



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 20, 2026 – 10:48 AM UTC

PDB ID : 5JX3 / pdb_00005jx3
Title : Wild type D4 in orthorhombic space group
Authors : Schormann, N.; Chattopadhyay, D.
Deposited on : 2016-05-12
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

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>.

The following versions of software and data (see [references ⓘ](#)) 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

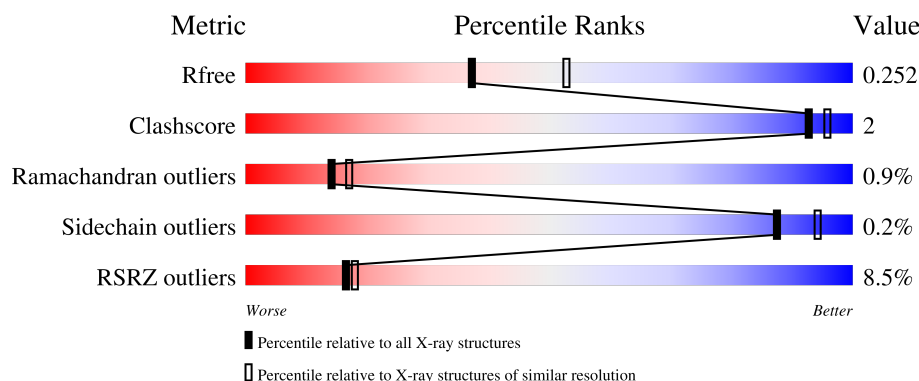
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

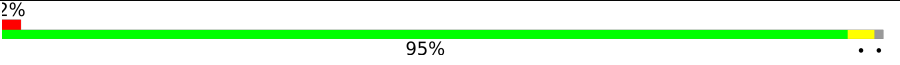
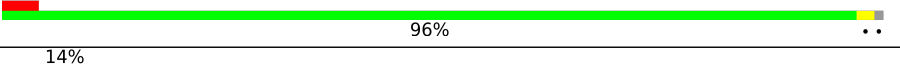
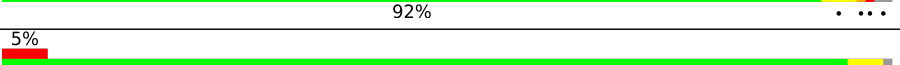
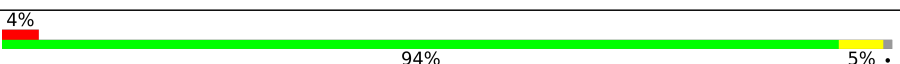
The reported resolution of this entry is 2.30 Å.

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.



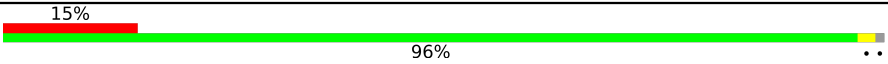
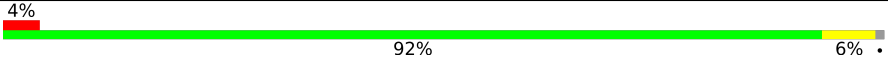
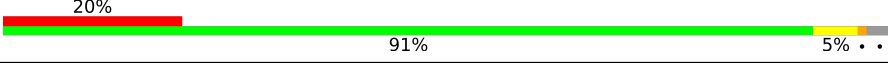
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	6319 (2.30-2.30)
Clashscore	190562	6919 (2.30-2.30)
Ramachandran outliers	187476	6854 (2.30-2.30)
Sidechain outliers	187428	6854 (2.30-2.30)
RSRZ outliers	180081	6325 (2.30-2.30)

