



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 19, 2016 – 10:25 PM GMT

PDB ID : 5CJX
Title : Crystal structure of 8ANC195 Fab in complex with BG505 SOSIP.664 HIV-1 Env trimer
Authors : Scharf, L.; Bjorkman, P.J.
Deposited on : 2015-07-15
Resolution : 3.58 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<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 : 1.7.1 (RC1), CSD as537be (2016)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026982
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
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) : rb-20026982

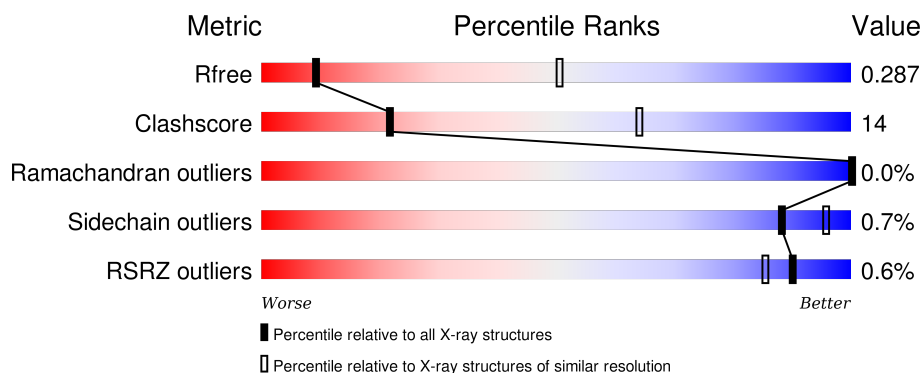
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.58 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}	91344	1261 (3.76-3.40)
Clashscore	102246	1026 (3.72-3.44)
Ramachandran outliers	100387	1028 (3.74-3.42)
Sidechain outliers	100360	1028 (3.74-3.42)
RSRZ outliers	91569	1268 (3.76-3.40)

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	244	<div> <div></div> <div>70% 22% 8%</div> </div>
1	D	244	<div> <div></div> <div>74% 18% 8%</div> </div>
1	H	244	<div> <div></div> <div>70% 23% 7%</div> </div>
2	B	153	<div> <div>%</div> <div>50% 31% 19%</div> </div>
2	J	153	<div> <div>%</div> <div>55% 25% 19%</div> </div>

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
2	X	153	
3	C	215	
3	E	215	
3	L	215	
4	G	479	
4	K	479	
4	Y	479	

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
5	NAG	B	1040	-	-	-	X
5	NAG	G	1020	-	-	X	-
5	NAG	G	1021	-	-	-	X
5	NAG	Y	1042	-	-	-	X
7	MAN	Y	1009	-	-	X	-

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 22299 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 8ANC195 G52K5 heavy chain, IG gamma-1 chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	224	Total	C	N	O	S	0	0	0
			1655	1049	278	323	5			
1	D	224	Total	C	N	O	S	0	0	0
			1614	1022	269	318	5			
1	H	227	Total	C	N	O	S	0	0	0
			1675	1063	282	325	5			

- Molecule 2 is a protein called BG505 Env gp41.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	124	Total	C	N	O	S	0	0	0
			956	602	164	184	6			
2	J	124	Total	C	N	O	S	0	0	0
			957	605	163	183	6			
2	X	121	Total	C	N	O	S	0	0	0
			945	596	165	178	6			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	559	PRO	ILE	engineered mutation	UNP Q2N0S6
B	605	CYS	THR	engineered mutation	UNP Q2N0S6
J	559	PRO	ILE	engineered mutation	UNP Q2N0S6
J	605	CYS	THR	engineered mutation	UNP Q2N0S6
X	559	PRO	ILE	engineered mutation	UNP Q2N0S6
X	605	CYS	THR	engineered mutation	UNP Q2N0S6

- Molecule 3 is a protein called 8ANC195 G52K5 light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	214	Total	C	N	O	S	0	0	0
			1593	996	267	325	5			

