



## wwPDB EM Map/Model Validation Report ⓘ

Aug 4, 2016 – 09:52 PM EDT

PDB ID : 5A7X  
EMDB ID: : EMD-3086  
Title : negative stain EM of BG505 SOSIP.664 in complex with sCD4, 17b, and 8ANC195  
Authors : Scharf, L.; Wang, H.; Gao, H.; Chen, S.; McDowall, A.; Bjorkman, P.  
Deposited on : 2015-07-10  
Resolution : 17.00 Å(reported)

This is a wwPDB EM Map/Model Validation Report for a publicly released PDB/EMDB entry.  
For rigid body fitted models, validation errors reported here could stem from errors in the original structure(s) used in the fitting.  
We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)  
A user guide is available at  
<http://wwpdb.org/validation/2016/EMValidationReportHelp>

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MolProbity : 4.02b-467  
Mogul : 1.7.1 (RC1), CSD as537be (2016)  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : rb-20027939

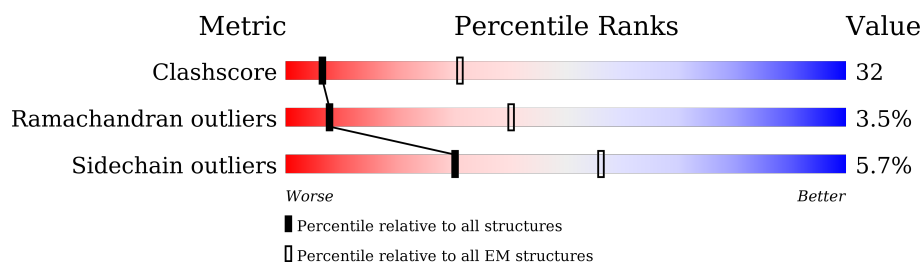
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 17.00 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)	EM structures (#Entries)
Clashscore	114402	924
Ramachandran outliers	111179	726
Sidechain outliers	111093	686

The table below summarises the geometric issues observed across the polymeric chains. The red, orange, yellow and green segments on the bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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  $\leq 5\%$ .

Mol	Chain	Length	Quality of chain
1	A	313	
1	E	313	
1	I	313	
2	B	181	
2	F	181	
2	J	181	
3	C	214	
3	G	214	
3	K	214	

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Mol	Chain	Length	Quality of chain
4	D	229	 38%56%6%
4	H	229	 41%53%6%
4	L	229	 40%54%6%
5	M	215	 87%12%
5	O	215	 86%13%
5	Q	215	 86%13%
6	N	244	 78%14%8%
6	P	244	 79%12%8%
6	R	244	 77%14%8%

## 2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 31872 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, 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 HIV-1 YU2 GP120.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	306	Total	C	N	O	S	0	0
			2385	1494	417	454	20		
1	E	306	Total	C	N	O	S	0	0
			2385	1494	417	454	20		
1	I	306	Total	C	N	O	S	0	0
			2385	1494	417	454	20		

- Molecule 2 is a protein called T-CELL SURFACE GLYCOPROTEIN CD4.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	181	Total	C	N	O	S	0	0
			1412	885	247	276	4		
2	F	181	Total	C	N	O	S	0	0
			1412	885	247	276	4		
2	J	181	Total	C	N	O	S	0	0
			1412	885	247	276	4		

- Molecule 3 is a protein called FAB OF BROADLY NEUTRALIZING ANTIBODY 17B.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	214	Total	C	N	O	S	0	0
			1647	1028	282	332	5		
3	G	214	Total	C	N	O	S	0	0
			1647	1028	282	332	5		
3	K	214	Total	C	N	O	S	0	0
			1647	1028	282	332	5		

- Molecule 4 is a protein called FAB OF BROADLY NEUTRALIZING ANTIBODY 17B.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	229	Total	C	N	O	S	0	0
			1722	1086	289	342	5		

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Mol	Chain	Residues	Atoms					AltConf	Trace
4	H	229	Total	C	N	O	S	0	0
			1722	1086	289	342	5		
4	L	229	Total	C	N	O	S	0	0
			1722	1086	289	342	5		

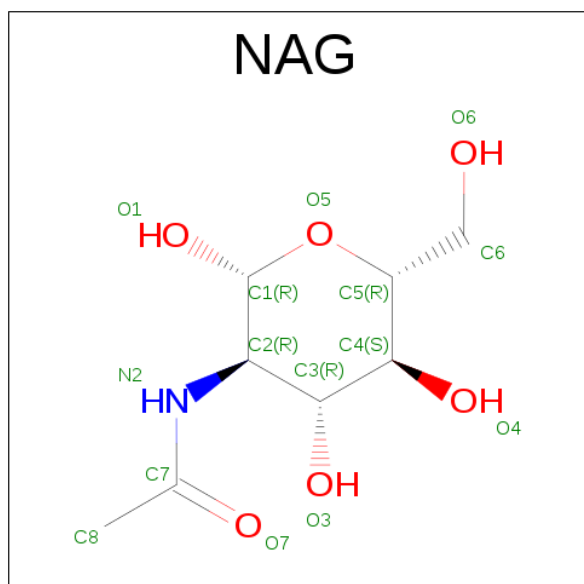
- Molecule 5 is a protein called FAB OF BROADLY NEUTRALIZING ANTIBODY 8ANC195.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	M	214	Total	C	N	O	S	0	0
			1605	1002	273	325	5		
5	O	214	Total	C	N	O	S	0	0
			1605	1002	273	325	5		
5	Q	214	Total	C	N	O	S	0	0
			1605	1002	273	325	5		

- Molecule 6 is a protein called FAB OF BROADLY NEUTRALIZING ANTIBODY 8ANC195.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	N	224	Total	C	N	O	S	0	0
			1643	1046	273	319	5		
6	P	224	Total	C	N	O	S	0	0
			1643	1046	273	319	5		
6	R	224	Total	C	N	O	S	0	0
			1643	1046	273	319	5		

- Molecule 7 is SUGAR (N-ACETYL-D-GLUCOSAMINE) (three-letter code: NAG) (formula:  $C_8H_{15}NO_6$ ).



