



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 06:27 AM GMT

PDB ID : 2WZS  
Title : STRUCTURE OF THE FAMILY GH92 INVERTING MANNOSIDASE  
BT3990 FROM BACTEROIDES THETA IOTAOMICRON VPI-5482 IN  
COMPLEX WITH MANNOIMIDAZOLE  
Authors : Zhu, Y.; Suits, M.D.L.; Thompson, A.; Chavan, S.; Dinev, Z.; Dumon,  
C.; Smith, N.; Moremen, K.W.; Xiang, Y.; Siriwardena, A.; Williams, S.J.;  
Gilbert, H.J.; Davies, G.J.  
Deposited on : 2009-12-02  
Resolution : 2.25 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](mailto:validation@mail.wwpdb.org)  
A user guide is available at  
<http://wwpdb.org/validation/2016/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 : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

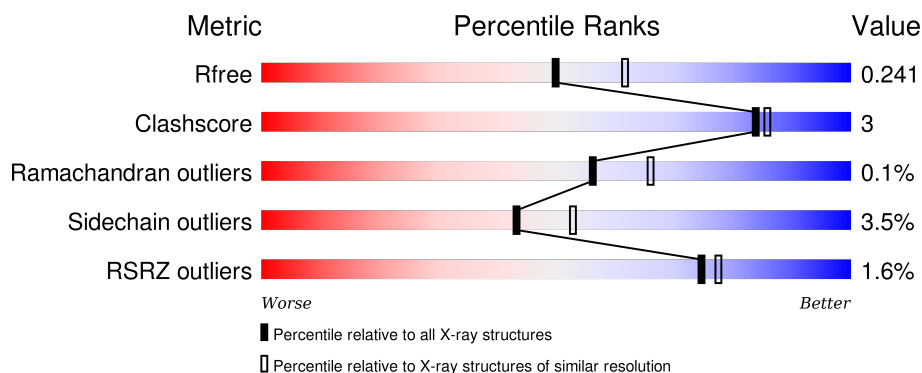
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.25 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))
$R_{free}$	91344	1640 (2.28-2.24)
Clashscore	102246	1095 (2.26-2.26)
Ramachandran outliers	100387	1063 (2.26-2.26)
Sidechain outliers	100360	1063 (2.26-2.26)
RSRZ outliers	91569	1647 (2.28-2.24)

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  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. 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	738	<div> <div>93%</div> <div>6%</div> </div>
1	B	738	<div> <div>92%</div> <div>7%</div> </div>
1	C	738	<div> <div>91%</div> <div>7%</div> </div>
1	D	738	<div> <div>94%</div> <div>6%</div> </div>
1	E	738	<div> <div>90%</div> <div>9%</div> </div>

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Length	Quality of chain
1	F	738	
1	G	738	
1	H	738	

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	CA	H	800	-	-	-	X
3	MVL	H	801	-	-	-	X
4	GOL	A	802	-	-	-	X
4	GOL	A	804	-	-	-	X
4	GOL	B	803	-	-	-	X
4	GOL	B	804	-	-	-	X
4	GOL	B	805	-	-	X	X
4	GOL	C	802	-	-	-	X
4	GOL	C	804	-	-	-	X
4	GOL	D	802	-	-	-	X
4	GOL	D	803	-	-	-	X
4	GOL	D	804	-	-	-	X
4	GOL	E	802	-	-	-	X
4	GOL	E	804	-	-	-	X
4	GOL	F	802	-	-	-	X

## 2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 49858 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 PUTATIVE ALPHA-1,2-MANNOSIDASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	736	Total	C	N	O	S	0	4	0
			5982	3837	985	1126	34			
1	B	736	Total	C	N	O	S	0	2	0
			5980	3835	984	1127	34			
1	C	736	Total	C	N	O	S	0	0	0
			5965	3824	983	1125	33			
1	D	738	Total	C	N	O	S	0	5	0
			6015	3862	987	1133	33			
1	E	736	Total	C	N	O	S	0	0	0
			5950	3816	982	1119	33			
1	F	735	Total	C	N	O	S	0	2	0
			5955	3820	981	1120	34			
1	G	736	Total	C	N	O	S	0	0	0
			5943	3810	977	1123	33			
1	H	736	Total	C	N	O	S	0	1	0
			5966	3825	982	1125	34			

- Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca).

