wwPDB X-ray Structure Validation Summary Report (i)

Oct 10, 2023 – 09:49 AM EDT

PDB ID	:	7K1F
Title	:	Crystal structure of human insulin degrading enzyme (IDE) in complex with compound BDM_88558
Authors	:	Liang, W.G.; Deprez, R.; Bosc, D.; Tang, W.
Deposited on	:	2020-09-07
Resolution	:	2.60 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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:

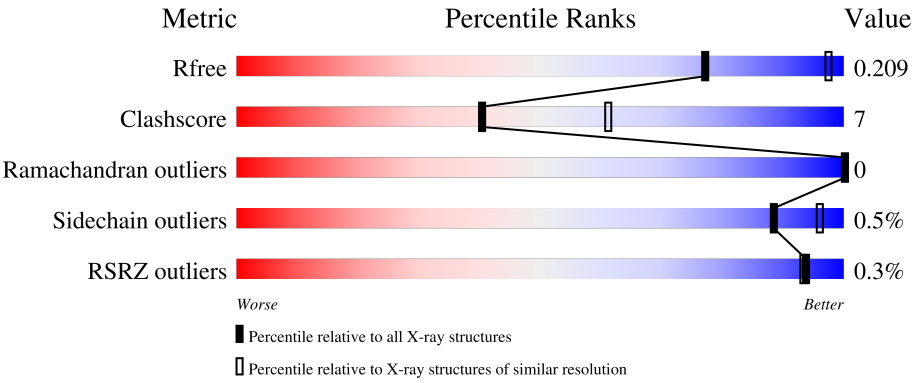
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35.1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35.1

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.60 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	3163 (2.60-2.60)
Clashscore	141614	3518 (2.60-2.60)
Ramachandran outliers	138981	3455 (2.60-2.60)
Sidechain outliers	138945	3455 (2.60-2.60)
RSRZ outliers	127900	3104 (2.60-2.60)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	990	81% 16% .
1	B	990	81% 16% .

2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 16499 atoms, of which 82 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 Insulin-degrading enzyme.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	956	Total	C	N	O	S	0	0	0
			7823	5039	1313	1449	22			
1	B	958	Total	C	N	O	S	0	0	0
			7834	5047	1315	1449	23			

There are 50 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	30	MET	-	initiating methionine	UNP P14735
A	31	HIS	-	expression tag	UNP P14735
A	32	HIS	-	expression tag	UNP P14735
A	33	HIS	-	expression tag	UNP P14735
A	34	HIS	-	expression tag	UNP P14735
A	35	HIS	-	expression tag	UNP P14735
A	36	HIS	-	expression tag	UNP P14735
A	37	ALA	-	expression tag	UNP P14735
A	38	ALA	-	expression tag	UNP P14735
A	39	GLY	-	expression tag	UNP P14735
A	40	ILE	-	expression tag	UNP P14735
A	41	PRO	-	expression tag	UNP P14735
A	110	LEU	CYS	engineered mutation	UNP P14735
A	171	SER	CYS	engineered mutation	UNP P14735
A	178	ALA	CYS	engineered mutation	UNP P14735
A	257	VAL	CYS	engineered mutation	UNP P14735
A	414	LEU	CYS	engineered mutation	UNP P14735
A	573	ASN	CYS	engineered mutation	UNP P14735
A	590	SER	CYS	engineered mutation	UNP P14735
A	789	SER	CYS	engineered mutation	UNP P14735
A	812	ALA	CYS	engineered mutation	UNP P14735
A	819	ALA	CYS	engineered mutation	UNP P14735
A	904	SER	CYS	engineered mutation	UNP P14735
A	966	ASN	CYS	engineered mutation	UNP P14735
A	974	ALA	CYS	engineered mutation	UNP P14735

