Full wwPDB X-ray Structure Validation Report (i)

Mar 17, 2026 – 11:54 PM UTC

PDB ID	:	1Q8F / pdb_00001q8f
Title	:	Crystal Structure of the E.coli pyrimidine nucleoside hydrolase yeiK
Authors	:	Giabbai, B.; Degano, M.
Deposited on	:	2003-08-21
Resolution	:	1.70 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*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (1)) were used in the production of this report:

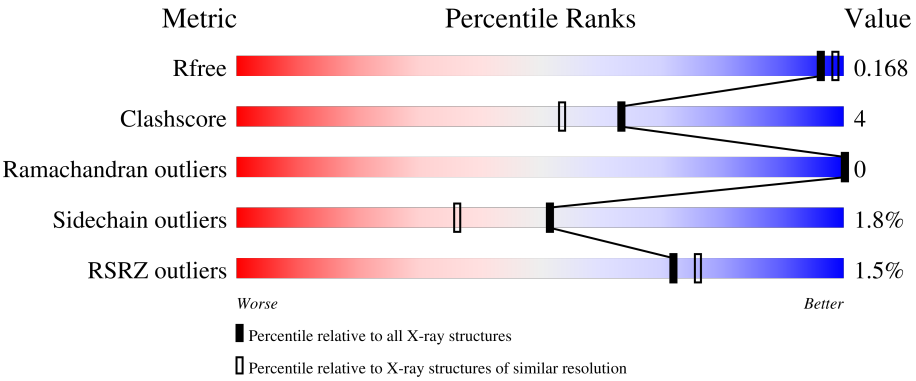
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 1.70 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}	180053	5551 (1.70-1.70)
Clashscore	190562	5924 (1.70-1.70)
Ramachandran outliers	187476	5846 (1.70-1.70)
Sidechain outliers	187428	5846 (1.70-1.70)
RSRZ outliers	180081	5554 (1.70-1.70)

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 >=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 <=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	313	93% 5%
1	B	313	4% 90% 8%
1	C	313	89% 9%
1	D	313	93% 5%

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
3	GOL	C	3007	-	-	X	-
3	GOL	D	3014	-	-	X	-

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 10415 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 Pyrimidine nucleoside hydrolase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	308	Total	C	N	O	S	0	0	0
			2315	1469	385	441	20			
1	B	308	Total	C	N	O	S	0	0	0
			2315	1469	385	441	20			
1	C	308	Total	C	N	O	S	0	0	0
			2315	1469	385	441	20			
1	D	308	Total	C	N	O	S	0	0	0
			2315	1469	385	441	20			

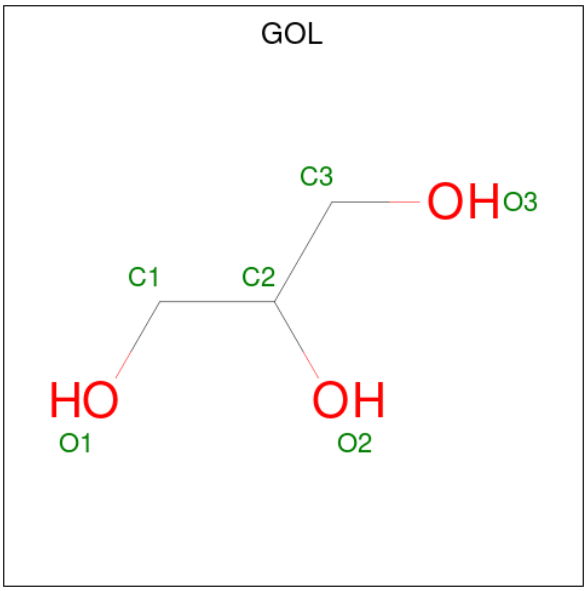
There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	84	ASP	GLU	cloning artifact	UNP P33022
B	84	ASP	GLU	cloning artifact	UNP P33022
C	84	ASP	GLU	cloning artifact	UNP P33022
D	84	ASP	GLU	cloning artifact	UNP P33022

- Molecule 2 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Ca	0	0
			1	1		
2	B	1	Total	Ca	0	0
			1	1		
2	C	1	Total	Ca	0	0
			1	1		
2	D	1	Total	Ca	0	0
			1	1		

- Molecule 3 is GLYCEROL (CCD ID: 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	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	B	1	Total	C	O	0	0
			6	3	3		
3	B	1	Total	C	O	0	0
			6	3	3		
3	C	1	Total	C	O	0	0
			6	3	3		
3	C	1	Total	C	O	0	0
			6	3	3		
3	C	1	Total	C	O	0	0
			6	3	3		
3	C	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		

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

- Molecule 4 is water.

