



# Full wwPDB X-ray Structure Validation Report ⓘ

Nov 2, 2017 – 04:06 PM EDT

PDB ID : 5N4C  
Title : Prolyl oligopeptidase B from *Galerina marginata* bound to 35mer hydrolysis and macrocyclization substrate - S577A mutant  
Authors : Czekster, C.M.; McMahon, S.A.; Ludewig, H.; Naismith, J.H.  
Deposited on : unknown  
Resolution : 2.19 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](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.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.7.2 (RC1), CSD as538be (2017)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20030345  
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)  
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) : rb-20030345

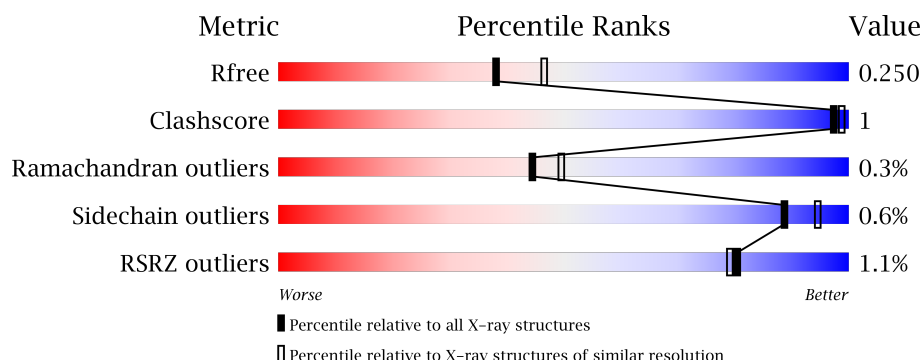
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.19 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))
$R_{free}$	100719	4002 (2.20-2.20)
Clashscore	112137	4730 (2.20-2.20)
Ramachandran outliers	110173	4656 (2.20-2.20)
Sidechain outliers	110143	4657 (2.20-2.20)
RSRZ outliers	101464	4033 (2.20-2.20)

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	730	<div> <div></div> <div>96%</div> <div>..</div> </div>
1	B	730	<div> <div></div> <div>96%</div> <div>..</div> </div>
1	C	730	<div> <div></div> <div>96%</div> <div>..</div> </div>
1	D	730	<div> <div></div> <div>95%</div> <div>..</div> </div>
2	E	35	<div> <div>6%</div> <div>77%</div> <div>9% 6% 9%</div> </div>

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Mol	Chain	Length	Quality of chain
2	F	35	<div><div></div><div>14%</div><div>77%</div><div>11%</div><div>•</div><div>9%</div></div>
2	G	35	<div><div></div><div>9%</div><div>86%</div><div>9%</div><div>6%</div></div>
2	H	35	<div><div></div><div>17%</div><div>86%</div><div>•</div><div>6%</div><div>6%</div></div>

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 25102 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 Prolyl oligopeptidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	722	Total	C	N	O	S	0	2	0
			5744	3679	968	1086	11			
1	B	721	Total	C	N	O	S	0	1	0
			5731	3669	966	1085	11			
1	C	721	Total	C	N	O	S	0	0	0
			5724	3665	964	1084	11			
1	D	720	Total	C	N	O	S	0	1	0
			5714	3656	961	1086	11			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	577	ALA	SER	engineered mutation	UNP H2E7Q8
B	577	ALA	SER	engineered mutation	UNP H2E7Q8
C	577	ALA	SER	engineered mutation	UNP H2E7Q8
D	577	ALA	SER	engineered mutation	UNP H2E7Q8

- Molecule 2 is a protein called Alpha-amanitin proprotein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	E	32	Total	C	N	O	S	0	0	0
			242	147	43	50	2			
2	F	32	Total	C	N	O	S	0	0	0
			245	151	43	50	1			
2	G	33	Total	C	N	O	S	0	0	0
			250	153	44	51	2			
2	H	33	Total	C	N	O	S	0	0	0
			250	153	44	51	2			

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: C<sub>3</sub>H<sub>8</sub>O<sub>3</sub>).