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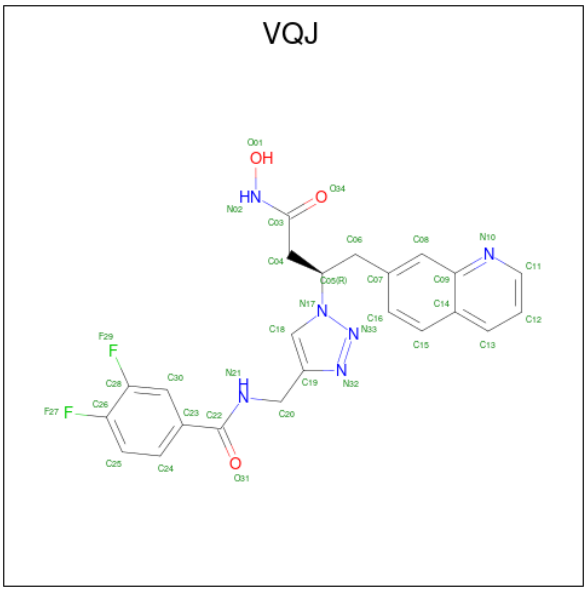
Chain	Residue	Modelled	Actual	Comment	Reference
B	30	MET	-	initiating methionine	UNP P14735
B	31	HIS	-	expression tag	UNP P14735
B	32	HIS	-	expression tag	UNP P14735
B	33	HIS	-	expression tag	UNP P14735
B	34	HIS	-	expression tag	UNP P14735
B	35	HIS	-	expression tag	UNP P14735
B	36	HIS	-	expression tag	UNP P14735
B	37	ALA	-	expression tag	UNP P14735
B	38	ALA	-	expression tag	UNP P14735
B	39	GLY	-	expression tag	UNP P14735
B	40	ILE	-	expression tag	UNP P14735
B	41	PRO	-	expression tag	UNP P14735
B	110	LEU	CYS	engineered mutation	UNP P14735
B	171	SER	CYS	engineered mutation	UNP P14735
B	178	ALA	CYS	engineered mutation	UNP P14735
B	257	VAL	CYS	engineered mutation	UNP P14735
B	414	LEU	CYS	engineered mutation	UNP P14735
B	573	ASN	CYS	engineered mutation	UNP P14735
B	590	SER	CYS	engineered mutation	UNP P14735
B	789	SER	CYS	engineered mutation	UNP P14735
B	812	ALA	CYS	engineered mutation	UNP P14735
B	819	ALA	CYS	engineered mutation	UNP P14735
B	904	SER	CYS	engineered mutation	UNP P14735
B	966	ASN	CYS	engineered mutation	UNP P14735
B	974	ALA	CYS	engineered mutation	UNP P14735

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

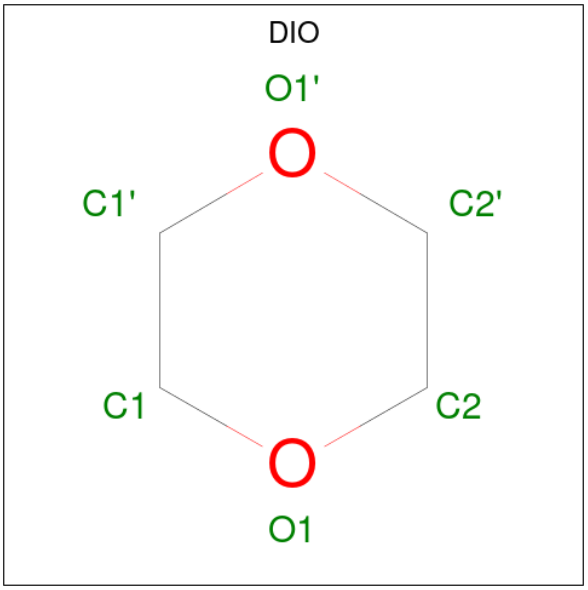
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Zn 1 1	0	0
2	B	1	Total Zn 1 1	0	0

- Molecule 3 is 3,4-difluoro-N-({1-[(2R)-4-(hydroxyamino)-4-oxo-1-(quinolin-7-yl)butan-2-yl]-1H-1,2,3-triazol-4-yl}methyl)benzamide (three-letter code: VQJ) (formula: $C_{23}H_{20}F_2N_6O_3$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C F N O 34 23 2 6 3	0	0
3	B	1	Total C F N O 34 23 2 6 3	0	0

- Molecule 4 is 1,4-DIETHYLENE DIOXIDE (three-letter code: DIO) (formula: $C_4H_8O_2$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C H O 14 4 8 2	0	0
4	A	1	Total C H O 14 4 8 2	0	0

