



# Full wwPDB X-ray Structure Validation Report ⓘ

Nov 1, 2023 – 04:17 PM JST

PDB ID : 5JYK  
Title : Deg9 crystal under 289K  
Authors : Ouyang, M.; Zhang, L.X.  
Deposited on : 2016-05-14  
Resolution : 2.30 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

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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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 : 1.8.5 (274361), CSD as541be (2020)  
Xtrriage (Phenix) : 1.13  
EDS : 2.36  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.36

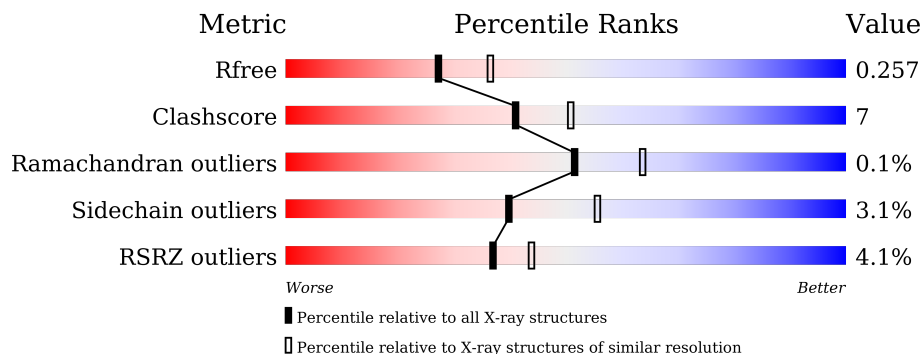
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.30 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	130704	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

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 of the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	566	 % 72% 9% 18%
1	B	566	 6% 59% 13% 27%

## 2 Entry composition i

There are 3 unique types of molecules in this entry. The entry contains 7294 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 Protease Do-like 9.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	465	3611	2311	602	682	16	0	6	0
1	B	412	3176	2031	535	598	12	0	7	0

There are 76 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	27	MET	-	expression tag	UNP Q9FL12
A	28	GLY	-	expression tag	UNP Q9FL12
A	29	SER	-	expression tag	UNP Q9FL12
A	30	SER	-	expression tag	UNP Q9FL12
A	31	HIS	-	expression tag	UNP Q9FL12
A	32	HIS	-	expression tag	UNP Q9FL12
A	33	HIS	-	expression tag	UNP Q9FL12
A	34	HIS	-	expression tag	UNP Q9FL12
A	35	HIS	-	expression tag	UNP Q9FL12
A	36	HIS	-	expression tag	UNP Q9FL12
A	37	SER	-	expression tag	UNP Q9FL12
A	38	SER	-	expression tag	UNP Q9FL12
A	39	GLY	-	expression tag	UNP Q9FL12
A	40	LEU	-	expression tag	UNP Q9FL12
A	41	VAL	-	expression tag	UNP Q9FL12
A	42	PRO	-	expression tag	UNP Q9FL12
A	43	ARG	-	expression tag	UNP Q9FL12
A	44	GLY	-	expression tag	UNP Q9FL12
A	45	SER	-	expression tag	UNP Q9FL12
A	46	HIS	-	expression tag	UNP Q9FL12
A	47	MET	-	expression tag	UNP Q9FL12
A	48	ALA	-	expression tag	UNP Q9FL12
A	49	SER	-	expression tag	UNP Q9FL12
A	50	MET	-	expression tag	UNP Q9FL12
A	51	THR	-	expression tag	UNP Q9FL12

