



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 11:33 AM GMT

PDB ID : 3P24  
Title : Structure of profragilysin-3 from Bacteroides fragilis  
Authors : Goulas, T.; Arolas, J.L.; Gomis-Ruth, F.X.  
Deposited on : 2010-10-01  
Resolution : 1.80 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 (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

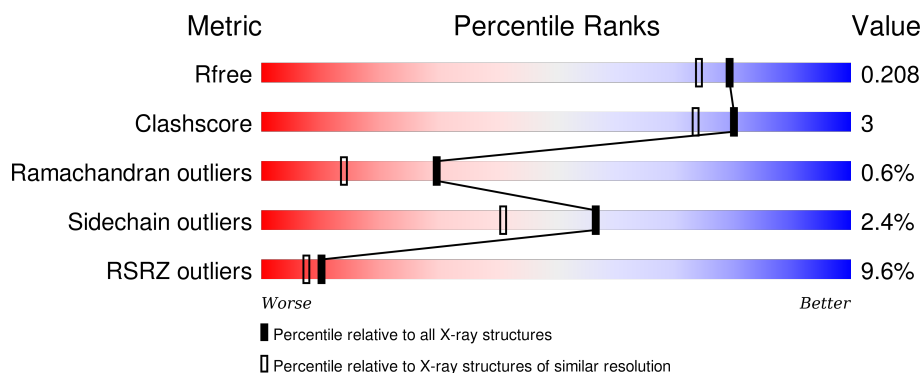
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.80 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	4533 (1.80-1.80)
Clashscore	102246	5383 (1.80-1.80)
Ramachandran outliers	100387	5320 (1.80-1.80)
Sidechain outliers	100360	5319 (1.80-1.80)
RSRZ outliers	91569	4547 (1.80-1.80)

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  $\geq 3$ , 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	397	<div> <div>7%</div> <div>82% 7% • 10%</div> </div>
1	B	397	<div> <div>9%</div> <div>81% 8% • 11%</div> </div>
1	C	397	<div> <div>8%</div> <div>82% 7% • 11%</div> </div>
1	D	397	<div> <div>10%</div> <div>80% 9% • 10%</div> </div>

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	PG4	D	501	-	-	-	X
3	GOL	A	503	-	-	-	X
3	GOL	A	505	-	-	-	X
3	GOL	B	506	-	-	-	X
4	AZI	A	511	-	-	-	X

## 2 Entry composition [i](#)

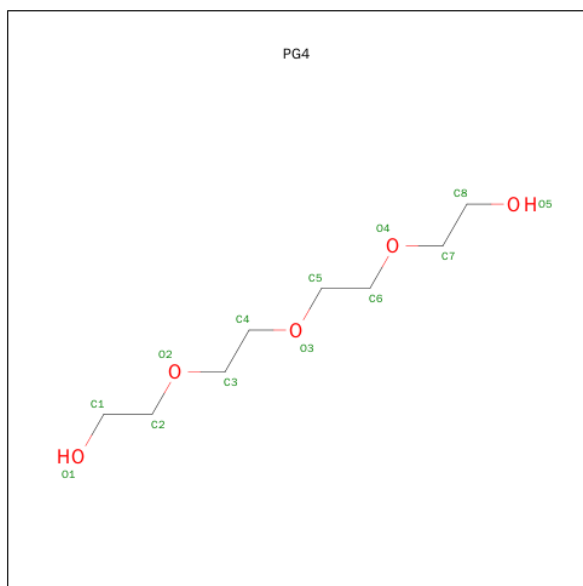
There are 6 unique types of molecules in this entry. The entry contains 12617 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 BFT-3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	357	Total	C	N	O	S	0	3	0
			2852	1809	475	554	14			
1	B	355	Total	C	N	O	S	0	3	0
			2836	1797	474	551	14			
1	C	354	Total	C	N	O	S	0	7	0
			2847	1809	472	552	14			
1	D	357	Total	C	N	O	S	0	6	0
			2860	1814	475	556	15			

- Molecule 2 is TETRAETHYLENE GLYCOL (three-letter code: PG4) (formula: C<sub>8</sub>H<sub>18</sub>O<sub>5</sub>).



