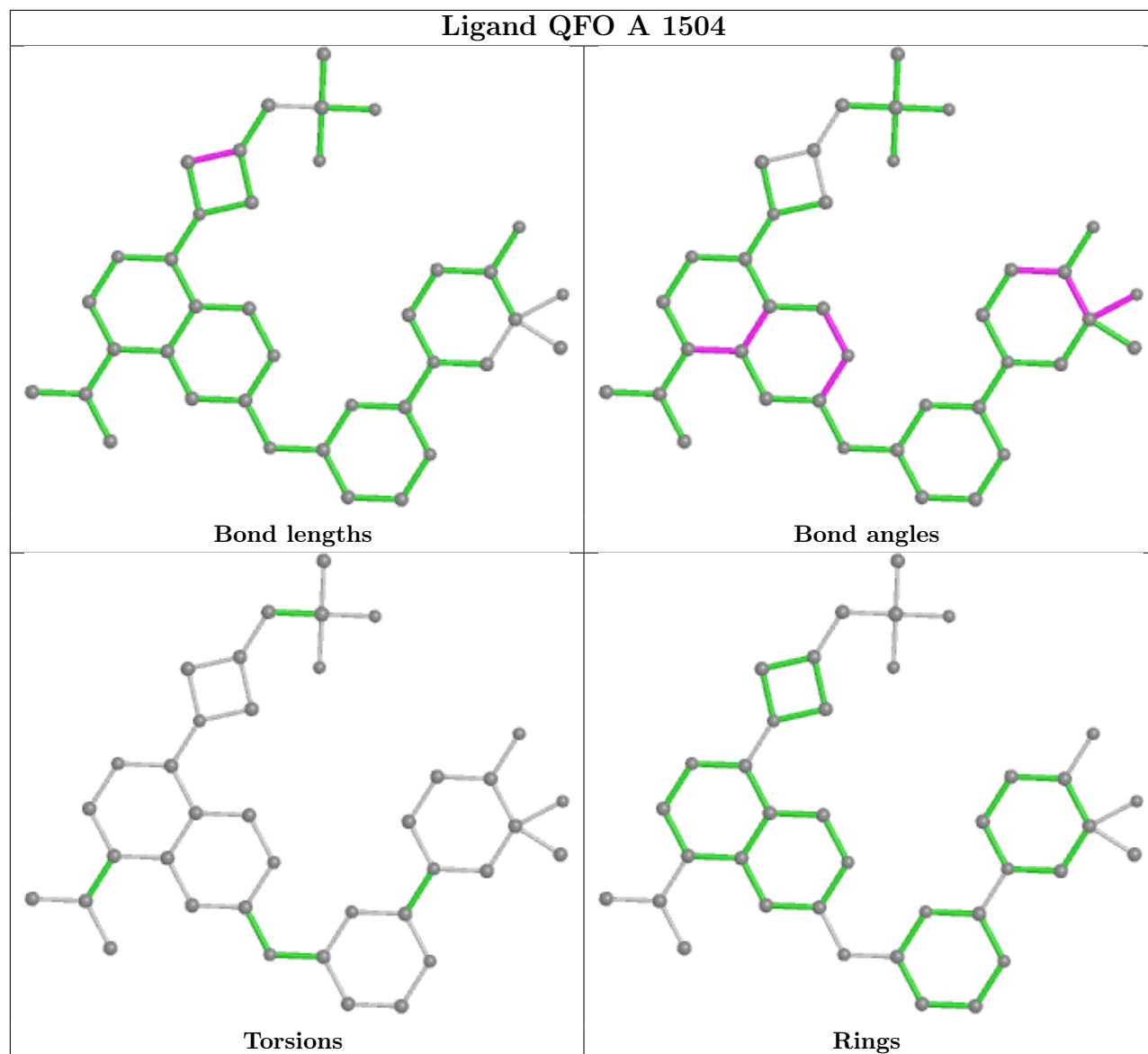
There are no ring outliers.