Mol	Chain	Residues	Atoms				AltConf
7	A	1	Total	C	N	O	0
			196	112	14	70	
7	A	1	Total	C	N	O	0
			196	112	14	70	
7	A	1	Total	C	N	O	0
			196	112	14	70	
7	A	1	Total	C	N	O	0
			196	112	14	70	
7	A	1	Total	C	N	O	0
			196	112	14	70	
7	A	1	Total	C	N	O	0
			196	112	14	70	
7	A	1	Total	C	N	O	0
			196	112	14	70	
7	A	1	Total	C	N	O	0
			196	112	14	70	
7	A	1	Total	C	N	O	0
			196	112	14	70	
7	A	1	Total	C	N	O	0
			196	112	14	70	
7	E	1	Total	C	N	O	0
			196	112	14	70	
7	E	1	Total	C	N	O	0
			196	112	14	70	
7	E	1	Total	C	N	O	0
			196	112	14	70	
7	E	1	Total	C	N	O	0
			196	112	14	70	
7	E	1	Total	C	N	O	0
			196	112	14	70	
7	E	1	Total	C	N	O	0
			196	112	14	70	
7	E	1	Total	C	N	O	0
			196	112	14	70	

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Mol	Chain	Residues	Atoms				AltConf
7	E	1	Total	C	N	O	0
			196	112	14	70	
7	E	1	Total	C	N	O	0
			196	112	14	70	
7	E	1	Total	C	N	O	0
			196	112	14	70	
7	E	1	Total	C	N	O	0
			196	112	14	70	
7	E	1	Total	C	N	O	0
			196	112	14	70	
7	E	1	Total	C	N	O	0
			196	112	14	70	
7	I	1	Total	C	N	O	0
			196	112	14	70	
7	I	1	Total	C	N	O	0
			196	112	14	70	
7	I	1	Total	C	N	O	0
			196	112	14	70	
7	I	1	Total	C	N	O	0
			196	112	14	70	
7	I	1	Total	C	N	O	0
			196	112	14	70	
7	I	1	Total	C	N	O	0
			196	112	14	70	
7	I	1	Total	C	N	O	0
			196	112	14	70	
7	I	1	Total	C	N	O	0
			196	112	14	70	
7	I	1	Total	C	N	O	0
			196	112	14	70	
7	I	1	Total	C	N	O	0
			196	112	14	70	
7	N	1	Total	C	N	O	0
			14	8	1	5	

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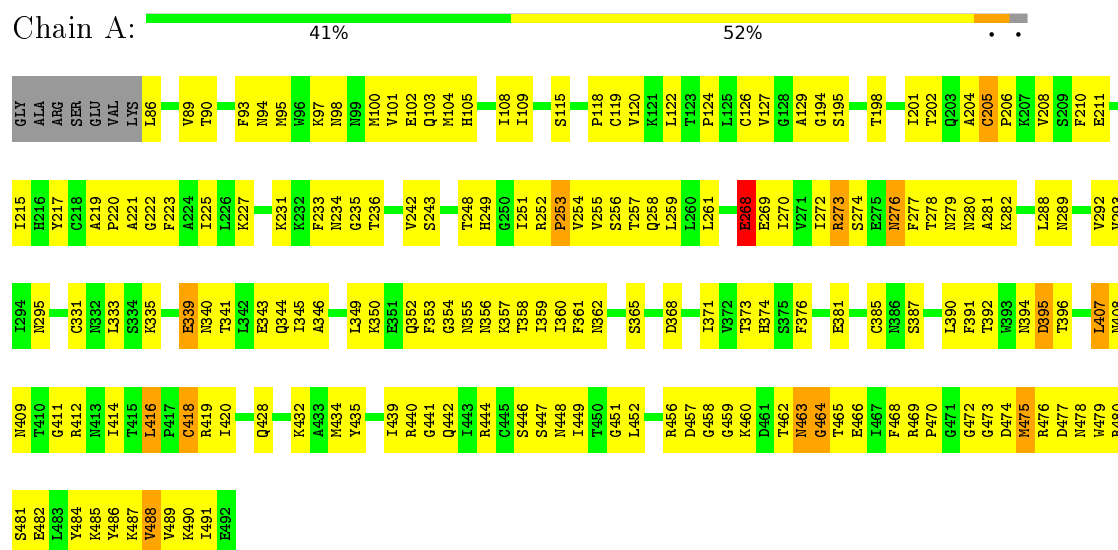
Mol	Chain	Residues	Atoms				AltConf
7	P	1	Total	C	N	O	0
			14	8	1	5	
7	R	1	Total	C	N	O	0
			14	8	1	5	



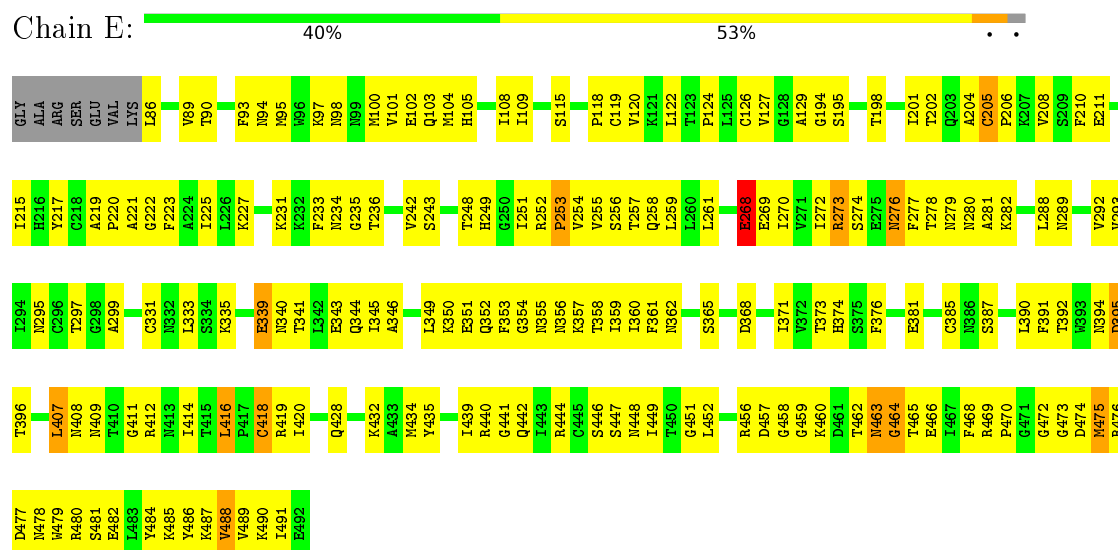
### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. 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. 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: HIV-1 YU2 GP120