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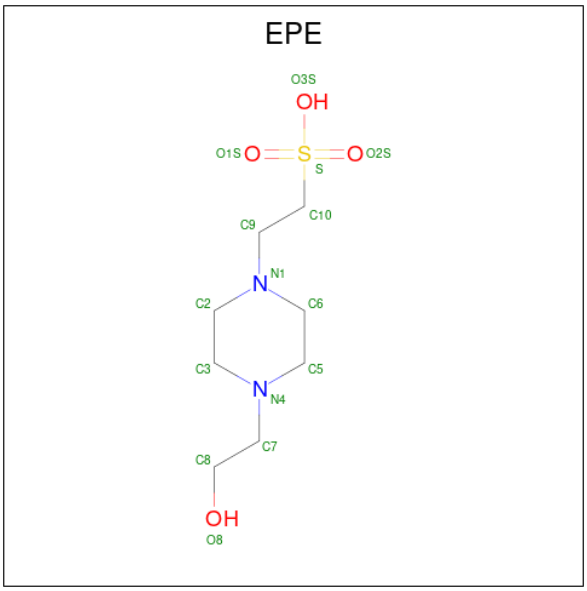
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C H O 14 4 8 2	0	0
4	B	1	Total C H O 14 4 8 2	0	0
4	B	1	Total C H O 14 4 8 2	0	0
4	B	1	Total C H O 14 4 8 2	0	0

- Molecule 5 is 4-(2-HYDROXYETHYL)-1-PIPERAZINE ETHANESULFONIC ACID (three-letter code: EPE) (formula: $C_8H_{18}N_2O_4S$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C H N O S 32 8 17 2 4 1	0	0
5	B	1	Total C H N O S 32 8 17 2 4 1	0	0

- Molecule 6 is water.

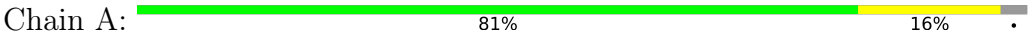
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	254	Total O 254 254	0	0
6	B	370	Total O 370 370	0	0

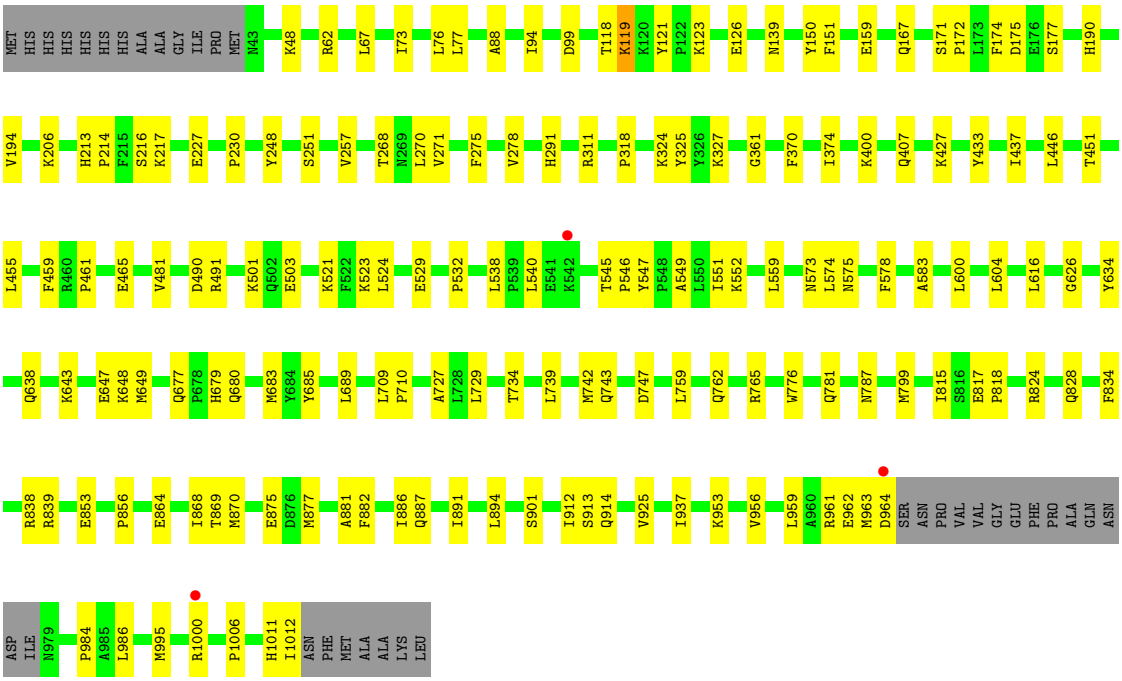
3 Residue-property plots (i)