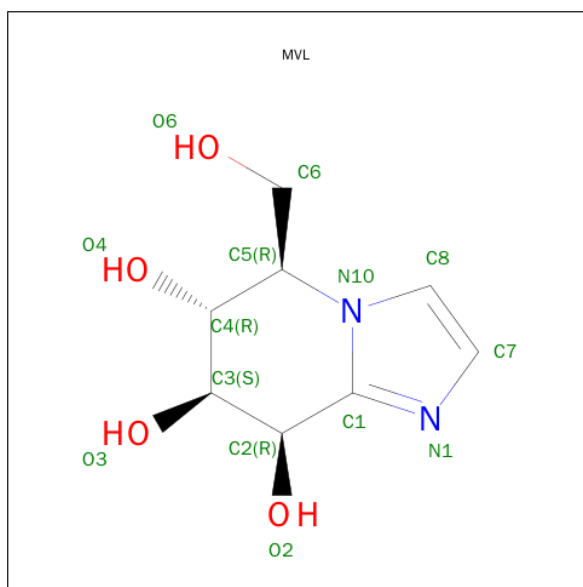
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	G	1	Total	Ca	0	0
			1	1		
2	D	1	Total	Ca	0	0
			1	1		
2	E	1	Total	Ca	0	0
			1	1		
2	H	1	Total	Ca	0	0
			1	1		
2	B	1	Total	Ca	0	0
			1	1		
2	C	1	Total	Ca	0	0
			1	1		

*Continued on next page...*

Continued from previous page...

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Ca	0	0
			1	1		
2	F	1	Total	Ca	0	0
			1	1		

- Molecule 3 is (5R,6R,7S,8R)-6,7,8-TRIHIDROXY-5-(HYDROXYMETHYL)-5,6,7,8-TE TRAHYDRO-1H-IMIDAZO[1,2-A]PYRIDIN-4-IUM (three-letter code: MVL) (formula: C<sub>8</sub>H<sub>12</sub>N<sub>2</sub>O<sub>4</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			14	8	2	4		
3	B	1	Total	C	N	O	0	0
			14	8	2	4		
3	C	1	Total	C	N	O	0	0
			14	8	2	4		
3	D	1	Total	C	N	O	0	0
			14	8	2	4		
3	E	1	Total	C	N	O	0	0
			14	8	2	4		
3	F	1	Total	C	N	O	0	0
			14	8	2	4		
3	G	1	Total	C	N	O	0	0
			14	8	2	4		
3	H	1	Total	C	N	O	0	0
			14	8	2	4		

- Molecule 4 is GLYCEROL (three-letter code: GOL) (formula:  $C_3H_8O_3$ ).



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

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	D	1	Total	C	O	0	0
			6	3	3		
4	D	1	Total	C	O	0	0
			6	3	3		
4	E	1	Total	C	O	0	0
			6	3	3		
4	E	1	Total	C	O	0	0
			6	3	3		
4	E	1	Total	C	O	0	0
			6	3	3		
4	F	1	Total	C	O	0	0
			6	3	3		

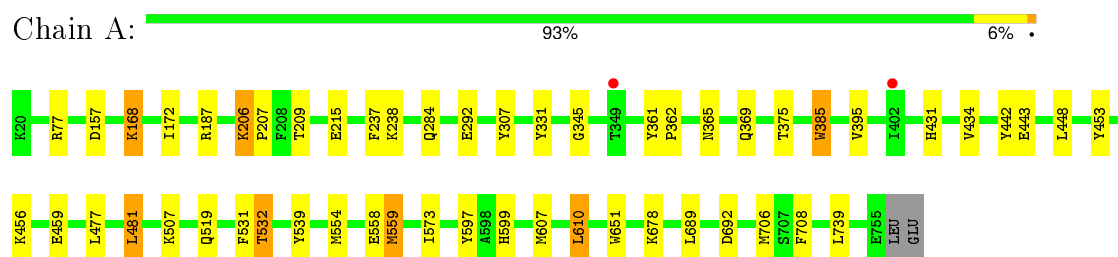
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	349	Total	O	0	0
			349	349		
5	B	320	Total	O	0	0
			320	320		
5	C	279	Total	O	0	0
			279	279		
5	D	323	Total	O	0	0
			323	323		
5	E	261	Total	O	0	0
			261	261		
5	F	179	Total	O	0	0
			179	179		
5	G	87	Total	O	0	0
			87	87		
5	H	70	Total	O	0	0
			70	70		