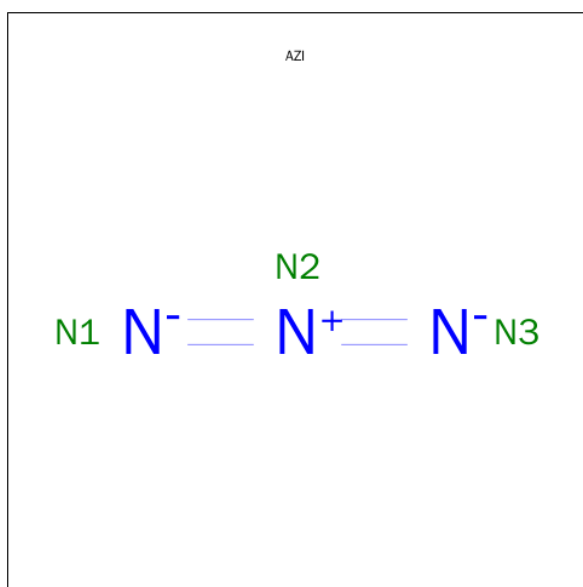
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			13	8	5		
2	D	1	Total	C	O	0	0
			13	8	5		

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula:  $C_3H_8O_3$ ).



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

- Molecule 4 is AZIDE ION (three-letter code: AZI) (formula:  $N_3$ ).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total N 3 3	0	0
4	A	1	Total N 3 3	0	0
4	B	1	Total N 3 3	0	0

- Molecule 5 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	B	1	Total Zn 1 1	0	0
5	A	1	Total Zn 1 1	0	0
5	D	1	Total Zn 1 1	0	0
5	C	1	Total Zn 1 1	0	0

- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	341	Total O 341 341	0	0
6	B	221	Total O 221 221	0	0

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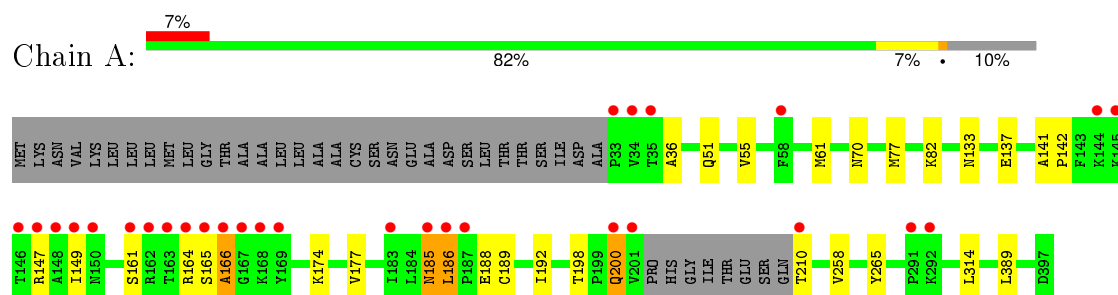
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	C	290	Total 290	O 290	0	0
6	D	295	Total 295	O 295	0	0