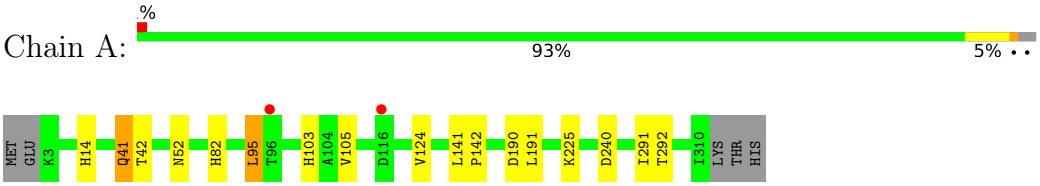
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	274	Total O 274 274	0	0
4	B	168	Total O 168 168	0	0
4	C	290	Total O 290 290	0	0
4	D	323	Total O 323 323	0	0

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.

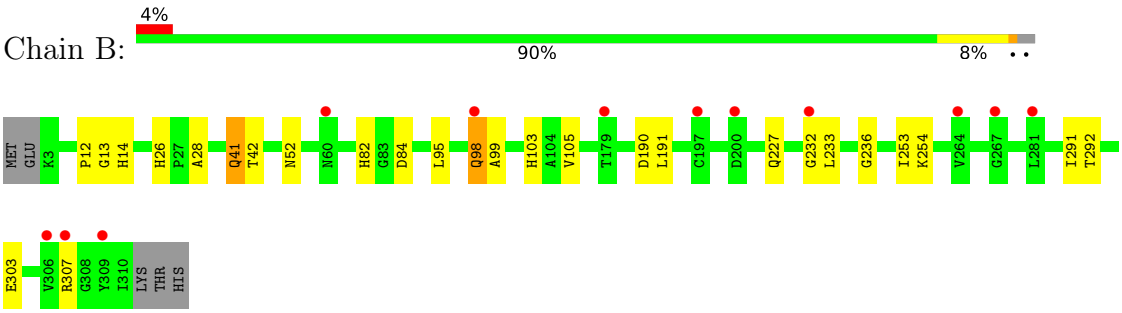
• Molecule 1: Pyrimidine nucleoside hydrolase

Chain A:



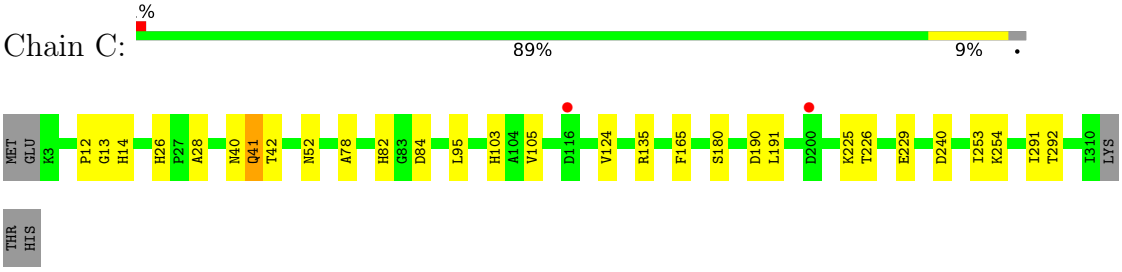
• Molecule 1: Pyrimidine nucleoside hydrolase

Chain B:



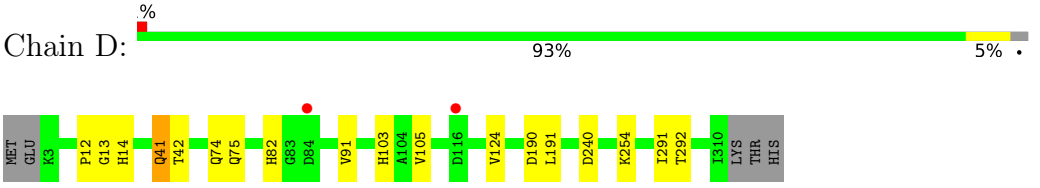
• Molecule 1: Pyrimidine nucleoside hydrolase