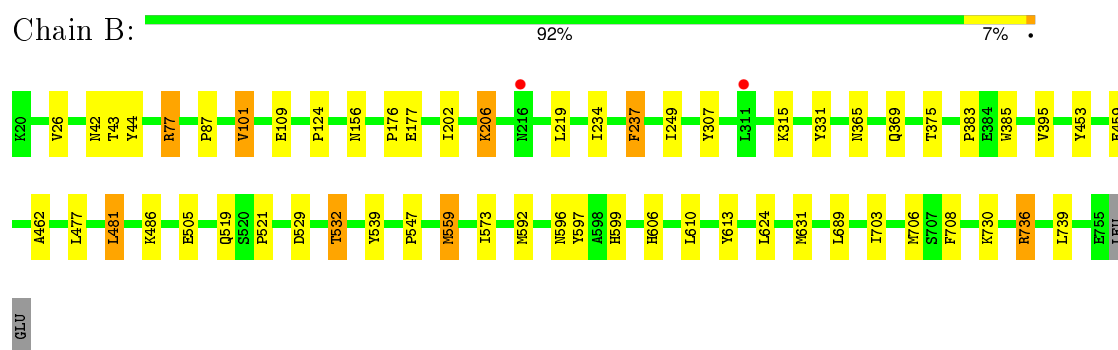
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

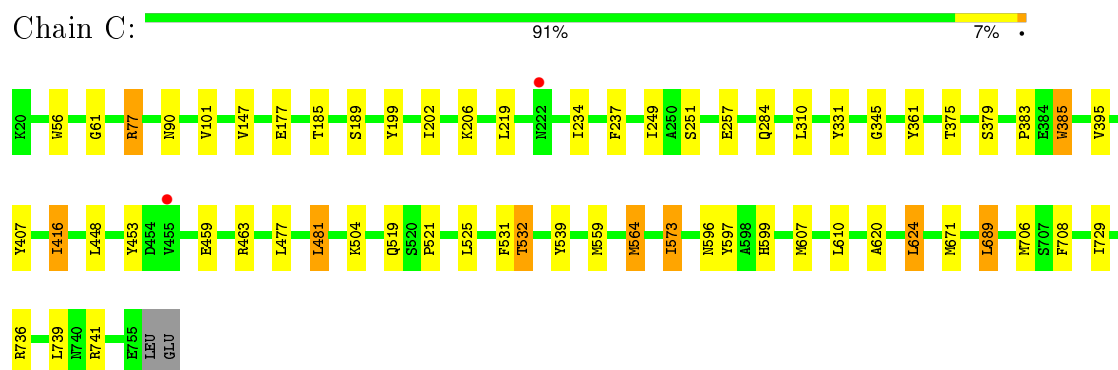
- Molecule 1: PUTATIVE ALPHA-1,2-MANNOSIDASE



