



wwPDB X-ray Structure Validation Summary Report ⓘ

May 15, 2020 – 11:59 am BST

PDB ID : 4GSC
Title : Structure analysis of insulin degrading enzyme with compound bdm41559 ((s)-2-[2-(carboxymethyl-phenethyl-amino)-acetylamino]-3-(1h-imidazol-4-yl)-propanoic acid methyl ester)
Authors : Guo, Q.; Deprez-Poulain, R.; Deprez, B.; Tang, W.J.
Deposited on : 2012-08-27
Resolution : 2.81 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 ⓘ 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

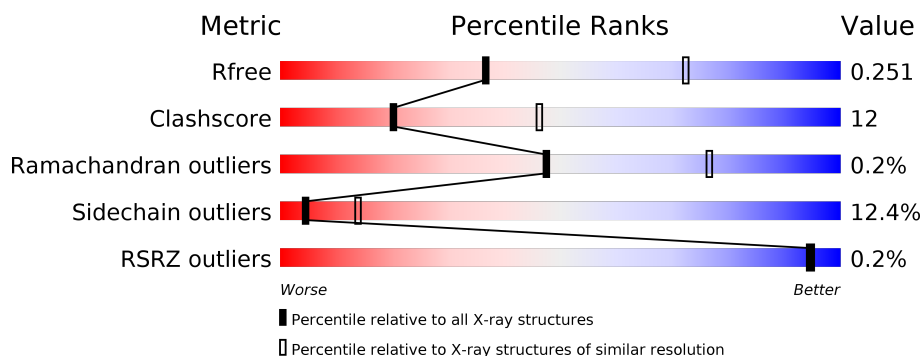
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION



The reported resolution of this entry is 2.81 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	3617 (2.84-2.80)
Clashscore	141614	4060 (2.84-2.80)
Ramachandran outliers	138981	3978 (2.84-2.80)
Sidechain outliers	138945	3980 (2.84-2.80)
RSRZ outliers	127900	3552 (2.84-2.80)

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	990	
1	B	990	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 15858 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 Insulin-degrading enzyme.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	958	Total	C	N	O	S	0	0	1
			7818	5035	1315	1445	23			
1	B	956	Total	C	N	O	S	0	0	1
			7802	5026	1312	1442	22			

There are 52 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	30	MET	-	EXPRESSION TAG	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	111	GLN	GLU	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

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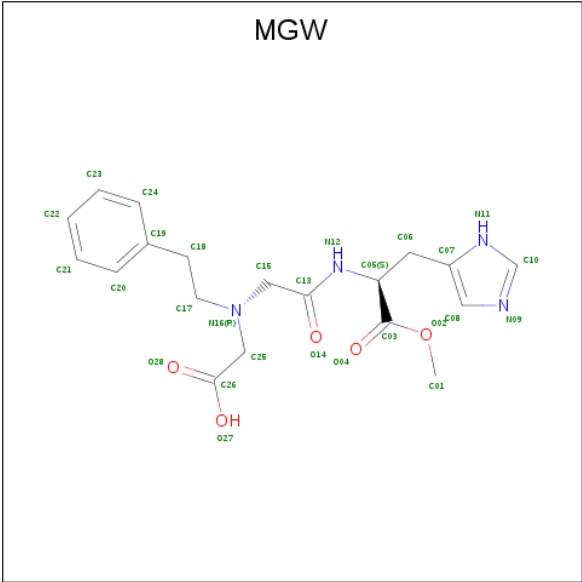
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Chain	Residue	Modelled	Actual	Comment	Reference
A	974	ALA	CYS	ENGINEERED MUTATION	UNP P14735
B	30	MET	-	EXPRESSION TAG	UNP P14735
B	31	HIS	-	EXPRESSION TAG	UNP P14735
B	32	HIS	-	EXPRESSION TAG	UNP P14735
B	33	HIS	-	EXPRESSION TAG	UNP P14735
B	34	HIS	-	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	111	GLN	GLU	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	B	1	Total Zn 1 1	0	0
2	A	1	Total Zn 1 1	0	0

- Molecule 3 is methyl N-(carboxymethyl)-N-(2-phenylethyl)glycyl-L-histidinate (three-letter code: MGW) (formula: C₁₉H₂₄N₄O₅).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			28	19	4	5		
3	B	1	Total	C	N	O	0	0
			28	19	4	5		


- Molecule 4 is water.

