



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 20, 2026 – 06:49 AM UTC

PDB ID : 9AUD / pdb_00009aud
Title : Immune receptor complex
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Deposited on : 2024-02-29
Resolution : 2.90 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

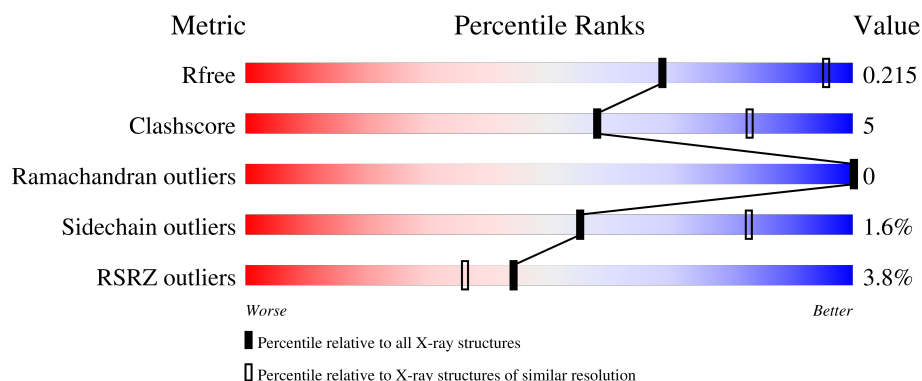
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.90 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	2481 (2.90-2.90)
Clashscore	190562	2690 (2.90-2.90)
Ramachandran outliers	187476	2623 (2.90-2.90)
Sidechain outliers	187428	2625 (2.90-2.90)
RSRZ outliers	180081	2481 (2.90-2.90)

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	C	188	0% 93% 6% ..
2	D	228	5% 67% 14% 18%
3	A	210	3% 70% 11% 19%
4	B	242	4% 89% 10% .

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 6196 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 II histocompatibility antigen, A-B alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	C	186	Total	C	N	O	S	0	3	0
			1487	961	235	288	3			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	181	THR	-	expression tag	UNP P14434
C	182	SER	-	expression tag	UNP P14434
C	183	GLY	-	expression tag	UNP P14434
C	184	LEU	-	expression tag	UNP P14434
C	185	GLU	-	expression tag	UNP P14434
C	186	VAL	-	expression tag	UNP P14434
C	187	LEU	-	expression tag	UNP P14434
C	188	PHE	-	expression tag	UNP P14434

- Molecule 2 is a protein called Nucleoprotein,H-2 class II histocompatibility antigen, A beta chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	186	Total	C	N	O	S	0	1	0
			1472	924	259	284	5			

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	-13C	GLY	-	linker	UNP O92607
D	-13D	SER	-	linker	UNP O92607
D	-13E	GLY	-	linker	UNP O92607
D	-13F	GLY	-	linker	UNP O92607
D	-13G	SER	-	linker	UNP O92607
D	-13H	ILE	-	linker	UNP O92607
D	-13I	GLU	-	linker	UNP O92607

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-13J	GLY	-	linker	UNP O92607
D	-13K	ARG	-	linker	UNP O92607
D	-13L	GLY	-	linker	UNP O92607
D	-13M	GLY	-	linker	UNP O92607
D	-13N	SER	-	linker	UNP O92607
D	-13O	GLY	-	linker	UNP O92607
D	-13P	ALA	-	linker	UNP O92607
D	-13Q	SER	-	linker	UNP O92607
D	187	THR	-	expression tag	UNP P14483
D	188	GLY	-	expression tag	UNP P14483
D	189	GLY	-	expression tag	UNP P14483
D	190	LEU	-	expression tag	UNP P14483
D	191	GLU	-	expression tag	UNP P14483
D	192	VAL	-	expression tag	UNP P14483
D	193	LEU	-	expression tag	UNP P14483
D	194	PHE	-	expression tag	UNP P14483
D	195	GLN	-	expression tag	UNP P14483