- Molecule 1: PUTATIVE ALPHA-1,2-MANNOSIDASE

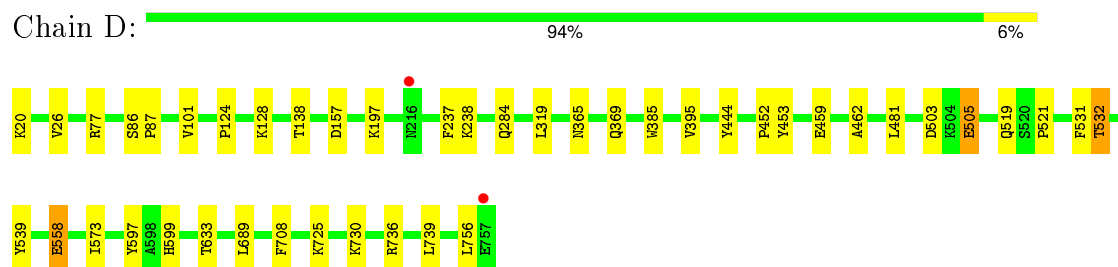


- Molecule 1: PUTATIVE ALPHA-1,2-MANNOSIDASE

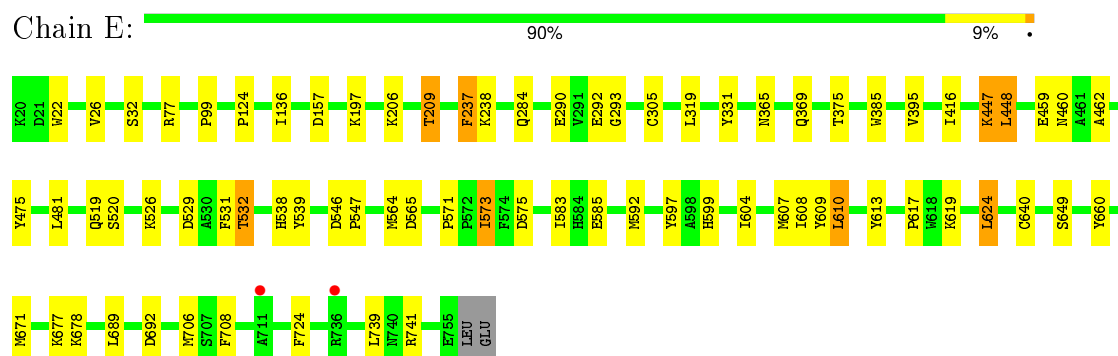


- Molecule 1: PUTATIVE ALPHA-1,2-MANNOSIDASE

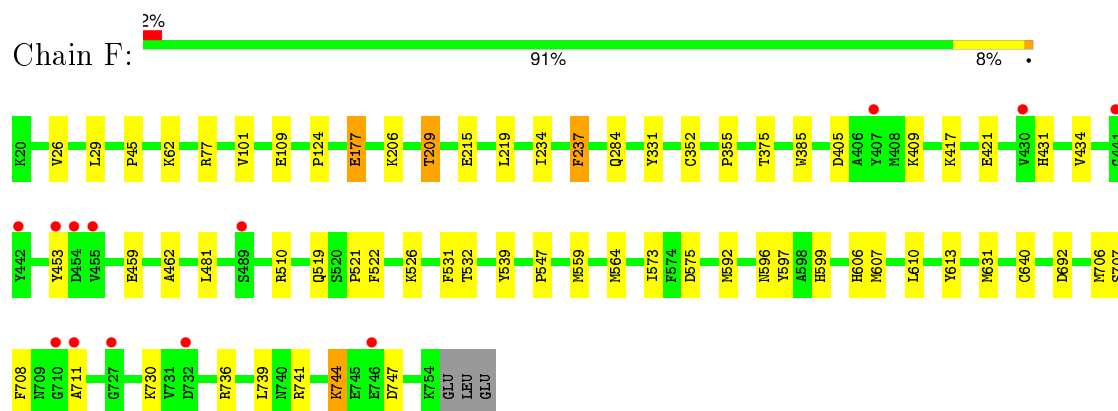




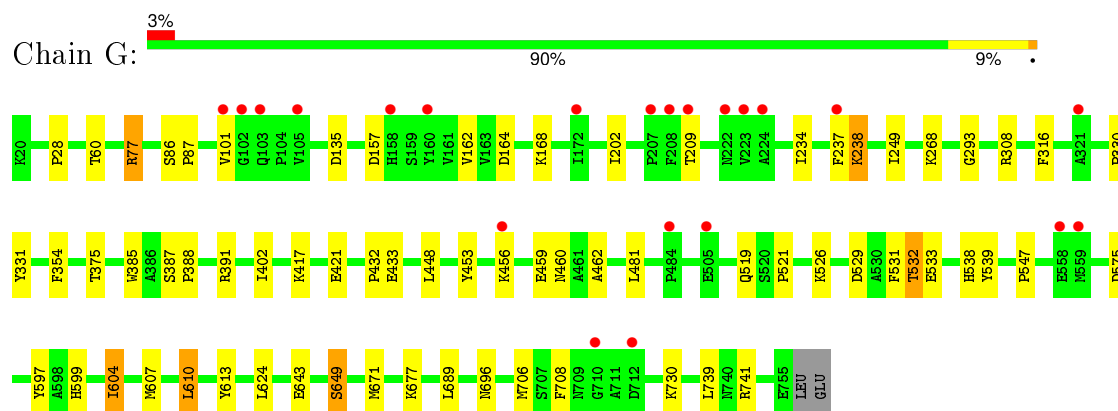
- Molecule 1: PUTATIVE ALPHA-1,2-MANNOSIDASE