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 ≥ 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	221	
1	B	221	
1	C	221	
1	D	221	
1	E	221	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	F	221	
1	G	221	
1	H	221	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 15051 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 Uracil-DNA glycosylase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	218	Total	C	N	O	S	0	0	0
			1770	1147	294	323	6			
1	B	218	Total	C	N	O	S	0	1	0
			1776	1150	295	325	6			
1	C	217	Total	C	N	O	S	0	2	0
			1762	1141	292	323	6			
1	D	219	Total	C	N	O	S	0	2	0
			1795	1161	300	328	6			
1	E	218	Total	C	N	O	S	0	1	0
			1779	1152	296	325	6			
1	F	218	Total	C	N	O	S	0	0	0
			1770	1147	294	323	6			
1	G	218	Total	C	N	O	S	0	2	0
			1785	1155	297	327	6			
1	H	215	Total	C	N	O	S	0	0	0
			1720	1118	281	315	6			

There are 40 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	GLY	-	expression tag	UNP P04303
A	-1	SER	-	expression tag	UNP P04303
A	0	HIS	-	expression tag	UNP P04303
A	17	ASN	ASP	see remark 999	UNP P04303
A	163	PHE	TYR	see remark 999	UNP P04303
B	-2	GLY	-	expression tag	UNP P04303
B	-1	SER	-	expression tag	UNP P04303
B	0	HIS	-	expression tag	UNP P04303
B	17	ASN	ASP	see remark 999	UNP P04303
B	163	PHE	TYR	see remark 999	UNP P04303
C	-2	GLY	-	expression tag	UNP P04303
C	-1	SER	-	expression tag	UNP P04303
C	0	HIS	-	expression tag	UNP P04303

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
C	17	ASN	ASP	see remark 999	UNP P04303
C	163	PHE	TYR	see remark 999	UNP P04303
D	-2	GLY	-	expression tag	UNP P04303
D	-1	SER	-	expression tag	UNP P04303
D	0	HIS	-	expression tag	UNP P04303
D	17	ASN	ASP	see remark 999	UNP P04303
D	163	PHE	TYR	see remark 999	UNP P04303
E	-2	GLY	-	expression tag	UNP P04303
E	-1	SER	-	expression tag	UNP P04303
E	0	HIS	-	expression tag	UNP P04303
E	17	ASN	ASP	see remark 999	UNP P04303
E	163	PHE	TYR	see remark 999	UNP P04303
F	-2	GLY	-	expression tag	UNP P04303
F	-1	SER	-	expression tag	UNP P04303
F	0	HIS	-	expression tag	UNP P04303
F	17	ASN	ASP	see remark 999	UNP P04303
F	163	PHE	TYR	see remark 999	UNP P04303
G	-2	GLY	-	expression tag	UNP P04303
G	-1	SER	-	expression tag	UNP P04303
G	0	HIS	-	expression tag	UNP P04303
G	17	ASN	ASP	see remark 999	UNP P04303
G	163	PHE	TYR	see remark 999	UNP P04303
H	-2	GLY	-	expression tag	UNP P04303
H	-1	SER	-	expression tag	UNP P04303
H	0	HIS	-	expression tag	UNP P04303
H	17	ASN	ASP	see remark 999	UNP P04303
H	163	PHE	TYR	see remark 999	UNP P04303

- Molecule 2 is GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃).



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

Continued on next page...

Continued from previous page...

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

- Molecule 3 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	D	1	Total	Cl	0	0
			1	1		
3	F	1	Total	Cl	0	0
			1	1		
3	G	1	Total	Cl	0	0
			1	1		
3	H	1	Total	Cl	0	0
			1	1		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	168	Total	O	0	0
			168	168		
4	B	107	Total	O	0	0
			107	107		
4	C	60	Total	O	0	0
			60	60		
4	D	127	Total	O	0	0
			127	127		
4	E	130	Total	O	0	0
			130	130		
4	F	60	Total	O	0	0
			60	60		
4	G	120	Total	O	0	0
			120	120		
4	H	28	Total	O	0	0
			28	28		

3 Residue-property plots

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.