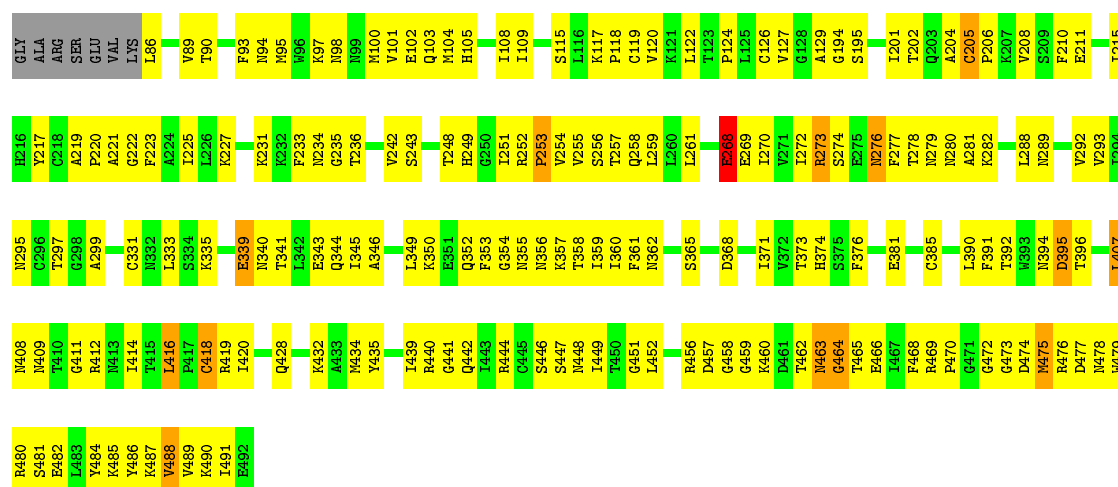


#### • Molecule 1: HIV-1 YU2 GP120

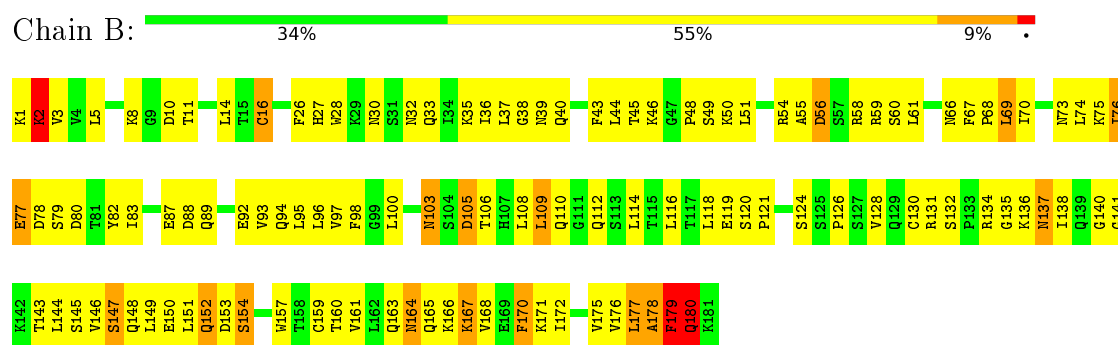


#### • Molecule 1: HIV-1 YU2 GP120





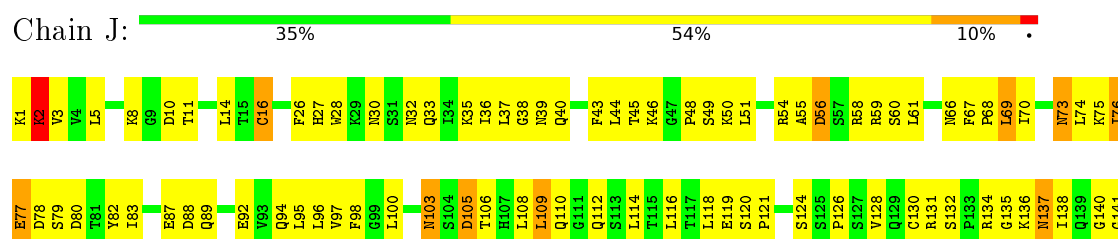
• Molecule 2: T-CELL SURFACE GLYCOPROTEIN CD4

