wwPDB X-ray Structure Validation Summary Report (i)

Nov 21, 2023 – 12:00 AM JST

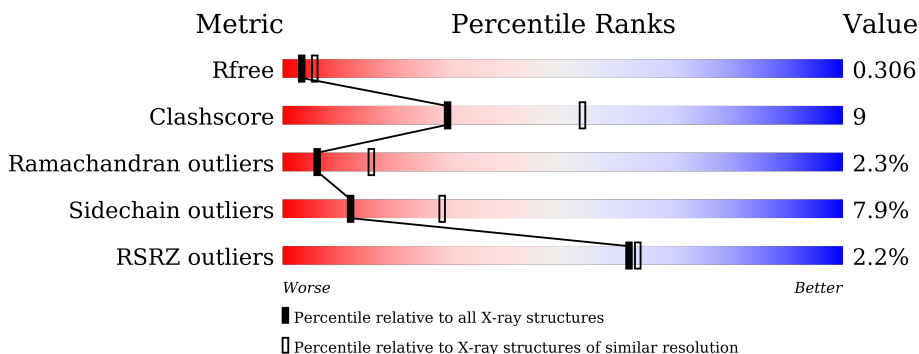|		
PDB ID	:	7E2E
Title	:	Crystal structure of the Estrogen-Related Receptor alpha (ERRalpha) ligand-binding domain (LBD) in complex with an agonist DS45500853 and a PGC-1alpha peptide
Authors	:	Ito, S.; Shinozuka, T.; Kimura, T.; Izumi, M.; Wakabayashi, K.
Deposited on	:	2021-02-05
Resolution	:	2.70 Å(reported)

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 2.70 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		0.306
Clashscore		9
Ramachandran outliers		2.3%
Sidechain outliers		7.9%
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	2808 (2.70-2.70)
Clashscore	141614	3122 (2.70-2.70)
Ramachandran outliers	138981	3069 (2.70-2.70)
Sidechain outliers	138945	3069 (2.70-2.70)
RSRZ outliers	127900	2737 (2.70-2.70)

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	245	63% / 22% / · / 12%
1	B	245	3% (top bar); 62% / 23% / · / 12%
2	P	12	8% (top bar); 58% / 33% / 8%
2	Q	12	58% / 42%

2 Entry composition ⓘ

There are 5 unique types of molecules in this entry. The entry contains 3610 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 Steroid hormone receptor ERR1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	216	Total	C	N	O	S	0	0	0
			1683	1079	286	310	8			
1	B	216	Total	C	N	O	S	0	0	0
			1683	1079	286	310	8			

There are 30 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	275	MET	-	initiating methionine	UNP P11474
A	276	ARG	-	expression tag	UNP P11474
A	277	GLY	-	expression tag	UNP P11474
A	278	SER	-	expression tag	UNP P11474
A	279	HIS	-	expression tag	UNP P11474
A	280	HIS	-	expression tag	UNP P11474
A	281	HIS	-	expression tag	UNP P11474
A	282	HIS	-	expression tag	UNP P11474
A	283	HIS	-	expression tag	UNP P11474
A	284	HIS	-	expression tag	UNP P11474
A	285	GLY	-	expression tag	UNP P11474
A	286	ILE	-	expression tag	UNP P11474
A	287	PRO	-	expression tag	UNP P11474
A	288	GLU	-	expression tag	UNP P11474
A	289	PHE	-	expression tag	UNP P11474
B	275	MET	-	initiating methionine	UNP P11474
B	276	ARG	-	expression tag	UNP P11474
B	277	GLY	-	expression tag	UNP P11474
B	278	SER	-	expression tag	UNP P11474
B	279	HIS	-	expression tag	UNP P11474
B	280	HIS	-	expression tag	UNP P11474
B	281	HIS	-	expression tag	UNP P11474
B	282	HIS	-	expression tag	UNP P11474
B	283	HIS	-	expression tag	UNP P11474
B	284	HIS	-	expression tag	UNP P11474