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: Insulin-degrading enzyme

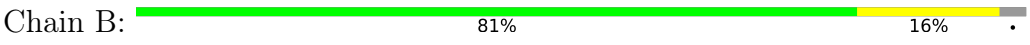
Chain A:





• Molecule 1: Insulin-degrading enzyme

Chain B:




E699
L709
P710
R711
L712
I716
R722
I725
E726
A727
T734
M742
E746
H752
L758
R765
Y766
L771
R774
G775
W776
E792
I793
Y794
Y795
Q796
M799
L808
E817
P818
R824
Q828
I832
V833
F834
R838
I843
Q844
G845
L846
R847
K854
H857
Y858
A865
I868
T869
K872
D876
M877
F882
W908
I912
Q915
K933
E934
Y940
K941
E942
A945
V946
D947
A948
P949
R950
R951
H952
K953
R961
E962
M963
ASP
SER
ASN
PRO
VAL
VAL
GLY
GLU
PHE
PRO
ALA
GLN
ASN
ASP
ILE
N979
P984
L1007
V1008
K1009
P1010
H1011
ILE
ASN
PHE
MET
ALA
ALA
LYS
LEU

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 65	Depositor
Cell constants a, b, c, α, β, γ	265.54Å 265.54Å 90.06Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	45.99 – 2.60 48.46 – 2.57	Depositor EDS
% Data completeness (in resolution range)	95.5 (45.99-2.60) 92.6 (48.46-2.57)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.84 (at 2.58Å)	Xtriage
Refinement program	PHENIX (1.18.2_3874)	Depositor
R, R_{free}	0.170 , 0.208 0.173 , 0.209	Depositor DCC
R_{free} test set	2001 reflections (1.74%)	wwPDB-VP
Wilson B-factor (Å^2)	38.3	Xtriage
Anisotropy	0.039	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 38.3	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	0.027 for h,-h-k,-l	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	16499	wwPDB-VP
Average B, all atoms (Å^2)	43.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.74% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: DIO, VQJ, ZN, EPE

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	0.45	0/8018	0.59	0/10846
1	B	0.49	0/8030	0.62	0/10862
All	All	0.47	0/16048	0.61	0/21708

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	7823	0	7764	114	0
1	B	7834	0	7779	114	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	34	0	0	0	0
3	B	34	0	0	0	0
4	A	18	24	24	3	0
4	B	18	24	24	1	0
5	A	15	17	18	1	0
5	B	15	17	17	0	0
6	A	254	0	0	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	B	370	0	0	5	0
All	All	16417	82	15626	226	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 7.

The worst 5 of 226 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:774:ARG:CZ	1:B:949:PRO:HA	1.58	1.32
1:B:192:LYS:HG3	1:B:677:GLN:HE22	1.27	0.95
1:B:774:ARG:NH1	1:B:949:PRO:HA	1.84	0.92
1:B:868:ILE:HD12	1:B:984:PRO:HD3	1.58	0.86
1:B:774:ARG:CZ	1:B:949:PRO:CA	2.52	0.82

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	952/990 (96%)	922 (97%)	30 (3%)	0	100	100
1	B	954/990 (96%)	923 (97%)	31 (3%)	0	100	100
All	All	1906/1980 (96%)	1845 (97%)	61 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	852/879 (97%)	850 (100%)	2 (0%)	93 98
1	B	853/879 (97%)	847 (99%)	6 (1%)	84 94
All	All	1705/1758 (97%)	1697 (100%)	8 (0%)	88 96

5 of 8 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	774	ARG
1	B	722	ARG
1	B	652	PHE
1	B	621	GLN
1	B	653	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	621	GLN
1	B	232	GLN
1	B	677	GLN
1	B	724	HIS
1	B	788	ASN

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)