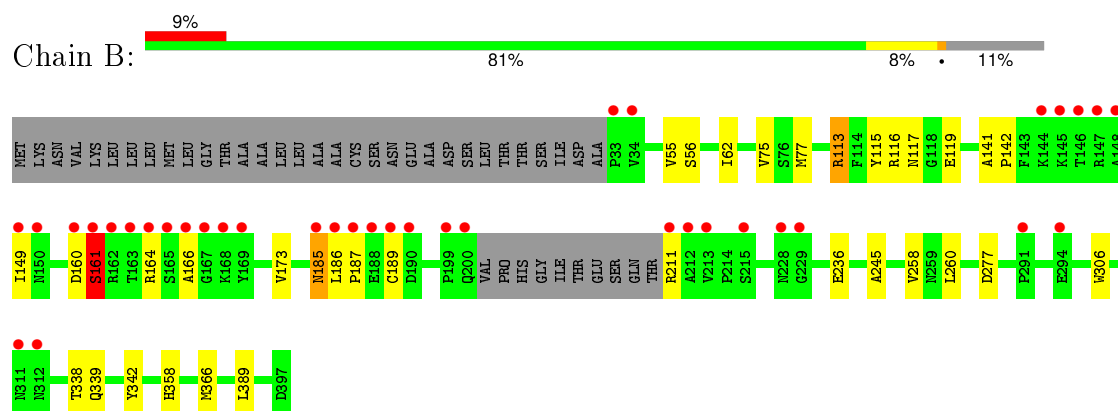
### 3 Residue-property plots

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.

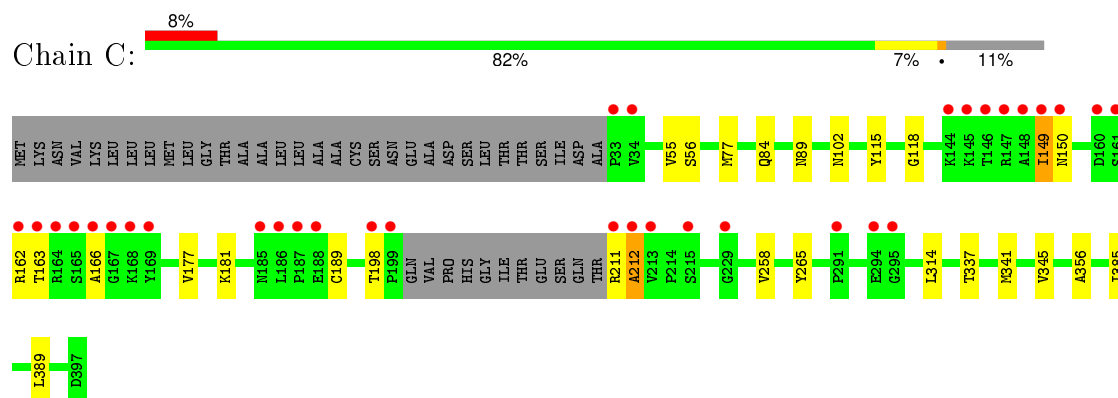
#### • Molecule 1: BFT-3



#### • Molecule 1: BFT-3

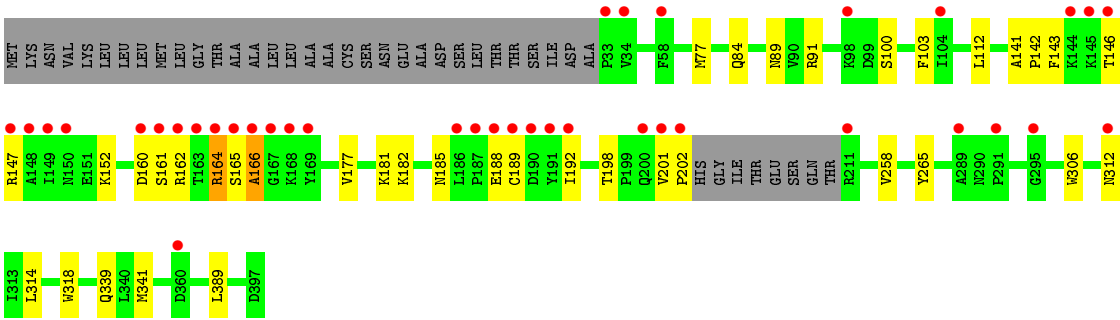
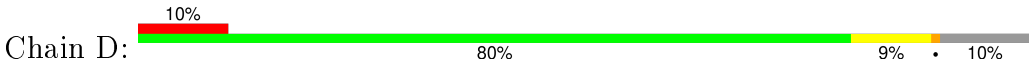