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| Chain	Residue	Modelled	Actual	Comment	Reference
B	285	GLY	-	expression tag	UNP P11474
B	286	ILE	-	expression tag	UNP P11474
B	287	PRO	-	expression tag	UNP P11474
B	288	GLU	-	expression tag	UNP P11474
B	289	PHE	-	expression tag	UNP P11474

- Molecule 2 is a protein called Peroxisome proliferator-activated receptor gamma coactivator 1-alpha.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	P	12	Total	C	N	O	0	0	0
			97	63	16	18			
2	Q	12	Total	C	N	O	0	0	0
			97	63	16	18			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
P	207	ALA	CYS	engineered mutation	UNP Q9UBK2
Q	207	ALA	CYS	engineered mutation	UNP Q9UBK2

- Molecule 3 is 1-[4-(3-tert-butyl-4-oxidanyl-phenoxy)phenyl]ethanone (three-letter code: HVO) (formula: $C_{18}H_{20}O_3$) (labeled as "Ligand of Interest" by depositor).
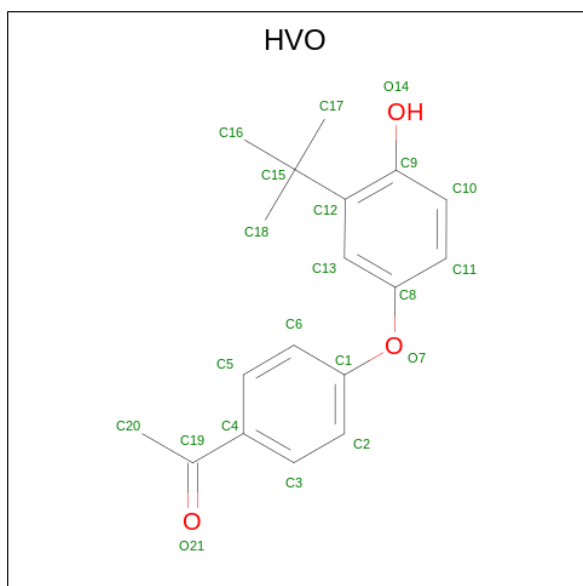
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total 21	C 18	O 3	0	0
3	B	1	Total 21	C 18	O 3	0	0

- Molecule 4 is IODIDE ION (three-letter code: IOD) (formula: I).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	P	1	Total 1	I 1	0	0

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	4	Total 4	O 4	0	0
5	B	3	Total 3	O 3	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.
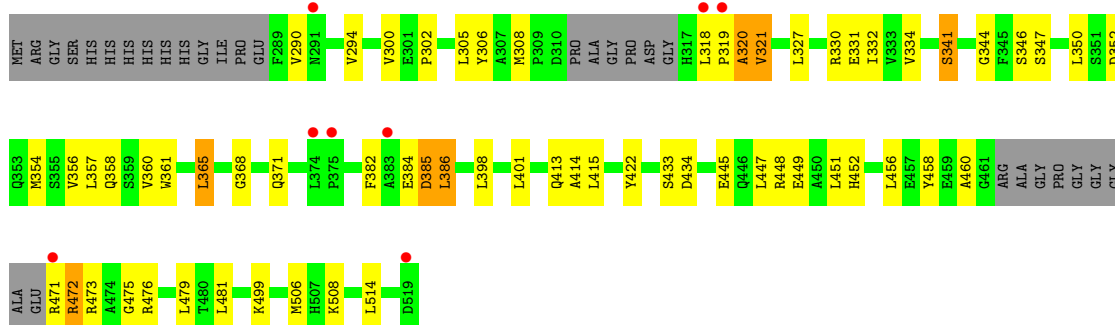
• Molecule 1: Steroid hormone receptor ERR1
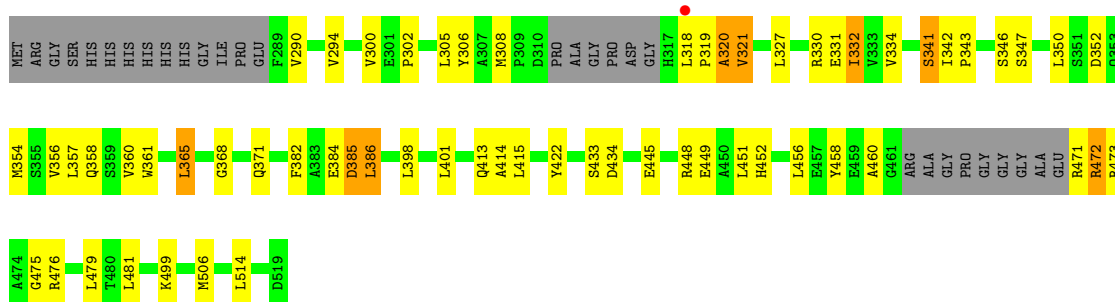
• Molecule 1: Steroid hormone receptor ERR1