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	E	214	Total	C	N	O	S	0	0	0
			1560	976	260	319	5			
3	L	214	Total	C	N	O	S	0	0	0
			1540	962	255	318	5			

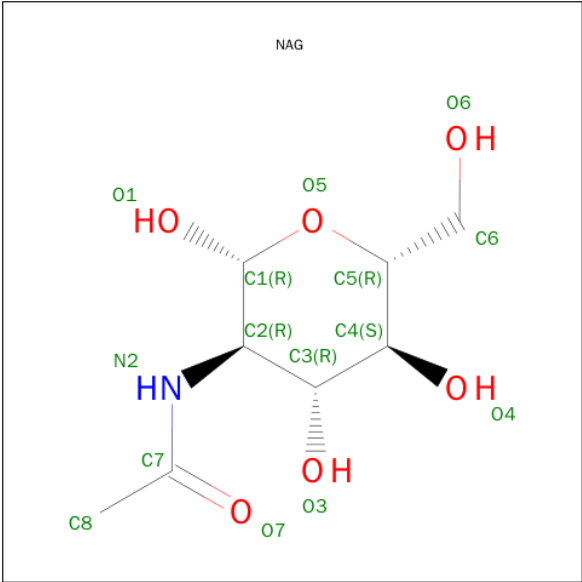
- Molecule 4 is a protein called BG505 Env gp120.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	G	398	Total	C	N	O	S	0	0	0
			2857	1807	480	546	24			
4	K	405	Total	C	N	O	S	0	0	0
			2984	1891	502	564	27			
4	Y	397	Total	C	N	O	S	0	0	0
			2947	1864	501	556	26			

There are 21 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	320M	ASN	THR	engineered mutation	UNP Q2N0S6
G	501	CYS	ALA	engineered mutation	UNP Q2N0S6
G	509	ARG	-	expression tag	UNP Q2N0S6
G	510	ARG	-	expression tag	UNP Q2N0S6
G	511	ARG	-	expression tag	UNP Q2N0S6
G	512	ARG	-	expression tag	UNP Q2N0S6
G	513	ARG	-	expression tag	UNP Q2N0S6
K	332	ASN	THR	engineered mutation	UNP Q2N0S6
K	501	CYS	ALA	engineered mutation	UNP Q2N0S6
K	509	ARG	-	expression tag	UNP Q2N0S6
K	510	ARG	-	expression tag	UNP Q2N0S6
K	511	ARG	-	expression tag	UNP Q2N0S6
K	512	ARG	-	expression tag	UNP Q2N0S6
K	513	ARG	-	expression tag	UNP Q2N0S6
Y	320M	ASN	THR	engineered mutation	UNP Q2N0S6
Y	501	CYS	ALA	engineered mutation	UNP Q2N0S6
Y	509	ARG	-	expression tag	UNP Q2N0S6
Y	510	ARG	-	expression tag	UNP Q2N0S6
Y	511	ARG	-	expression tag	UNP Q2N0S6
Y	512	ARG	-	expression tag	UNP Q2N0S6
Y	513	ARG	-	expression tag	UNP Q2N0S6

- Molecule 5 is N-ACETYL-D-GLUCOSAMINE (three-letter code: NAG) (formula: C₈H₁₅NO₆).



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

Continued on next page...

Continued from previous page...

