



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 15, 2017 – 04:49 am GMT

PDB ID : 3V4V
Title : crystal structure of a4b7 headpiece complexed with Fab ACT-1 and RO0505376
Authors : Yu, Y.; Zhu, J.; Springer, T.A.
Deposited on : 2011-12-15
Resolution : 3.10 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

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix)	:	1.9-1692
EDS	:	trunk28620
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	recalc28949

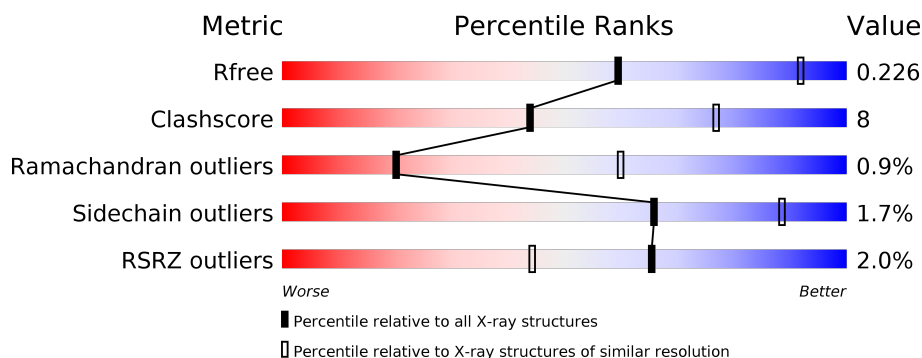
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.10 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}	100719	1001 (3.12-3.08)
Clashscore	112137	1099 (3.12-3.08)
Ramachandran outliers	110173	1057 (3.12-3.08)
Sidechain outliers	110143	1057 (3.12-3.08)
RSRZ outliers	101464	1006 (3.12-3.08)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	597	<div> <div style="width: 6%;"></div> <div style="width: 74%; background-color: green;"></div> <div style="width: 23%; background-color: yellow;"></div> <div style="width: 1%; background-color: orange;"></div> <div style="width: 1%; background-color: red;"></div> <div style="width: 1%; background-color: grey;"></div> </div> <div>74% 23% . .</div>
1	C	597	<div> <div style="width: 6%;"></div> <div style="width: 72%; background-color: green;"></div> <div style="width: 24%; background-color: yellow;"></div> <div style="width: 1%; background-color: orange;"></div> <div style="width: 1%; background-color: red;"></div> <div style="width: 1%; background-color: grey;"></div> </div> <div>72% 24% . .</div>
2	B	503	<div> <div style="width: 6%;"></div> <div style="width: 61%; background-color: green;"></div> <div style="width: 13%; background-color: yellow;"></div> <div style="width: 1%; background-color: orange;"></div> <div style="width: 1%; background-color: red;"></div> <div style="width: 20%; background-color: grey;"></div> </div> <div>61% 13% . 25%</div>
2	D	503	<div> <div style="width: 6%;"></div> <div style="width: 61%; background-color: green;"></div> <div style="width: 13%; background-color: yellow;"></div> <div style="width: 1%; background-color: orange;"></div> <div style="width: 1%; background-color: red;"></div> <div style="width: 20%; background-color: grey;"></div> </div> <div>61% 13% . 25%</div>
3	H	219	<div> <div style="width: 6%;"></div> <div style="width: 79%; background-color: green;"></div> <div style="width: 16%; background-color: yellow;"></div> <div style="width: 1%; background-color: orange;"></div> <div style="width: 1%; background-color: red;"></div> <div style="width: 1%; background-color: grey;"></div> </div> <div>6% 79% 16% . .</div>
3	M	219	<div> <div style="width: 82%; background-color: green;"></div> <div style="width: 14%; background-color: yellow;"></div> <div style="width: 1%; background-color: orange;"></div> <div style="width: 1%; background-color: red;"></div> <div style="width: 1%; background-color: grey;"></div> </div> <div>82% 14% . .</div>

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Mol	Chain	Length	Quality of chain
4	L	217	 8% 87% 13%
4	N	217	 86% 14%

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
10	ODU	D	4000	-	-	-	X
5	CA	D	2003	-	-	-	X
8	TRS	A	598	-	-	-	X

2 Entry composition

There are 11 unique types of molecules in this entry. The entry contains 21791 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 Integrin alpha-4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	582	Total	C	N	O	S	10	0	0
			4499	2837	776	864	22			
1	C	580	Total	C	N	O	S	10	0	0
			4489	2831	775	861	22			

There are 22 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	558	ALA	ARG	ENGINEERED MUTATION	UNP P13612
A	588	THR	-	EXPRESSION TAG	UNP P13612
A	589	GLY	-	EXPRESSION TAG	UNP P13612
A	590	GLY	-	EXPRESSION TAG	UNP P13612
A	591	LEU	-	EXPRESSION TAG	UNP P13612
A	592	GLU	-	EXPRESSION TAG	UNP P13612
A	593	ASN	-	EXPRESSION TAG	UNP P13612
A	594	LEU	-	EXPRESSION TAG	UNP P13612
A	595	TYR	-	EXPRESSION TAG	UNP P13612
A	596	PHE	-	EXPRESSION TAG	UNP P13612
A	597	GLN	-	EXPRESSION TAG	UNP P13612
C	558	ALA	ARG	ENGINEERED MUTATION	UNP P13612
C	588	THR	-	EXPRESSION TAG	UNP P13612
C	589	GLY	-	EXPRESSION TAG	UNP P13612
C	590	GLY	-	EXPRESSION TAG	UNP P13612
C	591	LEU	-	EXPRESSION TAG	UNP P13612
C	592	GLU	-	EXPRESSION TAG	UNP P13612
C	593	ASN	-	EXPRESSION TAG	UNP P13612
C	594	LEU	-	EXPRESSION TAG	UNP P13612
C	595	TYR	-	EXPRESSION TAG	UNP P13612
C	596	PHE	-	EXPRESSION TAG	UNP P13612
C	597	GLN	-	EXPRESSION TAG	UNP P13612

- Molecule 2 is a protein called Integrin beta-7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	375	Total	C	N	O	S	0	1	0
			2918	1826	521	559	12			
2	D	375	Total	C	N	O	S	0	1	0
			2919	1826	521	560	12			

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	494	SER	-	EXPRESSION TAG	UNP P26010
B	495	ARG	-	EXPRESSION TAG	UNP P26010
B	496	GLY	-	EXPRESSION TAG	UNP P26010
B	497	LEU	-	EXPRESSION TAG	UNP P26010
B	498	GLU	-	EXPRESSION TAG	UNP P26010
B	499	ASN	-	EXPRESSION TAG	UNP P26010
B	500	LEU	-	EXPRESSION TAG	UNP P26010
B	501	TYR	-	EXPRESSION TAG	UNP P26010
B	502	PHE	-	EXPRESSION TAG	UNP P26010
B	503	GLN	-	EXPRESSION TAG	UNP P26010
D	494	SER	-	EXPRESSION TAG	UNP P26010
D	495	ARG	-	EXPRESSION TAG	UNP P26010
D	496	GLY	-	EXPRESSION TAG	UNP P26010
D	497	LEU	-	EXPRESSION TAG	UNP P26010
D	498	GLU	-	EXPRESSION TAG	UNP P26010
D	499	ASN	-	EXPRESSION TAG	UNP P26010
D	500	LEU	-	EXPRESSION TAG	UNP P26010
D	501	TYR	-	EXPRESSION TAG	UNP P26010
D	502	PHE	-	EXPRESSION TAG	UNP P26010
D	503	GLN	-	EXPRESSION TAG	UNP P26010

- Molecule 3 is a protein called MONOCLONAL ANTIBODY Act-1 HEAVY CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	H	211	Total	C	N	O	S	0	0	0
			1607	1021	258	321	7			
3	M	213	Total	C	N	O	S	8	0	0
			1622	1030	261	324	7			

- Molecule 4 is a protein called MONOCLONAL ANTIBODY Act-1 LIGHT CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	L	217	Total	C	N	O	S	0	0	0
			1681	1054	282	339	6			

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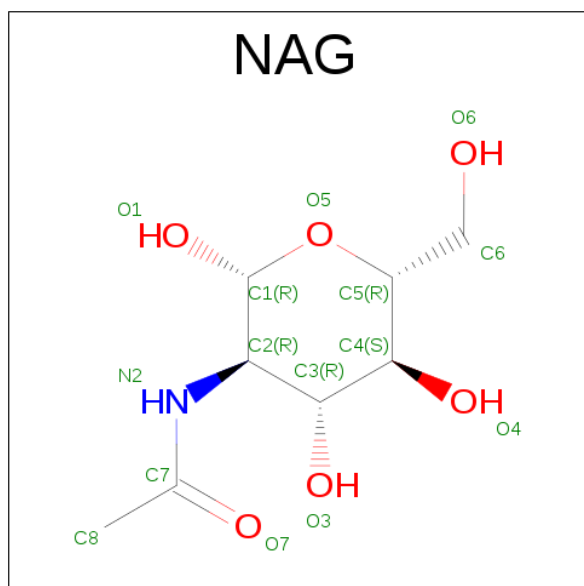
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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	N	217	Total	C	N	O	S	0	0	0
			1681	1054	282	339	6			

- Molecule 5 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	2	Total	Ca	0	0
			2	2		
5	A	3	Total	Ca	0	0
			3	3		
5	D	2	Total	Ca	0	0
			2	2		
5	C	3	Total	Ca	0	0
			3	3		

- Molecule 6 is SUGAR (N-ACETYL-D-GLUCOSAMINE) (three-letter code: NAG) (formula: C₈H₁₅NO₆).