• Molecule 2: Peroxisome proliferator-activated receptor gamma coactivator 1-alpha

• Molecule 2: Peroxisome proliferator-activated receptor gamma coactivator 1-alpha

4 Data and refinement statistics ⓘ

Property	Value	Source
Space group	P 43	Depositor
Cell constants a, b, c, α, β, γ	71.33Å 71.33Å 97.65Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.70 33.50 – 2.70	Depositor EDS
% Data completeness (in resolution range)	99.7 (20.00-2.70) 99.7 (33.50-2.70)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.88 (at 2.68Å)	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
R, R_{free}	0.250 , 0.305 0.251 , 0.306	Depositor DCC
R_{free} test set	1381 reflections (10.28%)	wwPDB-VP
Wilson B-factor (Å^2)	59.2	Xtriage
Anisotropy	0.302	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.29 , 24.0	EDS
L-test for twinning[2]	$< |L| > = 0.50, < L^2 > = 0.33$	Xtriage
Estimated twinning fraction	0.479 for h,-k,-l	Xtriage
F_o,F_c correlation	0.92	EDS
Total number of atoms	3610	wwPDB-VP
Average B, all atoms (Å^2)	67.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.18% 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: HVO, IOD

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	0.36	0/1707	0.63	0/2309
1	B	0.37	0/1707	0.64	0/2309
2	P	0.39	0/98	0.58	0/132
2	Q	0.39	0/98	0.60	0/132
All	All	0.37	0/3610	0.63	0/4882

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	1683	0	1733	37	0
1	B	1683	0	1733	36	0
2	P	97	0	104	3	0
2	Q	97	0	104	3	0
3	A	21	0	0	0	0
3	B	21	0	0	0	0
4	P	1	0	0	0	0
5	A	4	0	0	1	0
5	B	3	0	0	1	0
All	All	3610	0	3674	69	0

WORLDWIDE
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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.

The worst 5 of 69 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:318:LEU:HB3	1:A:319:PRO:HD2	1.44	1.00
1:B:318:LEU:HB3	1:B:319:PRO:HD2	1.44	0.96
1:A:330:ARG:O	1:A:334:VAL:HG23	1.88	0.73
1:A:456:LEU:HD22	1:B:472:ARG:HG3	1.72	0.72
1:B:330:ARG:O	1:B:334:VAL:HG23	1.90	0.72

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	210/245 (86%)	188 (90%)	17 (8%)	5 (2%)	6	15
1	B	210/245 (86%)	188 (90%)	17 (8%)	5 (2%)	6	15
2	P	10/12 (83%)	8 (80%)	2 (20%)	0	100	100
2	Q	10/12 (83%)	8 (80%)	2 (20%)	0	100	100
All	All	440/514 (86%)	392 (89%)	38 (9%)	10 (2%)	6	16

5 of 10 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	320	ALA
1	A	321	VAL
1	B	320	ALA
1	B	321	VAL
1	A	472	ARG

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	179/197 (91%)	165 (92%)	14 (8%)	12	29
1	B	179/197 (91%)	165 (92%)	14 (8%)	12	29
2	P	11/11 (100%)	10 (91%)	1 (9%)	9	21
2	Q	11/11 (100%)	10 (91%)	1 (9%)	9	21
All	All	380/416 (91%)	350 (92%)	30 (8%)	12	28

