



wwPDB X-ray Structure Validation Summary Report ⓘ

Apr 25, 2026 – 03:05 PM EDT

PDB ID : 3CH1 / pdb_00003ch1
Title : Crystal structure of H-2Db in complex with chimeric gp100
Authors : Badia-Martinez, D.; Achour, A.
Deposited on : 2008-03-06
Resolution : 2.30 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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

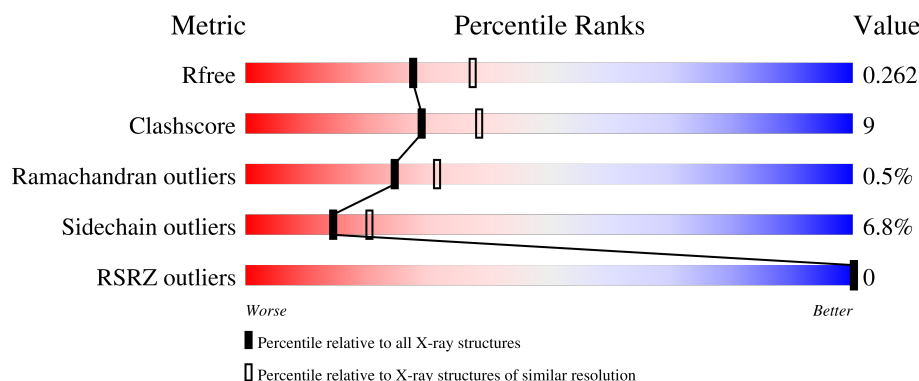
1 Overall quality at a glance

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	276	
1	D	276	
1	G	276	
1	J	276	
2	B	99	

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Mol	Chain	Length	Quality of chain
2	E	99	
2	H	99	
2	K	99	
3	C	9	
3	F	9	
3	I	9	
3	L	9	

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
4	GOL	A	279	-	-	X	-
4	GOL	G	278	-	-	X	-
4	GOL	I	10	-	-	X	-
4	GOL	J	281	-	-	X	-

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 13252 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 H-2 class I histocompatibility antigen, D-B alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	274	Total	C	N	O	S	3	0	0
			2253	1423	398	423	9			
1	D	273	Total	C	N	O	S	3	0	0
			2242	1414	397	422	9			
1	G	271	Total	C	N	O	S	0	1	0
			2237	1410	398	420	9			
1	J	272	Total	C	N	O	S	0	0	0
			2237	1411	396	421	9			

- Molecule 2 is a protein called Beta-2-microglobulin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	99	Total	C	N	O	S	0	1	0
			827	528	138	154	7			
2	E	99	Total	C	N	O	S	0	1	0
			827	528	138	154	7			
2	H	99	Total	C	N	O	S	0	0	0
			821	524	138	152	7			
2	K	99	Total	C	N	O	S	0	0	0
			821	524	138	152	7			

- Molecule 3 is a protein called nonameric peptide chimeric gp100.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	C	9	Total	C	N	O	0	1	0
			87	53	18	16			
3	F	9	Total	C	N	O	0	0	0
			79	48	15	16			
3	I	9	Total	C	N	O	0	0	0
			79	48	15	16			
3	L	9	Total	C	N	O	0	0	0
			79	48	15	16			

- Molecule 4 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



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

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	E	1	Total	C	O	0	0
			6	3	3		
4	E	1	Total	C	O	0	0
			6	3	3		
4	E	1	Total	C	O	0	0
			6	3	3		
4	G	1	Total	C	O	0	0
			6	3	3		
4	G	1	Total	C	O	0	0
			6	3	3		
4	J	1	Total	C	O	0	0
			6	3	3		
4	J	1	Total	C	O	0	0
			6	3	3		
4	J	1	Total	C	O	0	0
			6	3	3		
4	J	1	Total	C	O	0	0
			6	3	3		
4	J	1	Total	C	O	0	0
			6	3	3		
4	I	1	Total	C	O	0	0
			6	3	3		
4	I	1	Total	C	O	0	0
			6	3	3		

- Molecule 5 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	O	S	0	0
			5	4	1		
5	D	1	Total	O	S	0	0
			5	4	1		
5	J	1	Total	O	S	0	0
			5	4	1		
5	J	1	Total	O	S	0	0
			5	4	1		
5	J	1	Total	O	S	0	0
			5	4	1		