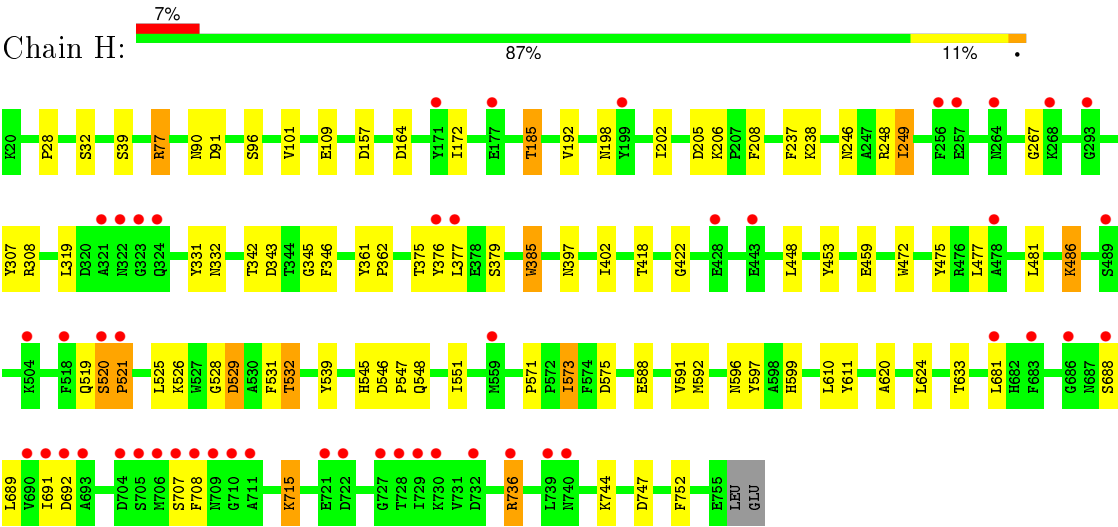
- Molecule 1: PUTATIVE ALPHA-1,2-MANNOSIDASE



- Molecule 1: PUTATIVE ALPHA-1,2-MANNOSIDASE



- Molecule 1: PUTATIVE ALPHA-1,2-MANNOSIDASE



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	109.19Å 152.39Å 221.45Å 90.00° 94.21° 90.00°	Depositor
Resolution (Å)	218.22 – 2.25 45.40 – 2.25	Depositor EDS
% Data completeness (in resolution range)	100.0 (218.22-2.25) 100.0 (45.40-2.25)	Depositor EDS
$R_{merge}$	0.17	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.99 (at 2.24Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, $R_{free}$	0.200 , 0.242 0.201 , 0.241	Depositor DCC
$R_{free}$ test set	17260 reflections (5.32%)	DCC
Wilson B-factor (Å <sup>2</sup> )	26.2	Xtriage
Anisotropy	0.328	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 36.1	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.30$	Xtriage
Outliers	0 of 341577 reflections	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	49858	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	23.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 10.58% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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: GOL, CA, MVL

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	0.49	0/6175	0.58	0/8376
1	B	0.47	0/6167	0.57	0/8364
1	C	0.46	0/6146	0.57	0/8338
1	D	0.47	0/6213	0.57	0/8429
1	E	0.50	0/6131	0.58	0/8320
1	F	0.52	0/6142	0.58	0/8334
1	G	0.54	0/6124	0.57	1/8314 (0.0%)
1	H	0.56	0/6150	0.57	1/8344 (0.0%)
All	All	0.50	0/49248	0.57	2/66819 (0.0%)

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	H	0	1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	164	ASP	CB-CG-OD1	5.45	123.21	118.30
1	H	689	LEU	CA-CB-CG	5.27	127.42	115.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	H	520	SER	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	5982	0	5660	27	0
1	B	5980	0	5658	39	0
1	C	5965	0	5632	32	0
1	D	6015	0	5693	21	0
1	E	5950	0	5611	42	0
1	F	5955	0	5622	36	0
1	G	5943	0	5584	34	0
1	H	5966	0	5630	51	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
2	E	1	0	0	0	0
2	F	1	0	0	0	0
2	G	1	0	0	0	0
2	H	1	0	0	0	0
3	A	14	0	10	1	0
3	B	14	0	10	0	0
3	C	14	0	10	0	0
3	D	14	0	10	1	0
3	E	14	0	10	0	0
3	F	14	0	10	1	0
3	G	14	0	10	1	0
3	H	14	0	10	0	0
4	A	18	0	24	0	0
4	B	24	0	32	10	0
4	C	24	0	32	0	0
4	D	24	0	32	1	0
4	E	18	0	24	2	0
4	F	6	0	8	0	0
5	A	349	0	0	1	0
5	B	320	0	0	4	0
5	C	279	0	0	1	0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	D	323	0	0	5	0
5	E	261	0	0	6	0
5	F	179	0	0	4	0
5	G	87	0	0	0	0
5	H	70	0	0	3	0
All	All	49858	0	45322	284	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 3.

