



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 8, 2026 – 05:34 PM UTC

PDB ID : 4I0P / pdb_00004i0p
Title : HLA-DO in complex with HLA-DM
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Deposited on : 2012-11-18
Resolution : 3.20 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

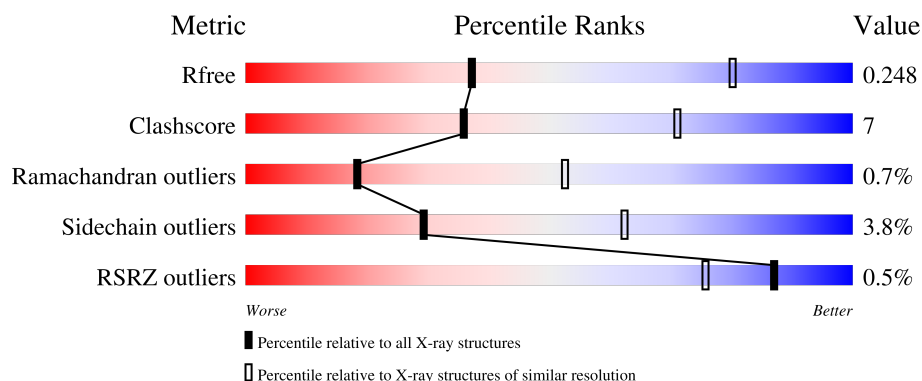
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.20 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	1466 (3.20-3.20)
Clashscore	190562	1573 (3.20-3.20)
Ramachandran outliers	187476	1548 (3.20-3.20)
Sidechain outliers	187428	1547 (3.20-3.20)
RSRZ outliers	180081	1466 (3.20-3.20)

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	188	80%19%.
1	E	188	% 81%18%.
2	B	191	% 82%15%..
2	F	191	% 82%16%..
3	C	181	83%13%. .

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Mol	Chain	Length	Quality of chain
3	G	181	83% 14%
4	D	189	% 75% 20%
4	H	189	% 83% 14%

2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 13370 atoms, of which 1306 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 HLA-DMA protein.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	188	Total	C	H	N	O	S	0	0	0
			1667	984	159	239	279	6			
1	E	188	Total	C	H	N	O	S	0	0	0
			1667	984	159	239	279	6			

- Molecule 2 is a protein called HLA class II histocompatibility antigen, DM beta chain.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	B	186	Total	C	H	N	O	S	0	0	0
			1630	938	155	252	274	11			
2	F	187	Total	C	H	N	O	S	0	0	0
			1638	944	155	253	275	11			

- Molecule 3 is a protein called HLA class II histocompatibility antigen, DO alpha chain.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
3	C	181	Total	C	H	N	O	S	0	0	0
			1609	939	152	251	264	3			
3	G	181	Total	C	H	N	O	S	0	0	0
			1609	939	152	251	264	3			

- Molecule 4 is a protein called HLA class II histocompatibility antigen, DO beta chain.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
4	D	188	Total	C	H	N	O	S	0	0	0
			1704	968	187	263	278	8			
4	H	189	Total	C	H	N	O	S	0	0	0
			1710	971	187	264	280	8			

- Molecule 5 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).



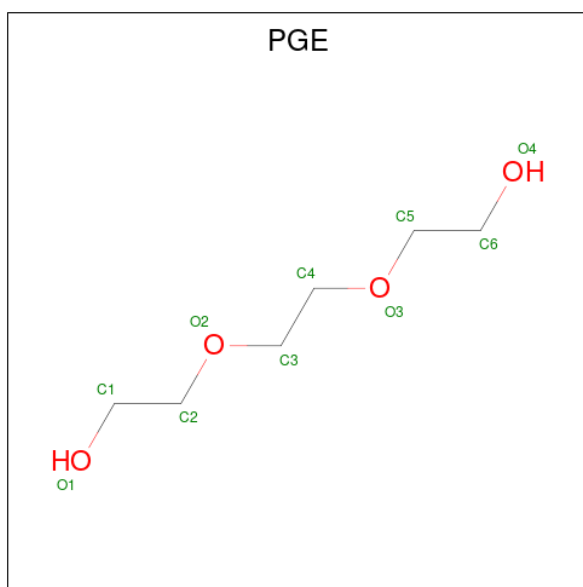
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	N	O	0	0
			14	8	1	5		
5	C	1	Total	C	N	O	0	0
			14	8	1	5		
5	D	1	Total	C	N	O	0	0
			14	8	1	5		
5	E	1	Total	C	N	O	0	0
			14	8	1	5		
5	G	1	Total	C	N	O	0	0
			14	8	1	5		
5	G	1	Total	C	N	O	0	0
			14	8	1	5		
5	H	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 6 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