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

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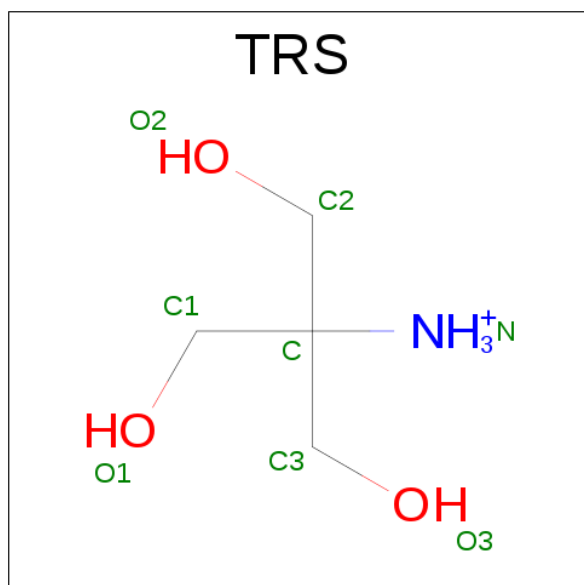
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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	B	1	Total	C	N	O	0	0
			14	8	1	5		
6	B	1	Total	C	N	O	0	0
			14	8	1	5		
6	C	1	Total	C	N	O	0	0
			14	8	1	5		
6	C	1	Total	C	N	O	0	0
			14	8	1	5		
6	C	1	Total	C	N	O	0	0
			14	8	1	5		
6	D	1	Total	C	N	O	0	0
	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

- Molecule 7 is a polymer of unknown type called SUGAR (4-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	A	4	Total	C	N	O	0	0
			50	28	2	20		
7	C	4	Total	C	N	O	0	0
			50	28	2	20		

- Molecule 8 is 2-AMINO-2-HYDROXYMETHYL-PROPANE-1,3-DIOL (three-letter code: TRS) (formula: $C_4H_{12}NO_3$).

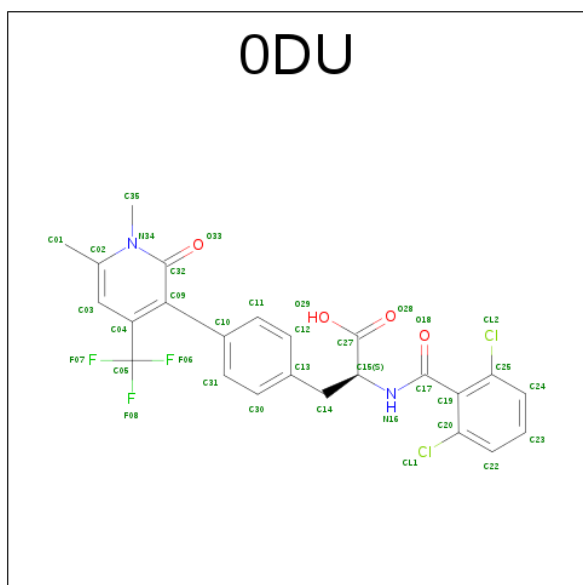


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
8	A	1	Total	C	N	O	0	0
			8	4	1	3		

- Molecule 9 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	B	1	Total	Mg	0	0
			1	1		
9	D	1	Total	Mg	0	0
			1	1		

- Molecule 10 is N-(2,6-DICHLOROBENZOYL)-4-[1,6-DIMETHYL-2-OXO-4-(TRIFLUOROMETHYL)-1,2-DIHYDROPYRIDIN-3-YL]-L-PHENYLALANINE (three-letter code: 0DU) (formula: C₂₄H₁₉Cl₂F₃N₂O₄).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
10	B	1	Total	C	Cl	F	N	O	0	0
			35	24	2	3	2	4		
10	D	1	Total	C	Cl	F	N	O	0	0
			35	24	2	3	2	4		

- Molecule 11 is water.

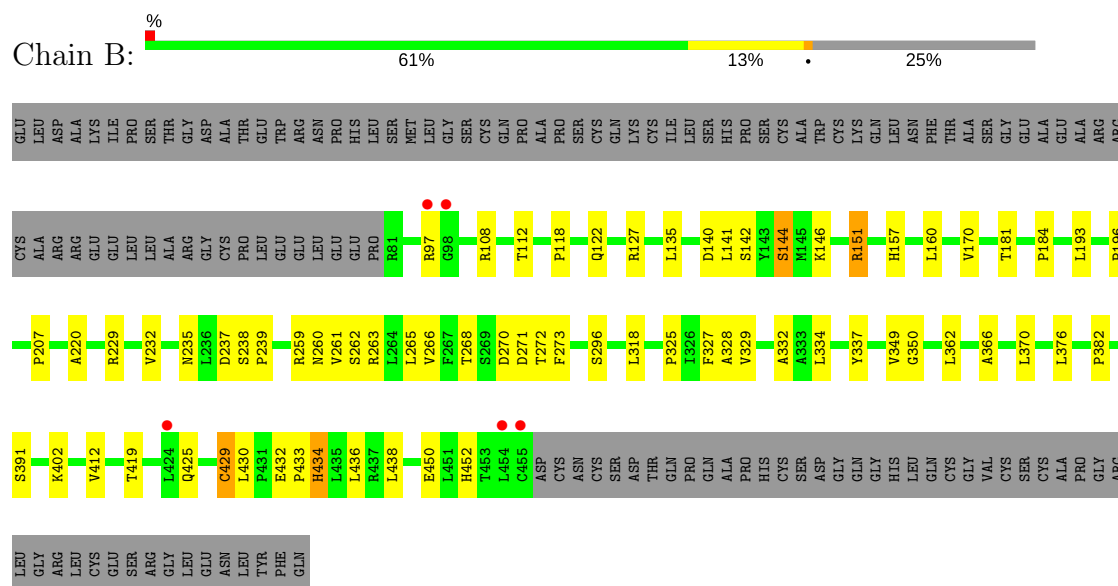
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
11	A	10	Total	O	0	0
			10	10		

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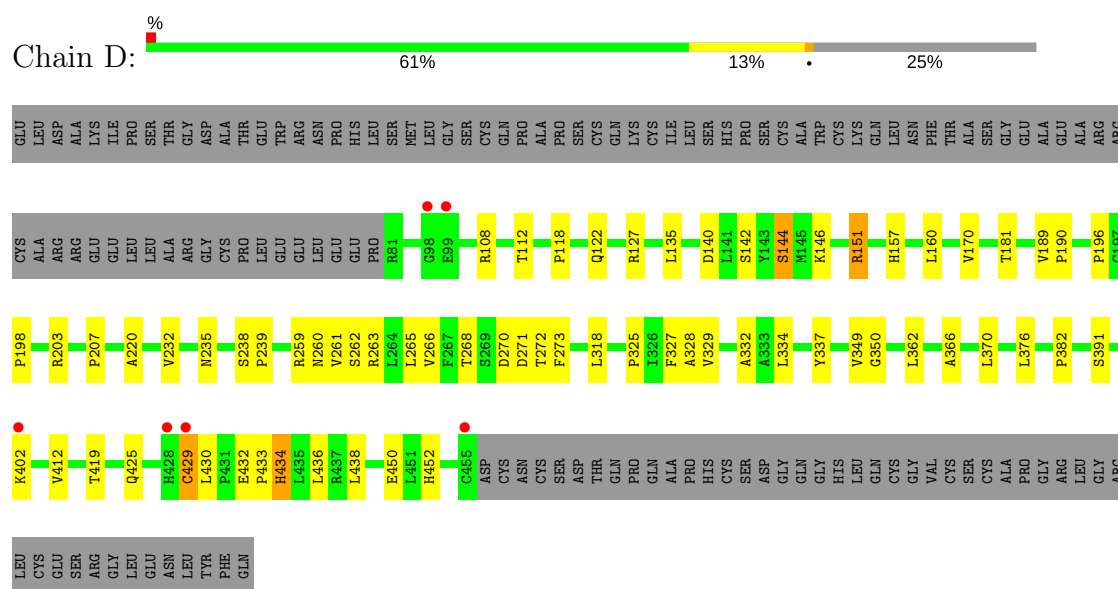
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
11	B	4	Total 4	O 4	0	0
11	H	1	Total 1	O 1	0	0
11	C	11	Total 11	O 11	0	0
11	D	5	Total 5	O 5	0	0