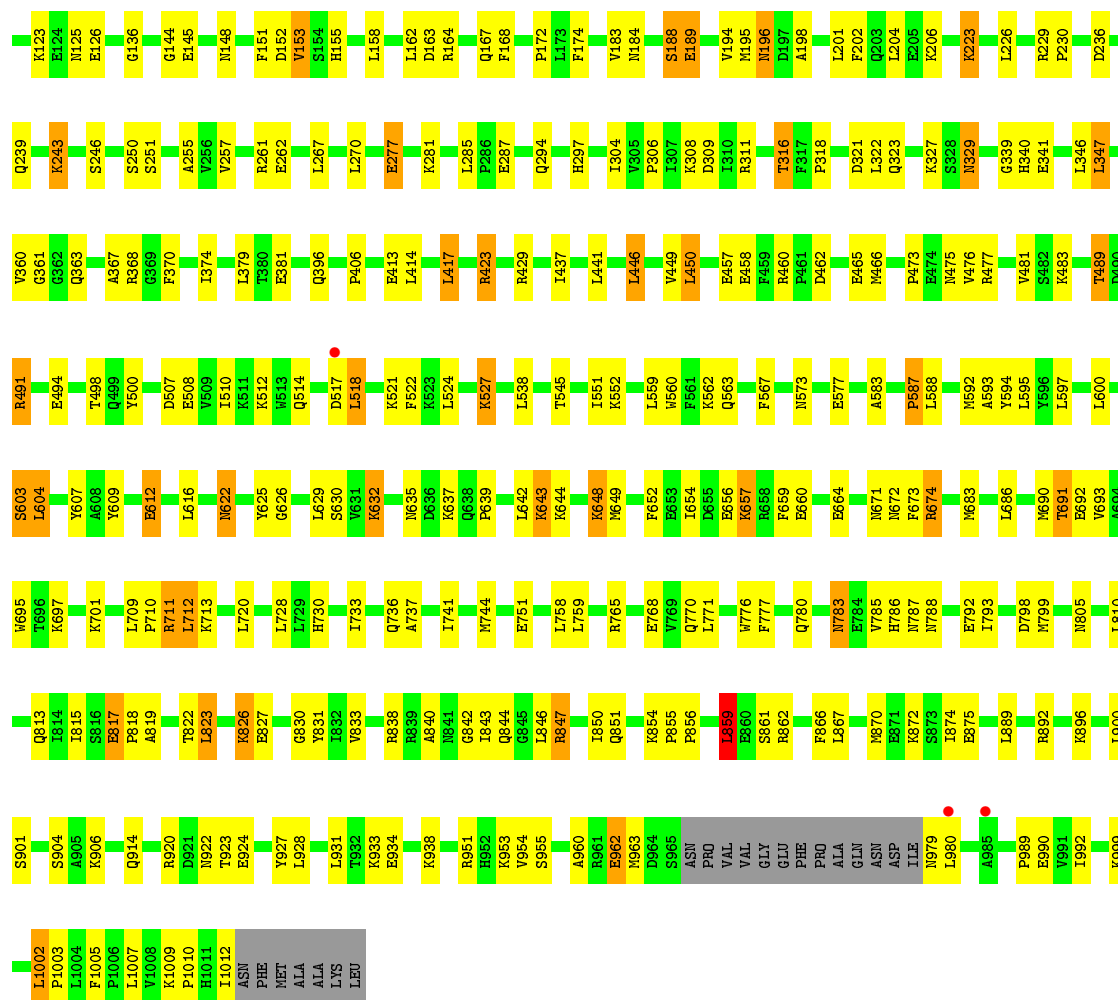
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	108	Total	O	0	0
			108	108		
4	B	72	Total	O	0	0
			72	72		

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.

