



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 07:01 AM GMT

PDB ID : 2Z71  
Title : Structure of truncated mutant CYS1GLY of penicillin V acylase from bacillus  
sphaericus co-crystallized with penicillin V  
Authors : Pathak, M.C.; Brannigan, J.; Dodson, G.G.; Suresh, C.G.  
Deposited on : 2007-08-10  
Resolution : 2.60 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) : **NOT EXECUTED**  
EDS : **NOT EXECUTED**  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

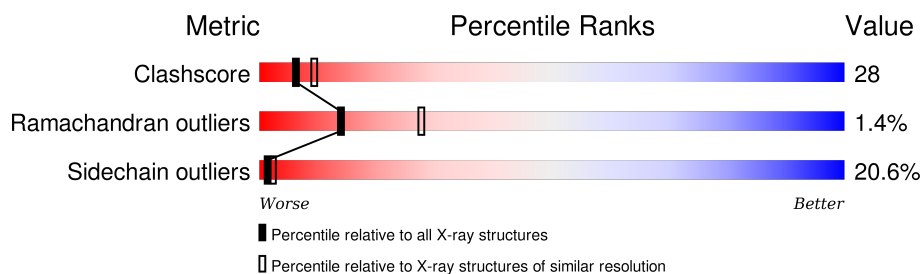
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.60 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	102246	2679 (2.60-2.60)
Ramachandran outliers	100387	2635 (2.60-2.60)
Sidechain outliers	100360	2635 (2.60-2.60)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments 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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	335	 43% 37% 13% 5% •
1	C	335	 47% 39% 11% ••

## 2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 5260 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.

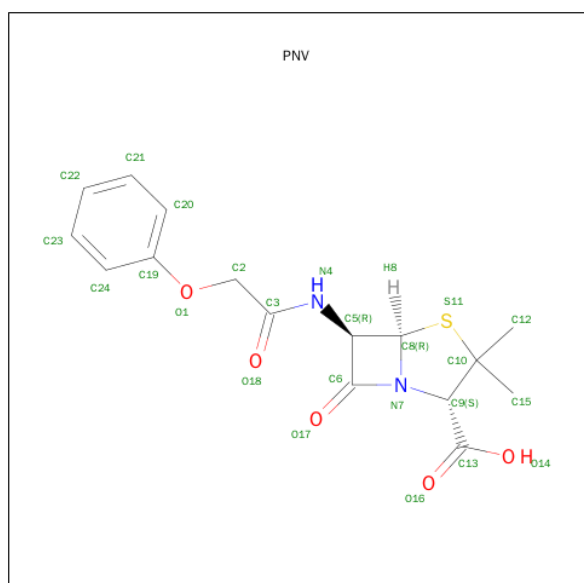
- Molecule 1 is a protein called Penicillin acylase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	330	Total	C	N	O	S	0	0	0
			2577	1640	423	502	12			
1	C	331	Total	C	N	O	S	0	0	0
			2584	1645	424	503	12			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	GLY	CYS	ENGINEERED	UNP P12256
A	98	ARG	THR	CONFLICT	UNP P12256
C	1	GLY	CYS	ENGINEERED	UNP P12256
C	98	ARG	THR	CONFLICT	UNP P12256

- Molecule 2 is (2S,5R,6R)-3,3-DIMETHYL-7-OXO-6-(2-PHENOXYACETAMIDO)-4-THIA-1-AZABICYCLO(3.2.0)HEPTANE-2-CARBOXYLIC ACID (three-letter code: PNV) (formula: C<sub>16</sub>H<sub>18</sub>N<sub>2</sub>O<sub>5</sub>S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	S	0	0
			24	16	2	5	1		
2	C	1	Total	C	N	O	S	0	0
			24	16	2	5	1		

- Molecule 3 is water.

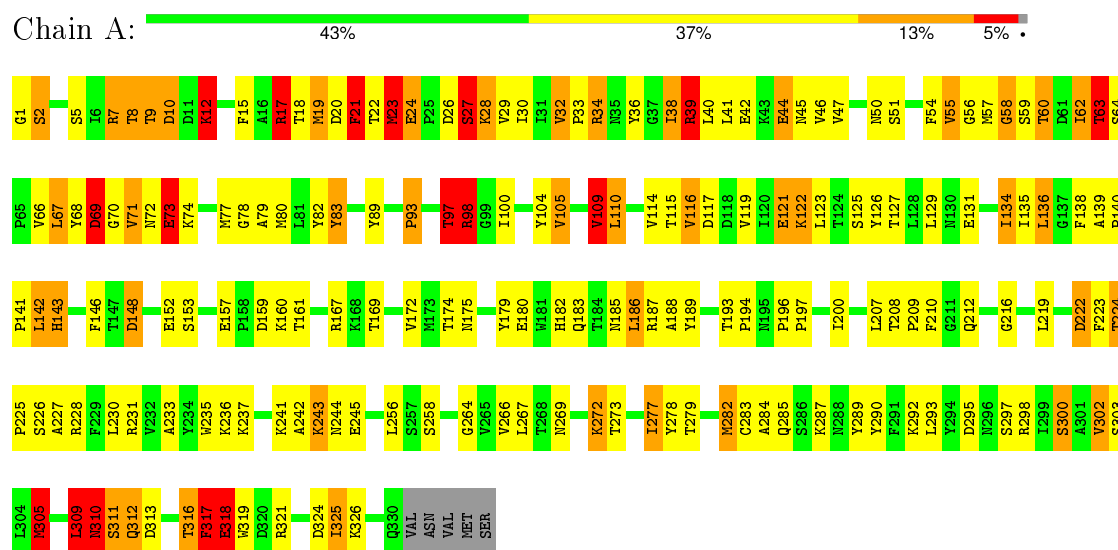
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	18	Total	O	0	0
			18	18		
3	C	33	Total	O	0	0
			33	33		

### 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.

Note EDS was not executed.