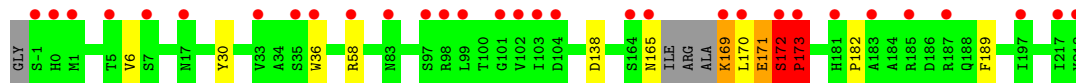
- Molecule 1: Uracil-DNA glycosylase



- Molecule 1: Uracil-DNA glycosylase



- Molecule 1: Uracil-DNA glycosylase



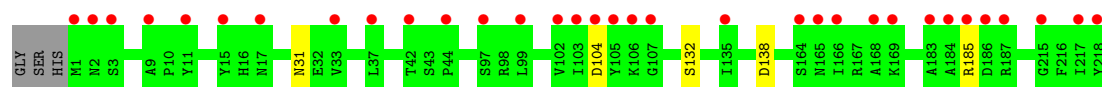
- Molecule 1: Uracil-DNA glycosylase



- Molecule 1: Uracil-DNA glycosylase



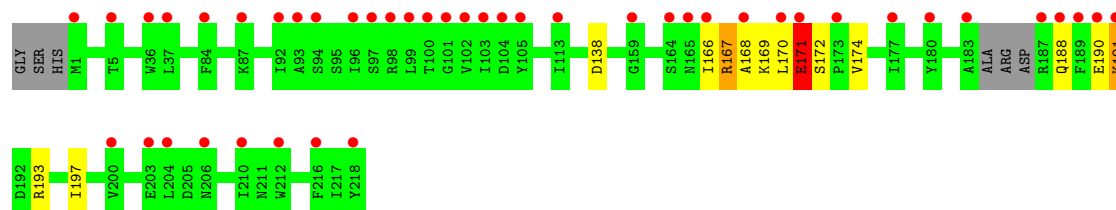
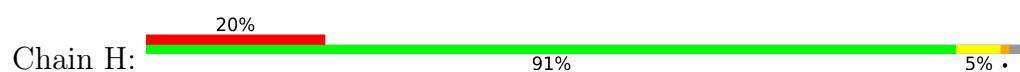
- Molecule 1: Uracil-DNA glycosylase



- Molecule 1: Uracil-DNA glycosylase



- Molecule 1: Uracil-DNA glycosylase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	117.77Å 134.06Å 139.10Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	32.24 – 2.30 32.24 – 2.30	Depositor EDS
% Data completeness (in resolution range)	99.9 (32.24-2.30) 99.9 (32.24-2.30)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.17 (at 2.29Å)	Xtriage
Refinement program	REFMAC 5.8.0131	Depositor
R, R_{free}	0.215 , 0.249 0.218 , 0.252	Depositor DCC
R_{free} test set	4905 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	28.6	Xtriage
Anisotropy	0.032	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 35.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.011 for -h,l,k	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	15051	wwPDB-VP
Average B, all atoms (Å ²)	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 10.91% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, CL

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	0.56	0/1819	0.78	0/2474
1	B	0.57	0/1825	0.77	0/2482
1	C	0.61	0/1811	0.95	6/2464 (0.2%)
1	D	0.57	0/1845	0.78	1/2509 (0.0%)
1	E	0.56	0/1828	0.78	0/2486
1	F	0.58	0/1819	0.78	0/2474
1	G	0.60	0/1834	0.80	2/2494 (0.1%)
1	H	0.61	0/1767	0.89	4/2406 (0.2%)
All	All	0.58	0/14548	0.82	13/19789 (0.1%)

There are no bond length outliers.