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

- Molecule 7 is TRIETHYLENE GLYCOL (CCD ID: PGE) (formula: $C_6H_{14}O_4$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	H	1	Total	C	O	0	0
			10	6	4		

- Molecule 8 is ACETATE ION (CCD ID: ACT) (formula: $C_2H_3O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	H	1	Total	C	O	0	0
			4	2	2		

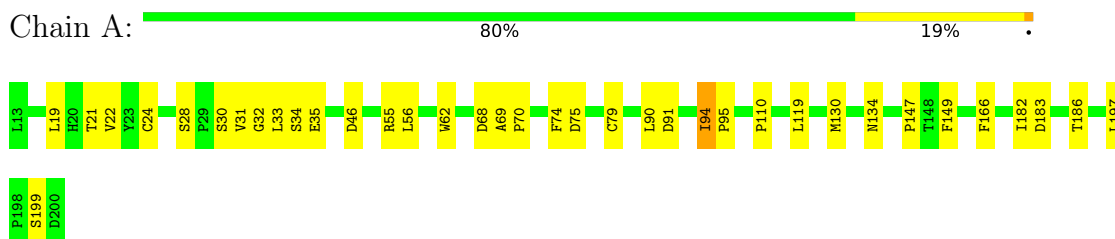
- Molecule 9 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	B	2	Total	O	0	0
			2	2		
9	C	1	Total	O	0	0
			1	1		
9	F	1	Total	O	0	0
			1	1		
9	G	2	Total	O	0	0
			2	2		

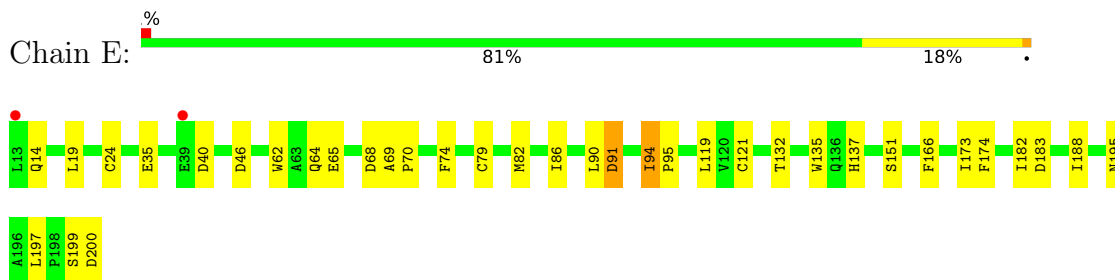
3 Residue-property plots

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.

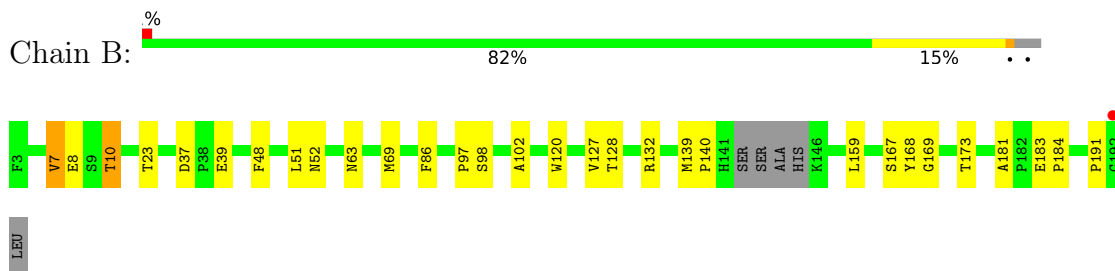
- Molecule 1: HLA-DMA protein

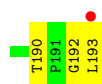


- Molecule 1: HLA-DMA protein



- Molecule 2: HLA class II histocompatibility antigen, DM beta chain





- Molecule 3: HLA class II histocompatibility antigen, DO alpha chain

Chain C: 83% 13% .



- Molecule 3: HLA class II histocompatibility antigen, DO alpha chain

Chain G: 83% 14% .



- Molecule 4: HLA class II histocompatibility antigen, DO beta chain

Chain D: 75% 20% . .



- Molecule 4: HLA class II histocompatibility antigen, DO beta chain

Chain H: 83% 14% .