5 of 30 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	P	211	LEU
1	B	481	LEU
1	B	341	SER
2	Q	211	LEU
1	B	422	TYR

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	446	GLN
1	B	446	GLN

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 ⓘ

Of 3 ligands modelled in this entry, 1 is monoatomic - leaving 2 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
3	HVO	A	601	-	22,22,22	0.79	0	32,32,32	0.80	0
3	HVO	B	601	-	22,22,22	0.77	0	32,32,32	0.86	1 (3%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	HVO	A	601	-	-	4/14/14/14	0/2/2/2
3	HVO	B	601	-	-	0/14/14/14	0/2/2/2

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	B	601	HVO	C15-C12-C9	2.65	123.88	122.26

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	601	HVO	O21-C19-C4-C5
3	A	601	HVO	O21-C19-C4-C3
3	A	601	HVO	C20-C19-C4-C3

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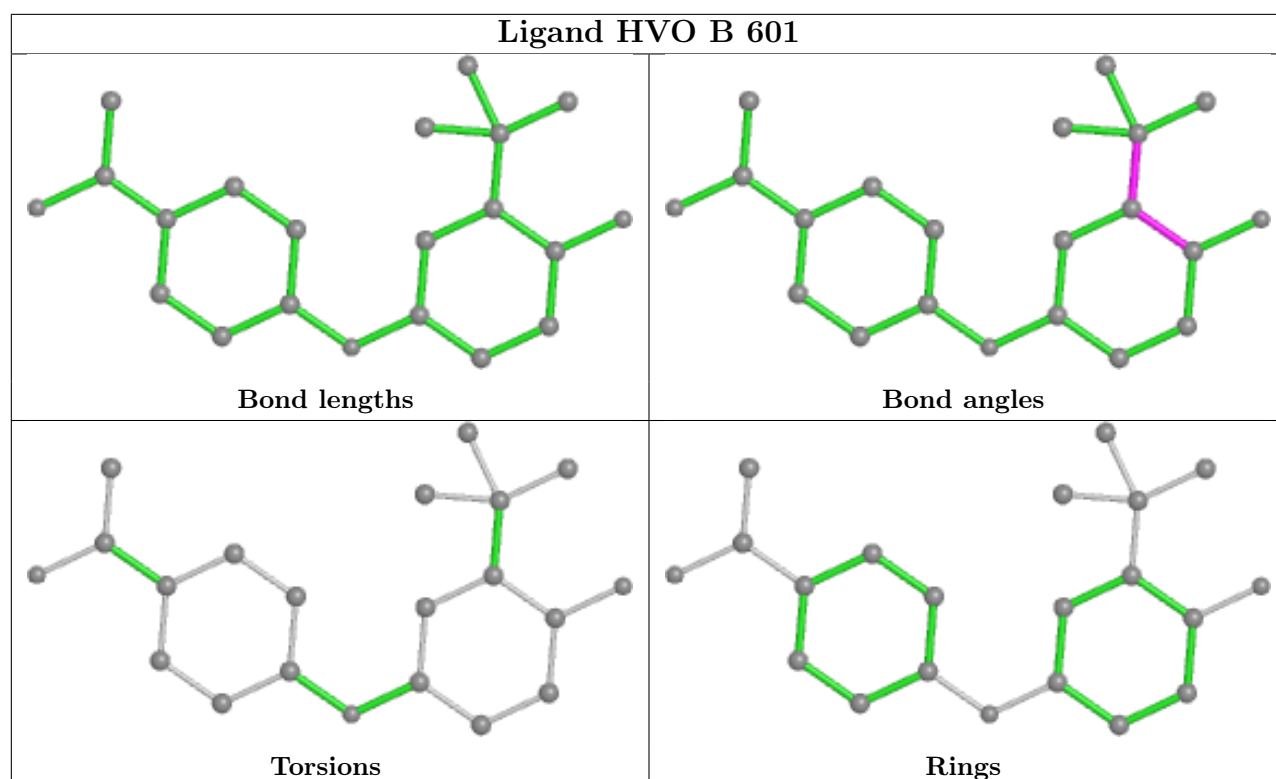| Mol	Chain	Res	Type	Atoms
3	A	601	HVO	C20-C19-C4-C5

There are no ring outliers.