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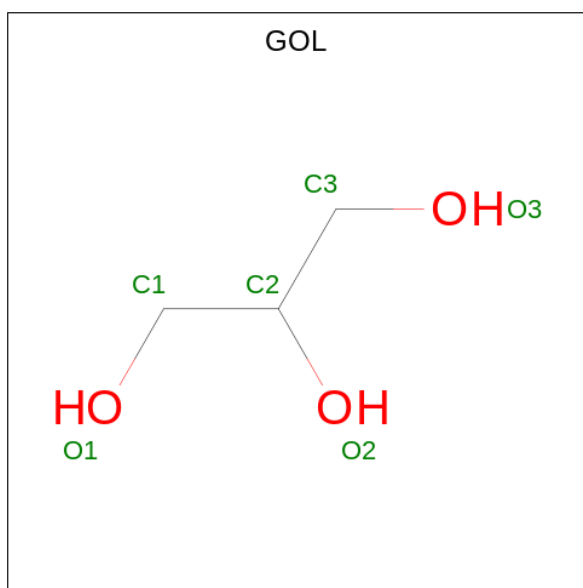
Chain	Residue	Modelled	Actual	Comment	Reference
A	52	GLY	-	expression tag	UNP Q9FL12
A	53	GLY	-	expression tag	UNP Q9FL12
A	54	GLN	-	expression tag	UNP Q9FL12
A	55	GLN	-	expression tag	UNP Q9FL12
A	56	MET	-	expression tag	UNP Q9FL12
A	57	GLY	-	expression tag	UNP Q9FL12
A	58	ARG	-	expression tag	UNP Q9FL12
A	59	GLY	-	expression tag	UNP Q9FL12
A	60	SER	-	expression tag	UNP Q9FL12
A	61	GLU	-	expression tag	UNP Q9FL12
A	62	PHE	-	expression tag	UNP Q9FL12
A	63	GLU	-	expression tag	UNP Q9FL12
A	64	LEU	-	expression tag	UNP Q9FL12
B	27	MET	-	expression tag	UNP Q9FL12
B	28	GLY	-	expression tag	UNP Q9FL12
B	29	SER	-	expression tag	UNP Q9FL12
B	30	SER	-	expression tag	UNP Q9FL12
B	31	HIS	-	expression tag	UNP Q9FL12
B	32	HIS	-	expression tag	UNP Q9FL12
B	33	HIS	-	expression tag	UNP Q9FL12
B	34	HIS	-	expression tag	UNP Q9FL12
B	35	HIS	-	expression tag	UNP Q9FL12
B	36	HIS	-	expression tag	UNP Q9FL12
B	37	SER	-	expression tag	UNP Q9FL12
B	38	SER	-	expression tag	UNP Q9FL12
B	39	GLY	-	expression tag	UNP Q9FL12
B	40	LEU	-	expression tag	UNP Q9FL12
B	41	VAL	-	expression tag	UNP Q9FL12
B	42	PRO	-	expression tag	UNP Q9FL12
B	43	ARG	-	expression tag	UNP Q9FL12
B	44	GLY	-	expression tag	UNP Q9FL12
B	45	SER	-	expression tag	UNP Q9FL12
B	46	HIS	-	expression tag	UNP Q9FL12
B	47	MET	-	expression tag	UNP Q9FL12
B	48	ALA	-	expression tag	UNP Q9FL12
B	49	SER	-	expression tag	UNP Q9FL12
B	50	MET	-	expression tag	UNP Q9FL12
B	51	THR	-	expression tag	UNP Q9FL12
B	52	GLY	-	expression tag	UNP Q9FL12
B	53	GLY	-	expression tag	UNP Q9FL12
B	54	GLN	-	expression tag	UNP Q9FL12
B	55	GLN	-	expression tag	UNP Q9FL12

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Chain	Residue	Modelled	Actual	Comment	Reference
B	56	MET	-	expression tag	UNP Q9FL12
B	57	GLY	-	expression tag	UNP Q9FL12
B	58	ARG	-	expression tag	UNP Q9FL12
B	59	GLY	-	expression tag	UNP Q9FL12
B	60	SER	-	expression tag	UNP Q9FL12
B	61	GLU	-	expression tag	UNP Q9FL12
B	62	PHE	-	expression tag	UNP Q9FL12
B	63	GLU	-	expression tag	UNP Q9FL12
B	64	LEU	-	expression tag	UNP Q9FL12

- Molecule 2 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
2	A	1	Total	C O	0	0
			6	3 3		