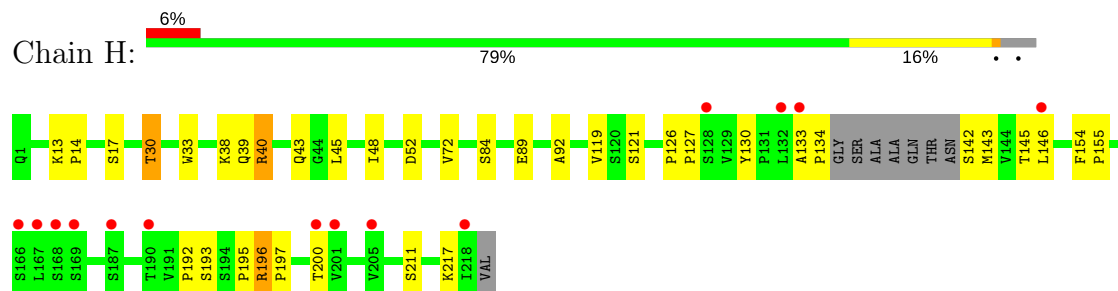
- Molecule 2: Integrin beta-7




- Molecule 2: Integrin beta-7

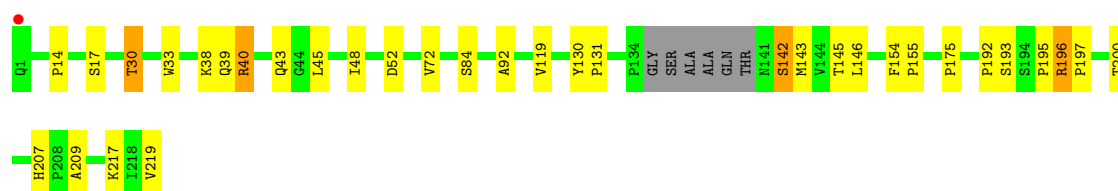


- Molecule 3: MONOCLONAL ANTIBODY Act-1 HEAVY CHAIN




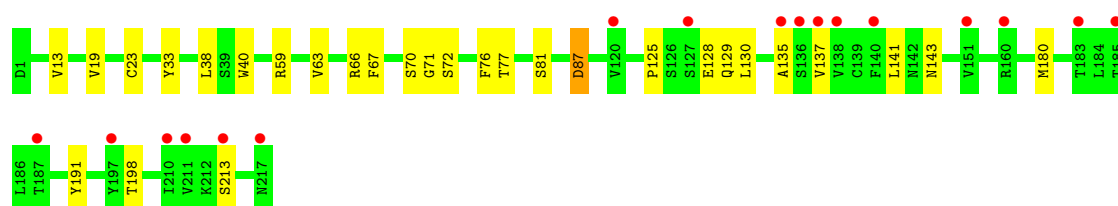
- Molecule 3: MONOCLONAL ANTIBODY Act-1 HEAVY CHAIN

Chain M:  82% 14%




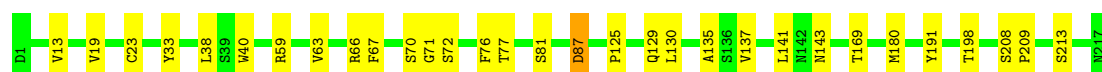
• Molecule 4: MONOCLONAL ANTIBODY Act-1 LIGHT CHAIN

Chain L:  8% 87% 13%



• Molecule 4: MONOCLONAL ANTIBODY Act-1 LIGHT CHAIN

Chain N:  86% 14%



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	127.58Å 123.53Å 154.16Å 90.00° 112.63° 90.00°	Depositor
Resolution (Å)	50.00 – 3.10 56.66 – 3.10	Depositor EDS
% Data completeness (in resolution range)	98.4 (50.00-3.10) 98.5 (56.66-3.10)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.59 (at 3.13Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7.2_869)	Depositor
R, R_{free}	0.197 , 0.231 0.188 , 0.226	Depositor DCC
R_{free} test set	1035 reflections (1.31%)	DCC
Wilson B-factor (Å ²)	76.3	Xtriage
Anisotropy	0.675	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.27 , 63.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	0.025 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	21791	wwPDB-VP
Average B, all atoms (Å ²)	120.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.89% 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: MG, BMA, NAG, CA, TRS, ODU, MAN

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	4/4599 (0.1%)	0.47	1/6228 (0.0%)
1	C	0.40	4/4589 (0.1%)	0.47	1/6214 (0.0%)
2	B	0.25	0/2980	0.44	0/4046
2	D	0.25	0/2981	0.44	0/4047
3	H	0.24	0/1652	0.57	3/2259 (0.1%)
3	M	0.23	0/1667	0.57	3/2280 (0.1%)
4	L	0.24	0/1722	0.41	0/2340
4	N	0.24	0/1722	0.41	0/2340
All	All	0.32	8/21912 (0.0%)	0.47	8/29754 (0.0%)

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	19	PHE	CE2-CZ	-11.35	1.15	1.37
1	A	19	PHE	CE1-CZ	-11.23	1.16	1.37
1	C	19	PHE	CE1-CZ	-11.21	1.16	1.37
1	A	19	PHE	CE2-CZ	-11.12	1.16	1.37
1	C	19	PHE	CG-CD2	-10.19	1.23	1.38
1	A	19	PHE	CG-CD1	-10.14	1.23	1.38
1	A	19	PHE	CG-CD2	-10.14	1.23	1.38
1	C	19	PHE	CG-CD1	-10.08	1.23	1.38

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	H	40	ARG	NE-CZ-NH2	-12.14	114.23	120.30
3	M	40	ARG	NE-CZ-NH1	-12.11	114.25	120.30
3	M	40	ARG	NE-CZ-NH2	12.09	126.34	120.30
3	H	40	ARG	NE-CZ-NH1	11.46	126.03	120.30
3	M	40	ARG	CD-NE-CZ	6.12	132.17	123.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	H	40	ARG	CD-NE-CZ	5.62	131.46	123.60
1	A	19	PHE	CB-CG-CD2	5.02	124.31	120.80
1	C	19	PHE	CD1-CG-CD2	-5.01	111.79	118.30

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	4499	0	4362	82	0
1	C	4489	0	4353	86	0
2	B	2918	0	2849	44	0
2	D	2919	0	2850	38	0
3	H	1607	0	1552	23	0
3	M	1622	0	1567	22	0
4	L	1681	0	1616	20	0
4	N	1681	0	1616	21	0
5	A	3	0	0	0	0
5	B	2	0	0	0	0
5	C	3	0	0	0	0
5	D	2	0	0	0	0
6	A	56	0	52	1	0
6	B	28	0	26	1	0
6	C	56	0	52	0	0
6	D	14	0	13	0	0
7	A	50	0	43	1	0
7	C	50	0	43	1	0
8	A	8	0	12	0	0
9	B	1	0	0	0	0
9	D	1	0	0	0	0
10	B	35	0	18	2	0
10	D	35	0	18	2	0
11	A	10	0	0	1	0
11	B	4	0	0	0	0
11	C	11	0	0	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
11	D	5	0	0	0	0
11	H	1	0	0	0	0
All	All	21791	0	21042	326	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 8.