#### • Molecule 1: BFT-3



#### • Molecule 1: BFT-3





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	82.74Å 69.14Å 158.91Å 90.00° 91.57° 90.00°	Depositor
Resolution (Å)	50.00 – 1.80 45.16 – 1.80	Depositor EDS
% Data completeness (in resolution range)	98.9 (50.00-1.80) 98.9 (45.16-1.80)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.74 (at 1.79Å)	Xtriage
Refinement program	REFMAC 5.5.0102	Depositor
R, $R_{free}$	0.170 , 0.204 0.177 , 0.208	Depositor DCC
$R_{free}$ test set	781 reflections (0.48%)	DCC
Wilson B-factor (Å <sup>2</sup> )	23.9	Xtriage
Anisotropy	0.134	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 49.9	EDS
Estimated twinning fraction	0.065 for h,-k,-l	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 164503 reflections	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	12617	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.29% 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: AZI, ZN, PG4, 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	0/2924	0.65	0/3959
1	B	0.51	0/2906	0.66	4/3932 (0.1%)
1	C	0.54	0/2935	0.64	0/3972
1	D	0.56	0/2944	0.65	0/3985
All	All	0.55	0/11709	0.65	4/15848 (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	B	0	1
1	C	0	1
All	All	0	2

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	113	ARG	NE-CZ-NH1	11.46	126.03	120.30
1	B	113	ARG	NE-CZ-NH2	-8.73	115.93	120.30
1	B	113	ARG	CD-NE-CZ	6.06	132.08	123.60
1	B	113	ARG	CG-CD-NE	5.81	124.01	111.80

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	149	ILE	Peptide
1	C	149	ILE	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	2852	0	2768	17	0
1	B	2836	0	2758	20	0
1	C	2847	0	2764	17	0
1	D	2860	0	2775	22	0
2	A	13	0	18	0	0
2	D	13	0	18	0	0
3	A	18	0	24	0	0
3	B	6	0	8	2	0
3	D	12	0	16	0	0
4	A	6	0	0	0	0
4	B	3	0	0	1	0
5	A	1	0	0	0	0
5	B	1	0	0	0	0
5	C	1	0	0	0	0
5	D	1	0	0	0	0
6	A	341	0	0	2	0
6	B	221	0	0	0	0
6	C	290	0	0	1	0
6	D	295	0	0	2	0
All	All	12617	0	11149	76	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.