Of 12 ligands modelled in this entry, 2 are monoatomic - leaving 10 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	$\#\|Z\| > 2$
5	EPE	B	1106	-	15,15,15	1.09	1 (6%)	18,20,20	1.82	4 (22%)
4	DIO	A	1104	-	6,6,6	0.68	0	6,6,6	0.72	0
5	EPE	A	1106	-	15,15,15	0.95	1 (6%)	18,20,20	1.91	5 (27%)
4	DIO	A	1103	-	6,6,6	0.65	0	6,6,6	0.65	0
4	DIO	B	1105	-	6,6,6	0.70	0	6,6,6	0.34	0
4	DIO	B	1104	-	6,6,6	0.62	0	6,6,6	1.05	1 (16%)
4	DIO	A	1105	-	6,6,6	0.66	0	6,6,6	0.41	0
4	DIO	B	1103	-	6,6,6	0.67	0	6,6,6	0.64	0
3	VQJ	A	1102	2	37,37,37	2.62	7 (18%)	42,51,51	1.25	3 (7%)
3	VQJ	B	1102	2	37,37,37	2.72	8 (21%)	42,51,51	1.53	5 (11%)

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
5	EPE	B	1106	-	-	6/9/19/19	0/1/1/1
4	DIO	A	1104	-	-	-	0/1/1/1
5	EPE	A	1106	-	-	7/9/19/19	0/1/1/1
4	DIO	A	1103	-	-	-	0/1/1/1
4	DIO	B	1105	-	-	-	0/1/1/1
4	DIO	B	1104	-	-	-	0/1/1/1
4	DIO	A	1105	-	-	-	0/1/1/1
4	DIO	B	1103	-	-	-	0/1/1/1
3	VQJ	A	1102	2	-	2/17/23/23	0/4/4/4
3	VQJ	B	1102	2	-	2/17/23/23	0/4/4/4

The worst 5 of 17 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	1102	VQJ	C03-N02	13.12	1.46	1.32
3	A	1102	VQJ	C03-N02	12.12	1.45	1.32
3	A	1102	VQJ	C22-N21	5.53	1.45	1.33
3	B	1102	VQJ	C18-C19	5.19	1.43	1.36
3	B	1102	VQJ	C22-N21	5.06	1.44	1.33

The worst 5 of 18 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	A	1102	VQJ	C18-C19-N32	-4.52	104.63	111.34
3	B	1102	VQJ	C18-C19-N32	-4.41	104.78	111.34
5	B	1106	EPE	C5-N4-C3	4.36	118.64	108.83
5	A	1106	EPE	C5-N4-C3	4.27	118.44	108.83
3	B	1102	VQJ	C04-C03-N02	4.09	121.34	115.14

There are no chirality outliers.

5 of 17 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	1102	VQJ	C03-C04-C05-N17
3	B	1102	VQJ	C03-C04-C05-C06
3	B	1102	VQJ	C03-C04-C05-N17
5	B	1106	EPE	C10-C9-N1-C2
5	B	1106	EPE	C10-C9-N1-C6

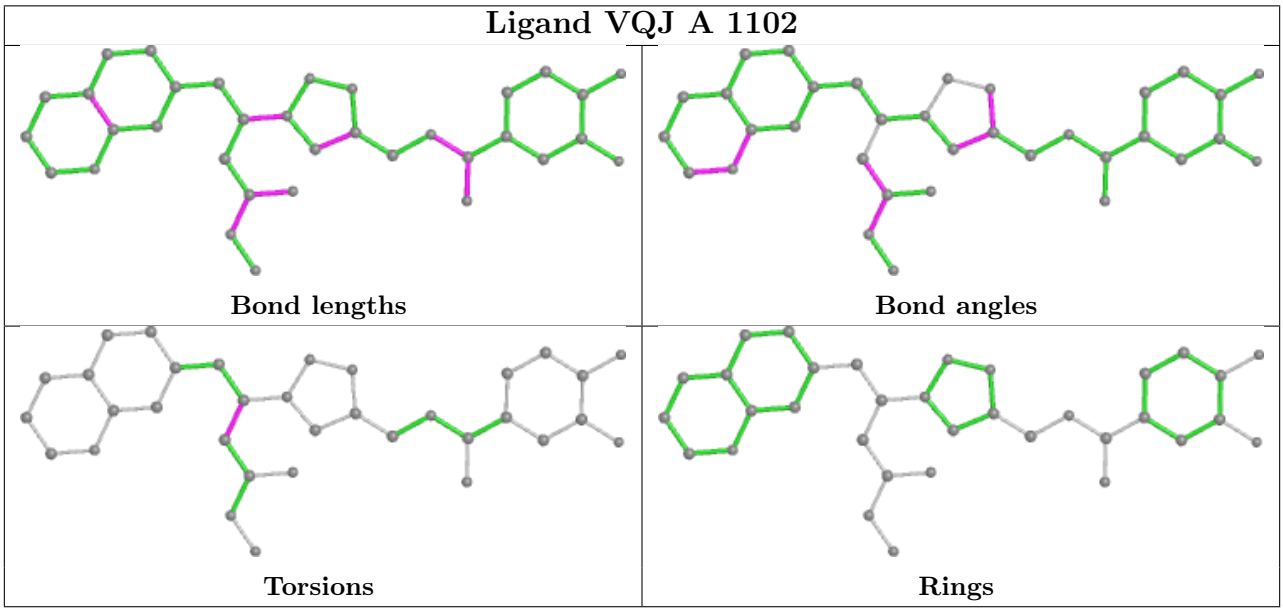
There are no ring outliers.