The worst 5 of 284 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:F:592[B]:MET:CE	1:F:592[B]:MET:HA	1.59	1.32
1:H:592[B]:MET:CE	1:H:592[B]:MET:HA	1.75	1.16
1:H:592[B]:MET:HE3	1:H:592[B]:MET:HA	1.35	1.06
1:F:592[B]:MET:HE3	1:F:592[B]:MET:HA	0.99	0.98
1:F:592[B]:MET:HE3	1:F:592[B]:MET:CA	1.96	0.93

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	738/738 (100%)	712 (96%)	26 (4%)	0	100	100
1	B	736/738 (100%)	708 (96%)	28 (4%)	0	100	100
1	C	734/738 (100%)	713 (97%)	21 (3%)	0	100	100
1	D	741/738 (100%)	715 (96%)	26 (4%)	0	100	100
1	E	734/738 (100%)	710 (97%)	23 (3%)	1 (0%)	56	66

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	F	735/738 (100%)	708 (96%)	27 (4%)	0	100	100
1	G	734/738 (100%)	699 (95%)	34 (5%)	1 (0%)	56	66
1	H	735/738 (100%)	699 (95%)	34 (5%)	2 (0%)	46	52
All	All	5887/5904 (100%)	5664 (96%)	219 (4%)	4 (0%)	56	66

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	H	521	PRO
1	G	529	ASP
1	H	529	ASP
1	E	529	ASP

### 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	637/637 (100%)	615 (96%)	22 (4%)	43	53
1	B	637/637 (100%)	615 (96%)	22 (4%)	43	53
1	C	634/637 (100%)	610 (96%)	24 (4%)	40	49
1	D	641/637 (101%)	620 (97%)	21 (3%)	45	56
1	E	630/637 (99%)	608 (96%)	22 (4%)	43	53
1	F	632/637 (99%)	612 (97%)	20 (3%)	46	57
1	G	629/637 (99%)	607 (96%)	22 (4%)	43	53
1	H	634/637 (100%)	605 (95%)	29 (5%)	33	37
All	All	5074/5096 (100%)	4892 (96%)	182 (4%)	43	51

5 of 182 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	689	LEU
1	E	520	SER

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	H	532	THR
1	D	730[A]	LYS
1	E	237	PHE

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

Mol	Chain	Res	Type
1	E	713	HIS
1	F	74	ASN
1	G	548	GLN
1	G	740	ASN
1	H	398	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 35 ligands modelled in this entry, 8 are monoatomic - leaving 27 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	MVL	A	801	2	11,15,15	0.77	0	12,22,22	1.74	2 (16%)



Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
4	GOL	A	802	-	5,5,5	0.46	0	5,5,5	0.33	0
4	GOL	A	803	-	5,5,5	0.31	0	5,5,5	0.19	0
4	GOL	A	804	-	5,5,5	0.34	0	5,5,5	0.28	0
3	MVL	B	801	2	11,15,15	0.64	0	12,22,22	1.57	1 (8%)
4	GOL	B	802	-	5,5,5	0.36	0	5,5,5	0.24	0
4	GOL	B	803	-	5,5,5	0.39	0	5,5,5	0.51	0
4	GOL	B	804	-	5,5,5	0.44	0	5,5,5	0.48	0
4	GOL	B	805	-	5,5,5	0.50	0	5,5,5	0.99	0
3	MVL	C	801	2	11,15,15	0.77	0	12,22,22	2.07	3 (25%)
4	GOL	C	802	-	5,5,5	0.25	0	5,5,5	0.34	0
4	GOL	C	803	-	5,5,5	0.40	0	5,5,5	0.53	0
4	GOL	C	804	-	5,5,5	0.38	0	5,5,5	0.26	0
4	GOL	C	805	-	5,5,5	0.39	0	5,5,5	0.21	0
3	MVL	D	801	2	11,15,15	0.81	0	12,22,22	1.75	2 (16%)
4	GOL	D	802	-	5,5,5	0.33	0	5,5,5	0.71	0
4	GOL	D	803	-	5,5,5	0.33	0	5,5,5	0.32	0
4	GOL	D	804	-	5,5,5	0.34	0	5,5,5	0.23	0
4	GOL	D	805	-	5,5,5	0.26	0	5,5,5	0.43	0
3	MVL	E	801	2	11,15,15	0.66	0	12,22,22	1.75	2 (16%)
4	GOL	E	802	-	5,5,5	0.32	0	5,5,5	0.18	0
4	GOL	E	803	-	5,5,5	0.32	0	5,5,5	0.43	0
4	GOL	E	804	-	5,5,5	0.30	0	5,5,5	0.27	0
3	MVL	F	801	2	11,15,15	0.69	0	12,22,22	1.93	2 (16%)
4	GOL	F	802	-	5,5,5	0.37	0	5,5,5	0.25	0
3	MVL	G	801	2	11,15,15	0.75	0	12,22,22	1.89	3 (25%)
3	MVL	H	801	2	11,15,15	0.72	0	12,22,22	1.79	2 (16%)

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	MVL	A	801	2	-	0/2/22/22	0/1/2/2
4	GOL	A	802	-	-	0/4/4/4	0/0/0/0
4	GOL	A	803	-	-	0/4/4/4	0/0/0/0
4	GOL	A	804	-	-	0/4/4/4	0/0/0/0
3	MVL	B	801	2	-	0/2/22/22	0/1/2/2
4	GOL	B	802	-	-	0/4/4/4	0/0/0/0
4	GOL	B	803	-	-	0/4/4/4	0/0/0/0
4	GOL	B	804	-	-	0/4/4/4	0/0/0/0

*Continued on next page...*

*Continued from previous page...*

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	GOL	B	805	-	-	0/4/4/4	0/0/0/0
3	MVL	C	801	2	-	0/2/22/22	0/1/2/2
4	GOL	C	802	-	-	0/4/4/4	0/0/0/0
4	GOL	C	803	-	-	0/4/4/4	0/0/0/0
4	GOL	C	804	-	-	0/4/4/4	0/0/0/0
4	GOL	C	805	-	-	0/4/4/4	0/0/0/0
3	MVL	D	801	2	-	0/2/22/22	0/1/2/2
4	GOL	D	802	-	-	0/4/4/4	0/0/0/0
4	GOL	D	803	-	-	0/4/4/4	0/0/0/0
4	GOL	D	804	-	-	0/4/4/4	0/0/0/0
4	GOL	D	805	-	-	0/4/4/4	0/0/0/0
3	MVL	E	801	2	-	0/2/22/22	0/1/2/2
4	GOL	E	802	-	-	0/4/4/4	0/0/0/0
4	GOL	E	803	-	-	0/4/4/4	0/0/0/0
4	GOL	E	804	-	-	0/4/4/4	0/0/0/0
3	MVL	F	801	2	-	0/2/22/22	0/1/2/2
4	GOL	F	802	-	-	0/4/4/4	0/0/0/0
3	MVL	G	801	2	-	0/2/22/22	0/1/2/2
3	MVL	H	801	2	-	0/2/22/22	0/1/2/2

There are no bond length outliers.

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	E	801	MVL	O3-C3-C4	-2.21	105.36	110.34
3	H	801	MVL	C3-C4-C5	2.02	114.11	111.39
3	D	801	MVL	C3-C4-C5	2.03	114.12	111.39
3	G	801	MVL	O2-C2-C3	2.08	112.96	108.63
3	A	801	MVL	C3-C4-C5	2.25	114.42	111.39

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

8 monomers are involved in 17 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	801	MVL	1	0
4	B	804	GOL	3	0
4	B	805	GOL	7	0
3	D	801	MVL	1	0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	D	802	GOL	1	0
4	E	804	GOL	2	0
3	F	801	MVL	1	0
3	G	801	MVL	1	0