All (76) 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:C:177:VAL:HG13	1:C:341:MET:HE2	1.26	1.10
1:B:160:ASP:HB3	1:B:166:ALA:HB2	1.31	1.08
1:D:177:VAL:HG13	1:D:341:MET:HE1	1.61	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:189:CYS:HB2	1:D:314:LEU:HD21	1.70	0.74
1:B:258:VAL:HG11	1:B:389:LEU:HD22	1.71	0.70
1:A:82:LYS:NZ	6:A:543:HOH:O	2.25	0.68
1:C:258[B]:VAL:HG11	1:C:389:LEU:HD22	1.78	0.66
1:C:84:GLN:HE21	1:C:89:ASN:HD22	1.45	0.65
1:C:177:VAL:CG1	1:C:341:MET:HE2	2.16	0.62
1:B:160:ASP:OD1	1:B:161:SER:N	2.34	0.61
1:D:189:CYS:CB	1:D:314:LEU:HD21	2.32	0.60
1:B:160:ASP:HB3	1:B:166:ALA:CB	2.21	0.59
1:D:177:VAL:HG21	6:D:1387:HOH:O	2.04	0.57
1:C:198:THR:HG21	6:C:905:HOH:O	2.05	0.56
1:D:84:GLN:HE21	1:D:89:ASN:HD22	1.53	0.56
1:D:103:PHE:CE1	1:D:112:LEU:HD13	2.40	0.56
1:D:162:ARG:NH1	6:D:1326:HOH:O	2.38	0.56
1:B:186:LEU:HD21	1:B:342:TYR:CE2	2.41	0.56
1:A:186:LEU:HD13	1:A:186:LEU:O	2.06	0.56
1:B:306:TRP:O	1:B:339:GLN:HG3	2.05	0.56
1:C:258[A]:VAL:HG21	1:C:389:LEU:HD22	1.88	0.55
1:C:56:SER:C	1:C:77:MET:HE3	2.27	0.55
1:A:133:ASN:O	1:A:137:GLU:HG3	2.06	0.54
1:D:189:CYS:HA	1:D:312:ASN:HB3	1.88	0.54
1:A:165:SER:O	1:A:166:ALA:HB3	2.07	0.54
1:B:116:ARG:HH21	3:B:506:GOL:H11	1.73	0.54
1:D:160:ASP:OD2	1:D:161:SER:N	2.40	0.53
1:A:141:ALA:HB3	1:A:142:PRO:HD3	1.91	0.53
1:D:258:VAL:HG11	1:D:389:LEU:HD22	1.92	0.52
1:A:258[A]:VAL:HG21	1:A:389:LEU:HD22	1.92	0.51
1:D:165:SER:O	1:D:166:ALA:HB3	2.11	0.51
1:B:117:ASN:OD1	3:B:506:GOL:H12	2.10	0.50
1:D:198:THR:HG23	1:D:318:TRP:CZ3	2.47	0.50
1:D:143:PHE:HA	1:D:146:THR:HG22	1.93	0.49
1:A:200:GLN:HA	1:A:200:GLN:HE21	1.78	0.48
1:A:165:SER:O	1:A:166:ALA:CB	2.62	0.48
1:C:211:ARG:O	1:C:212:ALA:HB2	2.14	0.48
1:D:182:LYS:O	1:D:185:ASN:ND2	2.47	0.48
1:B:62:ILE:HD12	1:B:75:VAL:HG21	1.95	0.47
1:A:174:LYS:HD2	1:A:174:LYS:C	2.35	0.47
1:C:181:LYS:HE2	1:C:341:MET:O	2.15	0.46
1:D:306:TRP:O	1:D:339:GLN:HG3	2.16	0.46
1:B:55:VAL:O	1:B:77:MET:CE	2.63	0.46
1:A:55:VAL:O	1:A:77:MET:HE3	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:164:ARG:HG3	1:D:164:ARG:O	2.16	0.45
1:A:185:ASN:O	1:A:185:ASN:CG	2.54	0.44
1:C:84:GLN:HE21	1:C:89:ASN:ND2	2.11	0.44
1:A:55:VAL:O	1:A:77:MET:CE	2.66	0.44
1:A:177:VAL:HG21	6:A:606:HOH:O	2.17	0.44
1:C:356:ALA:HB2	1:C:385:ILE:HD11	2.00	0.44
1:C:115[A]:TYR:CE2	1:C:118:GLY:HA2	2.52	0.44
1:D:165:SER:O	1:D:166:ALA:CB	2.66	0.43
1:B:115:TYR:HA	1:B:119:GLU:O	2.18	0.43
1:B:77:MET:HB3	4:B:509:AZI:N2	2.33	0.43
1:C:163:THR:HB	1:C:166:ALA:HB3	2.00	0.43
1:D:181:LYS:HE2	1:D:341:MET:O	2.19	0.43
1:B:55:VAL:O	1:B:77:MET:HE2	2.18	0.43
1:B:141:ALA:HB3	1:B:142:PRO:HD3	2.01	0.43
1:B:56:SER:C	1:B:77:MET:HE3	2.39	0.43
1:C:55:VAL:O	1:C:77:MET:HE2	2.19	0.43
1:A:186:LEU:HD22	1:A:188:GLU:HA	2.02	0.42
1:D:77[B]:MET:HE2	1:D:91:ARG:HD2	2.01	0.42
1:A:186:LEU:CD2	1:A:188:GLU:HA	2.50	0.42
1:C:337:THR:HG22	1:C:345:VAL:HG11	2.01	0.42
1:B:358:HIS:HA	1:B:366:MET:O	2.20	0.42
1:B:185:ASN:HD22	1:B:185:ASN:N	2.18	0.42
1:B:186:LEU:HD23	1:B:187:PRO:O	2.19	0.42
1:A:189:CYS:HB2	1:A:314:LEU:HD21	2.02	0.41
1:D:201:VAL:HG12	1:D:202:PRO:HD2	2.03	0.41
1:C:189:CYS:HB2	1:C:314:LEU:HD21	2.02	0.41
1:B:245:ALA:HA	1:B:260:LEU:HD12	2.03	0.41
1:D:141:ALA:HB3	1:D:142:PRO:HD3	2.03	0.41
1:C:115[A]:TYR:CZ	1:C:118:GLY:HA2	2.54	0.40
1:D:201:VAL:CG1	1:D:202:PRO:HD2	2.51	0.40
1:A:36:ALA:HB1	1:A:51:GLN:OE1	2.21	0.40
1:B:236:GLU:HB3	1:B:338:THR:O	2.22	0.40