#### • Molecule 1: Penicillin acylase



## 4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section will therefore be incomplete.

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	129.73Å 158.89Å 90.74Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.60	Depositor
% Data completeness (in resolution range)	89.7 (20.00-2.60)	Depositor
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
Refinement program	REFMAC 5.1.24	Depositor
R, $R_{free}$	0.239 , 0.270	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	5260	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	51.0	wwPDB-VP

## 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: PNV

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	1.93	50/2632 (1.9%)	0.85	15/3577 (0.4%)
1	C	1.96	60/2639 (2.3%)	0.72	8/3587 (0.2%)
All	All	1.95	110/5271 (2.1%)	0.78	23/7164 (0.3%)

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	A	0	8

All (110) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	247	GLU	CD-OE1	11.57	1.38	1.25
1	C	318	GLU	CD-OE2	11.01	1.37	1.25
1	A	284	ALA	CA-CB	-10.72	1.29	1.52
1	A	245	GLU	CD-OE2	9.47	1.36	1.25
1	C	181	TRP	CB-CG	8.34	1.65	1.50
1	C	180	GLU	CG-CD	8.30	1.64	1.51
1	A	104	TYR	CE2-CZ	-8.17	1.27	1.38
1	C	79	ALA	CA-CB	-7.92	1.35	1.52
1	A	51	SER	CB-OG	7.67	1.52	1.42
1	A	243	LYS	CD-CE	7.62	1.70	1.51
1	C	104	TYR	CE2-CZ	-7.54	1.28	1.38
1	C	292	LYS	CB-CG	-7.54	1.32	1.52
1	C	282	MET	CG-SD	7.54	2.00	1.81
1	C	6	ILE	C-O	7.53	1.37	1.23
1	A	121	GLU	CD-OE2	7.53	1.33	1.25
1	A	210	PHE	CB-CG	-7.33	1.38	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	290	TYR	CG-CD1	-7.26	1.29	1.39
1	A	73	GLU	CD-OE1	7.25	1.33	1.25
1	A	12	LYS	CE-NZ	7.22	1.67	1.49
1	C	186	LEU	C-O	-7.18	1.09	1.23
1	C	29	VAL	CB-CG2	-7.16	1.37	1.52
1	C	226	SER	CB-OG	-7.00	1.33	1.42
1	C	105	VAL	CB-CG1	6.90	1.67	1.52
1	C	92	GLU	CD-OE2	6.88	1.33	1.25
1	C	228	ARG	CD-NE	6.70	1.57	1.46
1	C	73	GLU	CD-OE1	6.68	1.33	1.25
1	A	216	GLY	C-O	-6.58	1.13	1.23
1	A	139	ALA	CA-CB	6.56	1.66	1.52
1	A	109	VAL	CB-CG1	-6.56	1.39	1.52
1	C	111	GLY	CA-C	6.55	1.62	1.51
1	A	180	GLU	CD-OE2	6.51	1.32	1.25
1	C	229	PHE	CE2-CZ	-6.43	1.25	1.37
1	A	21	PHE	CE1-CZ	6.36	1.49	1.37
1	A	89	TYR	CE1-CZ	-6.34	1.30	1.38
1	C	180	GLU	CD-OE1	6.33	1.32	1.25
1	C	189	TYR	CE2-CZ	-6.30	1.30	1.38
1	C	126	TYR	CD2-CE2	6.29	1.48	1.39
1	A	295	ASP	CB-CG	6.25	1.64	1.51
1	A	39	ARG	NE-CZ	6.25	1.41	1.33
1	A	17	ARG	CA-CB	-6.19	1.40	1.53
1	C	160	LYS	CG-CD	6.17	1.73	1.52
1	C	76	LEU	C-O	6.07	1.34	1.23
1	A	7	ARG	CZ-NH1	6.03	1.40	1.33
1	C	145	THR	CA-CB	-5.99	1.37	1.53
1	C	180	GLU	CD-OE2	5.97	1.32	1.25
1	A	119	VAL	CA-CB	-5.96	1.42	1.54
1	C	160	LYS	CD-CE	5.96	1.66	1.51
1	A	210	PHE	CE1-CZ	5.92	1.48	1.37
1	C	290	TYR	CE2-CZ	-5.92	1.30	1.38
1	C	258	SER	CB-OG	-5.92	1.34	1.42
1	A	290	TYR	CE2-CZ	-5.89	1.30	1.38
1	C	195	ASN	CB-CG	5.88	1.64	1.51
1	C	44	GLU	CD-OE2	5.85	1.32	1.25
1	A	55	VAL	C-O	5.85	1.34	1.23
1	C	103	VAL	CA-CB	5.84	1.67	1.54
1	A	272	LYS	CE-NZ	5.81	1.63	1.49
1	C	185	ASN	CB-CG	-5.80	1.37	1.51
1	C	234	TYR	CE1-CZ	-5.79	1.31	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	278	TYR	CE2-CZ	5.74	1.46	1.38
1	A	293	LEU	C-O	5.74	1.34	1.23
1	A	318	GLU	CG-CD	5.73	1.60	1.51
1	A	172	VAL	CB-CG2	5.71	1.64	1.52
1	C	13	SER	CA-CB	-5.71	1.44	1.52
1	C	185	ASN	CG-OD1	-5.66	1.11	1.24
1	C	39	ARG	CZ-NH1	5.60	1.40	1.33
1	C	1	GLY	C-O	-5.60	1.14	1.23
1	A	58	GLY	C-O	5.59	1.32	1.23
1	A	258	SER	CB-OG	-5.57	1.35	1.42
1	C	255	ILE	C-O	-5.57	1.12	1.23
1	A	233	ALA	CA-CB	-5.56	1.40	1.52
1	C	5	SER	CA-CB	-5.54	1.44	1.52
1	A	152	GLU	CD-OE1	5.54	1.31	1.25
1	C	157	GLU	CD-OE2	-5.54	1.19	1.25
1	C	219	LEU	C-O	-5.52	1.12	1.23
1	A	325	ILE	CA-CB	-5.52	1.42	1.54
1	A	317	PHE	CB-CG	5.50	1.60	1.51
1	A	321	ARG	CZ-NH2	5.49	1.40	1.33
1	C	69	ASP	CA-C	-5.46	1.38	1.52
1	A	188	ALA	CA-CB	-5.44	1.41	1.52
1	C	126	TYR	CE1-CZ	5.43	1.45	1.38
1	C	216	GLY	C-O	-5.41	1.15	1.23
1	C	173	MET	CA-C	-5.39	1.39	1.52
1	A	104	TYR	CG-CD1	-5.36	1.32	1.39
1	A	89	TYR	CG-CD2	-5.35	1.32	1.39
1	C	218	GLY	C-O	-5.32	1.15	1.23
1	A	326	LYS	CA-C	-5.31	1.39	1.52
1	A	290	TYR	CG-CD1	-5.27	1.32	1.39
1	C	289	TYR	C-N	5.26	1.46	1.34
1	C	46	VAL	CA-CB	-5.26	1.43	1.54
1	C	147	THR	CA-CB	-5.25	1.39	1.53
1	A	15	PHE	CE1-CZ	5.23	1.47	1.37
1	C	82	TYR	CZ-OH	5.23	1.46	1.37
1	A	292	LYS	CB-CG	-5.22	1.38	1.52
1	C	6	ILE	CB-CG2	-5.20	1.36	1.52
1	C	198	GLN	CG-CD	5.20	1.63	1.51
1	A	235	TRP	CB-CG	5.19	1.59	1.50
1	A	321	ARG	CZ-NH1	5.18	1.39	1.33
1	A	152	GLU	CD-OE2	5.17	1.31	1.25
1	C	17	ARG	CA-CB	-5.17	1.42	1.53
1	A	298	ARG	CA-C	-5.15	1.39	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	105	VAL	CB-CG1	-5.11	1.42	1.52
1	A	69	ASP	CB-CG	5.09	1.62	1.51
1	C	121	GLU	CD-OE1	5.09	1.31	1.25
1	C	83	TYR	CE1-CZ	-5.08	1.31	1.38
1	A	283	CYS	CB-SG	5.04	1.90	1.82
1	C	83	TYR	CE2-CZ	-5.04	1.32	1.38
1	C	20	ASP	C-O	-5.03	1.13	1.23
1	A	62	ILE	C-O	5.02	1.32	1.23
1	A	302	VAL	CA-CB	5.01	1.65	1.54
1	C	181	TRP	CE2-CZ2	5.01	1.48	1.39