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	61	Total	O	0	0
			61	61		
6	B	53	Total	O	0	0
			53	53		
6	D	73	Total	O	0	0
			73	73		
6	E	56	Total	O	0	0
			56	56		
6	G	76	Total	O	0	0
			76	76		
6	H	33	Total	O	0	0
			33	33		
6	J	79	Total	O	0	0
			79	79		

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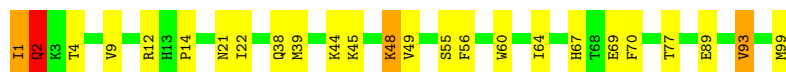
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	K	30	Total 30	O 30	0	0
6	C	2	Total 2	O 2	0	0
6	F	5	Total 5	O 5	0	0
6	I	8	Total 8	O 8	0	0
6	L	6	Total 6	O 6	0	0

- Molecule 1: H-2 class I histocompatibility antigen, D-B alpha chain

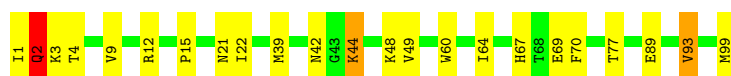
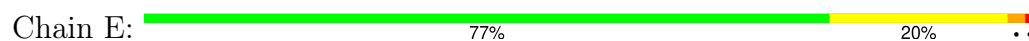




- Molecule 2: Beta-2-microglobulin



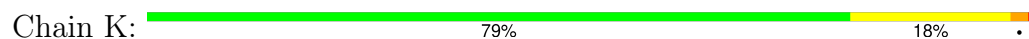
- Molecule 2: Beta-2-microglobulin



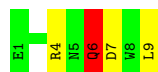
- Molecule 2: Beta-2-microglobulin



- Molecule 2: Beta-2-microglobulin



- Molecule 3: nonameric peptide chimeric gp100



- Molecule 3: nonameric peptide chimeric gp100

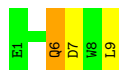


- Molecule 3: nonameric peptide chimeric gp100





- Molecule 3: nonameric peptide chimeric gp100



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	104.50Å 105.40Å 126.69Å 90.00° 90.08° 90.00°	Depositor
Resolution (Å)	48.60 – 2.30 48.60 – 2.30	Depositor EDS
% Data completeness (in resolution range)	99.9 (48.60-2.30) 99.5 (48.60-2.30)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.10 (at 2.29Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.231 , 0.264 0.230 , 0.262	Depositor DCC
R_{free} test set	6122 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	40.3	Xtriage
Anisotropy	0.110	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 28.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.019 for -k,-h,-l 0.018 for k,h,-l 0.488 for h,-k,-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	13252	wwPDB-VP
Average B, all atoms (Å ²)	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.90% 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: SO4, GOL

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.59	0/2319	0.83	1/3146 (0.0%)
1	D	0.59	0/2308	0.87	4/3131 (0.1%)
1	G	0.60	0/2305	0.81	0/3124
1	J	0.60	0/2302	0.87	3/3121 (0.1%)
2	B	0.64	0/856	0.80	1/1161 (0.1%)
2	E	0.64	0/856	0.80	1/1161 (0.1%)
2	H	0.62	0/847	0.82	1/1148 (0.1%)
2	K	0.61	0/847	0.83	3/1148 (0.3%)
3	C	0.59	0/92	0.67	0/122
3	F	0.63	0/81	0.68	0/108
3	I	0.53	0/81	0.70	0/108
3	L	0.56	0/81	0.71	0/108
All	All	0.60	0/12975	0.83	14/17586 (0.1%)

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	1

There are no bond length outliers.

The worst 5 of 14 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	J	170	ARG	NE-CZ-NH2	9.82	128.04	119.20
1	J	170	ARG	NE-CZ-NH1	-9.02	112.48	121.50
2	E	2	GLN	N-CA-C	7.13	121.65	110.17
1	J	170	ARG	CD-NE-CZ	6.87	134.02	124.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	18	GLU	N-CA-C	6.72	129.81	111.00