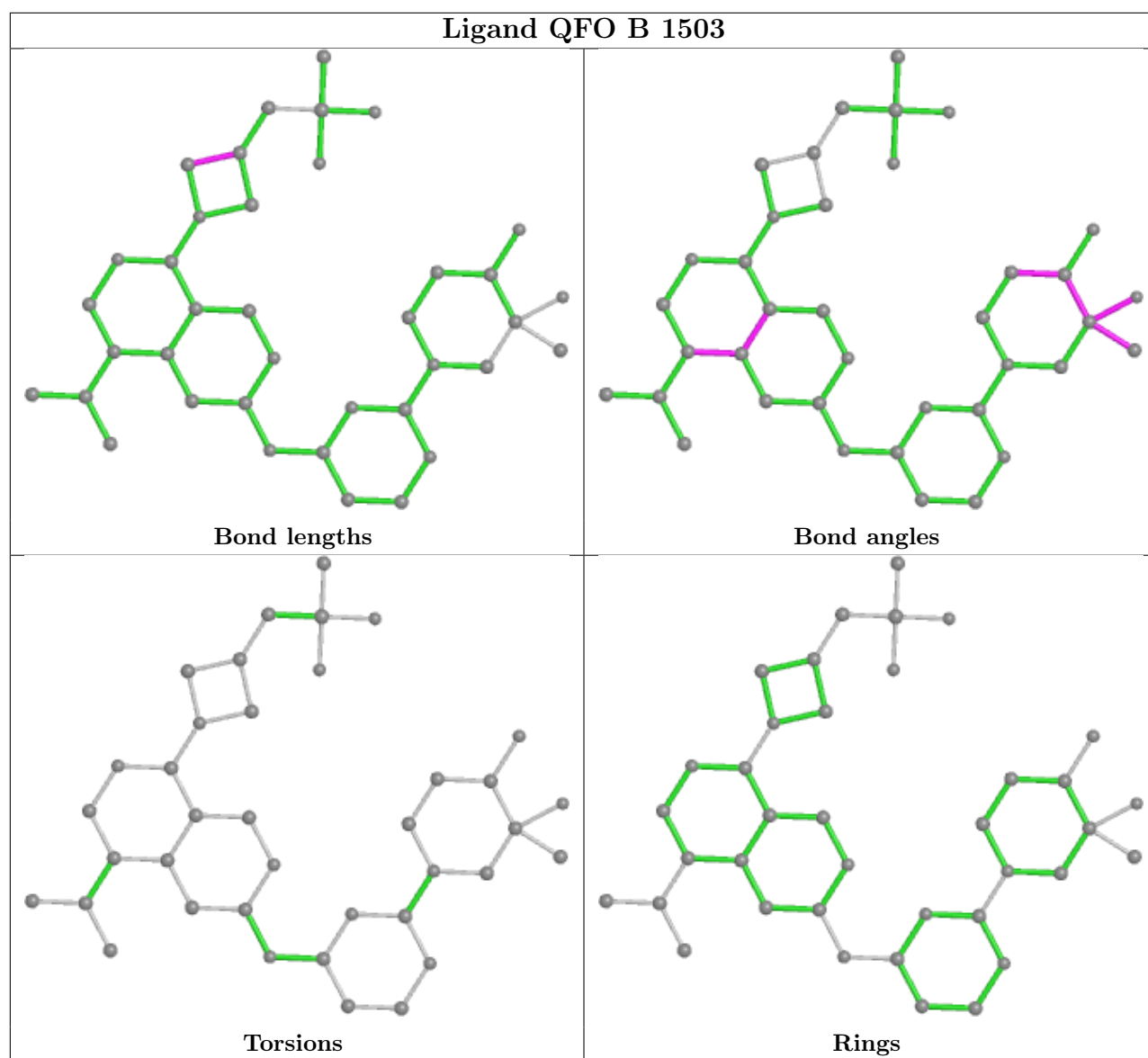
3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1502	GOL	1	0
3	B	1503	QFO	1	0
2	A	1501	GOL	1	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 [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	312/348 (89%)	0.01	13 (4%) 36 35	41, 60, 99, 145	0
1	B	313/348 (89%)	0.12	22 (7%) 16 15	42, 60, 102, 133	0
All	All	625/696 (89%)	0.07	35 (5%) 24 23	41, 60, 101, 145	0

All (35) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	702	ALA	7.3
1	A	735	GLY	5.8
1	A	1013	ALA	5.3
1	A	1014	ASP	5.0
1	A	988	HIS	4.9
1	B	1013	ALA	4.8
1	A	1011	VAL	4.2
1	B	735	GLY	4.1
1	B	988	HIS	3.8
1	B	1014	ASP	3.5
1	B	1011	VAL	3.3
1	B	821	ILE	3.2
1	A	1012	ASP	3.0
1	B	853	ILE	2.9
1	B	1009	ASP	2.9
1	A	736	GLU	2.9
1	B	1006	ASP	2.8
1	A	986	ARG	2.8
1	B	993[A]	THR	2.8
1	B	843	VAL	2.8
1	A	1006	ASP	2.7
1	A	1009	ASP	2.7
1	B	986	ARG	2.7
1	B	904	VAL	2.7