Chain C:



• Molecule 1: Pyrimidine nucleoside hydrolase

Chain D:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α, β, γ	44.81Å 85.71Å 90.68Å 112.95° 101.95° 85.92°	Depositor
Resolution (Å)	43.83 – 1.70 43.83 – 1.70	Depositor EDS
% Data completeness (in resolution range)	91.5 (43.83-1.70) 91.5 (43.83-1.70)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.05	Depositor
$< I/\sigma(I) >$ [1]	3.27 (at 1.70Å)	Xtriage
Refinement program	REFMAC 5.1.19	Depositor
R, R_{free}	0.153 , 0.170 0.153 , 0.168	Depositor DCC
R_{free} test set	1247 reflections (1.02%)	wwPDB-VP
Wilson B-factor (Å^2)	15.1	Xtriage
Anisotropy	0.180	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.38 , 48.0	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	10415	wwPDB-VP
Average B, all atoms (Å^2)	15.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.91% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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, CA

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	0.40	0/2360	0.84	0/3215
1	B	0.38	0/2360	0.85	1/3215 (0.0%)
1	C	0.41	0/2360	0.86	0/3215
1	D	0.43	0/2360	0.85	0/3215
All	All	0.41	0/9440	0.85	1/12860 (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

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	233	LEU	N-CA-C	5.64	118.73	109.76

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	232	GLY	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	2315	0	2321	10	0
1	B	2315	0	2321	14	0
1	C	2315	0	2321	30	0
1	D	2315	0	2321	14	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
3	A	30	0	39	1	0
3	B	18	0	23	1	0
3	C	24	0	32	20	0
3	D	24	0	32	5	0
4	A	274	0	0	0	0
4	B	168	0	0	0	0
4	C	290	0	0	9	0
4	D	323	0	0	2	1
All	All	10415	0	9410	75	1

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 4.