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	356/397 (90%)	349 (98%)	5 (1%)	2 (1%)	30	14
1	B	354/397 (89%)	343 (97%)	9 (2%)	2 (1%)	30	14
1	C	357/397 (90%)	349 (98%)	6 (2%)	2 (1%)	30	14
1	D	359/397 (90%)	343 (96%)	14 (4%)	2 (1%)	30	14
All	All	1426/1588 (90%)	1384 (97%)	34 (2%)	8 (1%)	30	14

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	166	ALA
1	D	166	ALA
1	C	149	ILE
1	B	189	CYS
1	C	212	ALA
1	A	192	ILE
1	B	161	SER
1	D	192	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	310/339 (91%)	297 (96%)	13 (4%)	36	18
1	B	308/339 (91%)	301 (98%)	7 (2%)	58	42
1	C	311/339 (92%)	306 (98%)	5 (2%)	70	59
1	D	313/339 (92%)	305 (97%)	8 (3%)	54	37
All	All	1242/1356 (92%)	1209 (97%)	33 (3%)	57	36

All (33) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	61	MET
1	A	70	ASN
1	A	147	ARG
1	A	149	ILE
1	A	161	SER
1	A	164	ARG
1	A	185	ASN
1	A	186	LEU
1	A	198	THR
1	A	200	GLN
1	A	210	THR
1	A	265[A]	TYR
1	A	265[B]	TYR
1	B	113	ARG
1	B	161	SER
1	B	164	ARG
1	B	173	VAL
1	B	185	ASN
1	B	211	ARG
1	B	277	ASP
1	C	102	ASN
1	C	150	ASN
1	C	162	ARG
1	C	265[A]	TYR
1	C	265[B]	TYR
1	D	100[A]	SER
1	D	100[B]	SER
1	D	147	ARG
1	D	152	LYS
1	D	164	ARG
1	D	188	GLU
1	D	265[A]	TYR
1	D	265[B]	TYR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	70	ASN
1	A	200	GLN
1	B	67	ASN
1	B	84	GLN
1	B	89	ASN
1	B	185	ASN