All (23) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	305	MET	CB-CA-C	13.57	137.55	110.40
1	A	97	THR	C-N-CA	-9.71	97.41	121.70
1	A	98	ARG	CA-C-N	-6.86	102.49	116.20
1	A	98	ARG	CD-NE-CZ	-6.66	114.27	123.60
1	A	310	ASN	O-C-N	-6.08	112.98	122.70
1	A	324	ASP	CB-CG-OD2	5.79	123.51	118.30
1	C	222	ASP	CB-CG-OD2	5.64	123.38	118.30
1	A	222	ASP	CB-CG-OD2	5.62	123.36	118.30
1	C	206	ASP	CB-CG-OD2	5.42	123.17	118.30
1	A	20	ASP	CB-CG-OD2	5.36	123.12	118.30
1	A	305	MET	CB-CG-SD	5.35	128.46	112.40
1	C	204	ASP	CB-CG-OD2	5.34	123.10	118.30
1	A	295	ASP	CB-CG-OD2	5.30	123.07	118.30
1	A	309	LEU	C-N-CA	-5.27	108.52	121.70
1	A	10	ASP	CB-CG-OD2	5.24	123.02	118.30
1	A	69	ASP	CB-CG-OD2	5.24	123.02	118.30
1	C	274	ASP	CB-CG-OD2	5.18	122.97	118.30
1	C	159	ASP	CB-CG-OD2	5.14	122.92	118.30
1	A	148	ASP	CB-CG-OD2	5.13	122.92	118.30
1	C	91	ASP	CB-CG-OD2	5.11	122.90	118.30
1	C	324	ASP	CB-CG-OD2	5.01	122.81	118.30
1	A	159	ASP	CB-CG-OD2	5.01	122.81	118.30
1	C	61	ASP	CB-CG-OD2	5.00	122.80	118.30

There are no chirality outliers.

All (8) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	310	ASN	Mainchain,Peptide
1	A	311	SER	Mainchain
1	A	317	PHE	Peptide
1	A	44	GLU	Peptide
1	A	98	ARG	Sidechain,Mainchain,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	2577	0	2553	184	0
1	C	2584	0	2562	110	0
2	A	24	0	17	4	0
2	C	24	0	16	8	0
3	A	18	0	0	1	0
3	C	33	0	0	1	0
All	All	5260	0	5148	290	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 28.

All (290) 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:305:MET:SD	1:C:305:MET:CE	2.03	1.46
1:A:24:GLU:HG3	1:A:277:ILE:CD1	1.49	1.41
1:A:24:GLU:CG	1:A:277:ILE:HD12	1.63	1.26
1:C:174:THR:CG2	1:C:175:ASN:H	1.50	1.20
1:A:26:ASP:O	1:A:27:SER:HB2	1.36	1.16
1:A:22:THR:O	1:A:23:MET:HB3	1.34	1.12
1:C:174:THR:HG22	1:C:175:ASN:N	1.48	1.12
1:A:317:PHE:HA	1:A:318:GLU:HB2	1.19	1.10
1:A:24:GLU:HB2	1:A:277:ILE:HG21	1.37	1.05
1:A:122:LYS:HD3	1:A:126:TYR:HE2	1.23	1.01
1:A:28:LYS:CD	1:A:30:ILE:HG12	1.93	0.99
1:A:9:THR:HG23	1:A:243:LYS:HA	1.41	0.98
1:C:4:LEU:HD12	1:C:4:LEU:N	1.79	0.97