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	170	LEU	N-CA-C	19.78	134.05	110.91
1	H	190	GLU	N-CA-C	-12.50	96.55	113.30
1	C	172	SER	C-N-CD	-8.93	100.95	120.60
1	G	187	ARG	N-CA-C	-7.82	94.14	110.80
1	C	171	GLU	N-CA-C	7.33	126.41	110.80
1	D	186	ASP	N-CA-C	6.09	120.32	113.01
1	H	191	LYS	N-CA-C	-5.93	104.73	111.14
1	G	186	ASP	N-CA-C	-5.74	98.58	110.80
1	C	169	LYS	CA-C-N	5.31	130.94	122.93
1	C	169	LYS	C-N-CA	5.31	130.94	122.93
1	H	190	GLU	CA-C-N	5.04	127.30	120.44
1	H	190	GLU	C-N-CA	5.04	127.30	120.44
1	C	173	PRO	N-CA-C	-5.03	99.01	112.10

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1770	0	1768	5	0
1	B	1776	0	1772	2	0
1	C	1762	0	1736	8	0
1	D	1795	0	1786	6	0
1	E	1779	0	1775	8	0
1	F	1770	0	1768	2	0
1	G	1785	0	1779	10	0
1	H	1720	0	1706	8	0
2	A	18	0	24	0	0
2	B	12	0	16	0	0
2	C	6	0	8	0	0
2	D	18	0	24	0	0
2	E	12	0	16	0	0
2	F	12	0	16	0	0
2	G	6	0	8	0	0
2	H	6	0	8	0	0
3	D	1	0	0	0	0
3	F	1	0	0	1	0
3	G	1	0	0	0	0
3	H	1	0	0	0	0
4	A	168	0	0	0	0
4	B	107	0	0	0	0
4	C	60	0	0	0	0
4	D	127	0	0	0	0
4	E	130	0	0	1	0
4	F	60	0	0	0	0
4	G	120	0	0	0	0
4	H	28	0	0	0	0
All	All	15051	0	14210	43	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 2.