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Mol	Chain	Res	Type
1	B	200	GLN
1	C	89	ASN
1	C	102	ASN
1	D	89	ASN
1	D	185	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 15 ligands modelled in this entry, 4 are monoatomic - leaving 11 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	$\# Z  > 2$
2	PG4	A	502	-	12,12,12	0.53	0	11,11,11	0.25	0
3	GOL	A	503	-	5,5,5	0.51	0	5,5,5	0.68	0
3	GOL	A	504	-	5,5,5	0.34	0	5,5,5	0.39	0
3	GOL	A	505	-	5,5,5	0.35	0	5,5,5	0.50	0
4	AZI	A	510	-	0,2,2	0.00	-	0,1,1	0.00	-
4	AZI	A	511	-	0,2,2	0.00	-	0,1,1	0.00	-
3	GOL	B	506	-	5,5,5	0.45	0	5,5,5	0.50	0
4	AZI	B	509	-	0,2,2	0.00	-	0,1,1	0.00	-
2	PG4	D	501	-	12,12,12	0.53	0	11,11,11	0.15	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	GOL	D	507	-	5,5,5	0.38	0	5,5,5	0.14	0
3	GOL	D	508	-	5,5,5	0.33	0	5,5,5	0.33	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
2	PG4	A	502	-	-	0/10/10/10	0/0/0/0
3	GOL	A	503	-	-	0/4/4/4	0/0/0/0
3	GOL	A	504	-	-	0/4/4/4	0/0/0/0
3	GOL	A	505	-	-	0/4/4/4	0/0/0/0
4	AZI	A	510	-	-	0/0/0/0	0/0/0/0
4	AZI	A	511	-	-	0/0/0/0	0/0/0/0
3	GOL	B	506	-	-	0/4/4/4	0/0/0/0
4	AZI	B	509	-	-	0/0/0/0	0/0/0/0
2	PG4	D	501	-	-	0/10/10/10	0/0/0/0
3	GOL	D	507	-	-	0/4/4/4	0/0/0/0
3	GOL	D	508	-	-	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.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	506	GOL	2	0
4	B	509	AZI	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	357/397 (89%)	0.41	29 (8%) 15 11	14, 25, 63, 80	0
1	B	355/397 (89%)	0.48	37 (10%) 8 6	16, 34, 72, 90	0
1	C	354/397 (89%)	0.34	33 (9%) 11 8	14, 28, 64, 83	0
1	D	357/397 (89%)	0.53	38 (10%) 8 6	14, 28, 70, 86	0
All	All	1423/1588 (89%)	0.44	137 (9%) 10 7	14, 29, 68, 90	0

All (137) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	166	ALA	13.2
1	B	166	ALA	12.0
1	D	163	THR	10.5
1	C	166	ALA	9.9
1	D	33	PRO	9.7
1	C	149	ILE	9.6
1	A	165	SER	9.3
1	B	186	LEU	9.2
1	A	166	ALA	9.2
1	B	149	ILE	9.1
1	C	162	ARG	8.7
1	B	162	ARG	8.6
1	D	201	VAL	8.6
1	B	165	SER	8.5
1	A	149	ILE	8.2
1	D	34	VAL	8.1
1	A	164	ARG	8.0
1	B	167	GLY	7.9
1	B	163	THR	7.8
1	C	33	PRO	7.7
1	D	162	ARG	7.7

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Mol	Chain	Res	Type	RSRZ
1	A	210	THR	7.6
1	D	165	SER	7.5
1	B	164	ARG	7.3
1	A	34	VAL	7.1
1	A	163	THR	7.1
1	C	164	ARG	7.0
1	A	201	VAL	6.8
1	D	149	ILE	6.6
1	C	161	SER	6.5
1	C	165	SER	6.4
1	B	34	VAL	6.4
1	C	163	THR	6.3
1	C	150	ASN	6.2
1	D	150	ASN	6.1
1	C	199	PRO	6.1
1	A	161	SER	6.0
1	D	187	PRO	6.0
1	B	33	PRO	5.8
1	B	169	TYR	5.7
1	D	161	SER	5.7
1	B	200	GLN	5.7
1	C	211	ARG	5.7
1	D	146	THR	5.6
1	C	147	ARG	5.4
1	C	167	GLY	5.4
1	A	33	PRO	5.4
1	D	167	GLY	5.4
1	B	211	ARG	5.4
1	B	147	ARG	5.3
1	B	161	SER	5.3
1	C	212	ALA	5.3
1	A	148	ALA	5.2
1	C	186	LEU	5.2
1	C	145	LYS	5.0
1	B	189	CYS	5.0
1	B	188	GLU	4.9
1	D	147	ARG	4.9
1	A	167	GLY	4.9
1	D	202	PRO	4.7
1	B	212	ALA	4.7
1	A	200	GLN	4.7
1	D	168	LYS	4.6