All (326) 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:M:196:ARG:HD2	3:M:197:PRO:HA	1.54	0.89
3:H:196:ARG:HD2	3:H:197:PRO:HA	1.55	0.85
1:C:442:HIS:HE1	1:C:583:ILE:HB	1.45	0.81
1:C:372:GLY:HA2	1:C:377:ILE:HG22	1.66	0.77
1:A:372:GLY:HA2	1:A:377:ILE:HG22	1.64	0.77
2:B:118:PRO:HB3	2:B:425:GLN:HB3	1.71	0.73
2:D:118:PRO:HB3	2:D:425:GLN:HB3	1.71	0.73
1:A:311:ASN:O	11:A:599:HOH:O	2.07	0.72
1:C:372:GLY:O	11:C:599:HOH:O	2.08	0.71
1:C:311:ASN:O	11:C:600:HOH:O	2.08	0.70
1:A:199:THR:O	1:A:201:LYS:N	2.25	0.70
1:C:199:THR:O	1:C:201:LYS:N	2.25	0.69
2:D:146:LYS:HA	2:D:232:VAL:HG11	1.75	0.69
2:B:296:SER:O	4:N:81:SER:OG	2.10	0.69
1:C:442:HIS:CE1	1:C:583:ILE:HB	2.27	0.69
2:B:135:LEU:HD11	2:B:266:VAL:HG23	1.74	0.68
2:B:146:LYS:HA	2:B:232:VAL:HG11	1.75	0.68
2:D:135:LEU:HD11	2:D:266:VAL:HG23	1.74	0.68
2:B:350:GLY:HA3	2:B:362:LEU:HD11	1.76	0.68
2:D:350:GLY:HA3	2:D:362:LEU:HD11	1.75	0.67
1:C:547:ALA:HB2	1:C:578:ILE:HD13	1.76	0.67
3:M:130:TYR:CG	4:N:129:GLN:HG2	2.30	0.66
2:B:229[B]:ARG:HE	4:L:33:TYR:HA	1.61	0.65
1:C:342:LEU:HD11	1:C:415:VAL:HG22	1.78	0.64
1:C:88:GLU:HB2	1:C:118:ILE:HG13	1.79	0.64
3:H:146:LEU:HD11	3:H:196:ARG:HE	1.61	0.64
1:A:88:GLU:HB2	1:A:118:ILE:HG13	1.79	0.64
1:C:9:LEU:HD12	1:C:427:LEU:HD23	1.80	0.64
1:A:342:LEU:HD11	1:A:415:VAL:HG22	1.79	0.64
1:A:9:LEU:HD12	1:A:427:LEU:HD23	1.81	0.63
3:M:146:LEU:HD11	3:M:196:ARG:HE	1.63	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:239:PRO:HB3	2:D:272:THR:HG23	1.79	0.63
1:C:476:VAL:HG13	1:C:519:SER:HB3	1.81	0.62
2:D:144:SER:OG	2:D:270:ASP:OD2	2.16	0.62
4:L:198:THR:HA	4:L:213:SER:HB3	1.83	0.61
2:B:239:PRO:HB3	2:B:272:THR:HG23	1.81	0.61
1:A:1:TYR:HA	1:A:383:GLN:HB2	1.83	0.61
2:B:142:SER:HB2	10:B:4000:ODU:O29	2.00	0.61
1:C:71:LEU:HB3	1:C:141:THR:HG21	1.82	0.60
1:A:287:PHE:HB3	1:A:311:ASN:ND2	2.16	0.60
4:N:198:THR:HA	4:N:213:SER:HB3	1.82	0.60
1:C:1:TYR:HA	1:C:383:GLN:HB2	1.84	0.60
3:H:39:GLN:HB2	3:H:45:LEU:HD23	1.82	0.60
3:H:17:SER:HB3	3:H:84:SER:HA	1.84	0.60
1:A:71:LEU:HB3	1:A:141:THR:HG21	1.83	0.60
1:A:442:HIS:HE1	1:A:583:ILE:HB	1.67	0.59
2:B:144:SER:OG	2:B:270:ASP:OD2	2.16	0.59
1:C:342:LEU:HB3	1:C:352:ASP:O	2.03	0.59
1:A:342:LEU:HB3	1:A:352:ASP:O	2.01	0.59
3:M:17:SER:HB3	3:M:84:SER:HA	1.85	0.59
3:M:39:GLN:HB2	3:M:45:LEU:HD23	1.84	0.59
1:C:489:ASP:O	1:C:493:LYS:HE3	2.03	0.59
2:D:318:LEU:HD13	2:D:325:PRO:HG3	1.85	0.59
1:C:287:PHE:HB3	1:C:311:ASN:ND2	2.17	0.58
2:D:238:SER:OG	10:D:4000:ODU:O33	2.15	0.58
1:C:340:VAL:HG21	1:C:402:SER:HA	1.86	0.58
1:C:280:VAL:O	1:C:289:ASP:HB2	2.03	0.58
1:A:280:VAL:O	1:A:289:ASP:HB2	2.04	0.58
2:B:238:SER:OG	10:B:4000:ODU:O33	2.19	0.58
1:A:489:ASP:O	1:A:493:LYS:HE3	2.03	0.57
2:B:318:LEU:HD13	2:B:325:PRO:HG3	1.85	0.57
1:C:302:GLU:HB3	1:C:334:ARG:HD3	1.87	0.57
1:A:89:ARG:NH2	6:A:3046:NAG:O6	2.36	0.57
2:D:268:THR:HG22	2:D:328:ALA:HB3	1.85	0.56
1:A:340:VAL:HG21	1:A:402:SER:HA	1.87	0.56
1:C:5:THR:HG21	1:C:389:GLN:HE21	1.70	0.56
1:A:549:HIS:HA	1:A:570:LEU:HD11	1.88	0.56
1:A:493:LYS:HB2	1:A:496:SER:HB2	1.87	0.56
2:B:268:THR:HG22	2:B:328:ALA:HB3	1.86	0.56
1:A:5:THR:HG21	1:A:389:GLN:HE21	1.70	0.56
1:C:173:TYR:OH	1:C:197:ILE:HD11	2.06	0.56
1:A:346:ASP:HB2	1:A:433:VAL:HG11	1.87	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:493:LYS:HB2	1:C:496:SER:HB2	1.87	0.55
1:C:1:TYR:CE2	1:C:574:LYS:HD2	2.42	0.55
2:D:160:LEU:HD22	2:D:220:ALA:HB2	1.88	0.55
1:A:173:TYR:OH	1:A:197:ILE:HD11	2.07	0.55
1:A:302:GLU:HB3	1:A:334:ARG:HD3	1.88	0.54
1:A:289:ASP:OD1	1:A:310:ILE:HA	2.07	0.54
2:B:160:LEU:HD22	2:B:220:ALA:HB2	1.89	0.54
1:C:179:VAL:HG22	1:C:194:VAL:HG12	1.90	0.54
1:C:289:ASP:OD1	1:C:310:ILE:HA	2.08	0.54
4:L:141:LEU:HD13	4:L:180:MET:HE3	1.89	0.54
1:A:117:ASN:HB3	1:A:127:LEU:HB2	1.89	0.54
1:A:545:GLU:HG2	1:A:580:LYS:HG2	1.90	0.54
1:A:442:HIS:CE1	1:A:583:ILE:HB	2.42	0.53
1:A:98:LEU:HD23	1:A:110:THR:HB	1.90	0.53
4:N:66:ARG:HB2	4:N:81:SER:HB3	1.89	0.53
4:L:66:ARG:HB2	4:L:81:SER:HB3	1.89	0.53
1:A:271:SER:HB2	1:A:297:GLN:HB2	1.91	0.53
4:N:141:LEU:HD13	4:N:180:MET:HE3	1.89	0.53
1:A:17:THR:HB	1:A:41:ALA:HB2	1.91	0.53
3:H:200:THR:HG23	3:H:217:LYS:HD3	1.90	0.53
1:C:117:ASN:HB3	1:C:127:LEU:HB2	1.90	0.53
3:M:200:THR:HG23	3:M:217:LYS:HD3	1.90	0.53
1:C:98:LEU:HD23	1:C:110:THR:HB	1.91	0.52
3:M:175:PRO:HD3	4:N:169:THR:HG22	1.91	0.52
4:L:87:ASP:OD1	4:L:87:ASP:N	2.42	0.52
1:C:17:THR:HB	1:C:41:ALA:HB2	1.91	0.52
1:C:543:GLN:HG2	1:C:582:THR:HB	1.90	0.52
3:H:146:LEU:HD11	3:H:196:ARG:NE	2.25	0.52
4:L:125:PRO:HD3	4:L:137:VAL:HG22	1.89	0.52
1:C:227:PHE:HD1	1:C:234:GLU:HB2	1.75	0.52
4:L:125:PRO:HG2	4:L:191:TYR:CE1	2.45	0.52
2:D:382:PRO:HD3	2:D:436:LEU:HD21	1.92	0.51
1:A:179:VAL:HG22	1:A:194:VAL:HG12	1.92	0.51
2:B:261:VAL:O	2:B:263:ARG:HG3	2.09	0.51
4:N:87:ASP:N	4:N:87:ASP:OD1	2.43	0.51
1:A:448:ARG:NH1	1:A:538:ILE:HG21	2.25	0.51
4:N:125:PRO:HD3	4:N:137:VAL:HG22	1.91	0.51
1:A:9:LEU:HB2	1:A:427:LEU:HB3	1.93	0.50
2:D:261:VAL:O	2:D:263:ARG:HG3	2.11	0.50
3:M:146:LEU:HD11	3:M:196:ARG:NE	2.26	0.50