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

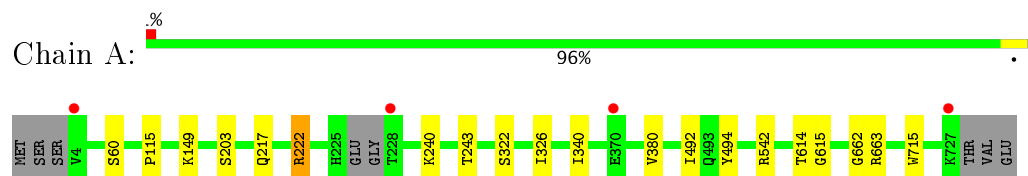
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	290	Total	O	0	0
			290	290		
4	E	11	Total	O	0	0
			11	11		
4	B	296	Total	O	0	0
			296	296		
4	C	289	Total	O	0	0
			289	289		
4	D	282	Total	O	0	0
			282	282		
4	F	7	Total	O	0	0
			7	7		
4	G	10	Total	O	0	0
			10	10		
4	H	11	Total	O	0	0
			11	11		

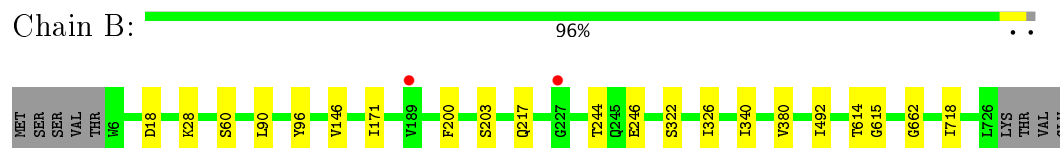
### 3 Residue-property plots [i](#)

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

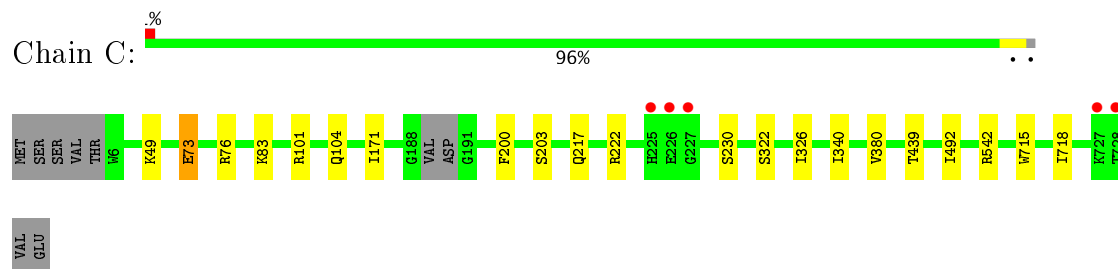
- Molecule 1: Prolyl oligopeptidase



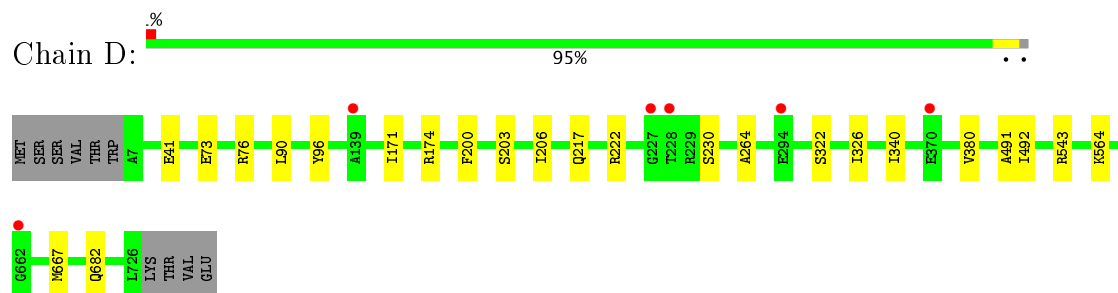
- Molecule 1: Prolyl oligopeptidase



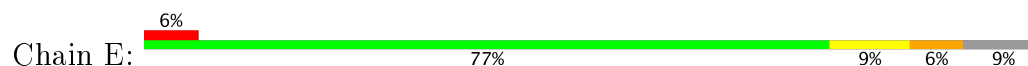
- Molecule 1: Prolyl oligopeptidase

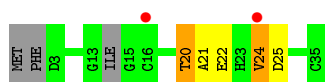


- Molecule 1: Prolyl oligopeptidase

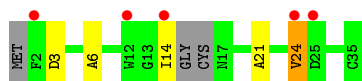
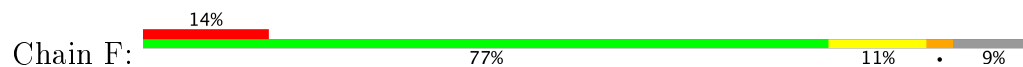