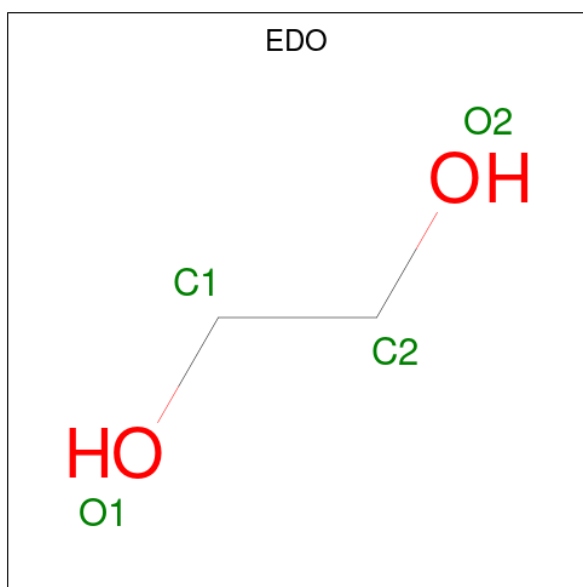
- Molecule 3 is a protein called NPLCK1-2_TCR TRAV6-5 alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	A	171	Total	C	N	O	S	0	0	0
			1255	787	204	260	4			

- Molecule 4 is a protein called NPLCK1-2 TCR TRBV1 Beta chain.

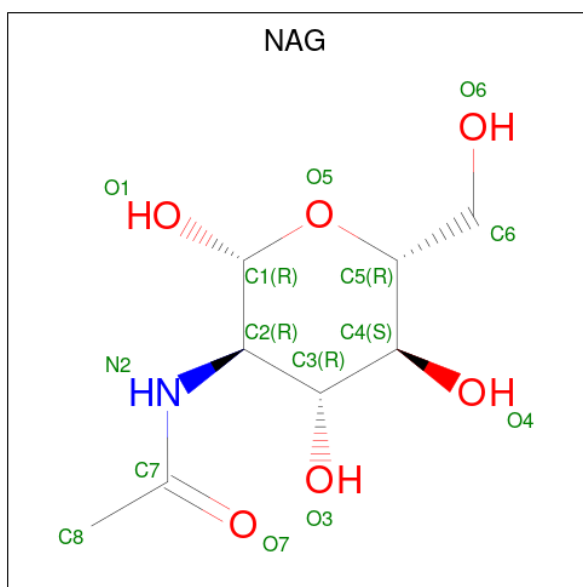
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	B	240	Total	C	N	O	S	0	2	0
			1888	1205	333	342	8			

- Molecule 5 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	C	1	Total	C	O	0	0
			4	2	2		
5	C	1	Total	C	O	0	0
			4	2	2		
5	C	1	Total	C	O	0	0
			4	2	2		
5	D	1	Total	C	O	0	0
			4	2	2		
5	B	1	Total	C	O	0	0
			4	2	2		
5	B	1	Total	C	O	0	0
			4	2	2		

- Molecule 6 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	C	1	Total	C	N	O	0	0
			14	8	1	5		
6	D	1	Total	C	N	O	0	0
			14	8	1	5		

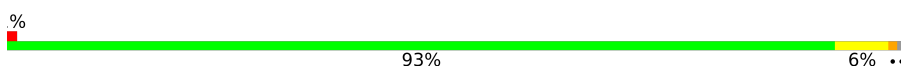
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	C	24	Total	O	0	0
			24	24		
7	D	9	Total	O	0	0
			9	9		
7	A	6	Total	O	0	0
			6	6		
7	B	3	Total	O	0	0
			3	3		

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.

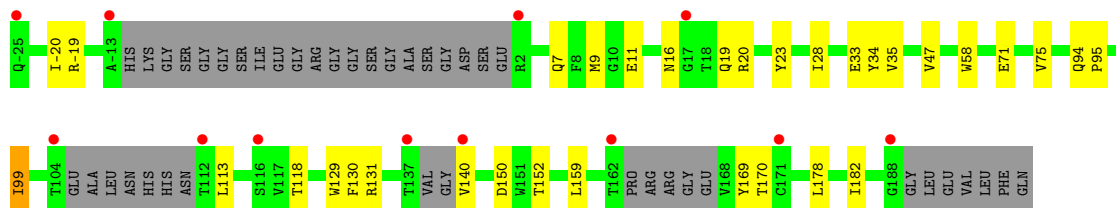
- Molecule 1: H-2 class II histocompatibility antigen, A-B alpha chain

Chain C:  93% 6% ..