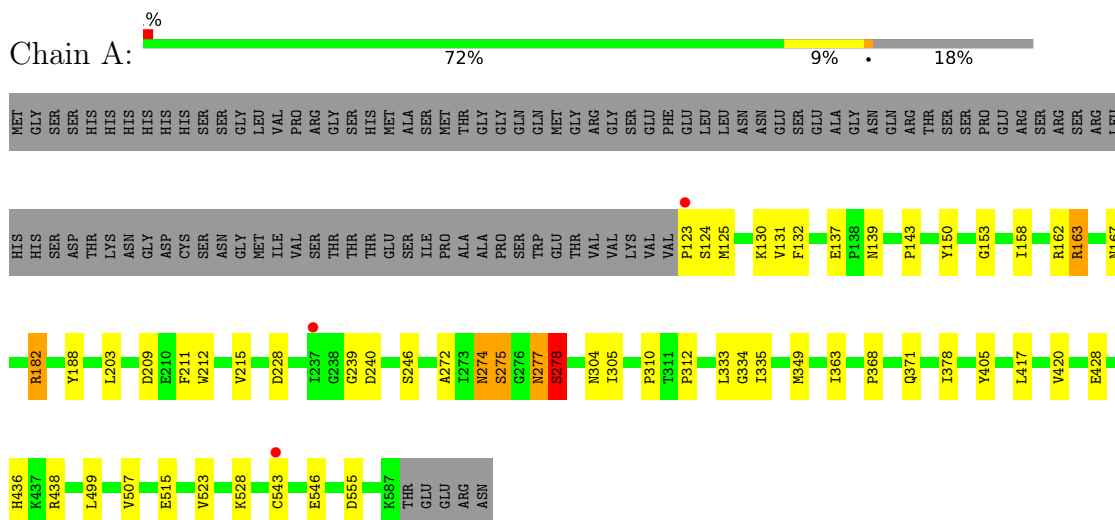
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	277	Total	O	0	0
			277	277		
3	B	224	Total	O	0	0
			224	224		

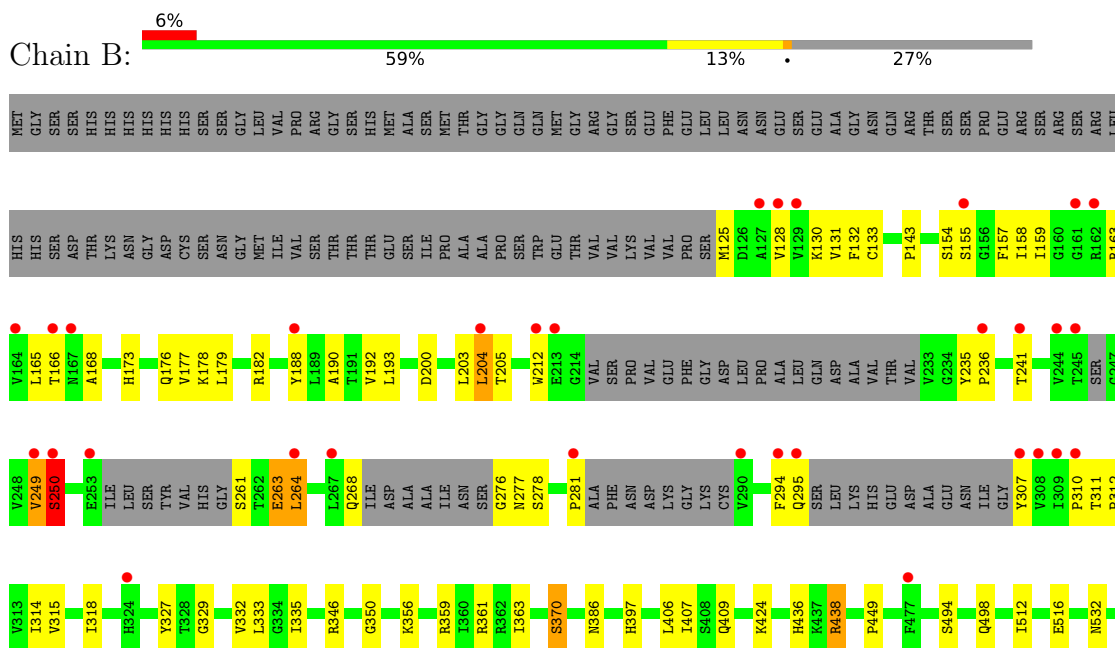
### 3 Residue-property plots [i](#)

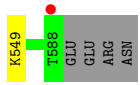
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: Protease Do-like 9



- Molecule 1: Protease Do-like 9





## 4 Data and refinement statistics i

Property	Value	Source
Space group	I 4	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	132.16Å 132.16Å 154.33Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	35.66 – 2.30 38.80 – 2.30	Depositor EDS
% Data completeness (in resolution range)	84.5 (35.66-2.30) 84.5 (38.80-2.30)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	5.76 (at 2.29Å)	Xtrriage
Refinement program	PHENIX 1.10.1_2155	Depositor
R, $R_{free}$	0.198 , 0.256 0.200 , 0.257	Depositor DCC
$R_{free}$ test set	2544 reflections (5.11%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	30.2	Xtrriage
Anisotropy	0.204	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 48.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.52$ , $\langle L^2 \rangle = 0.36$	Xtrriage
Estimated twinning fraction	0.017 for -h,k,-l	Xtrriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	7294	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	33.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.02% 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, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.