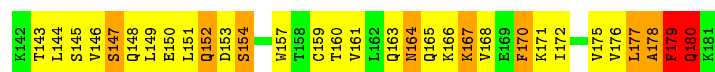


• Molecule 2: T-CELL SURFACE GLYCOPROTEIN CD4



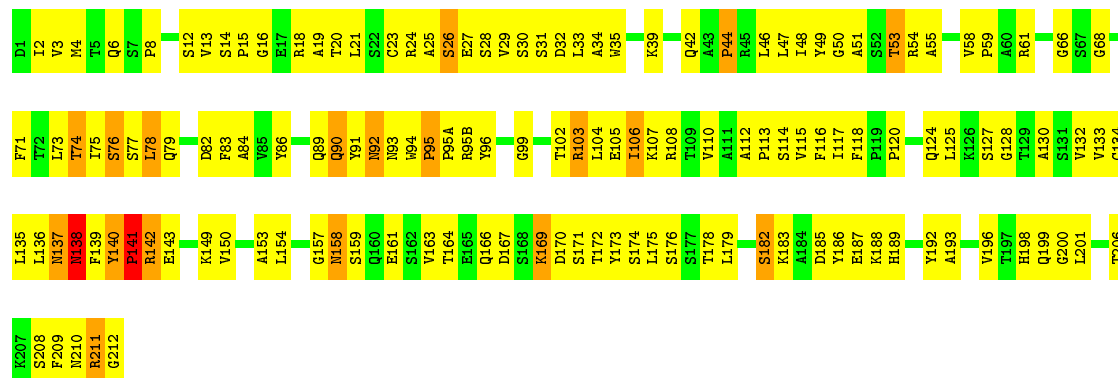
• Molecule 2: T-CELL SURFACE GLYCOPROTEIN CD4





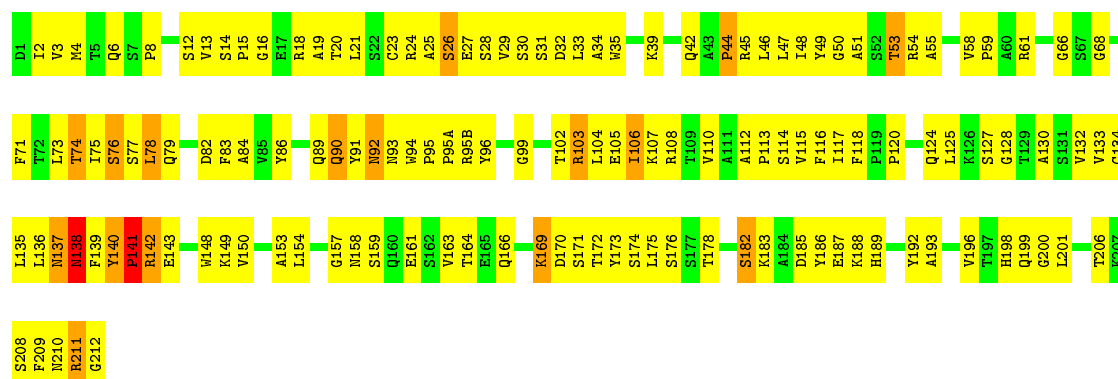
• Molecule 3: FAB OF BROADLY NEUTRALIZING ANTIBODY 17B

Chain C: 34% 57% 8%



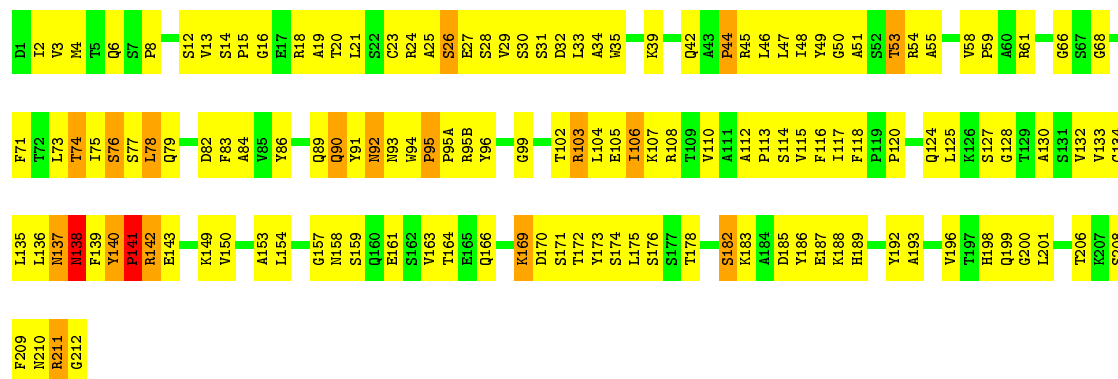
• Molecule 3: FAB OF BROADLY NEUTRALIZING ANTIBODY 17B