- Molecule 2: Alpha-amanitin proprotein

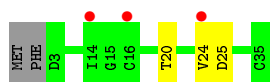
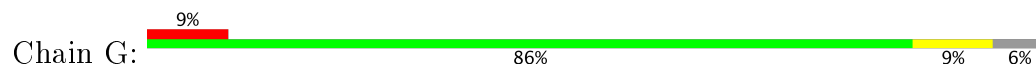




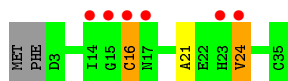
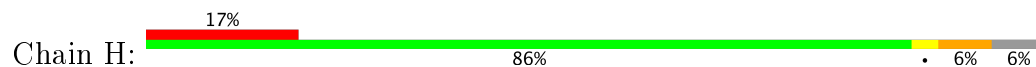
- Molecule 2: Alpha-amanitin proprotein



- Molecule 2: Alpha-amanitin proprotein



- Molecule 2: Alpha-amanitin proprotein



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	100.80Å 142.56Å 116.36Å 90.00° 90.29° 90.00°	Depositor
Resolution (Å)	90.14 – 2.19 90.14 – 2.19	Depositor EDS
% Data completeness (in resolution range)	96.8 (90.14-2.19) 96.8 (90.14-2.19)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.35 (at 2.18Å)	Xtriage
Refinement program	REFMAC 5.8.0155	Depositor
R, $R_{free}$	0.214 , 0.249 0.217 , 0.250	Depositor DCC
$R_{free}$ test set	7961 reflections (5.13%)	DCC
Wilson B-factor (Å <sup>2</sup> )	26.9	Xtriage
Anisotropy	0.731	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 16.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.52$ , $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	0.094 for h,-k,-l	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	25102	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 38.70 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 3.5427e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<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, 0.333 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: GOL

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z  > 5$	RMSZ	$\# Z  > 5$
1	A	0.59	0/5908	0.72	3/8022 (0.0%)
1	B	0.59	0/5893	0.72	0/8003
1	C	0.58	1/5882 (0.0%)	0.71	1/7986 (0.0%)
1	D	0.59	0/5874	0.72	1/7977 (0.0%)
2	E	0.71	0/247	0.82	0/337
2	F	0.69	0/250	0.75	0/342
2	G	0.70	0/256	0.83	0/351
2	H	0.72	0/256	0.74	0/351
All	All	0.59	1/24566 (0.0%)	0.72	5/33369 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	73	GLU	CD-OE2	5.23	1.31	1.25

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	149	LYS	CA-CB-CG	-5.41	101.49	113.40
1	D	174	ARG	NE-CZ-NH1	5.34	122.97	120.30
1	A	222	ARG	NE-CZ-NH2	-5.33	117.63	120.30
1	A	542	ARG	NE-CZ-NH1	5.20	122.90	120.30
1	C	542	ARG	NE-CZ-NH1	5.03	122.81	120.30

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	5744	0	5554	7	1
1	B	5731	0	5530	11	1
1	C	5724	0	5523	10	0
1	D	5714	0	5511	13	2
2	E	242	0	216	4	0
2	F	245	0	221	5	0
2	G	250	0	228	1	0
2	H	250	0	228	1	0
3	D	6	0	8	0	0
4	A	290	0	0	0	0
4	B	296	0	0	0	0
4	C	289	0	0	0	0
4	D	282	0	0	1	0
4	E	11	0	0	0	0
4	F	7	0	0	0	0
4	G	10	0	0	0	0
4	H	11	0	0	0	0
All	All	25102	0	23019	47	2

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 1.