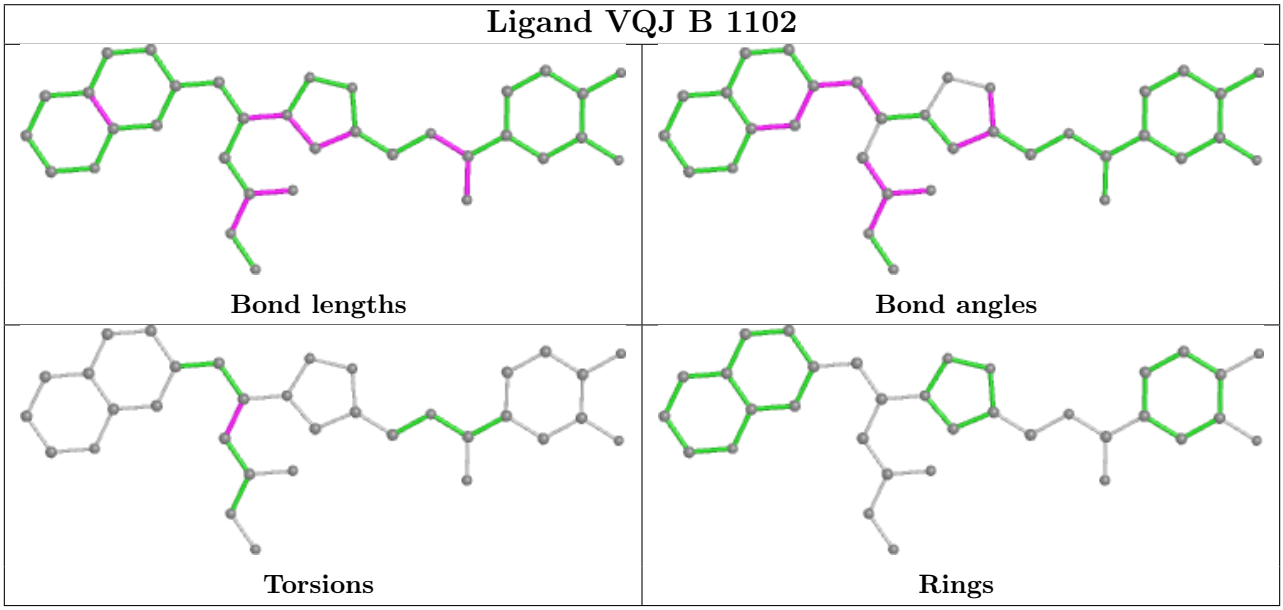
3 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1104	DIO	3	0
5	A	1106	EPE	1	0
4	B	1104	DIO	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 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.