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:28:LYS:HD2	1:A:30:ILE:CG1	1.95	0.97
1:A:24:GLU:CB	1:A:277:ILE:HG21	1.93	0.96
1:A:28:LYS:HD2	1:A:30:ILE:HG12	1.44	0.96
1:A:97:THR:HG21	1:A:127:THR:OG1	1.65	0.95
1:A:28:LYS:HZ2	1:A:30:ILE:HG12	1.30	0.94
1:A:9:THR:CG2	1:A:243:LYS:HA	1.98	0.94
1:A:310:ASN:H	1:A:311:SER:HB2	1.31	0.93
1:A:28:LYS:CD	1:A:30:ILE:CG1	2.46	0.93
1:A:24:GLU:CG	1:A:277:ILE:CD1	2.32	0.92
1:A:28:LYS:NZ	1:A:30:ILE:HG12	1.84	0.92
1:A:24:GLU:OE2	1:A:277:ILE:HB	1.69	0.92
1:A:228:ARG:HH12	2:A:903:PNV:H21	1.36	0.91
1:C:169:THR:HG22	1:C:171:GLY:H	1.35	0.91
1:A:8:THR:HG21	1:A:10:ASP:OD1	1.69	0.91
1:A:8:THR:HG22	1:A:10:ASP:H	1.35	0.90
1:A:24:GLU:HB2	1:A:277:ILE:HD13	1.52	0.89
1:C:106:ILE:HB	3:C:934:HOH:O	1.72	0.88
1:C:40:LEU:HD12	1:C:100:ILE:HD12	1.55	0.88
1:C:4:LEU:N	1:C:4:LEU:CD1	2.35	0.88
1:A:317:PHE:CA	1:A:318:GLU:HB2	2.04	0.86
1:C:180:GLU:O	1:C:184:THR:HG23	1.74	0.86
1:A:22:THR:O	1:A:23:MET:CB	2.20	0.86
1:A:115:THR:HG22	1:A:117:ASP:H	1.40	0.86
1:A:310:ASN:N	1:A:311:SER:HB2	1.90	0.85
1:A:26:ASP:O	1:A:27:SER:CB	2.24	0.84
1:C:22:THR:HG21	1:C:272:LYS:HD2	1.60	0.82
1:A:60:THR:CG2	1:A:60:THR:O	2.28	0.82
1:C:327:GLN:HG3	1:C:331:VAL:HB	1.62	0.82
1:A:223:PHE:O	1:A:228:ARG:HD3	1.80	0.82
1:A:38:ILE:HD11	1:A:50:ASN:HB3	1.60	0.81
1:C:327:GLN:CG	1:C:331:VAL:HB	2.10	0.80
1:A:312:GLN:HG2	1:A:313:ASP:N	1.98	0.79
1:A:46:VAL:HG11	1:A:98:ARG:CZ	2.14	0.77
1:A:105:VAL:O	1:A:109:VAL:HG12	1.83	0.77
1:A:24:GLU:CB	1:A:277:ILE:HD13	2.15	0.76
1:A:28:LYS:HD3	1:A:30:ILE:HG13	1.67	0.76
1:C:22:THR:HG21	1:C:272:LYS:CD	2.15	0.75
1:C:41:LEU:HD21	1:C:129:LEU:HD12	1.67	0.75
1:C:269:ASN:H	1:C:269:ASN:ND2	1.85	0.75
1:A:17:ARG:O	1:A:17:ARG:HG3	1.86	0.74
1:A:24:GLU:OE1	1:A:319:TRP:HH2	1.71	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:122:LYS:HD3	1:A:126:TYR:CE2	2.16	0.73
1:A:28:LYS:HE3	1:A:316:THR:OG1	1.88	0.73
1:A:46:VAL:HG11	1:A:98:ARG:NH1	2.03	0.73
1:A:222:ASP:OD1	1:A:224:THR:HB	1.89	0.72
1:C:174:THR:HG22	1:C:175:ASN:H	0.63	0.72
1:A:28:LYS:CD	1:A:30:ILE:HG13	2.19	0.71
1:C:82:TYR:CZ	2:C:904:PNV:H5	2.25	0.71
1:C:114:VAL:HG22	1:C:115:THR:HG23	1.73	0.71
1:C:288:ASN:ND2	1:C:303:SER:HA	2.05	0.71
1:C:4:LEU:HD23	1:C:236:LYS:HG3	1.72	0.70
1:A:60:THR:HG22	1:A:60:THR:O	1.90	0.70
1:C:45:ASN:N	1:C:45:ASN:HD22	1.88	0.70
1:A:225:PRO:HG3	2:A:903:PNV:H22	1.73	0.70
1:A:8:THR:CG2	1:A:10:ASP:OD1	2.40	0.70
1:C:228:ARG:HH11	1:C:228:ARG:HG2	1.57	0.70
1:A:28:LYS:CE	1:A:30:ILE:HG12	2.22	0.69
1:A:24:GLU:HG3	1:A:277:ILE:HD12	0.73	0.69
1:A:24:GLU:OE1	1:A:319:TRP:CH2	2.46	0.68
1:A:28:LYS:HE2	1:A:316:THR:HA	1.75	0.68
1:A:193:THR:HB	1:A:194:PRO:CD	2.24	0.68
1:A:39:ARG:HG2	1:A:41:LEU:O	1.94	0.68
1:A:8:THR:HG22	1:A:10:ASP:N	2.09	0.67
1:C:169:THR:HG22	1:C:171:GLY:N	2.09	0.67
1:C:288:ASN:HD22	1:C:303:SER:HA	1.59	0.67
1:A:93:PRO:HB3	1:A:97:THR:HG22	1.77	0.66
1:A:24:GLU:CG	1:A:277:ILE:HD13	2.26	0.66
1:C:57:MET:HB2	1:C:289:TYR:OH	1.97	0.65
1:A:300:SER:HB3	1:C:328:LEU:HD11	1.76	0.65
1:A:28:LYS:CE	1:A:316:THR:HA	2.27	0.65
1:C:45:ASN:N	1:C:45:ASN:ND2	2.45	0.64
1:C:180:GLU:O	1:C:184:THR:CG2	2.44	0.64
1:A:310:ASN:N	1:A:311:SER:CB	2.59	0.64
1:A:71:VAL:HG22	1:A:282:MET:HB3	1.79	0.63
1:C:22:THR:CG2	1:C:22:THR:O	2.46	0.63
1:C:272:LYS:HD2	2:C:904:PNV:H153	1.80	0.63
1:A:224:THR:HG22	1:A:227:ALA:H	1.64	0.63
1:A:22:THR:O	1:A:22:THR:HG23	1.99	0.62
1:A:71:VAL:CG2	1:A:282:MET:HB3	2.29	0.62
1:A:42:GLU:HB2	1:A:131:GLU:OE2	1.97	0.62
1:A:8:THR:CG2	1:A:10:ASP:H	2.09	0.62
1:A:264:GLY:H	1:A:273:THR:CG2	2.13	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:305:MET:SD	1:A:309:LEU:HD21	2.41	0.61
1:A:169:THR:HB	1:A:179:TYR:CZ	2.35	0.61
1:A:266:VAL:C	1:A:267:LEU:HD23	2.20	0.61
1:A:138:PHE:C	1:A:138:PHE:CD1	2.73	0.61
1:C:174:THR:CG2	1:C:175:ASN:N	2.23	0.61
1:A:69:ASP:HA	1:A:78:GLY:O	2.01	0.61
1:C:45:ASN:ND2	1:C:45:ASN:H	1.98	0.61
1:C:228:ARG:HH11	1:C:228:ARG:CG	2.14	0.60
1:C:268:THR:HG22	1:C:270:GLU:H	1.65	0.60
1:A:62:ILE:C	1:A:63:THR:HG22	2.21	0.60
1:A:68:TYR:O	1:A:79:ALA:HA	2.02	0.60