All (47) 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:244:THR:OG1	1:B:246:GLU:OE1	1.72	1.08
1:A:240:LYS:O	1:A:243:THR:HG22	1.83	0.79
1:B:146:VAL:HG13	2:F:14:ILE:CD1	2.17	0.74
1:C:73:GLU:OE1	1:C:76:ARG:NH1	2.29	0.65
1:C:101:ARG:H	1:C:104:GLN:HE21	1.43	0.65
1:D:73:GLU:OE1	1:D:76:ARG:NH1	2.30	0.65
1:B:146:VAL:CG1	2:F:14:ILE:CD1	2.77	0.62
2:F:3:ASP:HB3	2:F:6:ALA:HB3	1.81	0.62
1:D:492:ILE:N	1:D:492:ILE:HD12	2.15	0.61
1:D:222:ARG:NH1	1:D:230:SER:O	2.34	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:20:THR:HG23	2:E:22:GLU:H	1.69	0.57
1:B:146:VAL:CG1	2:F:14:ILE:HD13	2.36	0.56
1:C:222:ARG:NH1	1:C:230:SER:O	2.39	0.55
1:A:494:TYR:HE2	2:E:20:THR:HG21	1.72	0.54
1:C:326:ILE:HD12	1:C:340:ILE:HD12	1.92	0.52
1:C:203:SER:HB2	1:C:217:GLN:HB3	1.92	0.50
1:B:614:THR:HG21	1:B:662:GLY:O	2.12	0.50
1:A:203:SER:HB2	1:A:217:GLN:HB3	1.92	0.50
1:B:326:ILE:HD12	1:B:340:ILE:HD12	1.93	0.50
1:B:203:SER:HB2	1:B:217:GLN:HB3	1.92	0.50
1:D:203:SER:HB2	1:D:217:GLN:HB3	1.93	0.50
1:D:326:ILE:HD12	1:D:340:ILE:HD12	1.94	0.49
1:B:171:ILE:HD11	1:B:200:PHE:CD1	2.48	0.48
1:A:614:THR:HG21	1:A:662:GLY:O	2.13	0.48
1:D:171:ILE:HD11	1:D:200:PHE:CD1	2.49	0.48
1:A:326:ILE:HD12	1:A:340:ILE:HD12	1.96	0.48
1:D:491:ALA:C	1:D:492:ILE:HD12	2.35	0.46
1:C:73:GLU:CD	1:C:76:ARG:HH12	2.20	0.45
1:D:543:ARG:NH1	4:D:908:HOH:O	2.49	0.45
2:E:21:ALA:O	2:E:24:VAL:HG13	2.16	0.45
2:H:21:ALA:O	2:H:24:VAL:HG13	2.17	0.45
1:A:614:THR:HG23	1:A:615:GLY:H	1.82	0.45
2:F:21:ALA:O	2:F:24:VAL:HG13	2.17	0.45
2:E:20:THR:CG2	2:E:22:GLU:H	2.30	0.45
1:D:492:ILE:CD1	1:D:492:ILE:N	2.79	0.44
1:D:73:GLU:CD	1:D:76:ARG:HH12	2.20	0.44
1:B:492:ILE:CD1	1:B:718:ILE:HG21	2.48	0.44
1:D:41:GLU:HG2	1:D:667:MET:HG3	2.01	0.42
1:C:83:LYS:HD3	2:G:25:ASP:CG	2.40	0.42
1:C:492:ILE:HG13	1:C:715:TRP:HZ3	1.86	0.41
1:D:90:LEU:HD12	1:D:96:TYR:CE1	2.56	0.41
1:D:206:ILE:HD13	1:D:264:ALA:HB3	2.03	0.41
1:A:492:ILE:HG13	1:A:715:TRP:HZ3	1.86	0.41
1:B:614:THR:HG23	1:B:615:GLY:H	1.85	0.41
1:B:90:LEU:HD12	1:B:96:TYR:CE1	2.57	0.40
1:C:171:ILE:HD11	1:C:200:PHE:CD2	2.57	0.40
1:C:492:ILE:CD1	1:C:718:ILE:HG21	2.51	0.40

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:115:PRO:O	1:D:682:GLN:NE2[2_556]	1.80	0.40
1:B:18:ASP:O	1:D:564:LYS:NZ[2_556]	2.04	0.16

## 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	720/730 (99%)	698 (97%)	21 (3%)	1 (0%)	55	63
1	B	720/730 (99%)	699 (97%)	20 (3%)	1 (0%)	55	63
1	C	717/730 (98%)	699 (98%)	17 (2%)	1 (0%)	55	63
1	D	719/730 (98%)	698 (97%)	20 (3%)	1 (0%)	55	63
2	E	28/35 (80%)	24 (86%)	3 (11%)	1 (4%)	4	1
2	F	28/35 (80%)	24 (86%)	3 (11%)	1 (4%)	4	1
2	G	31/35 (89%)	26 (84%)	4 (13%)	1 (3%)	5	2
2	H	31/35 (89%)	26 (84%)	3 (10%)	2 (6%)	1	0
All	All	2994/3060 (98%)	2894 (97%)	91 (3%)	9 (0%)	44	49