5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95^{th} percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å^2)	Q<0.9
1	A	956/990 (96%)	-0.57	3 (0%)	94	93	34, 45, 60, 104	0
1	B	958/990 (96%)	-0.57	2 (0%)	95	95	27, 38, 56, 98	0
All	All	1914/1980 (96%)	-0.57	5 (0%)	94	93	27, 42, 59, 104	0

All (5) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	652	PHE	2.8
1	A	1000	ARG	2.7
1	B	774	ARG	2.7
1	A	542	LYS	2.5
1	A	964	ASP	2.3

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

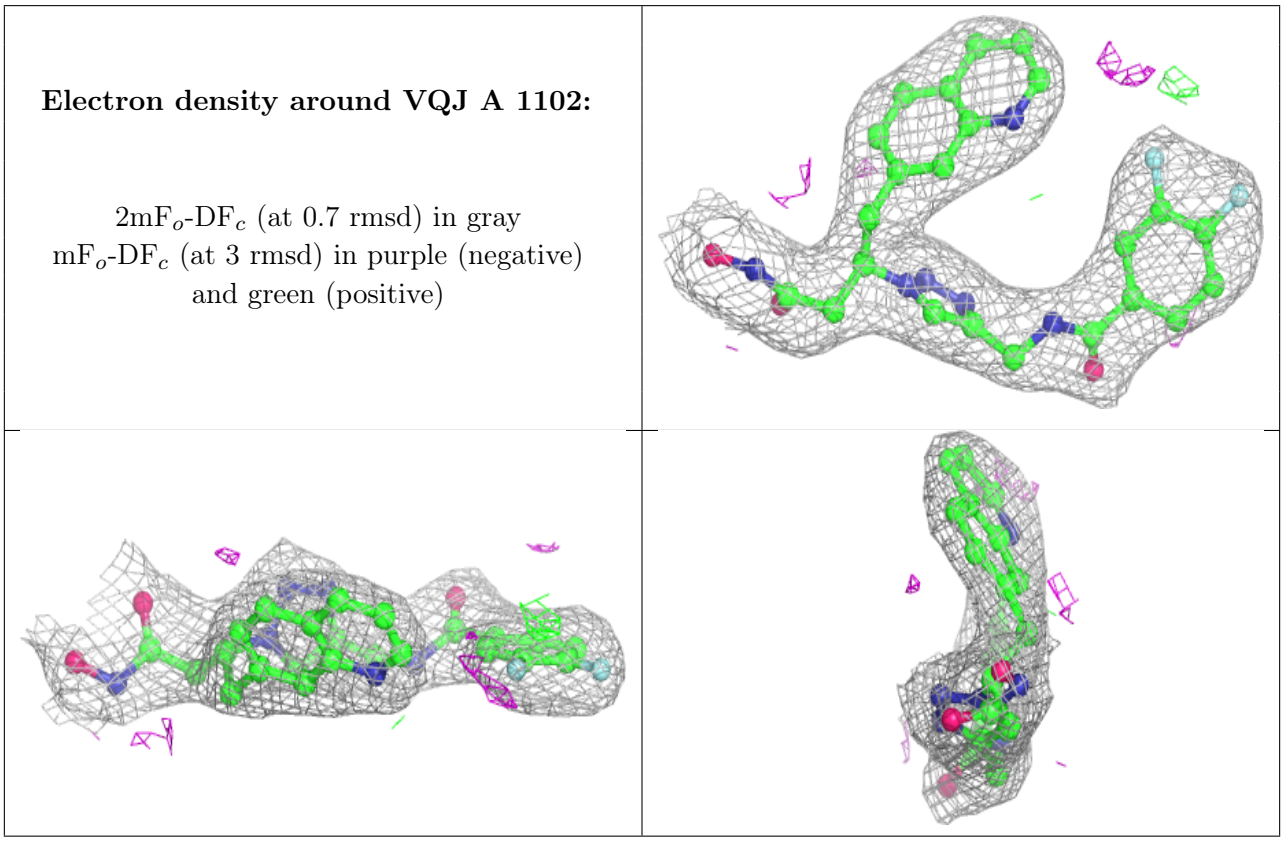
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9'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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
4	DIO	B	1104	6/6	0.80	0.20	57,73,91,91	0
4	DIO	A	1104	6/6	0.88	0.13	65,78,86,86	0
5	EPE	B	1106	15/15	0.89	0.26	62,76,89,91	0
5	EPE	A	1106	15/15	0.90	0.20	62,90,108,109	0
4	DIO	A	1105	6/6	0.93	0.17	49,66,86,86	0
4	DIO	B	1105	6/6	0.93	0.17	45,57,79,79	0
4	DIO	A	1103	6/6	0.95	0.12	52,63,78,78	0
2	ZN	B	1101	1/1	0.96	0.16	38,38,38,38	0
4	DIO	B	1103	6/6	0.96	0.10	52,63,73,73	0
3	VQJ	A	1102	34/34	0.97	0.12	37,43,49,52	0
3	VQJ	B	1102	34/34	0.98	0.12	34,39,44,46	0
2	ZN	A	1101	1/1	1.00	0.12	42,42,42,42	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.