All (75) 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)
3:C:3007:GOL:C1	4:C:3071:HOH:O	1.87	1.22
3:C:3007:GOL:O1	4:C:3071:HOH:O	1.76	1.00
3:C:3007:GOL:H12	4:C:3071:HOH:O	1.48	0.99
3:C:3007:GOL:O2	4:C:3282:HOH:O	1.64	0.94
1:D:75:GLN:H	3:D:3014:GOL:H31	1.33	0.93
1:C:78:ALA:HB1	3:C:3007:GOL:H32	1.59	0.84
1:C:135:ARG:HE	3:C:3012:GOL:H12	1.43	0.84
1:C:226:THR:HA	1:C:229:GLU:HG2	1.69	0.75
1:D:75:GLN:H	3:D:3014:GOL:C3	1.99	0.74
1:C:165:PHE:CB	3:C:3007:GOL:H2	2.18	0.74
1:C:26:HIS:HD2	1:C:28:ALA:H	1.36	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:225:LYS:HE2	4:C:3167:HOH:O	1.92	0.69
1:C:78:ALA:CB	3:C:3007:GOL:H32	2.24	0.67
1:A:82:HIS:HE1	3:A:3005:GOL:O1	1.77	0.67
1:C:82:HIS:HE1	4:C:3071:HOH:O	1.78	0.66
1:C:78:ALA:CB	3:C:3007:GOL:H11	2.25	0.65
1:B:26:HIS:HD2	1:B:28:ALA:H	1.45	0.65
1:C:103:HIS:HD2	1:C:105:VAL:H	1.45	0.64
1:D:82:HIS:HE1	3:D:3008:GOL:O1	1.81	0.64
1:D:14:HIS:ND1	1:D:82:HIS:HD2	1.96	0.64
1:D:75:GLN:N	3:D:3014:GOL:H31	2.11	0.63
1:C:14:HIS:ND1	1:C:82:HIS:HD2	1.97	0.62
1:C:40:ASN:ND2	3:C:3007:GOL:O1	2.33	0.61
1:B:103:HIS:HD2	1:B:105:VAL:H	1.51	0.58
1:A:14:HIS:ND1	1:A:82:HIS:HD2	2.01	0.58
1:B:14:HIS:ND1	1:B:82:HIS:HD2	2.01	0.58
1:B:303:GLU:OE2	1:B:307:ARG:NH1	2.37	0.57
1:C:165:PHE:HB2	3:C:3007:GOL:H2	1.87	0.57
1:C:225:LYS:HD2	4:C:3260:HOH:O	2.04	0.57
1:B:82:HIS:HE1	3:B:3006:GOL:O1	1.89	0.56
1:C:26:HIS:CD2	1:C:28:ALA:H	2.20	0.56
1:C:180:SER:HA	3:C:3012:GOL:H2	1.88	0.55
1:C:165:PHE:CG	3:C:3007:GOL:H2	2.43	0.54
3:C:3012:GOL:H11	4:D:3050:HOH:O	2.08	0.54
1:D:41:GLN:HE21	1:D:42:THR:H	1.56	0.54
1:D:103:HIS:HD2	1:D:105:VAL:H	1.56	0.53
1:D:74:GLN:HA	3:D:3014:GOL:H32	1.91	0.52
3:C:3007:GOL:C3	4:C:3158:HOH:O	2.48	0.52
1:A:103:HIS:HD2	1:A:105:VAL:H	1.58	0.52
1:A:52:ASN:ND2	1:A:95:LEU:HG	2.24	0.52
1:D:74:GLN:NE2	4:D:3330:HOH:O	2.31	0.51
1:B:98:GLN:HG3	1:B:99:ALA:N	2.26	0.51
1:B:291:ILE:HG22	1:B:292:THR:HG23	1.94	0.50
1:D:103:HIS:CD2	1:D:105:VAL:H	2.31	0.49
1:C:103:HIS:CD2	1:C:105:VAL:H	2.26	0.49
1:A:41:GLN:HE21	1:A:42:THR:H	1.61	0.48
1:B:191:LEU:HD11	1:B:253:ILE:HG23	1.95	0.48
1:B:26:HIS:CD2	1:B:28:ALA:H	2.29	0.48
1:C:52:ASN:ND2	1:C:95:LEU:HD13	2.28	0.48
1:B:103:HIS:CD2	1:B:105:VAL:H	2.30	0.48
1:C:291:ILE:HG22	1:C:292:THR:HG23	1.95	0.48
1:B:41:GLN:HE21	1:B:42:THR:H	1.62	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:82:HIS:HE1	3:C:3007:GOL:H12	1.78	0.47
1:C:191:LEU:HD11	1:C:253:ILE:HG23	1.97	0.46
1:C:52:ASN:HD22	1:C:95:LEU:HD13	1.79	0.46
1:A:291:ILE:HG22	1:A:292:THR:HG23	1.98	0.45
1:D:291:ILE:HG22	1:D:292:THR:HG23	1.98	0.45
1:C:82:HIS:CE1	3:C:3007:GOL:H12	2.52	0.45
1:B:227:GLN:HG3	1:B:236:GLY:HA2	1.99	0.44
1:D:124:VAL:HB	1:D:240:ASP:CG	2.43	0.44
1:B:12:PRO:HA	1:B:13:GLY:HA3	1.85	0.43
1:C:41:GLN:HE21	1:C:42:THR:H	1.64	0.43
1:C:124:VAL:HB	1:C:240:ASP:CG	2.42	0.43
1:A:141:LEU:HB2	1:A:142:PRO:HD3	2.01	0.43
1:A:124:VAL:HB	1:A:240:ASP:CG	2.43	0.43
1:A:191:LEU:C	1:A:191:LEU:HD23	2.44	0.43
1:B:52:ASN:HD22	1:B:52:ASN:HA	1.67	0.43
1:A:103:HIS:CD2	1:A:105:VAL:H	2.34	0.43
1:C:78:ALA:HB1	3:C:3007:GOL:H11	1.99	0.42
1:C:26:HIS:HE1	4:C:3156:HOH:O	2.03	0.42
1:D:12:PRO:HA	1:D:13:GLY:HA3	1.83	0.42
1:D:191:LEU:C	1:D:191:LEU:HD23	2.46	0.41
3:C:3003:GOL:O2	3:C:3007:GOL:O1	2.30	0.41
1:C:12:PRO:HA	1:C:13:GLY:HA3	1.82	0.40
1:C:82:HIS:HE1	3:C:3007:GOL:C1	2.34	0.40

All (1) 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)
4:D:3203:HOH:O	4:D:3337:HOH:O[1_655]	2.10	0.10