- Chain A: 66% 27%

	L859	L783	L642	Y500	G361	L131
R961	R961	L783	L642	Y500	G361	L131
E962	R862	R764	K644	I505	K364	H134
R963	L867	E768	I645	P506	R261	
D964	R870	R769	I646	D507	L264	S138
ASN	R871	L771	R648	E509	I374	N139
PRO	R872	L771	I654	I510	I375	A140
VAL	R873	R774	D655	K512	D389	N148
GLY	R874	R775	R656	H513		
GLU	R875	R776	R657	Q514	H393	F151
PHE	R880	R776	R658	Q514		
PRO	R881	R782	R659	K321	E404	S154
ALA	R884	R783	N783	G405	G405	H155
GLN	R885	E784	P406	P406	P286	
ASN	R887	R785	E664	Q407	E287	L158
ASP	R888	R786		E408		
ILE	R889		R668	K327		S171
N779	R890	T793	N671	L538	L414	V183
L980	R891	Y794	N672	Y547	L417	N184
S981	R892	T797	F673	P548		A185
Q882	R896	D798	R674	F422	F422	V186
			A675	M556		D187
P987		S801	E676	S557	K427	S188
		R802		K358	Y302	E189
E990	R906	L810	A682	L559	L441	K192
Q993	R910	I815	L688	K562	Y444	N196
R994	R911	S816	L689	Q563	P445	D197
N995	R912	R916	M690	N575	L446	A198
T996	R913	R917	T691	N576		D80
E997	R914	R918		F576	V449	R200
	R915		T696	E577	L450	L201
R1000		L823			T451	T83
G1001	D919	R824	L709	D586	A452	
L1002	R920	P710	R710	A452	F317	L204
P1003	D921	E827	R711	L595	P318	
F1005		Q828	L712	Y596	F459	H213
P1006	V925	L829	K713	L597	R460	P214
L1007	A926	G830		D462	P461	G95
	R927	R831	R722	L600	D462	S96
	L928			K601	M466	L97
P1010	R929	F834	E726	D802	V467	
H1011	R930		A727	S603	L468	L102
A1012	L931	R838	L728	L616	E341	I103
ASN	R932	I843	H730	L620	G342	
PHE	R933	Q844		I475	S345	L106
MET	E934	G845	Q736	V481	L346	S107
ALA		L846		N622	L347	H108
LYS	R937	R847	V745	F485		H112
	R938			L829		K119
LEU	R939	S852	K756	T489		K120
	R940	E853	P757	D490	K353	S246
	A945	R856	L758	K637	R491	A247
		L759	Q638	L759	V356	Y248
	V956	H857	P760	P639		E124
	R957	R858			E494	M125
						S250
						C254

- Chain B: 
- | Label | Color |
|-------|--------|
| MET | Green |
| HIS | Green |
| HIS | Green |
| HIS | Green |
| HIS | Green |
| HIS | Green |
| HIS | Green |
| ALA | Green |
| GLY | Green |
| ILE | Green |
| PRO | Green |
| MET | Green |
| ASP | Green |
| ILE44 | Yellow |
| P45 | Yellow |
| R49 | Yellow |
| I62 | Red |
| K61 | Green |
| R62 | Green |
| L67 | Orange |
| I73 | Green |
| K74 | Orange |
| V75 | Yellow |
| L76 | Yellow |
| L77 | Green |
| D80 | Yellow |
| T83 | Green |
| D84 | Green |
| K85 | Green |
| S86 | Green |
| S87 | Green |
| A88 | Yellow |
| V92 | Orange |
| H93 | Orange |
| S96 | Yellow |
| L97 | Yellow |
| S98 | Yellow |
| M102 | Orange |
| H108 | Green |
| F109 | Green |
| L110 | Green |
| Q111 | Yellow |
| L114 | Green |
| T118 | Green |
| K119 | Yellow |
| K120 | Yellow |



4 Data and refinement statistics

Property	Value	Source
Space group	P 65	Depositor
Cell constants a, b, c, α , β , γ	263.76 Å 263.76 Å 91.26 Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	49.85 – 2.81 49.85 – 2.81	Depositor EDS
% Data completeness (in resolution range)	89.4 (49.85-2.81) 89.4 (49.85-2.81)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.72 (at 2.81 Å)	Xtriage
Refinement program	REFMAC 5.5.0102	Depositor
R, R_{free}	0.195 , 0.253 0.196 , 0.251	Depositor DCC
R_{free} test set	3992 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å ²)	49.8	Xtriage
Anisotropy	0.047	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 44.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.027 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	15858	wwPDB-VP
Average B, all atoms (Å ²)	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.66% 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 [i](#)