## 5 Model quality i

### 5.1 Standard geometry i

Bond lengths and bond angles in the following residue types are not validated in this section: 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	0.43	1/3696 (0.0%)	0.59	1/5018 (0.0%)
1	B	0.40	0/3244	0.60	2/4396 (0.0%)
All	All	0.41	1/6940 (0.0%)	0.59	3/9414 (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	2

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	278	SER	C-N	-6.90	1.20	1.33

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	274	ASN	CB-CA-C	-5.98	98.44	110.40
1	B	264	LEU	CA-CB-CG	5.78	128.58	115.30
1	B	165	LEU	CA-CB-CG	5.02	126.84	115.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	249	VAL	Peptide

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Mol	Chain	Res	Type	Group
1	B	263	GLU	Peptide

## 5.2 Too-close contacts [i](#)

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	3611	0	3567	41	0
1	B	3176	0	3058	55	0
2	A	6	0	8	3	0
3	A	277	0	0	8	0
3	B	224	0	0	23	0
All	All	7294	0	6633	95	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 7.

All (95) 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:A:274:ASN:ND2	1:A:275:SER:O	1.88	1.06
1:B:178:LYS:O	3:B:601:HOH:O	1.88	0.91
1:A:272:ALA:HB2	1:A:304:ASN:HA	1.53	0.90
1:B:178:LYS:O	3:B:602:HOH:O	1.96	0.81
1:B:192:VAL:HG22	1:B:204:LEU:HD12	1.65	0.78
1:B:386[B]:ASN:OD1	3:B:603:HOH:O	2.02	0.76
1:B:176:GLN:O	3:B:604:HOH:O	2.04	0.74
1:A:167:ASN:OD1	1:A:278:SER:OG	2.05	0.73
1:B:132:PHE:O	3:B:602:HOH:O	2.05	0.72
1:B:177:VAL:HG13	1:B:190:ALA:HB3	1.73	0.71
1:B:264:LEU:HD11	1:B:310:PRO:HG2	1.73	0.71
1:A:130:LYS:NZ	1:A:239:GLY:O	2.24	0.70
1:A:163[A]:ARG:NH2	3:A:708:HOH:O	2.24	0.69
1:A:274:ASN:H	1:A:277:ASN:HD21	1.40	0.69
1:B:261:SER:N	3:B:612:HOH:O	2.26	0.68
1:B:350:GLY:HA3	1:B:424:LYS:HG3	1.76	0.67
1:A:123:PRO:HA	1:A:125:MET:H	1.61	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:546:GLU:OE1	3:A:701:HOH:O	2.15	0.64
1:B:549:LYS:NZ	3:B:613:HOH:O	2.29	0.64
1:B:157:PHE:O	3:B:605:HOH:O	2.16	0.62
1:B:333:LEU:HB2	1:B:407:ILE:HD13	1.81	0.62
1:B:158:ILE:HG23	1:B:212:TRP:HZ3	1.64	0.62
1:B:179:LEU:N	1:B:188:TYR:O	2.29	0.61
1:A:228:ASP:OD2	3:A:702:HOH:O	2.15	0.60
1:A:130:LYS:HD3	1:A:132:PHE:CZ	2.37	0.58
1:B:397:HIS:O	3:B:606:HOH:O	2.17	0.58
1:B:310:PRO:O	1:B:314:ILE:HG13	2.05	0.57
1:B:327:TYR:CZ	1:B:329:GLY:HA2	2.39	0.57
1:B:332:VAL:HG21	1:B:436:HIS:HB2	1.87	0.56
1:B:249:VAL:O	1:B:250:SER:HB2	2.05	0.56
1:B:182[B]:ARG:NH1	3:B:621:HOH:O	2.38	0.56
1:A:274:ASN:O	1:A:277:ASN:ND2	2.39	0.56
1:B:363:ILE:HG21	1:B:370:SER:HA	1.88	0.55
1:A:277:ASN:HD22	1:A:277:ASN:H	1.55	0.55