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	G	24	VAL
2	E	24	VAL
2	F	24	VAL
2	H	24	VAL
2	H	16	CYS
1	B	380	VAL
1	C	380	VAL
1	D	380	VAL
1	A	380	VAL

### 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	607/612 (99%)	603 (99%)	4 (1%)	87	93
1	B	604/612 (99%)	601 (100%)	3 (0%)	91	96
1	C	603/612 (98%)	600 (100%)	3 (0%)	91	96
1	D	603/612 (98%)	602 (100%)	1 (0%)	94	98
2	E	26/29 (90%)	24 (92%)	2 (8%)	15	15
2	F	26/29 (90%)	26 (100%)	0	100	100
2	G	27/29 (93%)	26 (96%)	1 (4%)	39	49
2	H	27/29 (93%)	26 (96%)	1 (4%)	39	49
All	All	2523/2564 (98%)	2508 (99%)	15 (1%)	89	94

All (15) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	60	SER
1	A	222	ARG
1	A	322	SER
1	A	663	ARG
2	E	20	THR
2	E	25	ASP
1	B	28	LYS
1	B	60	SER
1	B	322	SER
1	C	49	LYS
1	C	322	SER
1	C	439	THR
1	D	322	SER
2	G	20	THR
2	H	16	CYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
2	E	26	GLN
1	C	104	GLN
1	D	574	ASN

### 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 carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

1 ligand is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
3	GOL	D	801	-	5,5,5	0.22	0	5,5,5	0.34	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	GOL	D	801	-	-	0/4/4/4	0/0/0/0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 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	722/730 (98%)	-0.45	4 (0%) 89 88	19, 29, 48, 84	0
1	B	721/730 (98%)	-0.43	2 (0%) 93 93	17, 29, 51, 95	0
1	C	721/730 (98%)	-0.44	5 (0%) 87 86	17, 29, 51, 104	0
1	D	720/730 (98%)	-0.40	6 (0%) 86 85	19, 28, 52, 91	0
2	E	32/35 (91%)	0.37	2 (6%) 21 19	24, 46, 70, 82	0
2	F	32/35 (91%)	0.51	5 (15%) 2 2	25, 47, 62, 67	0
2	G	33/35 (94%)	0.37	3 (9%) 10 9	25, 45, 77, 79	0
2	H	33/35 (94%)	0.42	6 (18%) 1 1	25, 44, 79, 84	0
All	All	3014/3060 (98%)	-0.40	33 (1%) 80 79	17, 29, 54, 104	0

All (33) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	H	14	ILE	6.2
1	B	227	GLY	5.8
2	F	14	ILE	5.1
1	C	728	THR	5.1
1	A	4	VAL	4.9
2	G	14	ILE	4.3
1	D	227	GLY	3.9
1	C	227	GLY	3.7
2	H	16	CYS	3.3
1	D	228	THR	3.3
2	F	2	PHE	3.2
1	D	139	ALA	3.0
2	G	16	CYS	2.9
1	C	727	LYS	2.9
1	D	662	GLY	2.9
1	A	228	THR	2.7

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Mol	Chain	Res	Type	RSRZ
2	F	24	VAL	2.7
1	A	370	GLU	2.7
1	C	226	GLU	2.7
2	H	15	GLY	2.6
2	E	16	CYS	2.6
2	G	24	VAL	2.6
2	F	25	ASP	2.6
1	C	225	HIS	2.5
2	H	17	ASN	2.5
2	H	23	HIS	2.4
2	F	12	TRP	2.4
2	E	24	VAL	2.3
1	B	189	VAL	2.3
1	D	370	GLU	2.3
1	D	294	GLU	2.1
2	H	24	VAL	2.0
1	A	727	LYS	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. 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
3	GOL	D	801	6/6	0.95	0.11	0.33	39,42,45,47	0

## 6.5 Other polymers

There are no such residues in this entry.