5.1 Standard geometry [i](#)

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

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	0.93	6/8013 (0.1%)	0.94	18/10841 (0.2%)
1	B	0.89	7/7997 (0.1%)	0.89	9/10820 (0.1%)
All	All	0.91	13/16010 (0.1%)	0.92	27/21661 (0.1%)

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	B	0	1

The worst 5 of 13 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	189	GLU	CG-CD	9.95	1.66	1.51
1	A	577	GLU	CG-CD	8.22	1.64	1.51
1	B	189	GLU	CB-CG	6.35	1.64	1.52
1	B	577	GLU	CG-CD	6.04	1.61	1.51
1	B	660	GLU	CG-CD	5.89	1.60	1.51

The worst 5 of 27 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	189	GLU	OE1-CD-OE2	-8.31	113.32	123.30
1	B	489	THR	CB-CA-C	-7.75	90.66	111.60
1	B	153	VAL	CB-CA-C	6.52	123.79	111.40
1	B	52	ASN	N-CA-C	6.19	127.71	111.00
1	A	75	VAL	CB-CA-C	-6.11	99.78	111.40

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	52	ASN	Peptide

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	7818	0	7749	173	0
1	B	7802	0	7734	216	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	28	0	23	6	0
3	B	28	0	22	4	0
4	A	108	0	0	10	0
4	B	72	0	0	6	0
All	All	15858	0	15528	389	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 12.

The worst 5 of 389 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:527:LYS:HB2	1:B:527:LYS:NZ	1.62	1.15
1:A:892:ARG:HD3	4:A:1236:HOH:O	1.52	1.07
1:B:527:LYS:HB2	1:B:527:LYS:HZ3	1.06	1.07
1:A:108:HIS:CE1	1:A:189:GLU:OE1	2.09	1.02
1:A:112:HIS:NE2	1:A:189:GLU:OE1	1.91	1.01

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	954/990 (96%)	890 (93%)	61 (6%)	3 (0%)	41	70
1	B	952/990 (96%)	876 (92%)	75 (8%)	1 (0%)	51	80
All	All	1906/1980 (96%)	1766 (93%)	136 (7%)	4 (0%)	47	76

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	1010	PRO
1	A	636	ASP
1	A	1010	PRO
1	A	103	ILE

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	849/879 (97%)	745 (88%)	104 (12%)	5	14
1	B	847/879 (96%)	741 (88%)	106 (12%)	4	14
All	All	1696/1758 (96%)	1486 (88%)	210 (12%)	4	14

5 of 210 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	930	THR
1	B	148	ASN

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Mol	Chain	Res	Type
1	B	889	LEU
1	A	938	LYS
1	B	61	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 60 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	957	HIS
1	B	148	ASN
1	B	828	GLN
1	B	102	ASN
1	B	196	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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 2 are 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	MGW	A	1102	-	22,29,29	1.58	1 (4%)	28,37,37	1.89	9 (32%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	MGW	B	1102	-	22,29,29	1.59	2 (9%)	28,37,37	2.04	6 (21%)

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	MGW	A	1102	-	-	15/25/27/27	0/2/2/2
3	MGW	B	1102	-	-	8/25/27/27	0/2/2/2

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	1102	MGW	O02-C03	6.03	1.47	1.33
3	A	1102	MGW	O02-C03	6.01	1.47	1.33
3	B	1102	MGW	C05-N12	2.01	1.50	1.45

The worst 5 of 15 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	1102	MGW	C05-N12-C13	6.38	138.06	121.65
3	B	1102	MGW	C03-C05-N12	4.49	121.10	110.72
3	A	1102	MGW	O02-C03-C05	4.18	122.22	111.52
3	B	1102	MGW	C01-O02-C03	3.94	124.85	115.94
3	A	1102	MGW	C01-O02-C03	3.60	124.08	115.94

There are no chirality outliers.