All (43) 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:H:168:ALA:HA	1:H:171:GLU:OE2	1.64	0.97
1:C:172:SER:CB	1:C:173:PRO:HA	2.05	0.86
1:H:188:GLN:O	1:H:191:LYS:NZ	2.20	0.72
1:C:172:SER:CB	1:C:173:PRO:CA	2.70	0.69
1:E:199:ASN:O	1:E:203:GLU:HG2	1.95	0.66
1:G:185:ARG:O	1:G:186:ASP:HB2	1.96	0.66
1:E:199:ASN:O	1:E:203:GLU:CG	2.43	0.66
1:H:188:GLN:O	1:H:191:LYS:HG3	1.98	0.64
1:E:36:TRP:O	1:E:39:ARG:HD3	2.05	0.57
1:D:158:LEU:HD23	1:D:182:PRO:CG	2.35	0.55
1:H:166:ILE:O	1:H:167:ARG:CB	2.55	0.55
1:H:168:ALA:CA	1:H:171:GLU:OE2	2.50	0.53
1:G:187:ARG:O	1:G:188:GLN:HB2	2.08	0.52
1:D:158:LEU:HD23	1:D:182:PRO:CD	2.39	0.51
1:E:35:SER:HB2	1:G:35:SER:HB2	1.93	0.50
1:G:36:TRP:O	1:G:39:ARG:HD3	2.11	0.49
1:D:158:LEU:HD23	1:D:182:PRO:HD3	1.95	0.48
1:B:182:PRO:HA	1:B:189:PHE:CG	2.50	0.47
1:E:199:ASN:O	1:E:203:GLU:HG3	2.14	0.47
1:C:6:VAL:HG21	1:C:30:TYR:HD2	1.80	0.47
1:A:188:GLN:NE2	1:D:188:GLN:OE1	2.47	0.46
1:G:187:ARG:HD2	1:G:190:GLU:OE1	2.16	0.45
1:G:188:GLN:HA	1:G:188:GLN:OE1	2.15	0.45
1:G:182:PRO:HA	1:G:189:PHE:CG	2.52	0.44
1:A:149:THR:O	1:A:174:VAL:HG21	2.18	0.43
1:A:98:ARG:HD2	1:C:58:ARG:NE	2.32	0.43
1:G:204:LEU:HD11	1:H:197:ILE:HG21	2.01	0.43
1:G:131:LYS:NZ	1:G:162:ASP:OD1	2.50	0.42
1:H:172:SER:OG	1:H:174:VAL:HG12	2.19	0.42
1:E:149:THR:O	1:E:174:VAL:HG21	2.20	0.42
1:D:68:ASP:HB2	1:D:69:PRO:CD	2.50	0.42
1:G:25[A]:GLN:OE1	1:G:25[A]:GLN:HA	2.19	0.42
1:C:36:TRP:HZ2	1:F:132:SER:O	2.02	0.42
1:C:165:ASN:CB	1:C:169:LYS:CB	2.98	0.42
1:C:182:PRO:HA	1:C:189:PHE:CG	2.55	0.41
1:E:68:ASP:HB2	1:E:69:PRO:CD	2.50	0.41
1:A:182:PRO:HA	1:A:189:PHE:CG	2.55	0.41
1:B:1:MET:HE1	1:B:54:LYS:HG2	2.01	0.41
1:H:193:ARG:HG3	1:H:197:ILE:HD11	2.02	0.41
1:F:31:ASN:HA	3:F:303:CL:CL	2.58	0.41
1:E:139:LYS:NZ	4:E:405:HOH:O	2.54	0.41
1:C:169:LYS:N	1:D:171:GLU:HA	2.35	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:137:TRP:O	1:A:138:ASP:C	2.64	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	216/221 (98%)	212 (98%)	3 (1%)	1 (0%)	24	31
1	B	217/221 (98%)	212 (98%)	4 (2%)	1 (0%)	24	31
1	C	215/221 (97%)	205 (95%)	6 (3%)	4 (2%)	6	5
1	D	219/221 (99%)	215 (98%)	3 (1%)	1 (0%)	24	31
1	E	217/221 (98%)	212 (98%)	4 (2%)	1 (0%)	24	31
1	F	216/221 (98%)	208 (96%)	5 (2%)	3 (1%)	9	9
1	G	218/221 (99%)	212 (97%)	4 (2%)	2 (1%)	14	17
1	H	211/221 (96%)	205 (97%)	3 (1%)	3 (1%)	9	9
All	All	1729/1768 (98%)	1681 (97%)	32 (2%)	16 (1%)	14	17

All (16) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	138	ASP
1	C	171	GLU
1	C	172	SER
1	E	138	ASP
1	G	138	ASP
1	H	167	ARG
1	H	171	GLU
1	B	138	ASP
1	F	138	ASP

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	D	138	ASP
1	H	138	ASP
1	C	138	ASP
1	C	173	PRO
1	F	185	ARG
1	G	186	ASP
1	F	104	ASP

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	199/201 (99%)	199 (100%)	0	100	100
1	B	200/201 (100%)	200 (100%)	0	100	100
1	C	197/201 (98%)	197 (100%)	0	100	100
1	D	202/201 (100%)	202 (100%)	0	100	100
1	E	200/201 (100%)	200 (100%)	0	100	100
1	F	199/201 (99%)	199 (100%)	0	100	100
1	G	201/201 (100%)	201 (100%)	0	100	100
1	H	192/201 (96%)	189 (98%)	3 (2%)	55	73
All	All	1590/1608 (99%)	1587 (100%)	3 (0%)	87	94

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	H	169	LYS
1	H	170	LEU
1	H	171	GLU

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

Mol	Chain	Res	Type
1	A	17	ASN
1	A	25	GLN
1	A	55	GLN
1	A	188	GLN
1	B	181	HIS
1	B	188	GLN
1	C	25	GLN
1	D	2	ASN
1	D	55	GLN
1	D	188	GLN
1	E	165	ASN
1	E	188	GLN
1	F	55	GLN
1	F	181	HIS
1	G	55	GLN
1	H	8	HIS
1	H	16	HIS
1	H	55	GLN
1	H	181	HIS