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	83.26Å 147.10Å 95.96Å 90.00° 106.49° 90.00°	Depositor
Resolution (Å)	43.91 – 3.20 43.91 – 3.20	Depositor EDS
% Data completeness (in resolution range)	94.0 (43.91-3.20) 93.9 (43.91-3.20)	Depositor EDS
R_{merge}	0.68	Depositor
R_{sym}	0.68	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.92 (at 3.19Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8_1069)	Depositor
R, R_{free}	0.188 , 0.242 0.197 , 0.248	Depositor DCC
R_{free} test set	1856 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å ²)	49.0	Xtriage
Anisotropy	0.397	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 15.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	13370	wwPDB-VP
Average B, all atoms (Å ²)	28.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.06% 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: PGE, GOL, NAG, ACT

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	0.28	0/1561	0.68	0/2135
1	E	0.30	0/1561	0.69	1/2135 (0.0%)
2	B	0.30	0/1519	0.67	0/2079
2	F	0.29	0/1527	0.67	1/2090 (0.0%)
3	C	0.29	0/1502	0.68	1/2046 (0.0%)
3	G	0.28	0/1502	0.67	1/2046 (0.0%)
4	D	0.28	0/1557	0.66	0/2116
4	H	0.28	0/1563	0.66	0/2124
All	All	0.29	0/12292	0.67	4/16771 (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
3	C	0	1

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	52	ALA	N-CA-C	-6.27	101.00	110.28
3	G	52	ALA	N-CA-C	-6.00	101.39	110.28
1	E	188	ILE	N-CA-C	5.66	117.27	109.46
2	F	89	SER	N-CA-C	-5.35	105.53	111.36

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	C	51	PHE	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1508	159	1418	25	0
1	E	1508	159	1418	23	0
2	B	1475	155	1418	21	0
2	F	1483	155	1429	20	0
3	C	1457	152	1401	19	0
3	G	1457	152	1400	25	0
4	D	1517	187	1469	36	0
4	H	1523	187	1474	24	0
5	A	14	0	13	0	0
5	C	14	0	13	0	0
5	D	14	0	13	0	0
5	E	14	0	13	1	0
5	G	28	0	26	0	0
5	H	14	0	13	0	0
6	D	6	0	8	0	0
6	F	6	0	8	1	0
6	H	6	0	8	0	0
7	H	10	0	14	0	0
8	H	4	0	3	0	0
9	B	2	0	0	0	0
9	C	1	0	0	0	0
9	F	1	0	0	0	0
9	G	2	0	0	0	0
All	All	12064	1306	11559	172	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.

The worst 5 of 172 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:G:77:SER:O	3:G:79:ARG:N	2.12	0.82
4:D:189:ARG:HB2	4:D:190:ALA:O	1.91	0.70
2:F:110:ARG:NH1	4:H:185:SER:OG	2.30	0.65
2:B:63:ASN:HA	2:B:69:MET:HE3	1.77	0.65
2:F:167:SER:O	2:F:168:TYR:CB	2.45	0.64

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	186/188 (99%)	174 (94%)	12 (6%)	0	100	100
1	E	186/188 (99%)	174 (94%)	12 (6%)	0	100	100
2	B	182/191 (95%)	175 (96%)	5 (3%)	2 (1%)	11	43
2	F	183/191 (96%)	177 (97%)	5 (3%)	1 (0%)	24	59
3	C	179/181 (99%)	166 (93%)	12 (7%)	1 (1%)	21	56
3	G	179/181 (99%)	165 (92%)	12 (7%)	2 (1%)	11	43
4	D	186/189 (98%)	169 (91%)	15 (8%)	2 (1%)	11	43
4	H	187/189 (99%)	170 (91%)	15 (8%)	2 (1%)	11	43
All	All	1468/1498 (98%)	1370 (93%)	88 (6%)	10 (1%)	18	52

5 of 10 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	D	140	ALA
2	F	168	TYR
3	G	78	ASN
4	H	105	ARG
4	H	140	ALA

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	167/167 (100%)	162 (97%)	5 (3%)	36	66
1	E	167/167 (100%)	161 (96%)	6 (4%)	31	63
2	B	165/169 (98%)	162 (98%)	3 (2%)	51	74
2	F	166/169 (98%)	162 (98%)	4 (2%)	43	70
3	C	156/156 (100%)	148 (95%)	8 (5%)	21	54
3	G	156/156 (100%)	153 (98%)	3 (2%)	50	73
4	D	167/168 (99%)	154 (92%)	13 (8%)	11	41
4	H	168/168 (100%)	160 (95%)	8 (5%)	23	56
All	All	1312/1320 (99%)	1262 (96%)	50 (4%)	29	62

5 of 50 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	D	178	SER
2	F	9	SER
4	H	185	SER
1	E	40	ASP
1	E	132	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 12 such sidechains are listed below:

Mol	Chain	Res	Type
2	F	64	GLN
2	F	151	ASN
4	H	116	HIS
2	F	157	GLN
2	B	157	GLN

5.3.3 RNA ⓘ

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](#)