5 of 23 torsion outliers are listed below:

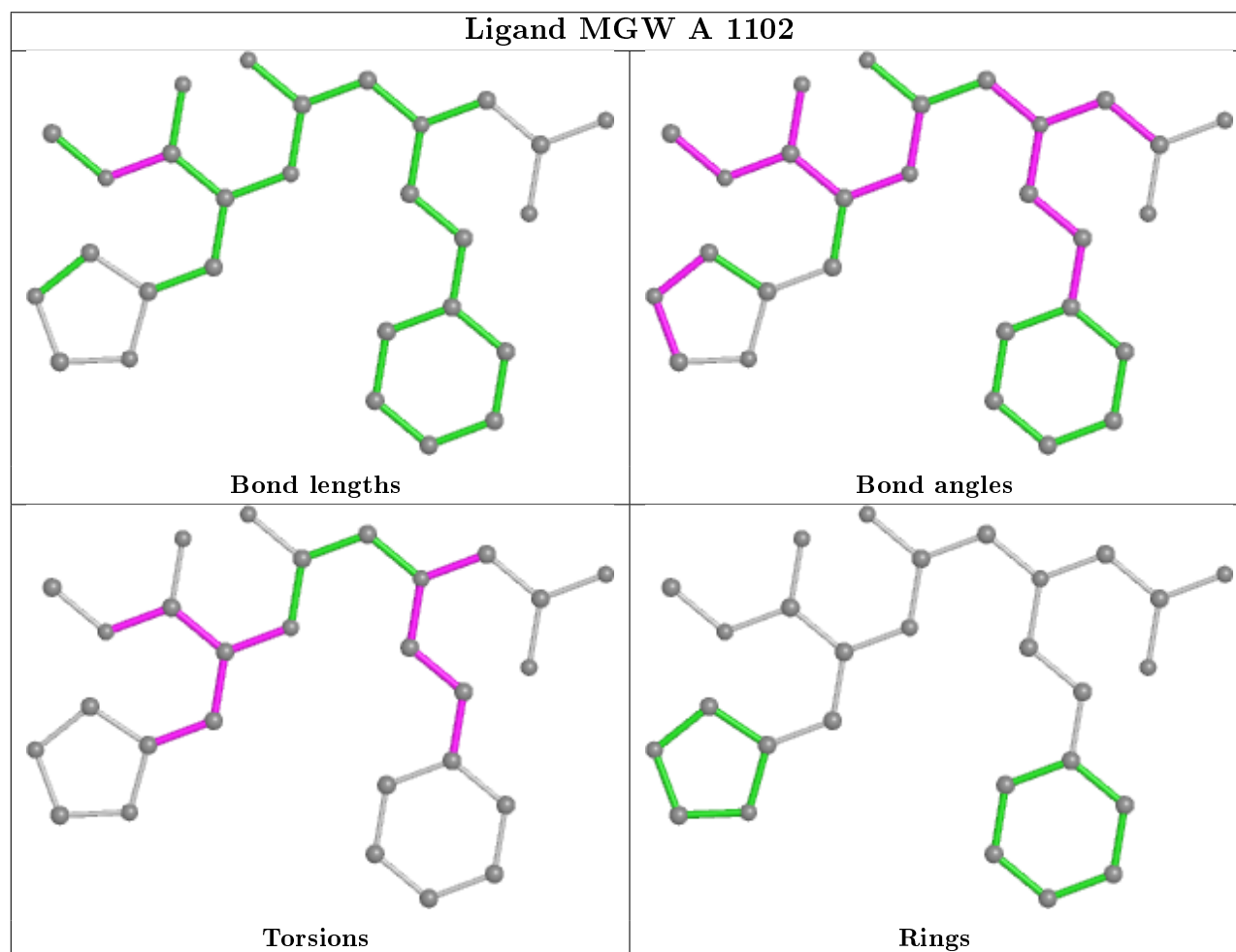
Mol	Chain	Res	Type	Atoms
3	A	1102	MGW	C06-C05-N12-C13
3	B	1102	MGW	N12-C05-C06-C07
3	A	1102	MGW	O04-C03-O02-C01
3	B	1102	MGW	O04-C03-O02-C01
3	A	1102	MGW	C05-C03-O02-C01