1:A:368:PRO:HA	1:A:371:GLN:HG2	1.89	0.54
1:A:310:PRO:HB2	1:A:312:PRO:HD2	1.89	0.54
1:B:235:TYR:O	1:B:277:ASN:HB2	2.06	0.54
1:A:162:ARG:HG3	1:A:212:TRP:CE2	2.43	0.54
1:A:333:LEU:H	2:A:601:GOL:H11	1.73	0.53
1:A:507:VAL:HG22	1:A:515:GLU:HG2	1.90	0.53
1:B:268:GLN:O	3:B:607:HOH:O	2.19	0.52
1:B:132:PHE:O	3:B:604:HOH:O	2.19	0.52
1:A:123:PRO:HA	1:A:125:MET:N	2.24	0.52
1:A:277:ASN:HD22	1:A:277:ASN:N	2.07	0.51
1:A:158:ILE:HG23	1:A:212:TRP:HZ3	1.75	0.51
1:B:278:SER:OG	1:B:294:PHE:HA	2.11	0.51
1:A:335:ILE:H	2:A:601:GOL:H12	1.77	0.50
1:B:143:PRO:HB3	1:B:449:PRO:HB2	1.93	0.50
1:A:543:CYS:O	3:A:703:HOH:O	2.19	0.50
1:B:278:SER:HB2	1:B:295:GLN:H	1.77	0.49
1:B:236:PRO:HD2	1:B:241:THR:O	2.11	0.49
1:A:528:LYS:NZ	3:A:720:HOH:O	2.38	0.49
1:B:335:ILE:HG22	1:B:363:ILE:HG12	1.95	0.49
1:A:378:ILE:O	1:A:420:VAL:HA	2.13	0.49
1:B:159:ILE:HG12	3:B:605:HOH:O	2.13	0.49
1:B:166:THR:OG1	3:B:608:HOH:O	2.19	0.49
1:B:311:THR:O	1:B:315:VAL:HG22	2.13	0.48
1:A:555:ASP:O	1:B:361:ARG:HG2	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:155[A]:SER:OG	1:B:277:ASN:HB3	2.14	0.48
1:B:346[B]:ARG:NH2	3:B:627:HOH:O	2.45	0.48
1:B:193:LEU:HD11	1:B:205:THR:HB	1.97	0.47
1:B:311:THR:N	1:B:312:PRO:HD2	2.29	0.47
1:A:182:ARG:H	1:A:182:ARG:HG3	1.48	0.47
1:A:209:ASP:OD1	3:A:704:HOH:O	2.20	0.47
1:B:276:GLY:HA2	1:B:277:ASN:HA	1.64	0.46
1:B:173:HIS:ND1	3:B:611:HOH:O	2.24	0.46
1:B:168:ALA:HB3	1:B:200:ASP:HA	1.98	0.46
1:A:240:ASP:HB2	3:A:721:HOH:O	2.15	0.46
1:A:436:HIS:CE1	1:A:438:ARG:HG3	2.51	0.45
1:B:159:ILE:HG13	1:B:163:ARG:HB2	1.98	0.45
1:B:193:LEU:N	1:B:203:LEU:O	2.43	0.45
1:A:131:VAL:O	1:A:153:GLY:HA2	2.17	0.45
1:A:334:GLY:H	2:A:601:GOL:C1	2.29	0.45
1:B:130:LYS:NZ	3:B:634:HOH:O	2.49	0.45
1:A:163[A]:ARG:HG2	1:A:203:LEU:HD11	1.99	0.45
1:B:133:CYS:HA	3:B:604:HOH:O	2.17	0.45
1:A:335:ILE:HG22	1:A:363:ILE:HG12	1.99	0.44
1:B:157:PHE:CG	1:B:281:PRO:HG3	2.53	0.44
1:B:131:VAL:HB	1:B:154:SER:OG	2.18	0.43
1:A:212:TRP:O	1:A:215:VAL:HG22	2.19	0.43
1:B:278:SER:HB3	3:B:771:HOH:O	2.18	0.43
1:A:137:GLU:OE2	1:A:150:TYR:OH	2.26	0.42
1:B:498:GLN:OE1	1:B:532:ASN:HB2	2.19	0.41
1:B:132:PHE:HD1	3:B:601:HOH:O	2.02	0.41
1:A:277:ASN:ND2	1:A:277:ASN:H	2.18	0.41
1:B:314:ILE:O	1:B:318:ILE:HG12	2.21	0.41
1:A:124:SER:HB2	3:A:884:HOH:O	2.20	0.41
1:B:356[A]:LYS:O	3:B:603:HOH:O	2.18	0.41
1:A:417:LEU:HD22	1:A:428:GLU:HG2	2.03	0.40
1:A:349[B]:MET:HE3	1:A:378:ILE:HD11	2.02	0.40
1:B:359:ARG:NH2	3:B:625:HOH:O	2.43	0.40
1:B:128:VAL:HG22	1:B:281:PRO:HG2	2.03	0.40
1:A:139:ASN:O	1:A:143:PRO:HA	2.22	0.40
1:A:188:TYR:CD2	1:A:211:PHE:HB2	2.56	0.40
1:B:438:ARG:HD3	3:B:675:HOH:O	2.20	0.40