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	306/313 (98%)	299 (98%)	7 (2%)	0	100	100
1	B	306/313 (98%)	297 (97%)	9 (3%)	0	100	100
1	C	306/313 (98%)	295 (96%)	11 (4%)	0	100	100
1	D	306/313 (98%)	298 (97%)	8 (3%)	0	100	100
All	All	1224/1252 (98%)	1189 (97%)	35 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	252/257 (98%)	248 (98%)	4 (2%)	55	41
1	B	252/257 (98%)	246 (98%)	6 (2%)	43	26
1	C	252/257 (98%)	248 (98%)	4 (2%)	55	41
1	D	252/257 (98%)	248 (98%)	4 (2%)	55	41
All	All	1008/1028 (98%)	990 (98%)	18 (2%)	51	36

All (18) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	41	GLN
1	A	95	LEU
1	A	190	ASP
1	A	225	LYS
1	B	41	GLN
1	B	84	ASP
1	B	95	LEU
1	B	98	GLN
1	B	190	ASP
1	B	254	LYS
1	C	41	GLN
1	C	84	ASP
1	C	190	ASP

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Mol	Chain	Res	Type
1	C	254	LYS
1	D	41	GLN
1	D	91	VAL
1	D	190	ASP
1	D	254	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (33) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	40	ASN
1	A	41	GLN
1	A	52	ASN
1	A	82	HIS
1	A	103	HIS
1	A	221	ASN
1	A	227	GLN
1	A	265	ASN
1	B	26	HIS
1	B	40	ASN
1	B	41	GLN
1	B	52	ASN
1	B	60	ASN
1	B	82	HIS
1	B	103	HIS
1	B	221	ASN
1	B	227	GLN
1	B	265	ASN
1	C	26	HIS
1	C	40	ASN
1	C	41	GLN
1	C	52	ASN
1	C	82	HIS
1	C	103	HIS
1	C	221	ASN
1	C	265	ASN
1	D	40	ASN
1	D	41	GLN
1	D	52	ASN
1	D	82	HIS
1	D	103	HIS
1	D	221	ASN
1	D	265	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 oligosaccharides in this entry.

5.6 Ligand geometry

Of 20 ligands modelled in this entry, 4 are monoatomic - leaving 16 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
3	GOL	B	3002	2	5,5,5	0.39	0	5,5,5	0.34	0
3	GOL	D	3004	2	5,5,5	0.32	0	5,5,5	0.60	0
3	GOL	D	3008	-	5,5,5	0.32	0	5,5,5	0.87	0
3	GOL	D	3014	-	5,5,5	0.24	0	5,5,5	0.63	0
3	GOL	B	3011	-	5,5,5	0.39	0	5,5,5	0.31	0
3	GOL	A	3015	-	5,5,5	0.39	0	5,5,5	0.49	0
3	GOL	D	3017	-	5,5,5	0.39	0	5,5,5	0.33	0
3	GOL	C	3003	2	5,5,5	0.32	0	5,5,5	0.50	0
3	GOL	A	3009	-	5,5,5	0.39	0	5,5,5	0.24	0
3	GOL	C	3012	-	5,5,5	0.41	0	5,5,5	0.93	0
3	GOL	A	3001	2	5,5,5	0.35	0	5,5,5	0.43	0
3	GOL	A	3005	-	5,5,5	0.30	0	5,5,5	0.63	0
3	GOL	B	3006	-	5,5,5	0.35	0	5,5,5	0.74	0
3	GOL	C	3007	-	5,5,5	0.43	0	5,5,5	0.50	0
3	GOL	A	3010	-	5,5,5	0.35	0	5,5,5	0.35	0
3	GOL	C	3016	-	5,5,5	0.31	0	5,5,5	0.61	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	B	3002	2	-	0/4/4/4	-
3	GOL	D	3004	2	-	0/4/4/4	-
3	GOL	D	3008	-	-	0/4/4/4	-
3	GOL	D	3014	-	-	2/4/4/4	-
3	GOL	B	3011	-	-	0/4/4/4	-
3	GOL	A	3015	-	-	0/4/4/4	-
3	GOL	D	3017	-	-	0/4/4/4	-
3	GOL	C	3003	2	-	0/4/4/4	-
3	GOL	A	3009	-	-	2/4/4/4	-
3	GOL	C	3012	-	-	3/4/4/4	-
3	GOL	A	3001	2	-	0/4/4/4	-
3	GOL	A	3005	-	-	0/4/4/4	-
3	GOL	B	3006	-	-	0/4/4/4	-
3	GOL	C	3007	-	-	4/4/4/4	-
3	GOL	A	3010	-	-	0/4/4/4	-
3	GOL	C	3016	-	-	0/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (11) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	C	3007	GOL	O1-C1-C2-C3
3	C	3007	GOL	C1-C2-C3-O3
3	C	3012	GOL	O1-C1-C2-C3
3	D	3014	GOL	C1-C2-C3-O3
3	C	3007	GOL	O2-C2-C3-O3
3	C	3012	GOL	O1-C1-C2-O2
3	D	3014	GOL	O2-C2-C3-O3
3	C	3007	GOL	O1-C1-C2-O2
3	A	3009	GOL	O1-C1-C2-C3
3	A	3009	GOL	O1-C1-C2-O2
3	C	3012	GOL	O2-C2-C3-O3