1:C:62:ILE:HD11	1:C:66:VAL:CG2	2.31	0.60
1:A:23:MET:CE	1:A:272:LYS:NZ	2.66	0.59
1:A:62:ILE:O	1:A:63:THR:HG22	2.01	0.59
1:C:272:LYS:CD	2:C:904:PNV:H153	2.32	0.59
1:A:264:GLY:H	1:A:273:THR:HG23	1.68	0.59
1:C:71:VAL:HG13	1:C:71:VAL:O	2.03	0.58
1:C:106:ILE:O	1:C:110:LEU:HB2	2.04	0.58
1:A:21:PHE:HB3	1:A:277:ILE:HD11	1.86	0.58
1:A:2:SER:HB3	1:A:174:THR:HG22	1.85	0.58
1:A:8:THR:CG2	1:A:9:THR:N	2.67	0.58
1:C:4:LEU:HD13	1:C:4:LEU:O	2.03	0.57
1:C:268:THR:CG2	1:C:269:ASN:N	2.67	0.57
1:A:312:GLN:CG	1:A:313:ASP:N	2.68	0.57
1:A:317:PHE:HA	1:A:318:GLU:CB	2.12	0.57
1:C:86:PHE:CZ	1:C:177:PRO:HB3	2.40	0.57
1:A:169:THR:HB	1:A:179:TYR:OH	2.05	0.56
1:C:102:PRO:O	1:C:105:VAL:HG13	2.05	0.56
1:A:189:TYR:CE1	1:A:230:LEU:HD11	2.40	0.56
1:C:327:GLN:HG2	1:C:331:VAL:HB	1.86	0.56
1:A:115:THR:HG22	1:A:117:ASP:N	2.14	0.56
1:A:45:ASN:O	1:A:47:VAL:HG12	2.05	0.55
1:A:71:VAL:HG13	1:A:77:MET:HG3	1.88	0.55
1:A:24:GLU:CB	1:A:277:ILE:CD1	2.79	0.55
1:A:34:ARG:HH21	1:A:309:LEU:HD23	1.72	0.55
1:A:10:ASP:OD1	1:A:12:LYS:HD3	2.07	0.55
1:C:308:ASN:O	1:C:311:SER:HB2	2.07	0.55
1:A:72:ASN:OD1	1:A:72:ASN:C	2.44	0.55
1:A:9:THR:HG22	1:A:242:ALA:O	2.06	0.55
1:C:174:THR:HG21	1:C:225:PRO:O	2.06	0.54
1:A:28:LYS:CE	1:A:316:THR:OG1	2.56	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:57:MET:HB2	1:A:289:TYR:OH	2.07	0.54
1:A:23:MET:CE	1:A:272:LYS:HZ1	2.20	0.54
1:C:169:THR:HG23	1:C:179:TYR:CE1	2.43	0.54
1:C:120:ILE:HG12	1:C:165:ILE:HG21	1.89	0.54
1:A:193:THR:HB	1:A:194:PRO:HD2	1.91	0.53
1:C:268:THR:HG22	1:C:270:GLU:N	2.23	0.53
1:C:4:LEU:HD12	1:C:4:LEU:H	1.64	0.53
1:C:6:ILE:HG12	1:C:252:LEU:HD21	1.90	0.53
1:A:325:ILE:HG21	1:C:301:ALA:HB2	1.90	0.52
1:C:268:THR:HG23	1:C:269:ASN:N	2.24	0.52
1:C:72:ASN:HB3	1:C:110:LEU:O	2.10	0.52
1:A:23:MET:O	1:A:23:MET:SD	2.67	0.52
1:A:224:THR:CG2	1:A:226:SER:OG	2.58	0.52
1:A:23:MET:HE1	1:A:272:LYS:NZ	2.24	0.52
1:C:232:VAL:O	1:C:236:LYS:HB2	2.09	0.52
1:A:38:ILE:CD1	1:A:50:ASN:HB3	2.36	0.52
1:A:228:ARG:HH12	2:A:903:PNV:C21	2.15	0.51
1:C:4:LEU:H	1:C:4:LEU:CD1	2.17	0.51
1:A:62:ILE:HG13	1:A:63:THR:H	1.75	0.51
1:A:200:ILE:HG13	1:A:207:LEU:HB2	1.93	0.51
1:C:272:LYS:CE	2:C:904:PNV:H153	2.41	0.51
1:A:58:GLY:HA3	1:A:66:VAL:O	2.11	0.50
1:A:109:VAL:HG11	1:A:146:PHE:CZ	2.46	0.50
1:A:140:PRO:O	1:A:142:LEU:HD22	2.11	0.50
1:C:22:THR:HG23	1:C:22:THR:O	2.11	0.50
1:A:302:VAL:HG11	1:A:317:PHE:CE1	2.47	0.50
1:C:94:LYS:O	1:C:97:THR:OG1	2.24	0.50
1:C:17:ARG:HD3	1:C:17:ARG:O	2.12	0.50
1:C:54:PHE:HB3	1:C:72:ASN:HA	1.92	0.50
1:C:201:MET:HG3	1:C:206:ASP:OD1	2.12	0.50
1:A:59:SER:OG	1:A:60:THR:N	2.45	0.49
1:A:60:THR:HG23	1:A:60:THR:O	2.09	0.49
1:C:270:GLU:OE1	2:C:904:PNV:H151	2.13	0.49
1:A:28:LYS:HE2	1:A:29:VAL:O	2.12	0.49
1:A:312:GLN:HE21	1:A:313:ASP:HB2	1.78	0.49
1:A:17:ARG:NH2	1:A:80:MET:O	2.45	0.49
1:A:208:THR:OG1	1:A:209:PRO:HD2	2.12	0.48
1:C:74:LYS:HD2	1:C:74:LYS:HA	1.62	0.48
1:A:17:ARG:O	1:A:17:ARG:CG	2.58	0.48
1:A:5:SER:O	1:A:236:LYS:NZ	2.35	0.48
1:C:42:GLU:OE1	1:C:63:THR:OG1	2.31	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:36:TYR:O	1:A:50:ASN:OD1	2.30	0.48
1:A:54:PHE:HA	1:A:72:ASN:HA	1.96	0.48
1:A:24:GLU:HB2	1:A:277:ILE:CG2	2.26	0.48
1:A:17:ARG:HH21	1:A:68:TYR:HB3	1.79	0.48
1:A:27:SER:HA	1:A:58:GLY:O	2.13	0.48
1:C:287:LYS:HD3	1:C:305:MET:HG2	1.96	0.48
1:C:268:THR:HG21	2:C:904:PNV:H151	1.96	0.48
1:C:175:ASN:OD1	2:C:904:PNV:H21	2.14	0.47
1:A:312:GLN:NE2	1:A:313:ASP:H	2.12	0.47
1:C:24:GLU:HA	1:C:25:PRO:HD2	1.76	0.47
1:C:82:TYR:CE2	2:C:904:PNV:H5	2.49	0.47
1:C:268:THR:HG23	1:C:269:ASN:H	1.79	0.47
1:A:23:MET:HE3	1:A:272:LYS:NZ	2.30	0.47
1:C:42:GLU:OE1	1:C:104:TYR:OH	2.27	0.47
1:C:16:ALA:HB2	1:C:252:LEU:HD13	1.97	0.47
1:A:266:VAL:O	1:A:267:LEU:HD23	2.15	0.47
1:A:24:GLU:CG	1:A:277:ILE:HG21	2.44	0.46
1:C:169:THR:HG23	1:C:179:TYR:CZ	2.50	0.46
1:C:45:ASN:O	1:C:47:VAL:HG23	2.14	0.46
1:C:69:ASP:HA	1:C:78:GLY:O	2.15	0.46
1:C:269:ASN:HD22	1:C:269:ASN:H	1.60	0.46
1:C:312:GLN:NE2	1:C:313:ASP:OD2	2.49	0.46
1:A:297:SER:O	1:C:297:SER:OG	2.34	0.46