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	181	ARG	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	2253	0	2123	26	0
1	D	2242	0	2106	32	0
1	G	2237	0	2102	37	0
1	J	2237	0	2100	42	0
2	B	827	0	802	21	0
2	E	827	0	802	22	0
2	H	821	0	796	21	0
2	K	821	0	796	17	0
3	C	87	0	83	3	0
3	F	79	0	70	2	0
3	I	79	0	70	6	0
3	L	79	0	70	3	0
4	A	42	0	56	9	0
4	B	12	0	16	1	0
4	D	12	0	16	0	0
4	E	30	0	40	7	0
4	G	12	0	16	6	0
4	I	12	0	16	6	0
4	J	36	0	48	13	0
5	A	5	0	0	1	0
5	D	5	0	0	0	0
5	J	15	0	0	0	0
6	A	61	0	0	1	0
6	B	53	0	0	2	0
6	C	2	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	D	73	0	0	2	0
6	E	56	0	0	2	0
6	F	5	0	0	0	0
6	G	76	0	0	4	0
6	H	33	0	0	1	0
6	I	8	0	0	3	0
6	J	79	0	0	4	0
6	K	30	0	0	1	0
6	L	6	0	0	0	0
All	All	13252	0	12128	216	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 9.

The worst 5 of 216 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)
4:A:279:GOL:H31	2:B:55:SER:HA	1.14	1.11
1:D:221:GLY:HA2	1:D:222:GLU:HB2	1.25	1.09
1:A:16:GLY:HA3	5:A:277:SO4:O1	1.55	1.07
4:J:281:GOL:C3	2:K:34:HIS:HB2	1.90	1.01
4:J:281:GOL:H31	2:K:34:HIS:CB	1.90	0.99

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	270/276 (98%)	257 (95%)	12 (4%)	1 (0%)	30 38
1	D	269/276 (98%)	254 (94%)	13 (5%)	2 (1%)	18 23

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	G	266/276 (96%)	255 (96%)	11 (4%)	0	100	100
1	J	266/276 (96%)	254 (96%)	9 (3%)	3 (1%)	11	13
2	B	98/99 (99%)	93 (95%)	5 (5%)	0	100	100
2	E	98/99 (99%)	94 (96%)	4 (4%)	0	100	100
2	H	97/99 (98%)	93 (96%)	4 (4%)	0	100	100
2	K	97/99 (98%)	93 (96%)	4 (4%)	0	100	100
3	C	8/9 (89%)	7 (88%)	0	1 (12%)	0	0
3	F	7/9 (78%)	6 (86%)	0	1 (14%)	0	0
3	I	7/9 (78%)	6 (86%)	1 (14%)	0	100	100
3	L	7/9 (78%)	6 (86%)	1 (14%)	0	100	100
All	All	1490/1536 (97%)	1418 (95%)	64 (4%)	8 (0%)	24	31

5 of 8 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	18	GLU
1	J	222	GLU
1	J	196	LYS
3	C	6	GLN
1	D	222	GLU

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	233/234 (100%)	221 (95%)	12 (5%)	21	31
1	D	231/234 (99%)	216 (94%)	15 (6%)	15	22
1	G	231/234 (99%)	217 (94%)	14 (6%)	17	24
1	J	231/234 (99%)	215 (93%)	16 (7%)	14	20
2	B	95/94 (101%)	85 (90%)	10 (10%)	6	8
2	E	95/94 (101%)	88 (93%)	7 (7%)	13	17

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	H	94/94 (100%)	86 (92%)	8 (8%)	10	13
2	K	94/94 (100%)	87 (93%)	7 (7%)	13	17
3	C	9/8 (112%)	8 (89%)	1 (11%)	6	7
3	F	8/8 (100%)	7 (88%)	1 (12%)	4	5
3	I	8/8 (100%)	7 (88%)	1 (12%)	4	5
3	L	8/8 (100%)	7 (88%)	1 (12%)	4	5
All	All	1337/1344 (100%)	1244 (93%)	93 (7%)	14	19

5 of 93 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	G	272	LEU
1	J	114	LEU
2	H	4	THR
2	H	93	VAL
1	J	234	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 32 such sidechains are listed below:

Mol	Chain	Res	Type
3	I	5	ASN
3	I	6	GLN
1	G	115	GLN
1	G	97	GLN
3	L	5	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