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 19 ligands modelled in this entry, 4 are monoatomic - leaving 15 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	GOL	B	302	-	5,5,5	0.42	0	5,5,5	0.53	0
2	GOL	A	401	-	5,5,5	0.30	0	5,5,5	0.58	0
2	GOL	G	301	-	5,5,5	0.45	0	5,5,5	0.44	0
2	GOL	F	302	-	5,5,5	0.29	0	5,5,5	0.33	0
2	GOL	A	402	-	5,5,5	0.30	0	5,5,5	0.46	0
2	GOL	D	301	-	5,5,5	0.29	0	5,5,5	0.26	0
2	GOL	D	303	-	5,5,5	0.37	0	5,5,5	0.42	0
2	GOL	F	301	-	5,5,5	0.35	0	5,5,5	0.26	0
2	GOL	E	301	-	5,5,5	0.37	0	5,5,5	0.57	0
2	GOL	D	302	-	5,5,5	0.33	0	5,5,5	0.42	0
2	GOL	E	302	-	5,5,5	0.40	0	5,5,5	0.25	0
2	GOL	H	301	-	5,5,5	0.38	0	5,5,5	0.58	0
2	GOL	C	301	-	5,5,5	0.32	0	5,5,5	0.17	0
2	GOL	B	301	-	5,5,5	0.31	0	5,5,5	0.42	0
2	GOL	A	403	-	5,5,5	0.52	0	5,5,5	0.63	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	B	302	-	-	0/4/4/4	-
2	GOL	A	401	-	-	3/4/4/4	-
2	GOL	G	301	-	-	0/4/4/4	-
2	GOL	F	302	-	-	2/4/4/4	-
2	GOL	A	402	-	-	2/4/4/4	-
2	GOL	D	301	-	-	0/4/4/4	-
2	GOL	D	303	-	-	2/4/4/4	-
2	GOL	F	301	-	-	4/4/4/4	-
2	GOL	E	301	-	-	2/4/4/4	-
2	GOL	D	302	-	-	2/4/4/4	-
2	GOL	E	302	-	-	2/4/4/4	-
2	GOL	H	301	-	-	2/4/4/4	-
2	GOL	C	301	-	-	0/4/4/4	-
2	GOL	B	301	-	-	4/4/4/4	-
2	GOL	A	403	-	-	1/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (26) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	401	GOL	C1-C2-C3-O3
2	D	302	GOL	O1-C1-C2-C3
2	D	303	GOL	C1-C2-C3-O3
2	D	303	GOL	O2-C2-C3-O3
2	E	302	GOL	O1-C1-C2-O2
2	E	302	GOL	O1-C1-C2-C3
2	F	301	GOL	C1-C2-C3-O3
2	F	301	GOL	O2-C2-C3-O3
2	F	302	GOL	O1-C1-C2-C3
2	H	301	GOL	O1-C1-C2-C3
2	A	402	GOL	C1-C2-C3-O3
2	B	301	GOL	O1-C1-C2-C3
2	B	301	GOL	C1-C2-C3-O3
2	E	301	GOL	O1-C1-C2-C3
2	F	301	GOL	O1-C1-C2-C3
2	B	301	GOL	O1-C1-C2-O2
2	D	302	GOL	O1-C1-C2-O2
2	F	302	GOL	O1-C1-C2-O2
2	H	301	GOL	O1-C1-C2-O2
2	E	301	GOL	O1-C1-C2-O2
2	A	401	GOL	O2-C2-C3-O3
2	A	403	GOL	O1-C1-C2-O2
2	B	301	GOL	O2-C2-C3-O3
2	A	402	GOL	O2-C2-C3-O3
2	F	301	GOL	O1-C1-C2-O2
2	A	401	GOL	O1-C1-C2-C3