Chain G: 34% 58% 7%

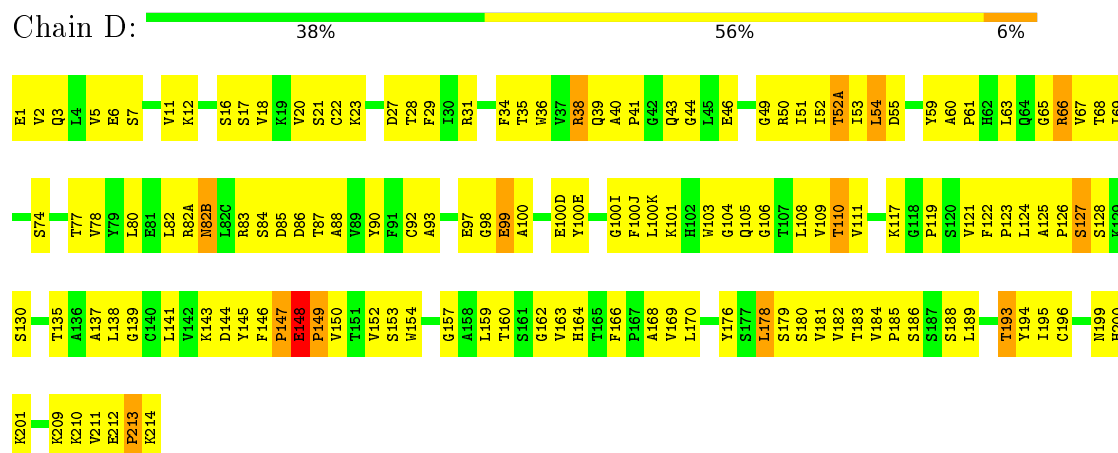


• Molecule 3: FAB OF BROADLY NEUTRALIZING ANTIBODY 17B

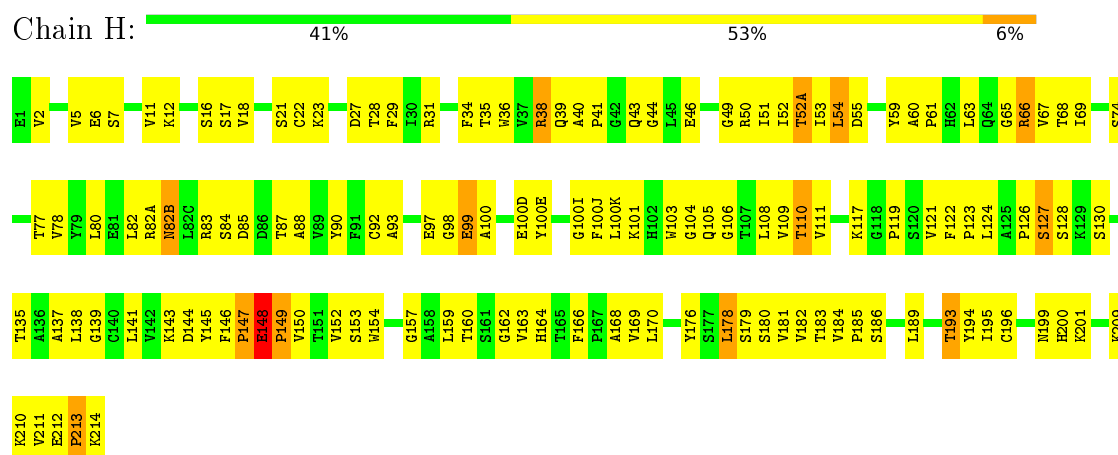
Chain K: 34% 57% 8%



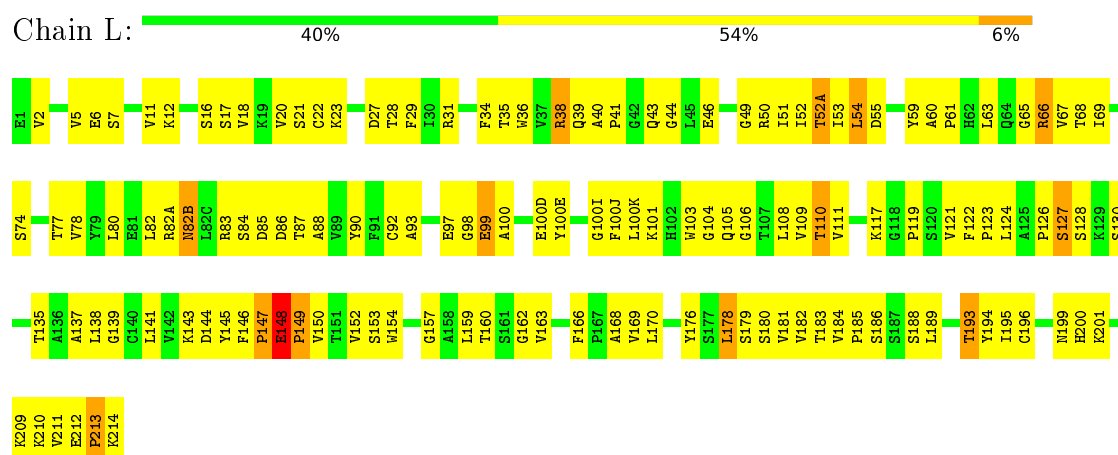
• Molecule 4: FAB OF BROADLY NEUTRALIZING ANTIBODY 17B



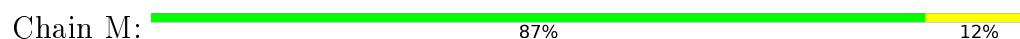
• Molecule 4: FAB OF BROADLY NEUTRALIZING ANTIBODY 17B



• Molecule 4: FAB OF BROADLY NEUTRALIZING ANTIBODY 17B



• Molecule 5: FAB OF BROADLY NEUTRALIZING ANTIBODY 8ANC195

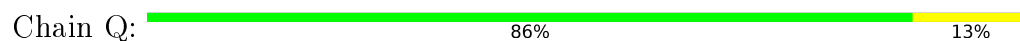




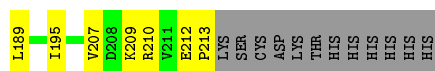
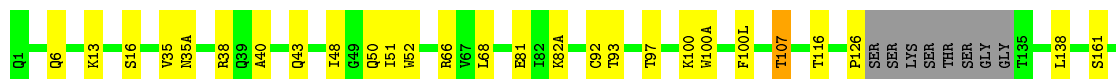
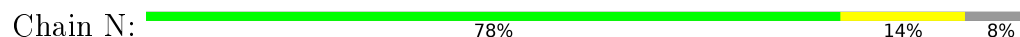
- Molecule 5: FAB OF BROADLY NEUTRALIZING ANTIBODY 8ANC195



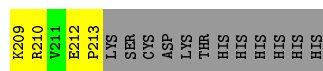
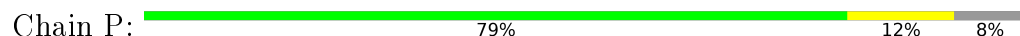
- Molecule 5: FAB OF BROADLY NEUTRALIZING ANTIBODY 8ANC195



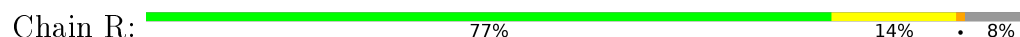
- Molecule 6: FAB OF BROADLY NEUTRALIZING ANTIBODY 8ANC195