31 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	$\# Z > 2$
4	GOL	J	282	-	5,5,5	0.34	0	5,5,5	0.51	0
4	GOL	E	100	-	5,5,5	0.38	0	5,5,5	0.52	0
4	GOL	E	101	-	5,5,5	0.39	0	5,5,5	0.48	0
4	GOL	A	279	-	5,5,5	0.50	0	5,5,5	1.11	1 (20%)
5	SO4	J	277	-	4,4,4	0.23	0	6,6,6	0.15	0
4	GOL	B	101	-	5,5,5	0.35	0	5,5,5	0.28	0
4	GOL	A	282	-	5,5,5	0.40	0	5,5,5	0.59	0
4	GOL	A	278	-	5,5,5	0.38	0	5,5,5	0.37	0
4	GOL	J	283	-	5,5,5	0.48	0	5,5,5	0.54	0
4	GOL	J	285	-	5,5,5	0.35	0	5,5,5	0.20	0
5	SO4	D	277	-	4,4,4	0.26	0	6,6,6	0.19	0
4	GOL	E	102	-	5,5,5	0.44	0	5,5,5	0.38	0
5	SO4	A	277	-	4,4,4	0.25	0	6,6,6	0.26	0
4	GOL	J	284	-	5,5,5	0.43	0	5,5,5	0.32	0
4	GOL	A	283	-	5,5,5	0.37	0	5,5,5	0.33	0
4	GOL	B	100	-	5,5,5	0.44	0	5,5,5	0.23	0
4	GOL	E	104	-	5,5,5	0.34	0	5,5,5	0.21	0
4	GOL	E	103	-	5,5,5	0.35	0	5,5,5	0.31	0
4	GOL	J	281	-	5,5,5	0.64	0	5,5,5	0.76	0
4	GOL	G	277	-	5,5,5	0.34	0	5,5,5	0.78	0
4	GOL	A	284	-	5,5,5	0.31	0	5,5,5	0.56	0
4	GOL	D	279	-	5,5,5	0.39	0	5,5,5	0.49	0
4	GOL	J	280	-	5,5,5	0.34	0	5,5,5	0.70	0
5	SO4	J	278	-	4,4,4	0.23	0	6,6,6	0.18	0
4	GOL	A	281	-	5,5,5	0.44	0	5,5,5	0.13	0
4	GOL	A	280	-	5,5,5	0.40	0	5,5,5	0.23	0
4	GOL	G	278	-	5,5,5	0.36	0	5,5,5	1.00	0
4	GOL	I	10	-	5,5,5	0.66	0	5,5,5	0.56	0
4	GOL	I	16	-	5,5,5	0.63	0	5,5,5	0.38	0
5	SO4	J	279	-	4,4,4	0.29	0	6,6,6	0.09	0
4	GOL	D	278	-	5,5,5	0.39	0	5,5,5	0.35	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
4	GOL	J	282	-	-	2/4/4/4	-
4	GOL	E	100	-	-	2/4/4/4	-
4	GOL	E	101	-	-	0/4/4/4	-
4	GOL	A	279	-	-	2/4/4/4	-
4	GOL	B	101	-	-	2/4/4/4	-
4	GOL	A	282	-	-	0/4/4/4	-
4	GOL	A	278	-	-	4/4/4/4	-
4	GOL	J	283	-	-	2/4/4/4	-
4	GOL	J	285	-	-	0/4/4/4	-
4	GOL	E	102	-	-	0/4/4/4	-
4	GOL	J	284	-	-	2/4/4/4	-
4	GOL	A	283	-	-	0/4/4/4	-
4	GOL	B	100	-	-	2/4/4/4	-
4	GOL	E	104	-	-	2/4/4/4	-
4	GOL	E	103	-	-	4/4/4/4	-
4	GOL	J	281	-	-	3/4/4/4	-
4	GOL	G	277	-	-	3/4/4/4	-
4	GOL	A	284	-	-	3/4/4/4	-
4	GOL	D	279	-	-	2/4/4/4	-
4	GOL	J	280	-	-	2/4/4/4	-
4	GOL	A	281	-	-	0/4/4/4	-
4	GOL	A	280	-	-	1/4/4/4	-
4	GOL	G	278	-	-	4/4/4/4	-
4	GOL	I	10	-	-	4/4/4/4	-
4	GOL	I	16	-	-	0/4/4/4	-
4	GOL	D	278	-	-	3/4/4/4	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	279	GOL	O3-C3-C2	2.07	119.69	110.38

There are no chirality outliers.

5 of 49 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	278	GOL	O1-C1-C2-C3
4	A	278	GOL	C1-C2-C3-O3
4	A	278	GOL	O2-C2-C3-O3
4	A	279	GOL	C1-C2-C3-O3
4	B	101	GOL	O1-C1-C2-C3

There are no ring outliers.