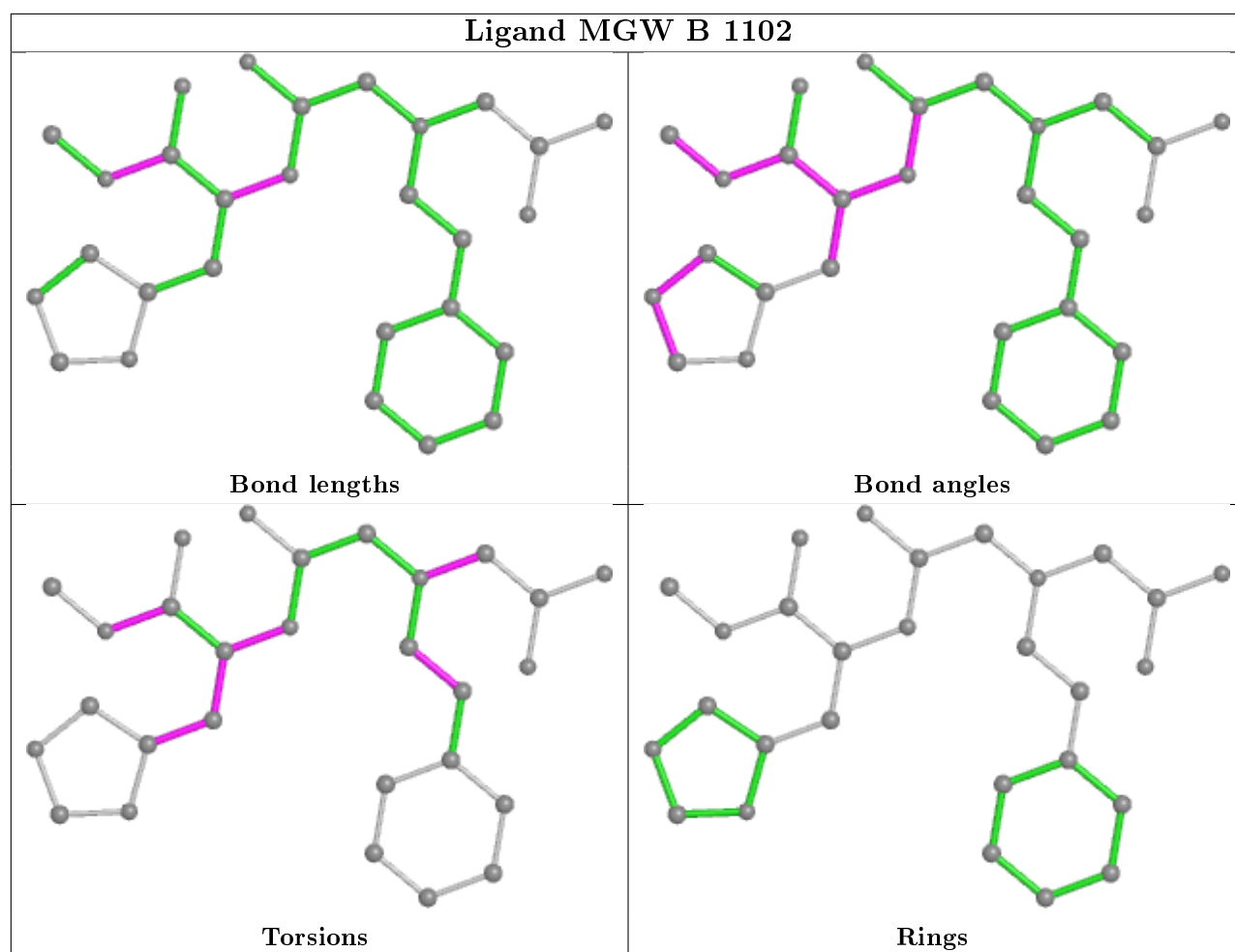
There are no ring outliers.