There are no ring outliers.

7 monomers are involved in 27 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	D	3008	GOL	1	0
3	D	3014	GOL	4	0
3	C	3003	GOL	1	0
3	C	3012	GOL	3	0
3	A	3005	GOL	1	0
3	B	3006	GOL	1	0
3	C	3007	GOL	17	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^{th} 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^2)	Q<0.9
1	A	308/313 (98%)	-0.34	2 (0%) 85 88	8, 13, 20, 27	0
1	B	308/313 (98%)	0.39	12 (3%) 43 47	9, 14, 22, 29	0
1	C	308/313 (98%)	-0.29	2 (0%) 85 88	6, 12, 20, 26	0
1	D	308/313 (98%)	-0.51	2 (0%) 85 88	7, 11, 19, 26	0
All	All	1232/1252 (98%)	-0.19	18 (1%) 72 76	6, 13, 21, 29	0

All (18) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	232	GLY	3.0
1	B	281	LEU	2.9
1	B	60	ASN	2.8
1	B	307	ARG	2.6
1	C	200	ASP	2.6
1	D	116	ASP	2.5
1	A	116	ASP	2.5
1	B	306	VAL	2.5
1	B	197	CYS	2.4
1	A	96	THR	2.3
1	B	200	ASP	2.3
1	D	84	ASP	2.3
1	B	309	TYR	2.2
1	B	179	THR	2.2
1	C	116	ASP	2.1
1	B	98	GLN	2.1
1	B	264	VAL	2.0
1	B	267	GLY	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 oligosaccharides 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^{th} 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^2)	Q<0.9
3	GOL	A	3009	6/6	0.71	0.26	83,84,84,84	0
3	GOL	C	3012	6/6	0.80	0.17	15,23,26,33	0
3	GOL	C	3007	6/6	0.81	0.20	41,44,45,47	0
3	GOL	D	3014	6/6	0.81	0.15	25,30,34,39	0
3	GOL	B	3006	6/6	0.83	0.13	32,34,35,36	0
3	GOL	A	3015	6/6	0.90	0.10	22,23,26,28	0
3	GOL	D	3008	6/6	0.93	0.10	21,21,23,23	0
3	GOL	A	3005	6/6	0.93	0.10	20,21,23,24	0
3	GOL	A	3001	6/6	0.94	0.08	13,17,19,22	0
3	GOL	B	3011	6/6	0.94	0.08	23,24,26,29	0
3	GOL	B	3002	6/6	0.94	0.08	18,22,24,26	0
3	GOL	C	3016	6/6	0.95	0.06	15,17,21,26	0
3	GOL	D	3004	6/6	0.95	0.07	12,15,18,20	0
3	GOL	A	3010	6/6	0.96	0.06	18,20,23,27	0
3	GOL	C	3003	6/6	0.96	0.07	12,15,18,21	0
2	CA	B	2002	1/1	0.97	0.04	19,19,19,19	0
3	GOL	D	3017	6/6	0.97	0.05	13,16,17,20	0
2	CA	C	2003	1/1	1.00	0.02	11,11,11,11	0
2	CA	D	2004	1/1	1.00	0.01	11,11,11,11	0
2	CA	A	2001	1/1	1.00	0.01	13,13,13,13	0

6.5 Other polymers (i)

There are no such residues in this entry.