15 monomers are involved in 43 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	J	282	GOL	2	0
4	E	101	GOL	2	0
4	A	279	GOL	5	0
4	B	101	GOL	1	0
4	J	283	GOL	2	0
4	E	102	GOL	2	0
5	A	277	SO4	1	0
4	E	104	GOL	3	0
4	J	281	GOL	8	0
4	A	284	GOL	3	0
4	J	280	GOL	1	0
4	A	280	GOL	1	0
4	G	278	GOL	6	0
4	I	10	GOL	4	0
4	I	16	GOL	2	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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	274/276 (99%)	-1.09	0 100 100	24, 46, 82, 86	1 (0%)
1	D	273/276 (98%)	-1.09	0 100 100	24, 46, 80, 86	1 (0%)
1	G	271/276 (98%)	-1.13	0 100 100	24, 45, 82, 88	1 (0%)
1	J	272/276 (98%)	-1.09	0 100 100	24, 45, 82, 88	0
2	B	99/99 (100%)	-1.32	0 100 100	27, 41, 54, 58	1 (1%)
2	E	99/99 (100%)	-1.33	0 100 100	27, 41, 54, 57	1 (1%)
2	H	99/99 (100%)	-1.25	0 100 100	27, 42, 55, 59	0
2	K	99/99 (100%)	-1.24	0 100 100	27, 42, 55, 58	0
3	C	9/9 (100%)	-1.31	0 100 100	21, 32, 38, 44	1 (11%)
3	F	9/9 (100%)	-1.35	0 100 100	31, 33, 40, 44	0
3	I	9/9 (100%)	-1.39	0 100 100	30, 32, 38, 43	0
3	L	9/9 (100%)	-1.38	0 100 100	31, 32, 38, 43	0
All	All	1522/1536 (99%)	-1.15	0 100 100	21, 44, 80, 88	6 (0%)

There are no RSRZ outliers to report.

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
4	GOL	A	283	6/6	0.94	0.12	145,145,145,145	0
4	GOL	B	101	6/6	0.97	0.10	88,89,89,89	0
4	GOL	A	279	6/6	0.98	0.16	39,42,43,45	0
4	GOL	B	100	6/6	0.98	0.09	38,46,48,49	0
4	GOL	A	281	6/6	0.98	0.10	79,81,82,82	0
4	GOL	D	278	6/6	0.98	0.05	67,67,67,68	0
4	GOL	E	102	6/6	0.98	0.08	69,71,71,71	0
4	GOL	E	103	6/6	0.98	0.07	79,79,80,80	0
4	GOL	E	104	6/6	0.98	0.10	94,95,96,96	0
4	GOL	G	278	6/6	0.98	0.17	54,55,55,56	0
4	GOL	J	281	6/6	0.98	0.17	55,58,58,58	0
4	GOL	J	284	6/6	0.98	0.07	85,85,85,85	0
4	GOL	J	285	6/6	0.98	0.08	87,89,89,89	0
4	GOL	I	16	6/6	0.98	0.09	47,49,51,52	0
5	SO4	J	277	5/5	0.98	0.06	120,120,120,120	0
4	GOL	A	282	6/6	0.99	0.06	41,46,47,47	0
4	GOL	G	277	6/6	0.99	0.04	36,37,39,40	0
4	GOL	A	280	6/6	0.99	0.08	51,54,55,55	0
4	GOL	J	280	6/6	0.99	0.06	34,35,36,40	0
4	GOL	D	279	6/6	0.99	0.06	41,46,46,47	0
4	GOL	J	282	6/6	0.99	0.07	74,75,75,77	0
4	GOL	J	283	6/6	0.99	0.06	61,64,65,66	0
4	GOL	E	100	6/6	0.99	0.07	73,75,75,76	0
4	GOL	E	101	6/6	0.99	0.03	51,52,52,54	0
4	GOL	I	10	6/6	0.99	0.17	48,49,50,51	0
4	GOL	A	284	6/6	0.99	0.05	48,49,50,50	0
5	SO4	A	277	5/5	0.99	0.07	63,63,65,65	0
5	SO4	D	277	5/5	0.99	0.08	62,62,63,64	0
4	GOL	A	278	6/6	0.99	0.05	70,71,73,74	0
5	SO4	J	278	5/5	0.99	0.07	137,137,137,137	0
5	SO4	J	279	5/5	0.99	0.04	75,75,75,76	0

6.5 Other polymers [i](#)

There are no such residues in this entry.