No monomer is involved in short contacts.

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 HVO A 601

Bond lengths

Bond angles

Torsions

Rings

Ligand HVO B 601

Bond lengths

Bond angles

Torsions

Rings
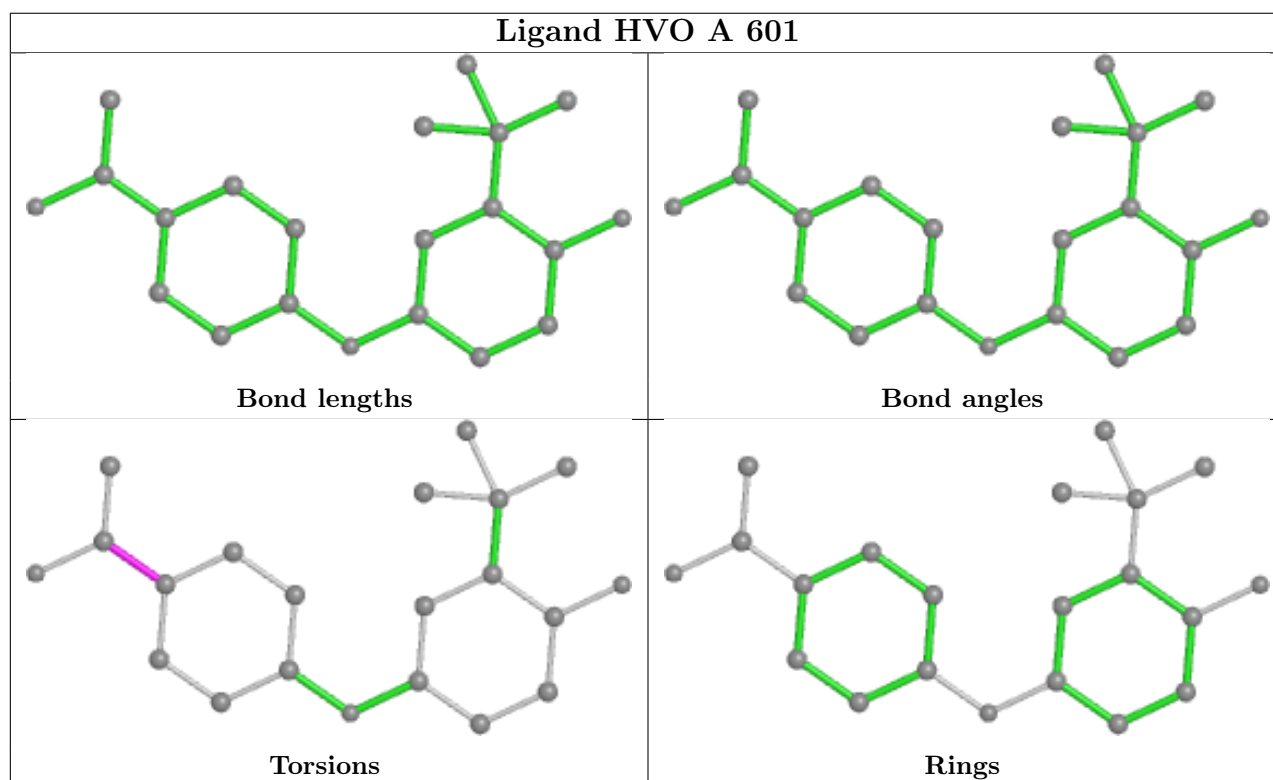
5.7 Other polymers (i)