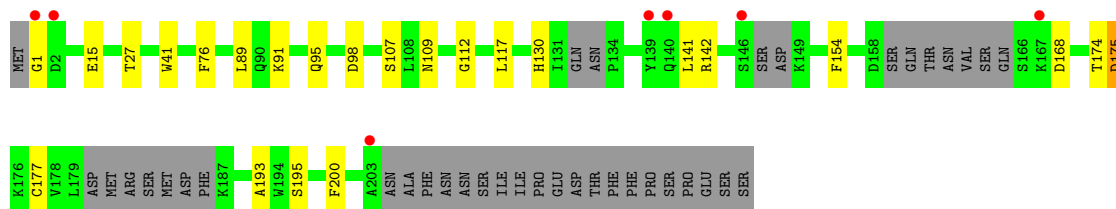
- Molecule 2: Nucleoprotein,H-2 class II histocompatibility antigen, A beta chain

Chain D:  67% 14% 18%

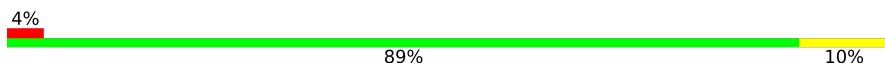


- Molecule 3: NPLCK1-2_TCR TRAV6-5 alpha chain

Chain A:  70% 11% 19%



- Molecule 4: NPLCK1-2 TCR TRBV1 Beta chain

Chain B:  89% 10% .





4 Data and refinement statistics

Property	Value	Source
Space group	H 3	Depositor
Cell constants a, b, c, α , β , γ	196.34Å 196.34Å 77.10Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	49.37 – 2.90 49.37 – 2.90	Depositor EDS
% Data completeness (in resolution range)	100.0 (49.37-2.90) 99.9 (49.37-2.90)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.50 (at 2.91Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487, PHENIX 1.20.1_4487	Depositor
R, R_{free}	0.183 , 0.216 0.184 , 0.215	Depositor DCC
R_{free} test set	1286 reflections (4.22%)	wwPDB-VP
Wilson B-factor (Å ²)	67.5	Xtriage
Anisotropy	0.473	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 63.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.016 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	6196	wwPDB-VP
Average B, all atoms (Å ²)	81.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.62% 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 [i](#)

5.1 Standard geometry [i](#)

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

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	C	0.07	0/1531	0.22	0/2096
2	D	0.08	0/1505	0.24	0/2055
3	A	0.09	0/1278	0.28	0/1734
4	B	0.07	0/1940	0.23	0/2657
All	All	0.08	0/6254	0.24	0/8542

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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	C	1487	0	1402	7	0
2	D	1472	0	1332	22	0
3	A	1255	0	1140	13	0
4	B	1888	0	1807	16	0
5	B	8	0	12	1	0
5	C	12	0	18	2	0
5	D	4	0	6	0	0
6	C	14	0	13	1	0
6	D	14	0	13	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	A	6	0	0	0	0
7	B	3	0	0	0	0
7	C	24	0	0	0	0
7	D	9	0	0	0	0
All	All	6196	0	5743	54	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 5.