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Mol	Chain	Res	Type	RSRZ
1	D	164	ARG	4.5
1	A	186	LEU	4.5
1	A	185	ASN	4.5
1	D	192	ILE	4.4
1	A	291	PRO	4.3
1	C	215	SER	4.3
1	B	148	ALA	4.3
1	C	34	VAL	4.3
1	A	146	THR	4.2
1	D	148	ALA	4.2
1	C	169	TYR	4.2
1	D	58	PHE	4.2
1	B	150	ASN	4.0
1	D	291	PRO	3.9
1	A	168	LYS	3.8
1	B	145	LYS	3.8
1	C	146	THR	3.8
1	A	162	ARG	3.8
1	D	200	GLN	3.8
1	D	189	CYS	3.7
1	C	291	PRO	3.7
1	B	146	THR	3.6
1	A	169	TYR	3.6
1	C	148	ALA	3.6
1	C	168	LYS	3.5
1	B	168	LYS	3.5
1	D	169	TYR	3.3
1	A	147	ARG	3.2
1	D	160	ASP	3.1
1	B	190	ASP	3.1
1	C	213	VAL	3.0
1	A	58	PHE	2.9
1	B	199	PRO	2.9
1	C	144	LYS	2.9
1	C	229	GLY	2.9
1	B	144	LYS	2.9
1	B	187	PRO	2.8
1	B	185	ASN	2.8
1	D	211	ARG	2.8
1	A	144	LYS	2.8
1	C	198	THR	2.8
1	B	294	GLU	2.8

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Mol	Chain	Res	Type	RSRZ
1	C	188	GLU	2.8
1	C	185	ASN	2.7
1	A	150	ASN	2.7
1	D	188	GLU	2.6
1	B	228	ASN	2.5
1	D	186	LEU	2.5
1	A	35	THR	2.5
1	C	187	PRO	2.5
1	B	213	VAL	2.4
1	B	312	ASN	2.4
1	A	145	LYS	2.4
1	D	144	LYS	2.4
1	B	229	GLY	2.4
1	D	295	GLY	2.4
1	B	291	PRO	2.4
1	B	160	ASP	2.3
1	B	311	ASN	2.3
1	C	294	GLU	2.2
1	A	187	PRO	2.2
1	D	190	ASP	2.1
1	D	104	ILE	2.1
1	D	145	LYS	2.1
1	B	215	SER	2.1
1	D	312	ASN	2.1
1	A	292	LYS	2.1
1	D	191	TYR	2.1
1	C	160	ASP	2.1
1	D	289	ALA	2.1
1	D	360	ASP	2.1
1	C	295	GLY	2.1
1	A	183	ILE	2.0
1	D	98	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	A	505	6/6	0.57	0.27	10.11	59,61,61,61	0
3	GOL	A	503	6/6	0.77	0.23	5.94	46,48,48,50	0
4	AZI	A	511	3/3	0.86	0.20	4.74	48,48,48,50	0
3	GOL	B	506	6/6	0.84	0.19	3.66	56,56,56,57	0
2	PG4	D	501	13/13	0.88	0.20	2.86	45,48,55,56	0
3	GOL	A	504	6/6	0.85	0.13	1.73	65,65,66,67	0
4	AZI	A	510	3/3	0.84	0.14	1.58	44,44,48,48	0
3	GOL	D	508	6/6	0.85	0.13	1.49	57,58,59,59	0
2	PG4	A	502	13/13	0.89	0.17	0.82	43,45,53,54	0
5	ZN	D	999	1/1	1.00	0.07	-1.26	26,26,26,26	0
5	ZN	C	999	1/1	1.00	0.07	-1.36	25,25,25,25	0
5	ZN	B	999	1/1	1.00	0.04	-1.95	34,34,34,34	0
5	ZN	A	999	1/1	1.00	0.08	-2.27	19,19,19,19	0
4	AZI	B	509	3/3	0.91	0.15	-	40,40,46,47	0
3	GOL	D	507	6/6	0.83	0.17	-	67,68,68,68	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.