4:N:125:PRO:HG2	4:N:191:TYR:CE1	2.46	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:431:ARG:HD2	1:C:567:GLN:O	2.11	0.50
1:C:9:LEU:HB2	1:C:427:LEU:HB3	1.93	0.50
1:C:53:GLY:O	1:C:94:LEU:HB3	2.11	0.50
1:A:184:GLY:HA2	1:A:188:TRP:CD1	2.47	0.50
3:H:130:TYR:CG	4:L:129:GLN:HG2	2.46	0.50
4:L:59:ARG:NH1	4:L:63:VAL:O	2.45	0.50
4:N:59:ARG:HD3	4:N:67:PHE:O	2.12	0.50
1:A:14:PRO:HB2	1:A:17:THR:HG21	1.92	0.50
2:B:157:HIS:HA	2:B:220:ALA:HB1	1.94	0.50
1:C:184:GLY:HA2	1:C:188:TRP:CD1	2.47	0.50
1:A:227:PHE:HD1	1:A:234:GLU:HB2	1.76	0.49
2:B:382:PRO:HD3	2:B:436:LEU:HD21	1.92	0.49
1:C:470:SER:HA	1:C:517:VAL:HG11	1.92	0.49
3:H:130:TYR:HD1	4:L:128:GLU:HB2	1.77	0.49
1:C:289:ASP:OD1	1:C:311:ASN:N	2.34	0.49
1:A:289:ASP:OD1	1:A:311:ASN:N	2.34	0.49
4:N:59:ARG:NH1	4:N:63:VAL:O	2.46	0.49
4:L:72:SER:HB3	4:N:71:GLY:HA2	1.94	0.49
1:A:488:LEU:HD13	1:A:500:PHE:HB3	1.93	0.49
1:C:25:LEU:HD12	1:C:403:GLY:HA2	1.94	0.49
1:C:488:LEU:HD13	1:C:500:PHE:HB3	1.93	0.49
4:L:59:ARG:HD3	4:L:67:PHE:O	2.11	0.49
2:B:151:ARG:HH11	2:B:151:ARG:HG3	1.78	0.49
3:M:38:LYS:HB2	3:M:48:ILE:HD11	1.94	0.49
3:M:40:ARG:HB2	3:M:43:GLN:HG3	1.94	0.49
2:B:196:PRO:HG3	2:B:207:PRO:HD3	1.94	0.49
1:C:271:SER:HB2	1:C:297:GLN:HB2	1.95	0.49
2:D:151:ARG:HH11	2:D:151:ARG:HG3	1.78	0.49
1:A:435:ILE:HG12	1:A:571:GLN:NE2	2.28	0.49
2:B:366:ALA:O	2:B:370:LEU:HB2	2.13	0.49
1:C:14:PRO:HB2	1:C:17:THR:HG21	1.94	0.49
1:C:388:LEU:HD12	1:C:392:LYS:HA	1.95	0.49
1:A:489:ASP:OD2	1:A:499:ARG:HD3	2.14	0.48
2:D:238:SER:N	2:D:239:PRO:HD2	2.28	0.48
4:L:125:PRO:HB3	4:L:135:ALA:HB1	1.95	0.48
2:D:376:LEU:HD11	2:D:438:LEU:HB3	1.95	0.48
3:H:192:PRO:HG2	3:H:195:PRO:HG3	1.95	0.48
1:A:53:GLY:O	1:A:94:LEU:HB3	2.12	0.48
3:H:38:LYS:HB2	3:H:48:ILE:HD11	1.95	0.48
1:A:85:CYS:HB2	1:A:151:TYR:CE1	2.49	0.48
1:C:5:THR:HG21	1:C:389:GLN:HB3	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:5:THR:HG21	1:A:389:GLN:HB3	1.96	0.48
2:B:376:LEU:HD11	2:B:438:LEU:HB3	1.94	0.48
3:H:30:THR:OG1	3:H:30:THR:O	2.29	0.48
1:C:254:ASP:OD2	1:C:259:ASN:ND2	2.46	0.48
2:D:140:ASP:OD2	2:D:142:SER:OG	2.28	0.48
2:D:157:HIS:HA	2:D:220:ALA:HB1	1.95	0.48
1:A:254:ASP:OD2	1:A:259:ASN:ND2	2.46	0.48
1:C:211:GLN:NE2	1:C:260:ILE:HD12	2.29	0.48
2:D:196:PRO:HG3	2:D:207:PRO:HD3	1.94	0.48
1:A:188:TRP:HZ2	2:B:184:PRO:HB2	1.79	0.47
1:C:85:CYS:HB2	1:C:151:TYR:CE1	2.49	0.47
1:C:491:ASN:C	1:C:493:LYS:H	2.16	0.47
1:A:25:LEU:HD12	1:A:403:GLY:HA2	1.94	0.47
3:M:142:SER:O	3:M:193:SER:OG	2.21	0.47
4:N:125:PRO:HB3	4:N:135:ALA:HB1	1.96	0.47
2:B:238:SER:N	2:B:239:PRO:HD2	2.29	0.47
2:B:332:ALA:C	2:B:334:LEU:H	2.18	0.47
1:C:165:CYS:HB2	1:C:182:ALA:HB1	1.96	0.47
3:M:192:PRO:HG2	3:M:195:PRO:HG3	1.95	0.47
1:A:211:GLN:NE2	1:A:260:ILE:HD12	2.30	0.47
4:L:70:SER:OG	4:L:77:THR:OG1	2.32	0.47
1:A:210:ASN:ND2	1:A:210:ASN:O	2.48	0.47
2:D:332:ALA:C	2:D:334:LEU:H	2.17	0.47
1:A:576:LYS:O	1:A:578:ILE:N	2.45	0.47
1:C:434:VAL:HG21	1:C:550:LEU:HD13	1.97	0.47
2:D:366:ALA:O	2:D:370:LEU:HB2	2.14	0.47
1:A:388:LEU:HD12	1:A:392:LYS:HA	1.95	0.47
1:A:469:PHE:HB2	1:A:517:VAL:HG21	1.95	0.47
1:C:100:ARG:NH2	1:C:103:GLY:O	2.48	0.47
1:A:491:ASN:C	1:A:493:LYS:H	2.17	0.47
1:C:489:ASP:OD2	1:C:499:ARG:HD3	2.14	0.47
1:A:370:TYR:CE1	1:A:381:PHE:HB3	2.50	0.47
4:N:23:CYS:HB2	4:N:40:TRP:CH2	2.49	0.47
1:A:165:CYS:HB2	1:A:182:ALA:HB1	1.97	0.46
1:C:210:ASN:O	1:C:210:ASN:ND2	2.49	0.46
1:C:181:GLY:HA3	1:C:219:GLY:O	2.16	0.46
1:A:431:ARG:HG2	1:A:566:LEU:HB3	1.98	0.46
1:C:314:SER:HB3	1:C:317:VAL:HB	1.98	0.46
1:C:396:MET:HG3	1:C:421:ARG:HG3	1.98	0.46
4:N:70:SER:OG	4:N:77:THR:OG1	2.32	0.46
1:C:370:TYR:CE1	1:C:381:PHE:HB3	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:H:40:ARG:HG2	3:H:92:ALA:HB2	1.97	0.46
4:L:23:CYS:HB2	4:L:40:TRP:CH2	2.50	0.46
2:B:140:ASP:OD2	2:B:142:SER:OG	2.29	0.46
1:C:371:ASN:HB3	11:C:599:HOH:O	2.14	0.45
1:C:484:TYR:OH	1:C:525:ARG:HD3	2.16	0.45
1:C:440:LEU:HD23	1:C:581:LYS:HG3	1.97	0.45
1:A:314:SER:HB3	1:A:317:VAL:HB	1.98	0.45
2:B:391:SER:H	2:B:402:LYS:HE3	1.81	0.45
3:M:207:HIS:CE1	3:M:209:ALA:HB3	2.51	0.45
1:A:100:ARG:NH2	1:A:103:GLY:O	2.48	0.45
1:A:396:MET:HG3	1:A:421:ARG:HG3	1.98	0.45
1:C:191:SER:O	1:C:192:LEU:HD23	2.17	0.45
4:L:71:GLY:HA2	4:N:72:SER:HB3	1.99	0.45
1:A:181:GLY:HA3	1:A:219:GLY:O	2.16	0.45
1:A:187:TYR:HB2	1:A:214:PHE:CD1	2.52	0.45
1:A:484:TYR:OH	1:A:525:ARG:HD3	2.17	0.45
1:A:28:HIS:O	1:A:30:ALA:N	2.50	0.45
1:C:187:TYR:HB2	1:C:214:PHE:CD1	2.51	0.45
2:D:329:VAL:HG11	2:D:337:TYR:CD2	2.52	0.45
1:A:515:ILE:HD13	1:A:525:ARG:HD2	1.99	0.45
2:D:122:GLN:HE21	2:D:419:THR:HG21	1.82	0.44
1:C:345:ILE:HG22	1:C:352:ASP:HB2	1.98	0.44
1:C:86:LEU:HB3	1:C:119:PHE:H	1.82	0.44
1:C:485:ASN:HB3	1:C:512:THR:HG22	1.99	0.44
2:B:151:ARG:HA	2:B:151:ARG:HD2	1.35	0.44
2:B:327:PHE:HB2	2:B:349:VAL:HG22	1.99	0.44
2:D:203:ARG:HD3	4:N:33:TYR:CZ	2.53	0.44
2:D:391:SER:H	2:D:402:LYS:HE3	1.82	0.44
3:M:143:MET:SD	3:M:192:PRO:HA	2.57	0.44
1:C:440:LEU:HD13	1:C:467:LEU:HD23	2.00	0.44