All (54) 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)
2:D:140:VAL:HG22	2:D:159:LEU:HA	1.77	0.66
2:D:-20:ILE:HG13	2:D:75:VAL:HG11	1.77	0.64
3:A:91:LYS:NZ	3:A:98:ASP:OD2	2.29	0.62
2:D:19:GLN:HE22	6:D:301:NAG:HN2	1.47	0.61
2:D:7:GLN:HB2	2:D:28:ILE:HB	1.81	0.61
6:D:301:NAG:H3	6:D:301:NAG:H83	1.85	0.59
2:D:99:ILE:HD11	2:D:129:TRP:CH2	2.39	0.58
4:B:81:VAL:HG12	4:B:83:THR:HG23	1.86	0.57
3:A:76:PHE:HB3	3:A:89:LEU:HD11	1.87	0.57
2:D:130:PHE:O	2:D:170:THR:OG1	2.24	0.56
6:C:203:NAG:H3	6:C:203:NAG:H83	1.87	0.56
1:C:105:ASN:OD1	1:C:106:THR:N	2.40	0.54
2:D:23:TYR:OH	2:D:71:GLU:OE1	2.22	0.54
3:A:107:SER:HB3	3:A:117:LEU:HD23	1.89	0.54
4:B:137:VAL:HG23	4:B:247:ALA:HB3	1.90	0.54
2:D:9:MET:HE2	2:D:11:GLU:OE2	2.08	0.53
2:D:113:LEU:HD23	2:D:159:LEU:HD23	1.91	0.53
4:B:140:PRO:HG3	4:B:151:ALA:HB1	1.90	0.53
1:C:75:LEU:HD21	2:D:34:TYR:CZ	2.45	0.52
1:C:98:PRO:HD3	2:D:118:THR:HG21	1.92	0.50
4:B:54:PHE:CE1	4:B:69:LYS:HB2	2.47	0.49
1:C:16:GLN:HE21	5:C:204:EDO:H12	1.78	0.49
4:B:120:ARG:NH1	4:B:163:ASP:OD2	2.46	0.49
3:A:142:ARG:HA	4:B:138:PHE:HD2	1.77	0.48
4:B:140:PRO:HD3	4:B:153:LEU:HG	1.95	0.48
3:A:175:ASP:OD1	3:A:175:ASP:N	2.47	0.47
2:D:20:ARG:HD3	2:D:20:ARG:HA	1.84	0.45
3:A:41:TRP:CE2	3:A:89:LEU:HB2	2.51	0.45
3:A:174:THR:HA	4:B:187[A]:LEU:HD11	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:21:ILE:HG22	5:C:204:EDO:H21	1.99	0.45
4:B:73:GLY:HA3	4:B:100:ARG:HH22	1.83	0.44
4:B:233:TRP:CD1	4:B:239:LYS:HG2	2.52	0.44
2:D:131:ARG:HA	2:D:169:TYR:HA	2.00	0.43
2:D:16:ASN:HB3	2:D:19:GLN:HB2	2.01	0.43
1:C:112:ASP:OD1	1:C:113:ASN:N	2.48	0.43
2:D:94:GLN:HA	2:D:95:PRO:HD3	1.90	0.42
4:B:132:PRO:HD3	4:B:240:PRO:HB3	2.01	0.42
4:B:123:VAL:H	5:B:402:EDO:H11	1.85	0.42
2:D:33:GLU:HG2	2:D:47:VAL:HG21	2.01	0.42
2:D:178:LEU:HD13	2:D:182:ILE:HG13	2.01	0.42
2:D:-19:ARG:NH2	3:A:112:GLY:O	2.53	0.42
3:A:15:GLU:HG3	3:A:95:GLN:HA	2.01	0.42
3:A:195:SER:HB3	3:A:200:PHE:CD2	2.54	0.42
4:B:71:LEU:HB2	4:B:72:PRO:HD2	2.01	0.42
4:B:40:SER:HB2	4:B:105:THR:OG1	2.19	0.41
4:B:73:GLY:HA3	4:B:100:ARG:NH2	2.35	0.41
1:C:9:THR:HB	1:C:27:GLU:HB2	2.02	0.41
3:A:154:PHE:HE1	3:A:193:ALA:HB3	1.86	0.41
2:D:35:VAL:HG11	2:D:58:TRP:HZ3	1.85	0.41
2:D:-19:ARG:NH1	3:A:109:ASN:O	2.54	0.41
2:D:99:ILE:HD12	2:D:99:ILE:HA	1.70	0.41
2:D:150:ASP:OD1	2:D:152:THR:OG1	2.33	0.41
4:B:163:ASP:OD1	4:B:163:ASP:N	2.53	0.41
3:A:1:GLY:HA2	3:A:27:THR:HA	2.03	0.40

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	C	187/188 (100%)	183 (98%)	4 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	D	177/228 (78%)	168 (95%)	9 (5%)	0	100	100
3	A	161/210 (77%)	153 (95%)	8 (5%)	0	100	100
4	B	240/242 (99%)	229 (95%)	11 (5%)	0	100	100
All	All	765/868 (88%)	733 (96%)	32 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	C	165/168 (98%)	162 (98%)	3 (2%)	51	80
2	D	154/202 (76%)	153 (99%)	1 (1%)	78	93
3	A	131/186 (70%)	126 (96%)	5 (4%)	29	64
4	B	199/216 (92%)	198 (100%)	1 (0%)	81	93
All	All	649/772 (84%)	639 (98%)	10 (2%)	55	84

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	9	THR
1	C	130	VAL
1	C	181	THR
2	D	99	ILE
3	A	130	HIS
3	A	141	LEU
3	A	168	ASP
3	A	175	ASP
3	A	177	CYS
4	B	17	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	C	59	GLN
2	D	78	HIS
4	B	109	GLN
4	B	128	ASN
4	B	235	GLN

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](#)