- Molecule 6: FAB OF BROADLY NEUTRALIZING ANTIBODY 8ANC195



- Molecule 6: FAB OF BROADLY NEUTRALIZING ANTIBODY 8ANC195



## 4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of particles used	Not provided	Depositor
Resolution determination method	Not provided	Depositor
CTF correction method	INDIVIDUAL PARTICLES	Depositor
Microscope	FEI TECNAI 12	Depositor
Voltage (kV)	120	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	Not provided	Depositor
Minimum defocus (nm)	Not provided	Depositor
Maximum defocus (nm)	Not provided	Depositor
Magnification	42000	Depositor
Image detector	GATAN ULTRASCAN 2K X 2K CCD	Depositor

## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

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

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  >2	RMSZ	# Z  >2
1	A	0.46	0/2432	0.66	0/3296
1	E	0.46	0/2432	0.66	0/3296
1	I	0.46	0/2432	0.66	0/3296
2	B	0.41	0/1432	0.72	2/1930 (0.1%)
2	F	0.41	0/1432	0.72	2/1930 (0.1%)
2	J	0.41	0/1432	0.72	2/1930 (0.1%)
3	C	0.43	0/1684	0.86	3/2288 (0.1%)
3	G	0.43	0/1684	0.86	3/2288 (0.1%)
3	K	0.43	0/1684	0.87	3/2288 (0.1%)
4	D	0.42	0/1762	0.64	0/2399
4	H	0.42	0/1762	0.64	0/2399
4	L	0.42	0/1762	0.64	0/2399
5	M	0.51	0/1640	0.60	0/2232
5	O	0.51	0/1640	0.60	0/2232
5	Q	0.51	0/1640	0.60	0/2232
6	N	0.54	1/1687 (0.1%)	0.60	1/2310 (0.0%)
6	P	0.54	1/1687 (0.1%)	0.61	1/2310 (0.0%)
6	R	0.54	1/1687 (0.1%)	0.60	1/2310 (0.0%)
All	All	0.46	3/31911 (0.0%)	0.68	18/43365 (0.0%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	P	213	PRO	N-CD	5.15	1.55	1.47
6	N	213	PRO	N-CD	5.15	1.55	1.47
6	R	213	PRO	N-CD	5.07	1.54	1.47

The worst 5 of 18 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	140	TYR	C-N-CD	-21.39	73.54	120.60

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Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
3	K	140	TYR	C-N-CD	-21.37	73.58	120.60
3	G	140	TYR	C-N-CD	-21.37	73.59	120.60
3	K	140	TYR	C-N-CA	13.74	179.70	122.00
3	G	140	TYR	C-N-CA	13.72	179.63	122.00

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	2385	0	2327	209	0
1	E	2385	0	2327	210	0
1	I	2385	0	2327	207	0
2	B	1412	0	1444	149	0
2	F	1412	0	1444	147	0
2	J	1412	0	1444	144	0
3	C	1647	0	1593	172	0
3	G	1647	0	1593	172	0
3	K	1647	0	1593	170	0
4	D	1722	0	1691	152	0
4	H	1722	0	1691	149	0
4	L	1722	0	1691	148	0
5	M	1605	0	1521	12	0
5	O	1605	0	1521	14	0
5	Q	1605	0	1521	14	0
6	N	1643	0	1586	21	0
6	P	1643	0	1586	19	0
6	R	1643	0	1586	21	0
7	A	196	0	180	20	0
7	E	196	0	180	19	0
7	I	196	0	180	20	0
7	N	14	0	13	0	0
7	P	14	0	13	0	0
7	R	14	0	13	0	0
All	All	31872	0	31065	2030	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 32.

The worst 5 of 2030 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:B:176:VAL:C	2:B:177:LEU:HD12	1.62	1.20
2:J:176:VAL:C	2:J:177:LEU:HD12	1.62	1.19
2:F:176:VAL:C	2:F:177:LEU:HD12	1.62	1.17
2:J:108:LEU:HD21	2:J:112:GLN:HB3	1.28	1.15
2:B:108:LEU:HD21	2:B:112:GLN:HB3	1.28	1.13

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 PDB entries followed by that with respect to all EM entries.

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	304/313 (97%)	242 (80%)	48 (16%)	14 (5%)	3	33
1	E	304/313 (97%)	242 (80%)	48 (16%)	14 (5%)	3	33
1	I	304/313 (97%)	242 (80%)	48 (16%)	14 (5%)	3	33
2	B	179/181 (99%)	127 (71%)	38 (21%)	14 (8%)	1	20
2	F	179/181 (99%)	127 (71%)	38 (21%)	14 (8%)	1	20
2	J	179/181 (99%)	128 (72%)	37 (21%)	14 (8%)	1	20
3	C	212/214 (99%)	171 (81%)	28 (13%)	13 (6%)	2	26
3	G	212/214 (99%)	171 (81%)	29 (14%)	12 (6%)	2	28
3	K	212/214 (99%)	171 (81%)	28 (13%)	13 (6%)	2	26
4	D	227/229 (99%)	185 (82%)	35 (15%)	7 (3%)	5	42
4	H	227/229 (99%)	185 (82%)	35 (15%)	7 (3%)	5	42
4	L	227/229 (99%)	184 (81%)	36 (16%)	7 (3%)	5	42

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	M	212/215 (99%)	211 (100%)	1 (0%)	0	100	100
5	O	212/215 (99%)	211 (100%)	1 (0%)	0	100	100
5	Q	212/215 (99%)	211 (100%)	1 (0%)	0	100	100
6	N	220/244 (90%)	219 (100%)	1 (0%)	0	100	100
6	P	220/244 (90%)	219 (100%)	1 (0%)	0	100	100
6	R	220/244 (90%)	219 (100%)	1 (0%)	0	100	100
All	All	4062/4188 (97%)	3465 (85%)	454 (11%)	143 (4%)	8	39

5 of 143 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	268	GLU
1	A	409	ASN
1	A	475	MET
2	B	109	LEU
2	B	165	GLN