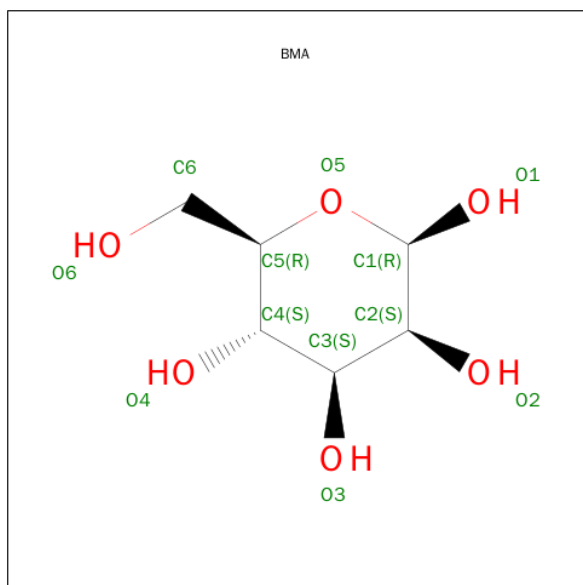
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	J	1	Total	C	N	O	0	0
			14	8	1	5		
5	J	1	Total	C	N	O	0	0
			14	8	1	5		
5	J	1	Total	C	N	O	0	0
			14	8	1	5		
5	J	1	Total	C	N	O	0	0
			14	8	1	5		
5	J	1	Total	C	N	O	0	0
			14	8	1	5		
5	K	1	Total	C	N	O	0	0
			14	8	1	5		
5	K	1	Total	C	N	O	0	0
			14	8	1	5		
5	K	1	Total	C	N	O	0	0
			14	8	1	5		
5	K	1	Total	C	N	O	0	0
			14	8	1	5		
5	K	1	Total	C	N	O	0	0
			14	8	1	5		
5	K	1	Total	C	N	O	0	0
			14	8	1	5		
5	K	1	Total	C	N	O	0	0
			14	8	1	5		
5	X	1	Total	C	N	O	0	0
			14	8	1	5		
5	X	1	Total	C	N	O	0	0
			14	8	1	5		
5	X	1	Total	C	N	O	0	0
			14	8	1	5		
5	X	1	Total	C	N	O	0	0
			14	8	1	5		
5	Y	1	Total	C	N	O	0	0
			14	8	1	5		
5	Y	1	Total	C	N	O	0	0
			14	8	1	5		
5	Y	1	Total	C	N	O	0	0
			14	8	1	5		
5	Y	1	Total	C	N	O	0	0
			14	8	1	5		
5	Y	1	Total	C	N	O	0	0
			14	8	1	5		

Continued on next page...

Continued from previous page...

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

- Molecule 6 is BETA-D-MANNOSE (three-letter code: BMA) (formula: $C_6H_{12}O_6$).



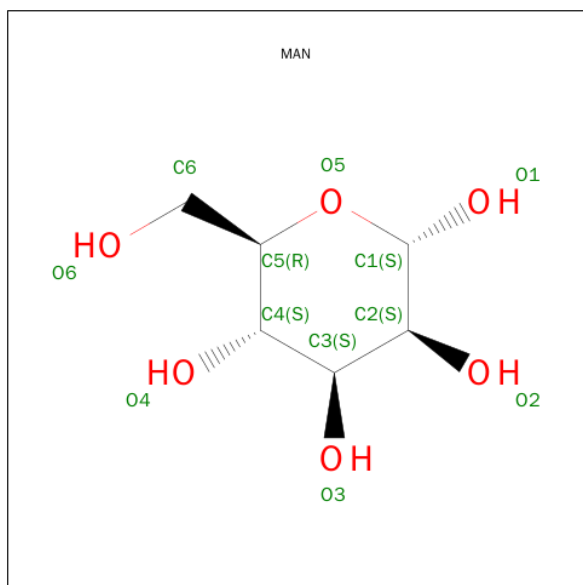
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	B	1	Total	C	O	0	0
			11	6	5		
6	G	1	Total	C	O	0	0
			11	6	5		
6	G	1	Total	C	O	0	0
			11	6	5		
6	J	1	Total	C	O	0	0
			11	6	5		
6	K	1	Total	C	O	0	0
			11	6	5		
6	K	1	Total	C	O	0	0
			11	6	5		
6	K	1	Total	C	O	0	0
			11	6	5		
6	X	1	Total	C	O	0	0
			11	6	5		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	Y	1	Total	C	O	0	0
			11	6	5		
6	Y	1	Total	C	O	0	0
			11	6	5		
6	Y	1	Total	C	O	0	0
			11	6	5		