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers ⓘ

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, 95th 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	218/221 (98%)	0.01	4 (1%) 67 69	13, 22, 41, 61	0
1	B	218/221 (98%)	0.35	8 (3%) 45 48	11, 31, 48, 68	1 (0%)
1	C	217/221 (98%)	1.04	31 (14%) 6 7	15, 38, 63, 82	2 (0%)
1	D	219/221 (99%)	0.34	12 (5%) 30 32	14, 26, 48, 71	2 (0%)
1	E	218/221 (98%)	0.21	8 (3%) 45 48	12, 25, 51, 75	1 (0%)
1	F	218/221 (98%)	1.08	33 (15%) 5 6	24, 40, 60, 84	0
1	G	218/221 (98%)	0.29	8 (3%) 45 48	11, 26, 53, 69	2 (0%)
1	H	215/221 (97%)	1.32	44 (20%) 2 3	28, 47, 68, 80	0
All	All	1741/1768 (98%)	0.58	148 (8%) 16 18	11, 32, 59, 84	8 (0%)

All (148) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	103	ILE	6.0
1	H	189	PHE	5.4
1	H	187	ARG	5.3
1	C	101	GLY	4.9
1	C	103	ILE	4.8
1	C	165	ASN	4.8
1	E	204	LEU	4.8
1	B	36	TRP	4.5
1	H	99	LEU	4.5
1	C	170	LEU	4.4
1	F	107	GLY	4.3
1	F	185	ARG	4.3
1	C	172	SER	4.2
1	H	183	ALA	4.2
1	H	98	ARG	4.2
1	F	106	LYS	4.1

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	H	170	LEU	4.1
1	C	0	HIS	4.0
1	H	93	ALA	3.9
1	H	168	ALA	3.9
1	C	164	SER	3.8
1	C	173	PRO	3.8
1	A	187	ARG	3.7
1	H	166	ILE	3.6
1	H	190	GLU	3.6
1	C	36	TRP	3.6
1	C	102	VAL	3.6
1	H	102	VAL	3.5
1	H	36	TRP	3.5
1	E	187	ARG	3.5
1	H	204	LEU	3.4
1	G	166	ILE	3.4
1	D	185	ARG	3.3
1	C	1	MET	3.3
1	F	168	ALA	3.3
1	F	1	MET	3.3
1	H	101	GLY	3.2
1	H	188	GLN	3.2
1	H	100	THR	3.2
1	F	164	SER	3.2
1	C	169	LYS	3.2
1	F	103	ILE	3.2
1	B	186	ASP	3.2
1	E	102	VAL	3.2
1	B	7	SER	3.1
1	D	184	ALA	3.1
1	B	37	LEU	3.1
1	F	218	TYR	3.1
1	F	135	ILE	3.1
1	H	103	ILE	3.0
1	G	168	ALA	3.0
1	C	218	TYR	3.0
1	G	103	ILE	3.0
1	H	1	MET	3.0
1	C	17	ASN	3.0
1	A	184	ALA	2.9
1	D	103	ILE	2.9
1	H	218	TYR	2.9

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	F	165	ASN	2.9
1	E	184	ALA	2.9
1	C	5	THR	2.9
1	C	58	ARG	2.9
1	H	212	TRP	2.9
1	C	35	SER	2.8
1	G	187	ARG	2.8
1	G	204	LEU	2.8
1	H	96	ILE	2.8
1	H	104	ASP	2.8
1	F	17	ASN	2.8
1	H	5	THR	2.7
1	F	2	ASN	2.7
1	H	105	TYR	2.7
1	H	216	PHE	2.7
1	H	203	GLU	2.7
1	C	104	ASP	2.7
1	C	-1	SER	2.7
1	A	186	ASP	2.6
1	H	173	PRO	2.6
1	C	185	ARG	2.6
1	D	186	ASP	2.6
1	D	164	SER	2.6
1	C	7	SER	2.6
1	F	11	TYR	2.6
1	F	105	TYR	2.6
1	H	206	ASN	2.5
1	C	181	HIS	2.5
1	F	102	VAL	2.5
1	C	187	ARG	2.5
1	E	101	GLY	2.5
1	D	25[A]	GLN	2.5
1	H	164	SER	2.5
1	B	185	ARG	2.5
1	H	37	LEU	2.5
1	B	184	ALA	2.5
1	D	206	ASN	2.5
1	F	184	ALA	2.5
1	H	92	ILE	2.5
1	C	99	LEU	2.5
1	D	0	HIS	2.5
1	F	187	ARG	2.4