2:D:151:ARG:HA	2:D:151:ARG:HD2	1.35	0.44
2:D:151:ARG:NH1	2:D:151:ARG:HG3	2.32	0.44
2:D:327:PHE:HB2	2:D:349:VAL:HG22	1.99	0.44
2:B:151:ARG:NH1	2:B:151:ARG:HG3	2.32	0.44
1:A:191:SER:O	1:A:192:LEU:HD23	2.18	0.43
1:C:436:VAL:HG11	1:C:570:LEU:HD22	2.00	0.43
1:C:124:GLU:HG3	1:C:156:LYS:HB2	2.00	0.43
1:C:28:HIS:O	1:C:30:ALA:N	2.51	0.43
1:A:408:ASP:OD2	1:A:429:ARG:HD2	2.18	0.43
3:H:126:PRO:HA	3:H:127:PRO:HD3	1.86	0.43
3:H:40:ARG:NH2	3:H:89:GLU:HB3	2.33	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:M:40:ARG:HG2	3:M:92:ALA:HB2	2.00	0.43
4:L:13:VAL:HG11	4:L:19:VAL:HG22	2.01	0.43
3:M:30:THR:O	3:M:30:THR:OG1	2.31	0.43
2:B:127:ARG:NH1	2:B:412:VAL:O	2.36	0.43
3:M:154:PHE:HA	3:M:155:PRO:HA	1.78	0.43
1:A:282:LEU:HD13	1:A:377:ILE:HG23	2.01	0.43
1:A:547:ALA:HB2	1:A:578:ILE:HG12	2.00	0.43
3:H:40:ARG:HB2	3:H:43:GLN:HG3	2.00	0.43
2:B:259:ARG:O	2:B:261:VAL:N	2.52	0.43
3:H:143:MET:SD	3:H:192:PRO:HA	2.59	0.43
2:B:329:VAL:HG11	2:B:337:TYR:CD2	2.54	0.43
1:A:345:ILE:HG22	1:A:352:ASP:HB2	1.99	0.42
2:D:151:ARG:HH11	2:D:151:ARG:CG	2.32	0.42
3:H:133:ALA:HA	3:H:134:PRO:HD3	1.87	0.42
4:N:38:LEU:HD22	4:N:76:PHE:CG	2.54	0.42
2:D:432:GLU:HB3	2:D:433:PRO:HD2	2.02	0.42
3:H:33:TRP:CH2	3:H:52:ASP:HB2	2.54	0.42
2:B:432:GLU:HB2	2:B:434:HIS:CD2	2.54	0.42
2:D:259:ARG:O	2:D:261:VAL:N	2.52	0.42
7:A:3196:NAG:H61	7:A:3197:NAG:N2	2.34	0.42
1:C:18:LEU:HB2	1:C:39:PRO:HD2	2.01	0.42
1:C:469:PHE:HB2	1:C:517:VAL:HG21	2.00	0.42
1:A:440:LEU:HD13	1:A:467:LEU:HD23	2.01	0.42
1:C:282:LEU:HD13	1:C:377:ILE:HG23	2.01	0.42
2:B:122:GLN:HE21	2:B:419:THR:HG21	1.83	0.42
1:C:408:ASP:HB3	1:C:563:PHE:HE2	1.85	0.42
1:A:86:LEU:HB3	1:A:119:PHE:H	1.85	0.42
1:A:124:GLU:HG3	1:A:156:LYS:HB2	2.01	0.42
2:B:151:ARG:HH11	2:B:151:ARG:CG	2.32	0.42
1:C:515:ILE:HD13	1:C:525:ARG:HD2	2.01	0.42
2:B:97:ARG:HG2	6:B:3415:NAG:O4	2.19	0.42
2:D:112:THR:HA	2:D:452:HIS:O	2.20	0.42
3:H:142:SER:O	3:H:193:SER:OG	2.20	0.42
3:M:197:PRO:HB3	3:M:219:VAL:HG22	2.01	0.42
1:A:115:TRP:HB3	1:A:130:GLY:HA2	2.01	0.42
1:C:431:ARG:NH2	1:C:569:ILE:HD12	2.35	0.42
2:D:127:ARG:NH1	2:D:412:VAL:O	2.45	0.42
1:A:412:TYR:CE1	1:A:432:PRO:HB3	2.54	0.42
2:B:432:GLU:HB3	2:B:433:PRO:HD2	2.02	0.42
3:H:130:TYR:CD1	4:L:128:GLU:HB2	2.55	0.42
4:N:13:VAL:HG11	4:N:19:VAL:HG22	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:238:GLY:HA3	1:A:274:GLY:O	2.19	0.41
1:C:238:GLY:HA3	1:C:274:GLY:O	2.20	0.41
4:L:38:LEU:HD22	4:L:76:PHE:CG	2.55	0.41
1:A:485:ASN:HB3	1:A:512:THR:HG22	2.02	0.41
3:H:14:PRO:HG3	3:H:119:VAL:HG12	2.02	0.41
4:L:198:THR:HA	4:L:213:SER:CB	2.49	0.41
3:M:33:TRP:CH2	3:M:52:ASP:HB2	2.55	0.41
1:A:118:ILE:O	1:A:121:ILE:HB	2.21	0.41
1:C:118:ILE:O	1:C:121:ILE:HB	2.20	0.41
2:D:430:LEU:HD13	2:D:434:HIS:ND1	2.36	0.41
2:D:432:GLU:HB2	2:D:434:HIS:CD2	2.55	0.41
1:A:1:TYR:HB3	1:A:382:SER:HB3	2.02	0.41
2:B:112:THR:HA	2:B:452:HIS:O	2.21	0.41
1:C:176:ASP:HB3	1:C:177:LEU:HD12	2.01	0.41
2:B:108:ARG:NH2	2:B:450:GLU:OE1	2.54	0.41
2:B:237:ASP:N	2:B:237:ASP:OD1	2.52	0.41
1:C:87:GLU:HG3	1:C:115:TRP:HE1	1.86	0.41
3:H:13:LYS:HG2	3:H:121:SER:HA	2.02	0.41
3:M:130:TYR:CD1	4:N:129:GLN:HG2	2.56	0.41
2:B:141:LEU:HA	2:B:141:LEU:HD23	1.89	0.41
7:C:3198:BMA:H2	7:C:3199:MAN:H62	2.03	0.41
1:C:408:ASP:OD2	1:C:429:ARG:HD2	2.20	0.41
1:A:1:TYR:OH	1:A:571:GLN:HA	2.21	0.41
1:C:115:TRP:HB3	1:C:130:GLY:HA2	2.01	0.41
1:C:446:VAL:HG23	1:C:585:PHE:HA	2.02	0.41
2:D:189:VAL:HA	2:D:190:PRO:HD3	1.94	0.41
2:B:193:LEU:HD23	2:B:193:LEU:HA	1.90	0.41
1:C:84:THR:HG21	1:C:154:TYR:H	1.86	0.41
2:D:108:ARG:NH2	2:D:450:GLU:OE1	2.54	0.41
3:M:130:TYR:HA	3:M:131:PRO:HD3	1.87	0.41
1:A:87:GLU:HG3	1:A:115:TRP:HE1	1.86	0.40
1:A:192:LEU:HD21	1:A:219:GLY:HA2	2.04	0.40
1:A:32:ARG:HD2	1:A:407:ALA:HA	2.03	0.40
1:C:32:ARG:HD2	1:C:407:ALA:HA	2.03	0.40
3:M:14:PRO:HG3	3:M:119:VAL:HG12	2.03	0.40
1:A:18:LEU:HB2	1:A:39:PRO:HD2	2.03	0.40
1:C:192:LEU:HD21	1:C:219:GLY:HA2	2.03	0.40
1:C:476:VAL:HG21	1:C:520:ARG:HE	1.87	0.40
2:B:272:THR:OG1	2:B:273:PHE:N	2.51	0.40
4:N:208:SER:HA	4:N:209:PRO:HD2	1.95	0.40
1:A:160:GLU:HB3	1:A:187:TYR:CE2	2.57	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:430:LEU:HD13	2:B:434:HIS:ND1	2.37	0.40
2:D:198:PRO:HD3	10:D:4000:ODU:CL2	2.59	0.40
1:A:84:THR:HG21	1:A:154:TYR:H	1.86	0.40
2:B:432:GLU:HB2	2:B:434:HIS:NE2	2.36	0.40
1:C:549:HIS:HA	1:C:570:LEU:HD11	2.03	0.40
1:C:75:SER:HA	1:C:76:PRO:HD3	1.96	0.40
2:D:272:THR:OG1	2:D:273:PHE:N	2.53	0.40
3:H:154:PHE:HA	3:H:155:PRO:HA	1.77	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	A	578/597 (97%)	523 (90%)	51 (9%)	4 (1%)	25	64
1	C	576/597 (96%)	521 (90%)	49 (8%)	6 (1%)	18	57
2	B	374/503 (74%)	337 (90%)	33 (9%)	4 (1%)	17	54
2	D	374/503 (74%)	333 (89%)	37 (10%)	4 (1%)	17	54
3	H	207/219 (94%)	185 (89%)	21 (10%)	1 (0%)	32	71
3	M	209/219 (95%)	189 (90%)	19 (9%)	1 (0%)	32	71
4	L	215/217 (99%)	197 (92%)	16 (7%)	2 (1%)	20	60
4	N	215/217 (99%)	196 (91%)	17 (8%)	2 (1%)	20	60
All	All	2748/3072 (90%)	2481 (90%)	243 (9%)	24 (1%)	20	60