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, 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(Å²)	Q<0.9
1	A	216/245 (88%)	0.06	1 (0%)	91	92	33, 65, 95, 132	0
1	B	216/245 (88%)	0.11	8 (3%)	41	41	35, 65, 94, 128	0
2	P	12/12 (100%)	0.34	1 (8%)	11	9	51, 68, 90, 94	0
2	Q	12/12 (100%)	0.09	0	100	100	51, 69, 87, 91	0
All	All	456/514 (88%)	0.09	10 (2%)	62	63	33, 65, 94, 132	0

The worst 5 of 10 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	471	ARG	3.6
1	A	318	LEU	3.5
1	B	318	LEU	3.3
2	P	216	THR	3.1
1	B	383	ALA	2.9

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

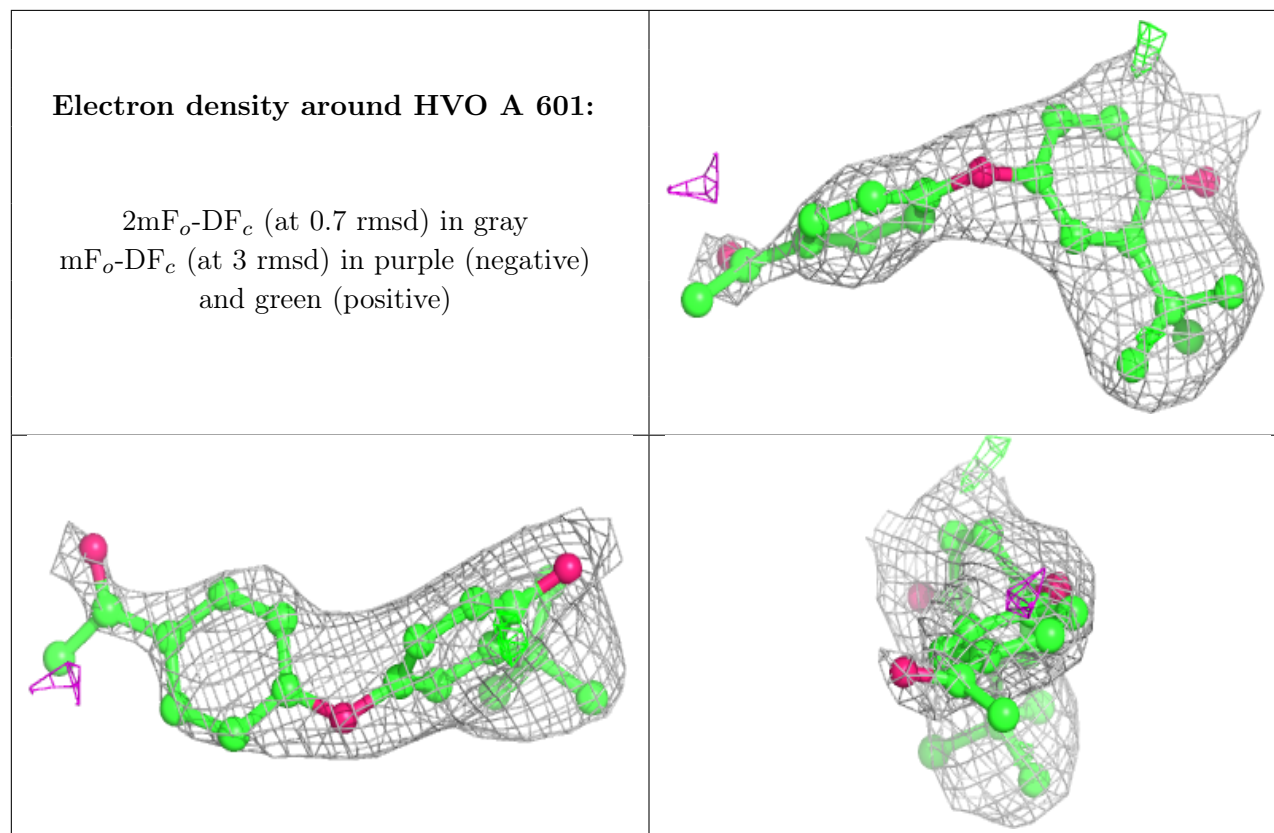There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates ⓘ