1:A:47:VAL:O	1:A:47:VAL:CG2	2.63	0.46
1:A:267:LEU:N	1:A:267:LEU:HD23	2.29	0.46
1:C:62:ILE:HD11	1:C:66:VAL:HG23	1.97	0.46
1:A:185:ASN:O	1:A:186:LEU:C	2.53	0.46
1:A:256:LEU:HD23	1:A:256:LEU:HA	1.69	0.46
1:A:32:VAL:CG1	1:A:54:PHE:CE1	2.99	0.46
1:C:22:THR:HG21	1:C:272:LYS:HD3	1.95	0.46
1:C:176:SER:CB	1:C:177:PRO:HA	2.44	0.46
1:C:122:LYS:HE3	1:C:126:TYR:CE2	2.51	0.46
1:A:1:GLY:N	1:A:175:ASN:OD1	2.44	0.45
1:A:115:THR:CG2	1:A:116:VAL:N	2.78	0.45
1:C:83:TYR:CZ	1:C:157:GLU:HG2	2.51	0.45
1:C:12:LYS:HG2	1:C:285:GLN:HB2	1.97	0.45
1:A:19:MET:HE3	1:A:24:GLU:OE2	2.16	0.45
1:A:241:LYS:HE3	1:A:241:LYS:HB3	1.72	0.45
1:A:62:ILE:C	1:A:63:THR:CG2	2.84	0.45
1:A:179:TYR:OH	1:A:183:GLN:NE2	2.50	0.45
1:C:268:THR:HG23	1:C:269:ASN:HD22	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:8:THR:HG22	1:A:9:THR:N	2.31	0.45
1:A:140:PRO:HA	1:A:141:PRO:HD2	1.62	0.44
1:A:12:LYS:HA	1:A:285:GLN:OE1	2.18	0.44
1:A:231:ARG:HD2	3:A:914:HOH:O	2.17	0.44
1:A:19:MET:HG3	1:A:278:TYR:CE2	2.52	0.44
1:A:29:VAL:HA	1:A:56:GLY:O	2.16	0.44
1:A:45:ASN:O	1:A:47:VAL:CG1	2.64	0.44
1:A:40:LEU:HD12	1:A:100:ILE:HD12	1.99	0.44
1:A:28:LYS:HD2	1:A:30:ILE:CD1	2.46	0.44
1:A:115:THR:HG22	1:A:116:VAL:N	2.31	0.44
1:C:268:THR:CG2	1:C:270:GLU:H	2.29	0.44
1:A:175:ASN:OD1	1:A:228:ARG:NH2	2.51	0.44
1:C:242:ALA:HB2	1:C:251:ASN:ND2	2.33	0.44
1:C:268:THR:HG21	1:C:270:GLU:OE1	2.18	0.44
1:A:39:ARG:HA	1:A:47:VAL:HB	1.99	0.44
1:C:145:THR:HG23	1:C:145:THR:O	2.16	0.44
1:A:17:ARG:NH1	1:A:19:MET:HG2	2.33	0.44
1:A:21:PHE:CB	1:A:277:ILE:HD11	2.48	0.43
1:A:23:MET:HE3	1:A:272:LYS:HZ1	1.81	0.43
1:A:42:GLU:OE2	1:A:63:THR:HG23	2.17	0.43
1:C:245:GLU:O	1:C:249:VAL:HG23	2.18	0.43
1:A:71:VAL:HG13	1:A:77:MET:CG	2.48	0.43
1:C:71:VAL:HA	1:C:76:LEU:O	2.18	0.43
1:A:54:PHE:HE1	1:A:67:LEU:HD13	1.83	0.43
1:A:143:HIS:HB2	1:A:157:GLU:HG2	2.01	0.43
1:C:232:VAL:HG23	1:C:259:VAL:HG11	2.00	0.43
1:C:4:LEU:C	1:C:4:LEU:HD13	2.37	0.43
1:A:70:GLY:C	1:A:110:LEU:HD11	2.38	0.43
1:C:145:THR:HB	1:C:173:MET:HE2	2.00	0.43
1:C:3:SER:C	1:C:4:LEU:HD12	2.36	0.43
1:A:55:VAL:O	1:A:70:GLY:HA2	2.19	0.43
1:C:50:ASN:OD1	1:C:50:ASN:N	2.52	0.43
1:C:115:THR:O	1:C:118:ASP:HB2	2.19	0.42
1:A:282:MET:HG2	1:A:289:TYR:HD2	1.84	0.42
1:C:24:GLU:HG2	1:C:24:GLU:O	2.19	0.42
1:A:185:ASN:O	1:A:187:ARG:N	2.52	0.42
1:A:135:ILE:H	1:A:135:ILE:HG12	1.67	0.42
1:A:148:ASP:OD1	1:A:148:ASP:C	2.57	0.42
2:A:903:PNV:C6	1:C:212:GLN:HE22	2.32	0.42
1:A:72:ASN:HB3	1:A:110:LEU:O	2.19	0.42
1:A:32:VAL:HA	1:A:33:PRO:HD3	1.97	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:175:ASN:HB2	1:A:225:PRO:HB3	2.01	0.41
1:A:73:GLU:H	1:A:73:GLU:HG3	1.53	0.41
1:A:24:GLU:OE2	1:A:277:ILE:CB	2.56	0.41
1:A:303:SER:HB2	1:C:331:VAL:HG22	2.03	0.41
1:A:196:PRO:HA	1:A:197:PRO:HD2	1.91	0.41
1:C:55:VAL:O	1:C:55:VAL:HG13	2.21	0.41
1:A:136:LEU:HD13	1:A:136:LEU:HA	1.86	0.41
1:A:17:ARG:NH2	1:A:68:TYR:HB3	2.35	0.41
1:A:224:THR:HG23	1:A:226:SER:H	1.85	0.41
1:A:47:VAL:O	1:A:47:VAL:HG22	2.21	0.41
1:A:8:THR:HB	1:A:12:LYS:O	2.21	0.41
1:C:170:ILE:HG13	1:C:172:VAL:HG13	2.03	0.41
1:C:269:ASN:N	1:C:269:ASN:ND2	2.60	0.41
1:C:62:ILE:HD12	1:C:104:TYR:OH	2.21	0.41
1:A:54:PHE:CD2	1:A:54:PHE:N	2.88	0.41
1:A:305:MET:SD	1:A:309:LEU:CD2	3.07	0.41
1:C:33:PRO:O	1:C:50:ASN:ND2	2.54	0.41
1:C:40:LEU:HD13	1:C:108:GLN:NE2	2.36	0.41
1:A:83:TYR:O	1:A:141:PRO:HB2	2.22	0.41
1:A:127:THR:O	1:A:129:LEU:HD13	2.21	0.40
1:A:175:ASN:O	1:A:182:HIS:HE1	2.05	0.40
1:C:238:TYR:O	1:C:239:THR:C	2.57	0.40
1:A:134:ILE:HG13	1:A:134:ILE:H	1.57	0.40
1:A:28:LYS:HG3	1:A:28:LYS:H	1.66	0.40
1:A:219:LEU:HA	1:A:219:LEU:HD12	1.87	0.40
1:C:277:ILE:HG12	1:C:277:ILE:H	1.65	0.40
1:A:50:ASN:N	1:A:50:ASN:OD1	2.48	0.40
1:A:98:ARG:HH11	1:A:98:ARG:HD3	1.58	0.40
1:C:101:ASN:OD1	1:C:102:PRO:HD2	2.21	0.40
1:A:219:LEU:HD21	1:A:231:ARG:HG2	2.03	0.40
1:C:193:THR:HB	1:C:194:PRO:CD	2.51	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	328/335 (98%)	297 (90%)	24 (7%)	7 (2%)	9	16
1	C	329/335 (98%)	302 (92%)	25 (8%)	2 (1%)	30	56
All	All	657/670 (98%)	599 (91%)	49 (8%)	9 (1%)	14	28