8 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	EDO	B	402	-	3,3,3	0.42	0	2,2,2	0.38	0
5	EDO	B	401	-	3,3,3	0.43	0	2,2,2	0.38	0
5	EDO	C	202	-	3,3,3	0.43	0	2,2,2	0.39	0
5	EDO	C	204	-	3,3,3	0.41	0	2,2,2	0.39	0
6	NAG	D	301	2	14,14,15	0.58	0	17,19,21	1.35	2 (11%)
5	EDO	D	302	-	3,3,3	0.42	0	2,2,2	0.37	0
6	NAG	C	203	1	14,14,15	1.01	1 (7%)	17,19,21	1.72	2 (11%)
5	EDO	C	201	-	3,3,3	0.43	0	2,2,2	0.37	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
5	EDO	B	402	-	-	0/1/1/1	-
5	EDO	B	401	-	-	0/1/1/1	-
5	EDO	C	202	-	-	0/1/1/1	-
5	EDO	C	204	-	-	0/1/1/1	-
6	NAG	D	301	2	-	5/6/23/26	0/1/1/1
5	EDO	D	302	-	-	0/1/1/1	-
6	NAG	C	203	1	-	6/6/23/26	0/1/1/1
5	EDO	C	201	-	-	0/1/1/1	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	C	203	NAG	O5-C1	3.14	1.49	1.43

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	C	203	NAG	C1-O5-C5	4.64	118.41	112.19
6	D	301	NAG	C2-N2-C7	4.59	129.05	122.90
6	C	203	NAG	C2-N2-C7	4.57	129.03	122.90
6	D	301	NAG	C1-C2-N2	2.19	113.89	110.43

There are no chirality outliers.

All (11) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	C	203	NAG	C8-C7-N2-C2
6	C	203	NAG	O7-C7-N2-C2
6	D	301	NAG	C8-C7-N2-C2
6	D	301	NAG	O7-C7-N2-C2
6	C	203	NAG	C4-C5-C6-O6
6	C	203	NAG	O5-C5-C6-O6
6	D	301	NAG	O5-C5-C6-O6
6	C	203	NAG	C1-C2-N2-C7
6	D	301	NAG	C1-C2-N2-C7
6	C	203	NAG	C3-C2-N2-C7
6	D	301	NAG	C3-C2-N2-C7

There are no ring outliers.

4 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	402	EDO	1	0
5	C	204	EDO	2	0
6	D	301	NAG	2	0
6	C	203	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	C	186/188 (98%)	-0.09	2 (1%) 78 71	27, 61, 100, 144	3 (1%)
2	D	186/228 (81%)	0.28	12 (6%) 25 20	43, 72, 148, 169	1 (0%)
3	A	171/210 (81%)	0.45	7 (4%) 41 33	47, 95, 132, 155	0
4	B	240/242 (99%)	0.27	9 (3%) 44 36	28, 82, 134, 156	2 (0%)
All	All	783/868 (90%)	0.22	30 (3%) 44 36	27, 78, 135, 169	6 (0%)

All (30) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	162	THR	6.5
3	A	1	GLY	5.2
3	A	146	SER	2.9
2	D	188	GLY	2.8
3	A	203	ALA	2.8
4	B	1	VAL	2.7
4	B	252	ARG	2.6
4	B	216	ASN	2.6
2	D	112	THR	2.6
4	B	209	THR	2.5
2	D	140	VAL	2.4
4	B	253	ALA	2.4
1	C	186	VAL	2.4
4	B	149	GLN	2.4
2	D	116	SER	2.3
2	D	104	THR	2.3
2	D	-13	ALA	2.2
2	D	17	GLY	2.2
4	B	228	SER	2.2
2	D	2	ARG	2.1
3	A	2	ASP	2.1

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Mol	Chain	Res	Type	RSRZ
1	C	132[A]	ASP	2.1
2	D	137	THR	2.1
3	A	140	GLN	2.1
4	B	218	PHE	2.1
3	A	139	TYR	2.1
2	D	-25	GLN	2.0
4	B	250	TRP	2.0
3	A	167	LYS	2.0
2	D	171	CYS	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
6	NAG	D	301	14/15	0.55	0.14	103,124,130,133	0
6	NAG	C	203	14/15	0.57	0.16	86,108,127,134	0
5	EDO	C	202	4/4	0.82	0.20	62,82,91,93	0
5	EDO	C	201	4/4	0.88	0.12	58,63,68,70	0
5	EDO	B	402	4/4	0.89	0.14	75,83,85,91	0
5	EDO	C	204	4/4	0.94	0.13	38,50,58,67	0
5	EDO	D	302	4/4	0.94	0.12	57,62,73,77	0
5	EDO	B	401	4/4	0.94	0.12	58,62,70,80	0

6.5 Other polymers [i](#)

There are no such residues in this entry.