### 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 PDB entries followed by that with respect to all EM entries.

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	271/276 (98%)	257 (95%)	14 (5%)	29	65
1	E	271/276 (98%)	257 (95%)	14 (5%)	29	65
1	I	271/276 (98%)	257 (95%)	14 (5%)	29	65
2	B	164/164 (100%)	149 (91%)	15 (9%)	12	43
2	F	164/164 (100%)	149 (91%)	15 (9%)	12	43
2	J	164/164 (100%)	149 (91%)	15 (9%)	12	43
3	C	184/184 (100%)	174 (95%)	10 (5%)	27	64
3	G	184/184 (100%)	174 (95%)	10 (5%)	27	64
3	K	184/184 (100%)	174 (95%)	10 (5%)	27	64
4	D	193/193 (100%)	183 (95%)	10 (5%)	29	65

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	H	193/193 (100%)	183 (95%)	10 (5%)	29	65
4	L	193/193 (100%)	183 (95%)	10 (5%)	29	65
5	M	174/182 (96%)	164 (94%)	10 (6%)	25	62
5	O	174/182 (96%)	164 (94%)	10 (6%)	25	62
5	Q	174/182 (96%)	164 (94%)	10 (6%)	25	62
6	N	183/210 (87%)	175 (96%)	8 (4%)	35	69
6	P	183/210 (87%)	175 (96%)	8 (4%)	35	69
6	R	183/210 (87%)	175 (96%)	8 (4%)	35	69
All	All	3507/3627 (97%)	3306 (94%)	201 (6%)	30	62

5 of 201 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	H	66	ARG
2	J	1	LYS
5	Q	50	ARG
4	H	105	GLN
1	I	268	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 69 such sidechains are listed below:

Mol	Chain	Res	Type
2	F	73	ASN
4	H	82(B)	ASN
5	M	155	GLN
2	F	103	ASN
3	G	100	GLN

### 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 carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

45 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$
7	NAG	A	588	1	12,12,15	0.58	0	11,15,21	0.79	0
7	NAG	A	697	1	14,14,15	0.64	0	15,19,21	0.71	0
7	NAG	A	734	1	14,14,15	0.59	0	15,19,21	0.55	0
7	NAG	A	741	1	12,12,15	0.47	0	11,15,21	0.61	0
7	NAG	A	762	1	14,14,15	0.60	0	15,19,21	0.84	1 (6%)
7	NAG	A	776	1	14,14,15	0.58	0	15,19,21	0.84	1 (6%)
7	NAG	A	789	1	14,14,15	0.64	0	15,19,21	0.97	1 (6%)
7	NAG	A	795	1	14,14,15	0.52	0	15,19,21	0.74	0
7	NAG	A	856	1	14,14,15	0.74	0	15,19,21	0.83	1 (6%)
7	NAG	A	886	1	14,14,15	0.66	0	15,19,21	1.18	2 (13%)
7	NAG	A	894	1	14,14,15	0.63	0	15,19,21	0.84	1 (6%)
7	NAG	A	908	1	14,14,15	0.62	0	15,19,21	0.68	1 (6%)
7	NAG	A	948	1	14,14,15	0.87	1 (7%)	15,19,21	1.05	1 (6%)
7	NAG	A	963	1	14,14,15	0.73	0	15,19,21	0.75	0
7	NAG	E	588	1	12,12,15	0.59	0	11,15,21	0.78	0
7	NAG	E	697	1	14,14,15	0.63	0	15,19,21	0.72	1 (6%)
7	NAG	E	734	1	14,14,15	0.61	0	15,19,21	0.55	0
7	NAG	E	741	1	12,12,15	0.46	0	11,15,21	0.63	0
7	NAG	E	762	1	14,14,15	0.61	0	15,19,21	0.83	1 (6%)
7	NAG	E	776	1	14,14,15	0.58	0	15,19,21	0.83	1 (6%)
7	NAG	E	789	1	14,14,15	0.64	0	15,19,21	0.97	1 (6%)
7	NAG	E	795	1	14,14,15	0.52	0	15,19,21	0.74	0
7	NAG	E	856	1	14,14,15	0.73	0	15,19,21	0.84	1 (6%)
7	NAG	E	886	1	14,14,15	0.65	0	15,19,21	1.17	2 (13%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
7	NAG	E	894	1	14,14,15	0.65	0	15,19,21	0.82	1 (6%)
7	NAG	E	908	1	14,14,15	0.60	0	15,19,21	0.67	1 (6%)
7	NAG	E	948	1	14,14,15	0.89	1 (7%)	15,19,21	1.05	1 (6%)
7	NAG	E	963	1	14,14,15	0.72	0	15,19,21	0.76	0
7	NAG	I	588	1	12,12,15	0.57	0	11,15,21	0.78	0
7	NAG	I	697	1	14,14,15	0.63	0	15,19,21	0.71	0
7	NAG	I	734	1	14,14,15	0.60	0	15,19,21	0.56	0
7	NAG	I	741	1	12,12,15	0.46	0	11,15,21	0.62	0
7	NAG	I	762	1	14,14,15	0.59	0	15,19,21	0.83	1 (6%)
7	NAG	I	776	1	14,14,15	0.57	0	15,19,21	0.84	1 (6%)
7	NAG	I	789	1	14,14,15	0.64	0	15,19,21	0.99	1 (6%)
7	NAG	I	795	1	14,14,15	0.51	0	15,19,21	0.74	0
7	NAG	I	856	1	14,14,15	0.75	0	15,19,21	0.84	1 (6%)
7	NAG	I	886	1	14,14,15	0.66	0	15,19,21	1.18	2 (13%)
7	NAG	I	894	1	14,14,15	0.63	0	15,19,21	0.84	1 (6%)
7	NAG	I	908	1	14,14,15	0.59	0	15,19,21	0.68	1 (6%)
7	NAG	I	948	1	14,14,15	0.89	1 (7%)	15,19,21	1.05	1 (6%)
7	NAG	I	963	1	14,14,15	0.73	0	15,19,21	0.75	0
7	NAG	N	1000	6	14,14,15	1.63	1 (7%)	15,19,21	1.30	1 (6%)
7	NAG	P	1000	6	14,14,15	1.64	1 (7%)	15,19,21	1.29	1 (6%)
7	NAG	R	1000	6	14,14,15	1.63	1 (7%)	15,19,21	1.29	1 (6%)