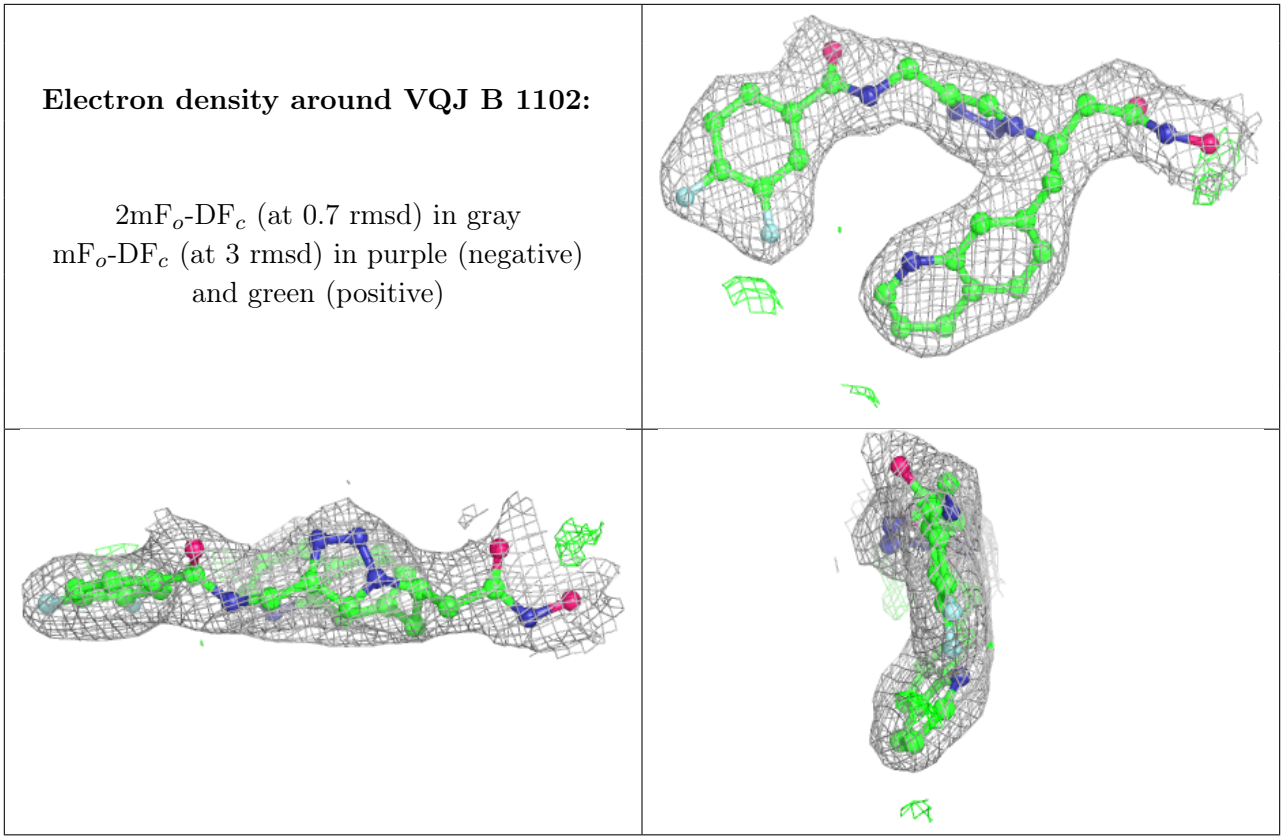
Electron density around VQJ A 1102:

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



Electron density around VQJ B 1102:

$2mF_o$-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.