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	23	MET
1	A	27	SER
1	A	83	TYR
1	C	23	MET
1	C	211	GLY
1	A	186	LEU
1	A	318	GLU
1	A	63	THR
1	A	93	PRO

### 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	286/291 (98%)	224 (78%)	62 (22%)	1	2
1	C	287/291 (99%)	231 (80%)	56 (20%)	2	3
All	All	573/582 (98%)	455 (79%)	118 (21%)	1	2

All (118) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	SER
1	A	7	ARG
1	A	8	THR
1	A	9	THR

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Mol	Chain	Res	Type
1	A	12	LYS
1	A	17	ARG
1	A	18	THR
1	A	19	MET
1	A	21	PHE
1	A	23	MET
1	A	24	GLU
1	A	27	SER
1	A	28	LYS
1	A	32	VAL
1	A	34	ARG
1	A	38	ILE
1	A	39	ARG
1	A	44	GLU
1	A	60	THR
1	A	63	THR
1	A	64	SER
1	A	67	LEU
1	A	69	ASP
1	A	71	VAL
1	A	73	GLU
1	A	74	LYS
1	A	82	TYR
1	A	97	THR
1	A	98	ARG
1	A	109	VAL
1	A	110	LEU
1	A	114	VAL
1	A	116	VAL
1	A	121	GLU
1	A	122	LYS
1	A	123	LEU
1	A	125	SER
1	A	134	ILE
1	A	136	LEU
1	A	142	LEU
1	A	143	HIS
1	A	153	SER
1	A	160	LYS
1	A	161	THR
1	A	167	ARG
1	A	212	GLN