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	588	1	-	0/15/15/26	0/0/0/1
7	NAG	A	697	1	-	1/6/23/26	0/1/1/1
7	NAG	A	734	1	-	0/6/23/26	0/1/1/1
7	NAG	A	741	1	-	0/15/15/26	0/0/0/1
7	NAG	A	762	1	-	0/6/23/26	0/1/1/1
7	NAG	A	776	1	-	0/6/23/26	0/1/1/1
7	NAG	A	789	1	-	1/6/23/26	0/1/1/1
7	NAG	A	795	1	-	0/6/23/26	0/1/1/1
7	NAG	A	856	1	-	0/6/23/26	0/1/1/1
7	NAG	A	886	1	-	0/6/23/26	0/1/1/1
7	NAG	A	894	1	-	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	NAG	A	908	1	-	0/6/23/26	0/1/1/1
7	NAG	A	948	1	-	0/6/23/26	0/1/1/1
7	NAG	A	963	1	-	1/6/23/26	0/1/1/1
7	NAG	E	588	1	-	0/15/15/26	0/0/0/1
7	NAG	E	697	1	-	1/6/23/26	0/1/1/1
7	NAG	E	734	1	-	0/6/23/26	0/1/1/1
7	NAG	E	741	1	-	0/15/15/26	0/0/0/1
7	NAG	E	762	1	-	0/6/23/26	0/1/1/1
7	NAG	E	776	1	-	0/6/23/26	0/1/1/1
7	NAG	E	789	1	-	1/6/23/26	0/1/1/1
7	NAG	E	795	1	-	0/6/23/26	0/1/1/1
7	NAG	E	856	1	-	0/6/23/26	0/1/1/1
7	NAG	E	886	1	-	0/6/23/26	0/1/1/1
7	NAG	E	894	1	-	0/6/23/26	0/1/1/1
7	NAG	E	908	1	-	0/6/23/26	0/1/1/1
7	NAG	E	948	1	-	0/6/23/26	0/1/1/1
7	NAG	E	963	1	-	1/6/23/26	0/1/1/1
7	NAG	I	588	1	-	0/15/15/26	0/0/0/1
7	NAG	I	697	1	-	1/6/23/26	0/1/1/1
7	NAG	I	734	1	-	0/6/23/26	0/1/1/1
7	NAG	I	741	1	-	0/15/15/26	0/0/0/1
7	NAG	I	762	1	-	0/6/23/26	0/1/1/1
7	NAG	I	776	1	-	0/6/23/26	0/1/1/1
7	NAG	I	789	1	-	1/6/23/26	0/1/1/1
7	NAG	I	795	1	-	0/6/23/26	0/1/1/1
7	NAG	I	856	1	-	0/6/23/26	0/1/1/1
7	NAG	I	886	1	-	0/6/23/26	0/1/1/1
7	NAG	I	894	1	-	0/6/23/26	0/1/1/1
7	NAG	I	908	1	-	0/6/23/26	0/1/1/1
7	NAG	I	948	1	-	0/6/23/26	0/1/1/1
7	NAG	I	963	1	-	1/6/23/26	0/1/1/1
7	NAG	N	1000	6	-	0/6/23/26	0/1/1/1
7	NAG	P	1000	6	-	0/6/23/26	0/1/1/1
7	NAG	R	1000	6	-	0/6/23/26	0/1/1/1

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	P	1000	NAG	O5-C1	-5.79	1.34	1.43
7	N	1000	NAG	O5-C1	-5.78	1.34	1.43
7	R	1000	NAG	O5-C1	-5.76	1.34	1.43
7	A	948	NAG	C1-C2	2.55	1.56	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	E	948	NAG	C1-C2	2.57	1.56	1.52

The worst 5 of 31 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	P	1000	NAG	C1-O5-C5	-4.32	105.78	112.14
7	N	1000	NAG	C1-O5-C5	-4.31	105.81	112.14
7	R	1000	NAG	C1-O5-C5	-4.30	105.82	112.14
7	I	886	NAG	C2-N2-C7	-3.10	119.08	123.11
7	A	886	NAG	C2-N2-C7	-3.06	119.12	123.11

There are no chirality outliers.

5 of 9 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	I	963	NAG	O7-C7-N2-C2
7	E	963	NAG	O7-C7-N2-C2
7	A	963	NAG	O7-C7-N2-C2
7	A	697	NAG	O7-C7-N2-C2
7	I	697	NAG	O7-C7-N2-C2

There are no ring outliers.

27 monomers are involved in 59 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	A	741	NAG	1	0
7	A	762	NAG	1	0
7	A	776	NAG	1	0
7	A	789	NAG	5	0
7	A	856	NAG	1	0
7	A	894	NAG	3	0
7	A	908	NAG	3	0
7	A	948	NAG	3	0
7	A	963	NAG	2	0
7	E	741	NAG	1	0
7	E	762	NAG	1	0
7	E	776	NAG	1	0
7	E	789	NAG	5	0
7	E	856	NAG	1	0
7	E	894	NAG	3	0
7	E	908	NAG	3	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	E	948	NAG	3	0
7	E	963	NAG	1	0
7	I	741	NAG	1	0
7	I	762	NAG	1	0
7	I	776	NAG	1	0
7	I	789	NAG	5	0
7	I	856	NAG	1	0
7	I	894	NAG	3	0
7	I	908	NAG	4	0
7	I	948	NAG	3	0
7	I	963	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.