## 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<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	736/738 (99%)	-0.10	2 (0%) 94 95	14, 22, 33, 41	0
1	B	736/738 (99%)	-0.14	2 (0%) 94 95	13, 21, 32, 39	0
1	C	736/738 (99%)	-0.20	2 (0%) 94 95	13, 22, 33, 41	0
1	D	738/738 (100%)	-0.14	2 (0%) 94 95	13, 21, 32, 50	0
1	E	736/738 (99%)	-0.15	2 (0%) 94 95	15, 23, 34, 43	0
1	F	735/738 (99%)	-0.04	13 (1%) 71 75	15, 24, 35, 41	0
1	G	736/738 (99%)	-0.00	22 (2%) 54 58	17, 24, 35, 49	0
1	H	736/738 (99%)	0.26	49 (6%) 21 23	17, 25, 35, 47	0
All	All	5889/5904 (99%)	-0.06	94 (1%) 74 77	13, 23, 34, 50	0

The worst 5 of 94 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	H	710	GLY	5.5
1	H	321	ALA	4.3
1	H	520	SER	3.8
1	H	739	LEU	3.6
1	H	711	ALA	3.6

### 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> 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	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
4	GOL	E	804	6/6	0.87	0.33	12.00	40,41,42,44	0
4	GOL	D	803	6/6	0.83	0.20	9.09	49,50,51,52	0
4	GOL	D	802	6/6	0.81	0.20	8.54	40,41,41,43	0
4	GOL	F	802	6/6	0.87	0.17	7.48	53,53,54,54	0
4	GOL	C	804	6/6	0.80	0.19	6.00	64,64,64,65	0
4	GOL	D	804	6/6	0.91	0.16	5.12	38,40,40,41	0
3	MVL	H	801	14/14	0.89	0.18	4.97	33,34,34,36	0
4	GOL	B	803	6/6	0.77	0.17	4.75	44,45,45,47	0
4	GOL	A	804	6/6	0.80	0.17	4.35	45,45,46,47	0
4	GOL	A	802	6/6	0.91	0.23	3.70	52,53,53,54	0
4	GOL	B	805	6/6	0.86	0.26	3.11	29,31,32,34	0
4	GOL	B	804	6/6	0.84	0.17	2.93	37,39,39,40	0
2	CA	H	800	1/1	0.98	0.18	2.55	33,33,33,33	0
4	GOL	C	802	6/6	0.90	0.16	2.35	36,37,37,38	0
4	GOL	E	802	6/6	0.89	0.17	2.17	49,50,51,51	0
4	GOL	C	805	6/6	0.89	0.13	1.90	38,39,40,40	0
4	GOL	E	803	6/6	0.83	0.14	1.64	48,48,49,49	0
4	GOL	B	802	6/6	0.90	0.16	1.40	39,40,41,41	0
2	CA	D	800	1/1	1.00	0.18	1.18	17,17,17,17	0
2	CA	G	800	1/1	0.99	0.13	0.66	28,28,28,28	0
3	MVL	G	801	14/14	0.96	0.12	0.65	27,31,32,33	0
2	CA	B	800	1/1	0.99	0.19	0.27	17,17,17,17	0
3	MVL	F	801	14/14	0.95	0.11	-0.24	21,25,29,29	0
3	MVL	C	801	14/14	0.96	0.12	-0.43	17,19,21,22	0
3	MVL	B	801	14/14	0.96	0.17	-0.45	9,14,15,16	0
3	MVL	D	801	14/14	0.97	0.14	-0.46	14,17,18,20	0
2	CA	F	800	1/1	0.98	0.11	-0.61	23,23,23,23	0
2	CA	C	800	1/1	1.00	0.13	-0.75	22,22,22,22	0
3	MVL	A	801	14/14	0.97	0.12	-0.90	12,15,16,17	0
3	MVL	E	801	14/14	0.97	0.12	-0.98	13,15,17,18	0
2	CA	A	800	1/1	0.99	0.13	-1.03	20,20,20,20	0
2	CA	E	800	1/1	0.99	0.10	-1.68	18,18,18,18	0
4	GOL	D	805	6/6	0.95	0.08	-3.48	32,33,34,34	0
4	GOL	C	803	6/6	0.72	0.20	-	51,51,51,52	0

*Continued on next page...*

*Continued from previous page...*

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
4	GOL	A	803	6/6	0.72	0.19	-	56,57,57,57	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.