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Mol	Chain	Res	Type	RSRZ
1	B	983	GLY	2.5
1	B	873	GLY	2.5
1	A	993	THR	2.3
1	B	900	TYR	2.2
1	B	921	SER	2.1
1	A	982	GLN	2.1
1	B	917	GLY	2.1
1	A	853	ILE	2.1
1	B	946	ILE	2.1
1	B	922	GLU	2.1
1	B	784	SER	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](#)

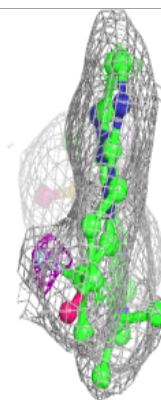
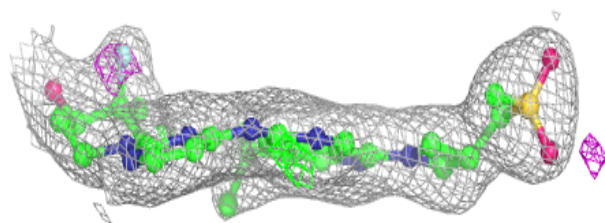
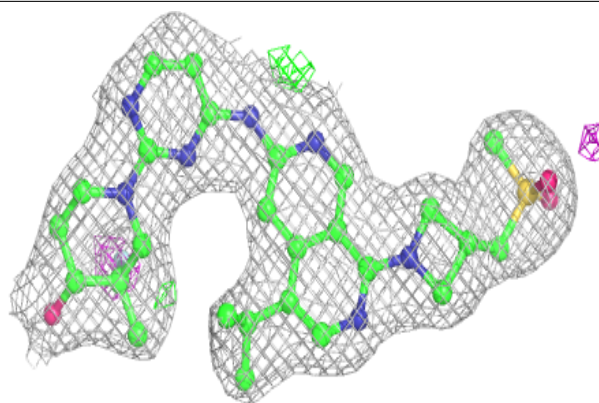
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q<0.9' lists 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	GOL	A	1502	6/6	0.86	0.16	62,84,88,89	0
2	GOL	B	1502	6/6	0.87	0.17	64,85,91,96	0
2	GOL	A	1503	6/6	0.88	0.36	78,89,97,101	0
2	GOL	A	1505	6/6	0.89	0.16	77,91,99,103	0
2	GOL	B	1501	6/6	0.90	0.16	58,74,92,97	0
2	GOL	A	1501	6/6	0.93	0.20	60,64,69,79	0
3	QFO	A	1504	38/38	0.96	0.14	40,51,63,76	0
3	QFO	B	1503	38/38	0.96	0.14	39,56,65,75	0

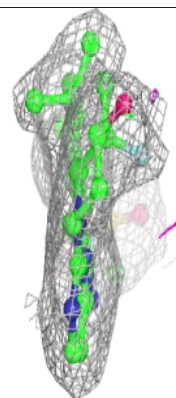
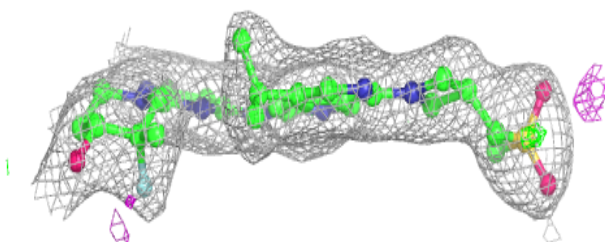
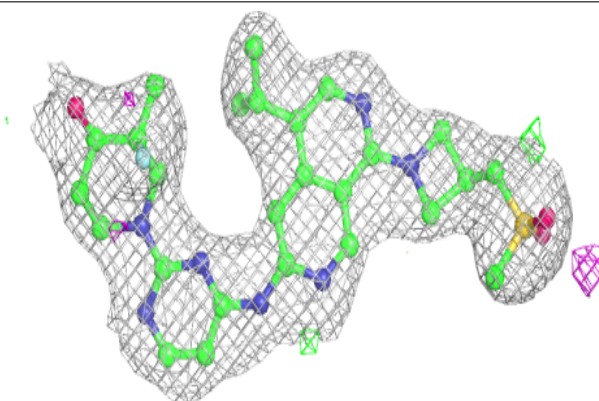
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around QFO A 1504:

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

**Electron density around QFO B 1503:**

$2mF_o-DF_c$ (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.