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Mol	Chain	Res	Type
1	A	224	THR
1	A	237	LYS
1	A	244	ASN
1	A	269	ASN
1	A	277	ILE
1	A	279	THR
1	A	282	MET
1	A	287	LYS
1	A	300	SER
1	A	305	MET
1	A	309	LEU
1	A	310	ASN
1	A	312	GLN
1	A	316	THR
1	A	317	PHE
1	A	318	GLU
1	C	2	SER
1	C	4	LEU
1	C	7	ARG
1	C	13	SER
1	C	17	ARG
1	C	19	MET
1	C	22	THR
1	C	23	MET
1	C	24	GLU
1	C	28	LYS
1	C	34	ARG
1	C	39	ARG
1	C	40	LEU
1	C	43	LYS
1	C	45	ASN
1	C	60	THR
1	C	74	LYS
1	C	82	TYR
1	C	95	LYS
1	C	110	LEU
1	C	114	VAL
1	C	116	VAL
1	C	117	ASP
1	C	124	THR
1	C	128	LEU
1	C	143	HIS

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Mol	Chain	Res	Type
1	C	160	LYS
1	C	161	THR
1	C	163	ILE
1	C	167	ARG
1	C	168	LYS
1	C	172	VAL
1	C	173	MET
1	C	176	SER
1	C	183	GLN
1	C	184	THR
1	C	201	MET
1	C	208	THR
1	C	212	GLN
1	C	228	ARG
1	C	235	TRP
1	C	246	THR
1	C	247	GLU
1	C	263	LYS
1	C	268	THR
1	C	269	ASN
1	C	273	THR
1	C	287	LYS
1	C	293	LEU
1	C	297	SER
1	C	303	SER
1	C	304	LEU
1	C	305	MET
1	C	311	SER
1	C	314	LEU
1	C	322	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (19) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	35	ASN
1	A	49	ASN
1	A	130	ASN
1	A	182	HIS
1	A	183	GLN
1	A	185	ASN
1	A	198	GLN
1	A	212	GLN

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Mol	Chain	Res	Type
1	A	251	ASN
1	A	260	ASN
1	A	312	GLN
1	C	45	ASN
1	C	108	GLN
1	C	183	GLN
1	C	185	ASN
1	C	269	ASN
1	C	288	ASN
1	C	310	ASN
1	C	312	GLN

### 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](#)

2 ligands are 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
2	PNV	A	903	-	23,26,26	1.18	3 (13%)	34,39,39	3.14	11 (32%)
2	PNV	C	904	-	23,26,26	1.45	4 (17%)	34,39,39	3.41	16 (47%)

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	PNV	A	903	-	-	0/9/44/44	0/3/3/3
2	PNV	C	904	-	-	0/9/44/44	0/3/3/3

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	904	PNV	C10-S11	-3.82	1.77	1.85
2	A	903	PNV	C10-S11	-3.27	1.78	1.85
2	C	904	PNV	C8-S11	-3.10	1.76	1.81
2	C	904	PNV	C6-N7	-2.70	1.31	1.37
2	A	903	PNV	C8-S11	-2.61	1.77	1.81
2	A	903	PNV	C6-N7	-2.30	1.32	1.37
2	C	904	PNV	C5-C6	-2.02	1.49	1.54

All (27) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	903	PNV	S11-C8-N7	-9.39	92.37	105.09
2	C	904	PNV	S11-C8-N7	-7.73	94.62	105.09
2	C	904	PNV	C5-C8-N7	-5.57	80.80	87.98
2	C	904	PNV	C2-C3-N4	-3.71	109.66	116.21
2	A	903	PNV	C5-C8-N7	-3.43	83.56	87.98
2	C	904	PNV	C10-C9-N7	-2.51	102.67	106.45
2	C	904	PNV	C5-C6-N7	-2.39	88.61	91.87
2	C	904	PNV	C15-C10-C9	-2.34	106.30	111.56
2	A	903	PNV	C10-C9-N7	-2.12	103.26	106.45
2	C	904	PNV	C8-C5-C6	2.23	89.04	85.20
2	C	904	PNV	C12-C10-C9	2.29	116.70	111.56
2	A	903	PNV	O17-C6-N7	3.45	136.59	131.64
2	C	904	PNV	C9-N7-C6	3.47	134.13	125.99
2	A	903	PNV	C6-C5-N4	3.59	125.80	115.36
2	C	904	PNV	C8-C5-N4	3.75	126.51	118.21
2	A	903	PNV	C8-N7-C6	3.77	98.82	93.89
2	A	903	PNV	C5-C8-S11	3.91	125.54	119.40
2	A	903	PNV	C9-N7-C6	4.79	137.25	125.99
2	C	904	PNV	O17-C6-N7	5.01	138.84	131.64
2	A	903	PNV	C2-O1-C19	5.06	127.18	117.62
2	C	904	PNV	C8-N7-C6	5.08	100.53	93.89

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	903	PNV	C8-N7-C9	5.60	123.04	117.36
2	C	904	PNV	C5-C8-S11	6.05	128.91	119.40
2	C	904	PNV	C2-O1-C19	6.34	129.60	117.62
2	C	904	PNV	C5-N4-C3	6.56	134.70	121.78
2	C	904	PNV	C8-N7-C9	6.89	124.34	117.36
2	A	903	PNV	C5-N4-C3	7.98	137.48	121.78

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	903	PNV	4	0
2	C	904	PNV	8	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 ⓘ

EDS was not executed - this section will therefore be empty.

### 6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

EDS was not executed - this section will therefore be empty.

### 6.3 Carbohydrates ⓘ

EDS was not executed - this section will therefore be empty.

### 6.4 Ligands ⓘ

EDS was not executed - this section will therefore be empty.

### 6.5 Other polymers ⓘ

EDS was not executed - this section will therefore be empty.