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	469/566 (83%)	460 (98%)	9 (2%)	0	100	100
1	B	405/566 (72%)	384 (95%)	20 (5%)	1 (0%)	47	58
All	All	874/1132 (77%)	844 (97%)	29 (3%)	1 (0%)	51	64

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	250	SER

### 5.3.2 Protein sidechains [i](#)

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	391/490 (80%)	380 (97%)	11 (3%)	43	60
1	B	329/490 (67%)	317 (96%)	12 (4%)	35	49
All	All	720/980 (74%)	697 (97%)	23 (3%)	40	54

All (23) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	163[A]	ARG
1	A	163[B]	ARG
1	A	182	ARG
1	A	246	SER
1	A	275	SER

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Mol	Chain	Res	Type
1	A	277	ASN
1	A	278	SER
1	A	305	ILE
1	A	405	TYR
1	A	499	LEU
1	A	523	VAL
1	B	125	MET
1	B	204	LEU
1	B	250	SER
1	B	263	GLU
1	B	307	TYR
1	B	370	SER
1	B	406	LEU
1	B	409	GLN
1	B	438	ARG
1	B	494	SER
1	B	512	ILE
1	B	516	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	277	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 monosaccharides in this entry.

### 5.6 Ligand geometry [i](#)

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
2	GOL	A	601	-	5,5,5	0.48	0	5,5,5	0.22	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	GOL	A	601	-	-	2/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	601	GOL	O1-C1-C2-C3
2	A	601	GOL	O1-C1-C2-O2

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	601	GOL	3	0

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues

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	465/566 (82%)	-0.38	3 (0%) 89 92	14, 27, 47, 72	0
1	B	412/566 (72%)	0.11	33 (8%) 12 16	13, 32, 71, 86	3 (0%)
All	All	877/1132 (77%)	-0.15	36 (4%) 37 44	13, 29, 65, 86	3 (0%)

All (36) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	244	VAL	6.4
1	B	128	VAL	6.2
1	B	129	VAL	6.1
1	B	127	ALA	5.5
1	B	245	THR	4.7
1	B	236	PRO	4.6
1	B	267	LEU	4.6
1	B	308	VAL	4.5
1	B	281	PRO	4.3
1	B	161	GLY	4.2
1	B	309	ILE	3.8
1	B	310	PRO	3.7
1	B	295	GLN	3.7
1	B	588	THR	3.5
1	B	241	THR	3.3
1	A	123	PRO	3.2
1	B	188	TYR	3.1
1	B	162	ARG	2.9
1	B	253	GLU	2.8
1	B	307	TYR	2.7
1	B	164	VAL	2.7
1	B	250	SER	2.6
1	B	213	GLU	2.5
1	B	249	VAL	2.4

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Mol	Chain	Res	Type	RSRZ
1	B	477	PHE	2.4
1	B	155[A]	SER	2.3
1	B	204	LEU	2.3
1	A	543	CYS	2.3
1	B	324	HIS	2.2
1	B	166	THR	2.2
1	A	237	ILE	2.2
1	B	294	PHE	2.1
1	B	212	TRP	2.1
1	B	290	VAL	2.0
1	B	167	ASN	2.0
1	B	264	LEU	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 monosaccharides in this entry.

## 6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 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	B-factors(Å <sup>2</sup> )	Q<0.9
2	GOL	A	601	6/6	0.89	0.14	23,34,39,43	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.