All (24) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	200	ASN
1	C	200	ASN

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Mol	Chain	Res	Type
1	C	577	ASP
1	C	578	ILE
3	M	142	SER
1	A	78	GLY
4	L	87	ASP
1	C	78	GLY
4	N	87	ASP
1	A	29	GLY
2	B	434	HIS
1	C	29	GLY
2	D	434	HIS
1	A	577	ASP
2	B	429	CYS
3	H	211	SER
2	D	429	CYS
2	B	260	ASN
2	B	262	SER
4	L	143	ASN
1	C	575	GLU
2	D	262	SER
4	N	143	ASN
2	D	260	ASN

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	487/500 (97%)	481 (99%)	6 (1%)	75	91
1	C	486/500 (97%)	478 (98%)	8 (2%)	68	89
2	B	324/431 (75%)	316 (98%)	8 (2%)	53	83
2	D	324/431 (75%)	316 (98%)	8 (2%)	53	83
3	H	183/188 (97%)	179 (98%)	4 (2%)	57	85
3	M	185/188 (98%)	181 (98%)	4 (2%)	57	85
4	L	194/194 (100%)	193 (100%)	1 (0%)	91	96

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	N	194/194 (100%)	193 (100%)	1 (0%)	91	96
All	All	2377/2626 (90%)	2337 (98%)	40 (2%)	66	88

All (40) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	125	ASN
1	A	138	ASP
1	A	173	TYR
1	A	197	ILE
1	A	272	TYR
1	A	421	ARG
2	B	144	SER
2	B	151	ARG
2	B	170	VAL
2	B	181	THR
2	B	235	ASN
2	B	265	LEU
2	B	271	ASP
2	B	429	CYS
3	H	30	THR
3	H	72	VAL
3	H	145	THR
3	H	196	ARG
4	L	130	LEU
1	C	125	ASN
1	C	138	ASP
1	C	173	TYR
1	C	197	ILE
1	C	272	TYR
1	C	421	ARG
1	C	472	LYS
1	C	566	LEU
2	D	144	SER
2	D	151	ARG
2	D	170	VAL
2	D	181	THR
2	D	235	ASN
2	D	265	LEU
2	D	271	ASP
2	D	429	CYS
3	M	30	THR

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Mol	Chain	Res	Type
3	M	72	VAL
3	M	145	THR
3	M	196	ARG
4	N	130	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (23) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	42	ASN
1	A	125	ASN
1	A	209	GLN
1	A	210	ASN
1	A	211	GLN
1	A	244	GLN
1	A	347	ASN
1	A	389	GLN
1	A	404	GLN
1	A	571	GLN
2	B	122	GLN
1	C	42	ASN
1	C	125	ASN
1	C	209	GLN
1	C	210	ASN
1	C	211	GLN
1	C	244	GLN
1	C	389	GLN
1	C	404	GLN
1	C	442	HIS
2	D	122	GLN
2	D	324	GLN
4	N	142	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

8 carbohydrates 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	$\# Z > 2$
7	NAG	A	3196	1,7	14,14,15	0.56	0	15,19,21	1.03	1 (6%)
7	NAG	A	3197	7	14,14,15	0.57	0	15,19,21	0.72	0
7	BMA	A	3198	7	11,11,12	0.53	0	13,15,17	0.63	0
7	MAN	A	3199	7	11,11,12	0.56	0	13,15,17	0.51	0
7	NAG	C	3196	1,7	14,14,15	0.53	0	15,19,21	1.31	1 (6%)
7	NAG	C	3197	7	14,14,15	0.57	0	15,19,21	0.76	0
7	BMA	C	3198	7	11,11,12	0.57	0	13,15,17	0.61	0
7	MAN	C	3199	7	11,11,12	0.59	0	13,15,17	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
7	NAG	A	3196	1,7	-	0/6/23/26	0/1/1/1
7	NAG	A	3197	7	-	0/6/23/26	0/1/1/1
7	BMA	A	3198	7	-	0/2/19/22	0/1/1/1
7	MAN	A	3199	7	-	0/2/19/22	1/1/1/1
7	NAG	C	3196	1,7	-	0/6/23/26	0/1/1/1
7	NAG	C	3197	7	-	0/6/23/26	0/1/1/1
7	BMA	C	3198	7	-	0/2/19/22	0/1/1/1
7	MAN	C	3199	7	-	0/2/19/22	1/1/1/1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	A	3196	NAG	C1-O5-C5	2.51	115.62	112.17
7	C	3196	NAG	C2-N2-C7	2.95	127.25	122.94

There are no chirality outliers.

There are no torsion outliers.

All (2) ring outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	C	3199	MAN	C1-C2-C3-C4-C5-O5
7	A	3199	MAN	C1-C2-C3-C4-C5-O5

4 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	A	3196	NAG	1	0
7	A	3197	NAG	1	0
7	C	3198	BMA	1	0
7	C	3199	MAN	1	0

5.6 Ligand geometry [i](#)

Of 26 ligands modelled in this entry, 12 are monoatomic - leaving 14 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	$\# Z > 2$
6	NAG	A	3046	1	14,14,15	0.56	0	15,19,21	0.73	0
6	NAG	A	3105	1	14,14,15	0.55	0	15,19,21	0.65	0
6	NAG	A	3447	1	14,14,15	0.45	0	15,19,21	1.18	1 (6%)
6	NAG	A	3485	1	14,14,15	0.40	0	15,19,21	1.69	3 (20%)
8	TRS	A	598	-	7,7,7	1.42	0	9,9,9	1.66	2 (22%)
6	NAG	B	3260	2	14,14,15	0.61	0	15,19,21	0.63	0
6	NAG	B	3415	2	14,14,15	0.52	0	15,19,21	1.22	1 (6%)
10	ODU	B	4000	9	34,37,37	2.03	7 (20%)	45,55,55	1.36	7 (15%)
6	NAG	C	3046	1	14,14,15	0.54	0	15,19,21	0.93	1 (6%)
6	NAG	C	3105	1	14,14,15	0.54	0	15,19,21	1.00	2 (13%)
6	NAG	C	3447	1	14,14,15	0.53	0	15,19,21	0.57	0
6	NAG	C	3485	1	14,14,15	0.48	0	15,19,21	2.26	2 (13%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	NAG	D	3260	2	14,14,15	0.56	0	15,19,21	0.63	0
10	ODU	D	4000	-	34,37,37	2.03	6 (17%)	45,55,55	1.25	6 (13%)

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
6	NAG	A	3046	1	-	0/6/23/26	0/1/1/1
6	NAG	A	3105	1	-	0/6/23/26	0/1/1/1
6	NAG	A	3447	1	-	0/6/23/26	0/1/1/1
6	NAG	A	3485	1	-	0/6/23/26	0/1/1/1
8	TRS	A	598	-	-	0/9/9/9	0/0/0/0
6	NAG	B	3260	2	-	0/6/23/26	0/1/1/1
6	NAG	B	3415	2	-	0/6/23/26	0/1/1/1
10	ODU	B	4000	9	-	0/22/26/26	0/3/3/3
6	NAG	C	3046	1	-	0/6/23/26	0/1/1/1
6	NAG	C	3105	1	-	0/6/23/26	0/1/1/1
6	NAG	C	3447	1	-	0/6/23/26	0/1/1/1
6	NAG	C	3485	1	-	0/6/23/26	0/1/1/1
6	NAG	D	3260	2	-	0/6/23/26	0/1/1/1
10	ODU	D	4000	-	-	0/22/26/26	0/3/3/3