- Molecule 7 is ALPHA-D-MANNOSE (three-letter code: MAN) (formula: C₆H₁₂O₆).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	B	1	Total	C	O	0	0
			11	6	5		
7	B	1	Total	C	O	0	0
			11	6	5		
7	G	1	Total	C	O	0	0
			11	6	5		
7	G	1	Total	C	O	0	0
			11	6	5		
7	G	1	Total	C	O	0	0
			11	6	5		
7	G	1	Total	C	O	0	0
			11	6	5		
7	G	1	Total	C	O	0	0
			11	6	5		

Continued on next page...

Continued from previous page...


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	G	1	Total	C	O	0	0
			11	6	5		
7	G	1	Total	C	O	0	0
			11	6	5		
7	G	1	Total	C	O	0	0
			11	6	5		
7	G	1	Total	C	O	0	0
			11	6	5		
7	J	1	Total	C	O	0	0
			11	6	5		
7	K	1	Total	C	O	0	0
			11	6	5		
7	K	1	Total	C	O	0	0
			11	6	5		
7	K	1	Total	C	O	0	0
			11	6	5		
7	K	1	Total	C	O	0	0
			11	6	5		
7	K	1	Total	C	O	0	0
			11	6	5		
7	K	1	Total	C	O	0	0
			11	6	5		
7	K	1	Total	C	O	0	0
			11	6	5		
7	K	1	Total	C	O	0	0
			11	6	5		
7	X	1	Total	C	O	0	0
			11	6	5		
7	Y	1	Total	C	O	0	0
			11	6	5		
7	Y	1	Total	C	O	0	0
			11	6	5		
7	Y	1	Total	C	O	0	0
			11	6	5		
7	Y	1	Total	C	O	0	0
			11	6	5		

Continued on next page...


Continued from previous page...

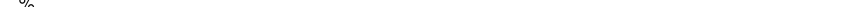
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	Y	1	Total	C	O	0	0
			11	6	5		
7	Y	1	Total	C	O	0	0
			11	6	5		
7	Y	1	Total	C	O	0	0
			11	6	5		
7	Y	1	Total	C	O	0	0
			11	6	5		

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 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.

- Chain A: 

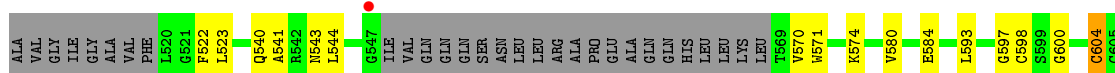
- [illegible]

- Chain H: 
- | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|------|-------|-------|-------|-------|-------|-------|-------|------|------|------|------|------|------|------|------|-----|-----|-----|-----|-----|------|------|------|------|------|------|------|------|------|------|------|------|------|-----|-----|------|-----|-----|-----|-----|-----|-----|-----|
| Q1 | Q6 | V11 | K23 | A24 | Y25 | Y33 | A34 | V35 | R35A | R38 | Q39 | A40 | Q43 | I48 | W52 | R54 | W55 | R56 | S57 | S60 | R64 | G65 | R66 | V67 | A71 | V72 | D73 | L74 | V75 | G76 | P77B | P77C | I77D | S78 | E81 | L82C | D86 | C92 | T93 | T94 | T95 | S96 | T97 |
| R100 | W100A | H100E | H100F | V100I | M100J | A100K | F100L | S101 | S102 | T107 | V111 | P119 | P126 | S127 | S128 | LYS | SER | THR | SER | GLY | T135 | Y145 | F146 | P147 | L159 | V182 | H200 | R210 | V211 | E212 | P213 | K214 | SER | CYS | ASP | LYS | THR | HIS | HIS | HIS | HIS | HIS | |