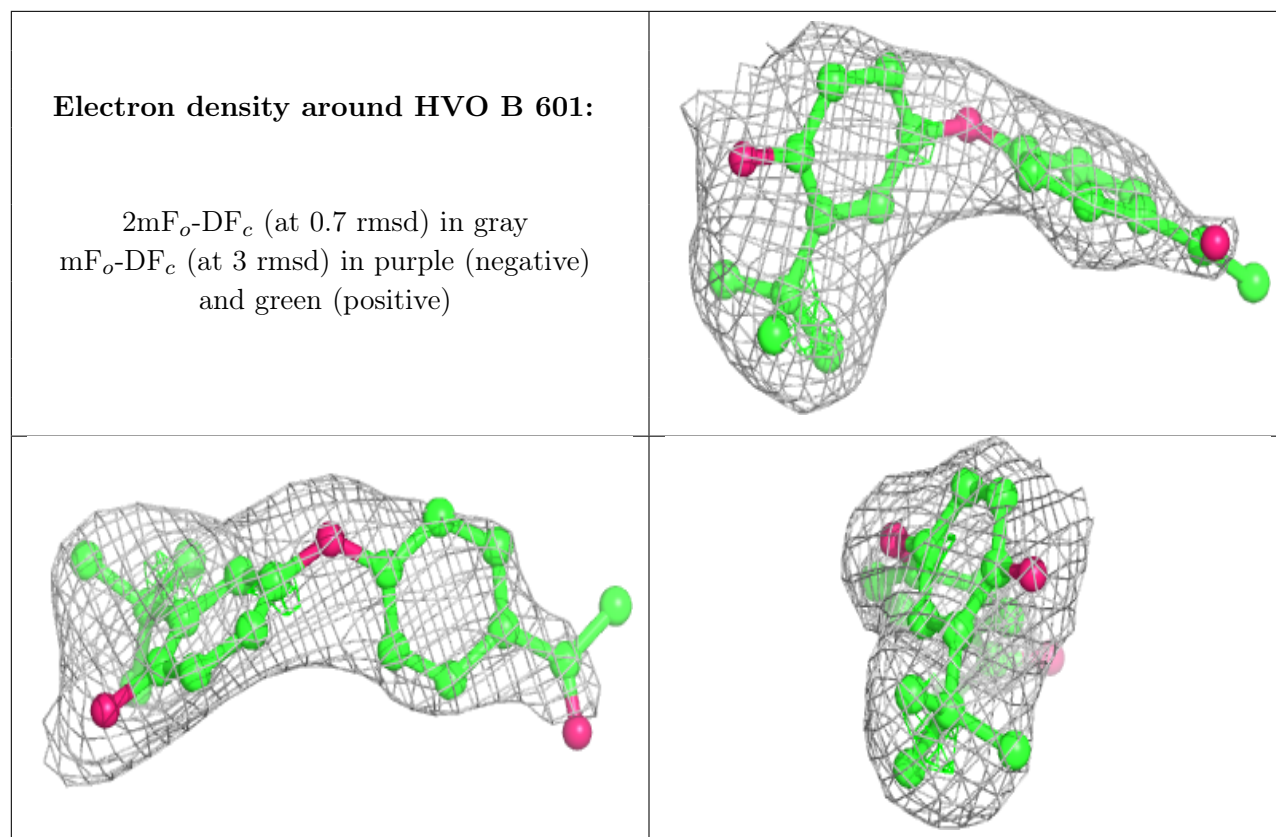There are no monosaccharides in this entry.

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
3	HVO	A	601	21/21	0.87	0.28	76,85,101,104	0
3	HVO	B	601	21/21	0.89	0.27	67,82,104,106	0
4	IOD	P	301	1/1	0.99	0.09	63,63,63,63	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 HVO A 601:

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

Electron density around HVO B 601:

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

6.5 Other polymers ⓘ

There are no such residues in this entry.