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
10	B	4000	ODU	C32-N34	-2.90	1.34	1.38
10	D	4000	ODU	C32-N34	-2.81	1.34	1.38
10	B	4000	ODU	C32-C09	-2.25	1.39	1.44
10	B	4000	ODU	C15-N16	-2.24	1.43	1.46
10	D	4000	ODU	C32-C09	-2.08	1.39	1.44
10	B	4000	ODU	C14-C13	2.03	1.56	1.51
10	B	4000	ODU	C19-C17	2.38	1.54	1.51
10	D	4000	ODU	C14-C13	2.42	1.57	1.51
10	D	4000	ODU	C19-C17	2.54	1.54	1.51
10	B	4000	ODU	C17-N16	5.72	1.47	1.34
10	D	4000	ODU	C17-N16	6.12	1.48	1.34
10	D	4000	ODU	O33-C32	7.82	1.44	1.24
10	B	4000	ODU	O33-C32	8.02	1.44	1.24

All (25) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	A	3485	NAG	O5-C1-C2	-4.83	104.75	111.47
6	A	3485	NAG	C1-O5-C5	-2.75	108.37	112.17
10	B	4000	ODU	F08-C05-C04	-2.71	107.81	112.69
10	D	4000	ODU	F07-C05-C04	-2.52	108.16	112.69
10	B	4000	ODU	C01-C02-C03	-2.49	115.96	121.61
10	D	4000	ODU	F06-C05-C04	-2.36	108.44	112.69
10	B	4000	ODU	F06-C05-C04	-2.32	108.52	112.69
10	D	4000	ODU	C01-C02-C03	-2.25	116.50	121.61
10	B	4000	ODU	C30-C31-C10	-2.23	117.87	121.10
10	D	4000	ODU	C24-C25-C19	-2.12	119.08	121.84
6	A	3485	NAG	C6-C5-C4	-2.07	108.16	113.00
10	B	4000	ODU	C24-C25-C19	-2.05	119.17	121.84
10	D	4000	ODU	C22-C20-C19	-2.01	119.22	121.84
10	B	4000	ODU	C22-C20-C19	-2.00	119.23	121.84
6	C	3105	NAG	C1-O5-C5	2.14	115.12	112.17
6	C	3046	NAG	O5-C1-C2	2.21	114.55	111.47
6	C	3105	NAG	O5-C1-C2	2.33	114.71	111.47
8	A	598	TRS	O2-C2-C	2.65	118.14	110.47
8	A	598	TRS	O3-C3-C	2.99	119.13	110.47
10	B	4000	ODU	C25-C19-C20	3.21	121.06	116.72
10	D	4000	ODU	C25-C19-C20	3.23	121.09	116.72
6	B	3415	NAG	C1-O5-C5	3.45	116.92	112.17
6	A	3447	NAG	C1-O5-C5	3.93	117.59	112.17
6	C	3485	NAG	C1-O5-C5	5.59	119.87	112.17
6	C	3485	NAG	O5-C1-C2	5.91	119.69	111.47

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	3046	NAG	1	0
6	B	3415	NAG	1	0
10	B	4000	ODU	2	0
10	D	4000	ODU	2	0

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	582/597 (97%)	-0.05	5 (0%) 84 69	60, 104, 178, 229	2 (0%)
1	C	580/597 (97%)	-0.16	7 (1%) 79 61	64, 108, 188, 230	2 (0%)
2	B	375/503 (74%)	-0.08	5 (1%) 77 59	60, 110, 184, 229	0
2	D	375/503 (74%)	-0.18	6 (1%) 72 51	69, 112, 182, 231	0
3	H	211/219 (96%)	0.30	14 (6%) 19 7	67, 138, 211, 237	0
3	M	213/219 (97%)	-0.14	1 (0%) 90 80	73, 124, 192, 218	2 (0%)
4	L	217/217 (100%)	0.26	17 (7%) 14 5	74, 139, 197, 218	0
4	N	217/217 (100%)	-0.10	0 100 100	70, 119, 185, 215	0
All	All	2770/3072 (90%)	-0.06	55 (1%) 65 44	60, 114, 190, 237	6 (0%)

All (55) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	455	CYS	5.3
3	H	200	THR	4.2
3	H	132	LEU	4.0
3	H	133	ALA	3.9
2	D	99	GLU	3.8
2	D	98	GLY	3.7
1	C	586	ALA	3.6
3	H	218	ILE	3.6
1	C	494	ALA	3.6
4	L	210	ILE	3.5
4	L	138	VAL	3.5
3	H	205	VAL	3.4
3	M	1	GLN	3.3
2	B	98	GLY	3.3
1	C	536	ARG	3.2
1	C	495	GLU	3.1

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Mol	Chain	Res	Type	RSRZ
2	B	455	CYS	3.1
4	L	217	ASN	3.1
1	C	492	ARG	3.1
1	C	474	LYS	3.0
4	L	211	VAL	3.0
4	L	187	THR	3.0
3	H	201	VAL	3.0
2	B	454	LEU	3.0
3	H	168	SER	2.9
3	H	146	LEU	2.8
4	L	160	ARG	2.8
1	A	442	HIS	2.8
1	A	564	PRO	2.7
3	H	167	LEU	2.7
4	L	120	VAL	2.7
4	L	185	THR	2.7
3	H	190	THR	2.7
3	H	166	SER	2.6
3	H	169	SER	2.6
2	D	402	LYS	2.6
4	L	183	THR	2.6
1	A	494	ALA	2.5
2	D	429	CYS	2.4
1	A	492	ARG	2.4
4	L	135	ALA	2.3
3	H	187	SER	2.3
3	H	128	SER	2.3
4	L	136	SER	2.2
4	L	197	TYR	2.2
4	L	140	PHE	2.2
2	B	424	LEU	2.2
2	D	428	HIS	2.2
4	L	127	SER	2.1
1	C	587	ARG	2.1
4	L	151	VAL	2.1
1	A	495	GLU	2.1
2	B	97	ARG	2.1
4	L	137	VAL	2.0
4	L	213	SER	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](#)

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
7	NAG	C	3196	14/15	0.94	0.17	-0.43	64,144,168,188	0
7	NAG	A	3196	14/15	0.93	0.16	-0.93	101,133,184,193	0
7	NAG	C	3197	14/15	0.85	0.21	-	119,177,211,242	0
7	BMA	A	3198	11/12	0.80	0.14	-	109,185,229,238	0
7	NAG	A	3197	14/15	0.83	0.24	-	127,183,213,232	0
7	MAN	A	3199	11/12	0.80	0.26	-	116,197,216,219	0
7	BMA	C	3198	11/12	0.40	0.41	-	164,262,307,328	0
7	MAN	C	3199	11/12	0.48	0.56	-	170,228,288,305	0

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
8	TRS	A	598	8/8	0.90	0.34	3.39	80,145,172,174	0
5	CA	D	2003	1/1	0.96	0.23	2.23	83,83,83,83	0
10	0DU	D	4000	35/35	0.96	0.27	2.08	55,119,193,221	0
9	MG	B	2001	1/1	0.95	0.23	1.88	49,49,49,49	0
5	CA	C	2005	1/1	0.89	0.23	1.88	96,96,96,96	0
6	NAG	A	3485	14/15	0.83	0.31	1.61	93,177,211,223	0
5	CA	B	2003	1/1	0.94	0.26	1.53	69,69,69,69	0
5	CA	A	2005	1/1	0.95	0.30	1.39	86,86,86,86	0
5	CA	A	2006	1/1	0.86	0.24	1.06	92,92,92,92	0
5	CA	A	2007	1/1	0.97	0.23	1.03	79,79,79,79	0
9	MG	D	2001	1/1	0.92	0.19	0.90	61,61,61,61	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
10	ODU	B	4000	35/35	0.97	0.22	0.77	46,96,152,165	0
5	CA	C	2007	1/1	0.89	0.21	0.66	99,99,99,99	0
6	NAG	C	3447	14/15	0.88	0.36	0.63	109,182,221,228	0
6	NAG	C	3485	14/15	0.84	0.24	0.37	153,180,207,207	0
5	CA	C	2006	1/1	0.71	0.24	0.25	102,102,102,102	0
6	NAG	B	3415	14/15	0.89	0.30	-0.11	112,171,206,231	0
6	NAG	A	3447	14/15	0.90	0.22	-0.14	102,171,199,199	0
6	NAG	C	3046	14/15	0.96	0.17	-0.52	83,118,139,161	0
5	CA	D	2002	1/1	0.81	0.09	-1.32	145,145,145,145	0
6	NAG	A	3046	14/15	0.95	0.15	-1.35	78,103,135,141	0
5	CA	B	2002	1/1	0.68	0.09	-2.28	140,140,140,140	0
6	NAG	D	3260	14/15	0.86	0.19	-	102,175,224,228	0
6	NAG	A	3105	14/15	0.86	0.23	-	94,159,196,207	0
6	NAG	B	3260	14/15	0.83	0.21	-	142,184,201,204	0
6	NAG	C	3105	14/15	0.90	0.14	-	75,163,185,186	0

6.5 Other polymers

There are no such residues in this entry.