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	C	33	VAL	2.4
1	H	87	LYS	2.4
1	C	83	ASN	2.4
1	H	165	ASN	2.4
1	E	171	GLU	2.4
1	F	3	SER	2.4
1	H	171	GLU	2.4
1	H	180	TYR	2.3
1	F	183	ALA	2.3
1	B	35	SER	2.3
1	F	33	VAL	2.3
1	C	97	SER	2.3
1	C	98	ARG	2.3
1	F	99	LEU	2.3
1	D	1	MET	2.3
1	F	37	LEU	2.3
1	G	185	ARG	2.3
1	A	103	ILE	2.3
1	F	169	LYS	2.3
1	F	215	GLY	2.2
1	G	167	ARG	2.2
1	G	104	ASP	2.2
1	D	168	ALA	2.2
1	H	191	LYS	2.2
1	F	104	ASP	2.2
1	F	217	ILE	2.2
1	H	177	ILE	2.2
1	C	183	ALA	2.2
1	E	185	ARG	2.1
1	F	15	TYR	2.1
1	H	210	ILE	2.1
1	H	159	GLY	2.1
1	H	94	SER	2.1
1	H	97	SER	2.1
1	B	169	LYS	2.1
1	H	84	PHE	2.1
1	F	9	ALA	2.1
1	F	97	SER	2.1
1	C	217	ILE	2.1
1	F	44	PRO	2.1
1	D	183	ALA	2.1
1	H	113	ILE	2.1

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	H	200	VAL	2.1
1	F	42	THR	2.0
1	D	204	LEU	2.0
1	F	186	ASP	2.0
1	C	197	ILE	2.0
1	F	166	ILE	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, 95th 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
2	GOL	B	302	6/6	0.63	0.23	47,48,50,50	0
2	GOL	F	302	6/6	0.70	0.24	59,61,61,62	0
2	GOL	F	301	6/6	0.72	0.23	55,57,57,58	0
2	GOL	E	301	6/6	0.76	0.20	25,28,29,30	0
2	GOL	D	303	6/6	0.80	0.20	39,41,41,41	0
2	GOL	A	403	6/6	0.81	0.16	27,28,29,29	0
2	GOL	G	301	6/6	0.83	0.15	29,32,33,35	0
2	GOL	H	301	6/6	0.83	0.16	41,44,45,46	0
2	GOL	A	402	6/6	0.85	0.12	23,24,25,26	0
2	GOL	E	302	6/6	0.85	0.20	69,70,70,71	0
2	GOL	B	301	6/6	0.85	0.17	39,40,41,41	0
2	GOL	D	301	6/6	0.86	0.13	30,33,34,35	0
2	GOL	A	401	6/6	0.88	0.15	31,31,32,32	0
2	GOL	D	302	6/6	0.91	0.09	24,27,28,29	0
3	CL	F	303	1/1	0.91	0.18	52,52,52,52	0
2	GOL	C	301	6/6	0.92	0.14	36,37,38,39	0
3	CL	G	302	1/1	0.94	0.13	47,47,47,47	0

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	CL	D	304	1/1	0.96	0.17	50,50,50,50	0
3	CL	H	302	1/1	0.98	0.10	44,44,44,44	0

6.5 Other polymers [i](#)

There are no such residues in this entry.