12 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	$\# Z > 2$
5	NAG	D	201	4	14,14,15	0.62	0	17,19,21	1.27	2 (11%)
6	GOL	D	202	-	5,5,5	0.37	0	5,5,5	0.28	0
5	NAG	A	301	1	14,14,15	0.45	0	17,19,21	0.97	1 (5%)
5	NAG	H	201	4	14,14,15	0.58	0	17,19,21	0.86	0
7	PGE	H	202	-	9,9,9	0.65	0	8,8,8	0.69	0
6	GOL	F	201	-	5,5,5	0.43	0	5,5,5	0.15	0
6	GOL	H	204	-	5,5,5	0.37	0	5,5,5	0.28	0
5	NAG	G	202	3	14,14,15	0.45	0	17,19,21	1.10	1 (5%)
5	NAG	C	201	3	14,14,15	0.53	0	17,19,21	0.99	1 (5%)
5	NAG	G	201	3	14,14,15	0.51	0	17,19,21	0.90	0
8	ACT	H	203	-	3,3,3	0.81	0	3,3,3	1.36	0
5	NAG	E	301	1	14,14,15	0.49	0	17,19,21	0.90	1 (5%)

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
5	NAG	D	201	4	-	2/6/23/26	0/1/1/1
6	GOL	D	202	-	-	0/4/4/4	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	NAG	A	301	1	-	1/6/23/26	0/1/1/1
5	NAG	H	201	4	-	0/6/23/26	0/1/1/1
7	PGE	H	202	-	-	2/7/7/7	-
6	GOL	F	201	-	-	2/4/4/4	-
6	GOL	H	204	-	-	2/4/4/4	-
5	NAG	G	202	3	-	0/6/23/26	0/1/1/1
5	NAG	C	201	3	-	1/6/23/26	0/1/1/1
5	NAG	G	201	3	-	0/6/23/26	0/1/1/1
5	NAG	E	301	1	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	G	202	NAG	C1-O5-C5	3.82	117.31	112.19
5	D	201	NAG	C3-C4-C5	3.48	116.54	110.23
5	A	301	NAG	C1-O5-C5	3.12	116.37	112.19
5	C	201	NAG	C3-C4-C5	2.66	115.05	110.23
5	E	301	NAG	C1-O5-C5	2.55	115.61	112.19

There are no chirality outliers.

5 of 10 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	F	201	GOL	O1-C1-C2-C3
6	H	204	GOL	O1-C1-C2-C3
7	H	202	PGE	O3-C5-C6-O4
5	D	201	NAG	C4-C5-C6-O6
6	F	201	GOL	O1-C1-C2-O2

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	F	201	GOL	1	0
5	E	301	NAG	1	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	188/188 (100%)	-0.21	0 100 100	12, 29, 54, 73	0
1	E	188/188 (100%)	-0.30	2 (1%) 78 61	8, 27, 51, 73	0
2	B	186/191 (97%)	-0.26	1 (0%) 87 76	13, 30, 54, 71	0
2	F	187/191 (97%)	-0.21	2 (1%) 78 61	13, 29, 56, 89	0
3	C	181/181 (100%)	-0.30	0 100 100	11, 23, 41, 61	0
3	G	181/181 (100%)	-0.35	0 100 100	9, 20, 34, 48	0
4	D	188/189 (99%)	-0.29	1 (0%) 87 76	8, 25, 54, 76	0
4	H	189/189 (100%)	-0.34	1 (0%) 87 76	11, 27, 52, 65	0
All	All	1488/1498 (99%)	-0.28	7 (0%) 87 76	8, 26, 52, 89	0

The worst 5 of 7 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
4	D	4	PRO	3.0
4	H	4	PRO	2.8
2	F	193	LEU	2.6
1	E	39	GLU	2.5
2	F	139	MET	2.5

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
5	NAG	G	201	14/15	0.40	0.17	63,81,86,86	0
5	NAG	D	201	14/15	0.58	0.16	66,85,95,98	0
5	NAG	H	201	14/15	0.75	0.13	25,34,44,46	0
8	ACT	H	203	4/4	0.82	0.14	27,41,41,47	0
5	NAG	C	201	14/15	0.84	0.11	29,45,57,61	0
5	NAG	E	301	14/15	0.85	0.10	40,53,61,63	0
6	GOL	D	202	6/6	0.87	0.10	21,25,31,47	0
5	NAG	G	202	14/15	0.87	0.11	14,29,46,55	0
7	PGE	H	202	10/10	0.91	0.12	12,16,20,25	0
5	NAG	A	301	14/15	0.92	0.09	55,64,69,78	0
6	GOL	F	201	6/6	0.94	0.11	29,41,48,53	0
6	GOL	H	204	6/6	0.94	0.12	13,19,34,42	0

6.5 Other polymers [i](#)

There are no such residues in this entry.