2 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1102	MGW	6	0
3	B	1102	MGW	4	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less 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	958/990 (96%)	-0.35	0 100 100	25, 41, 58, 88	0
1	B	956/990 (96%)	-0.25	3 (0%) 94 93	32, 47, 65, 82	0
All	All	1914/1980 (96%)	-0.30	3 (0%) 95 94	25, 44, 62, 88	0

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	517	ASP	2.2
1	B	980	LEU	2.1
1	B	985	ALA	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 carbohydrates 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
3	MGW	B	1102	28/28	0.79	0.29	79,87,102,102	0
3	MGW	A	1102	28/28	0.83	0.29	64,80,86,87	0

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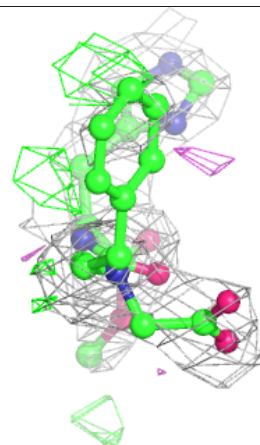
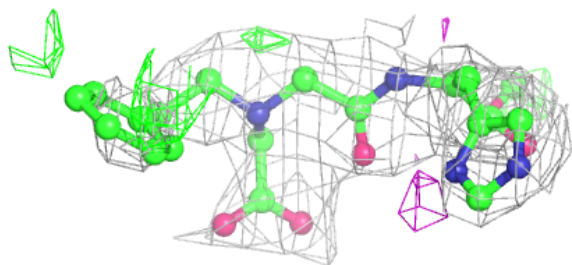
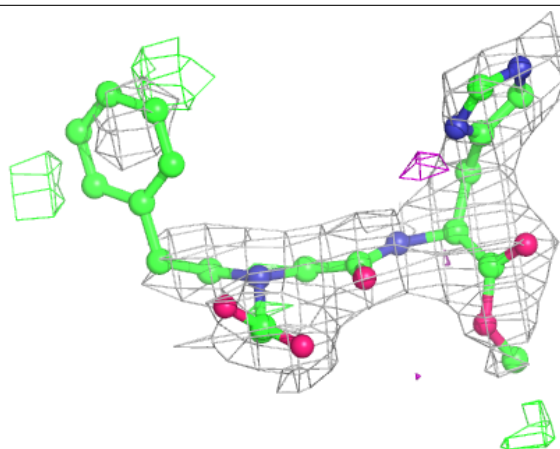
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	ZN	A	1101	1/1	0.87	0.18	2,2,2,2	0
2	ZN	B	1101	1/1	0.89	0.15	2,2,2,2	0

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.

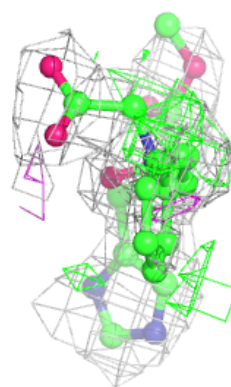
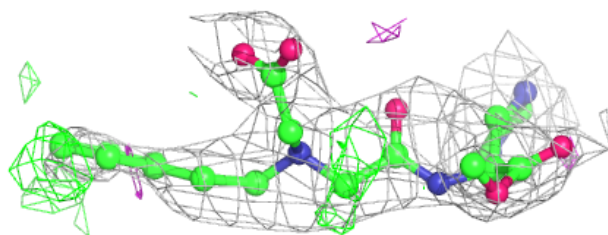
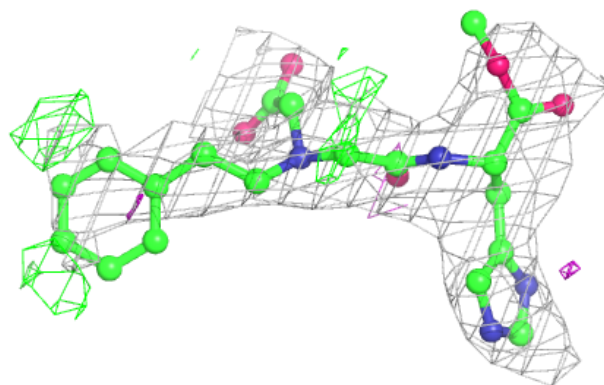
Electron density around MGW B 1102:

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



Electron density around MGW 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)



6.5 Other polymers [i](#)

There are no such residues in this entry.