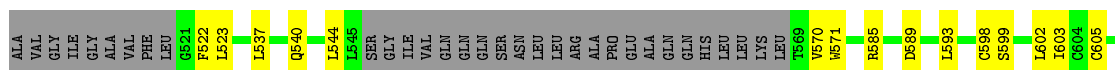
- Chain B: 



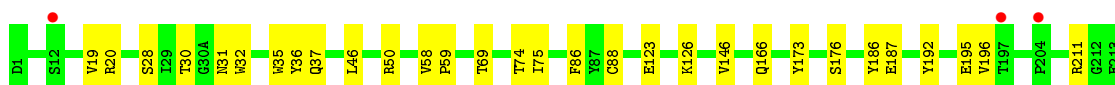
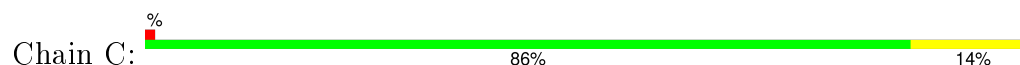
• Molecule 2: BG505 Env gp41



• Molecule 2: BG505 Env gp41

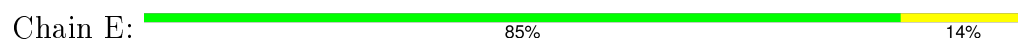


• Molecule 3: 8ANC195 G52K5 light chain



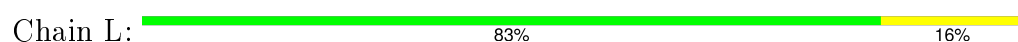
CYS

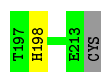
• Molecule 3: 8ANC195 G52K5 light chain



CYS

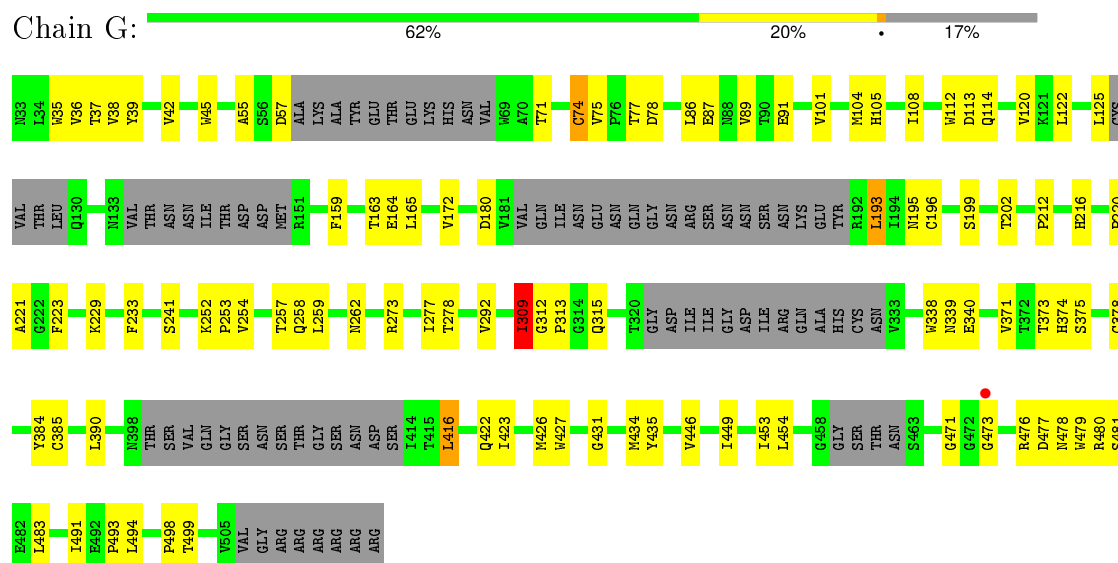
• Molecule 3: 8ANC195 G52K5 light chain





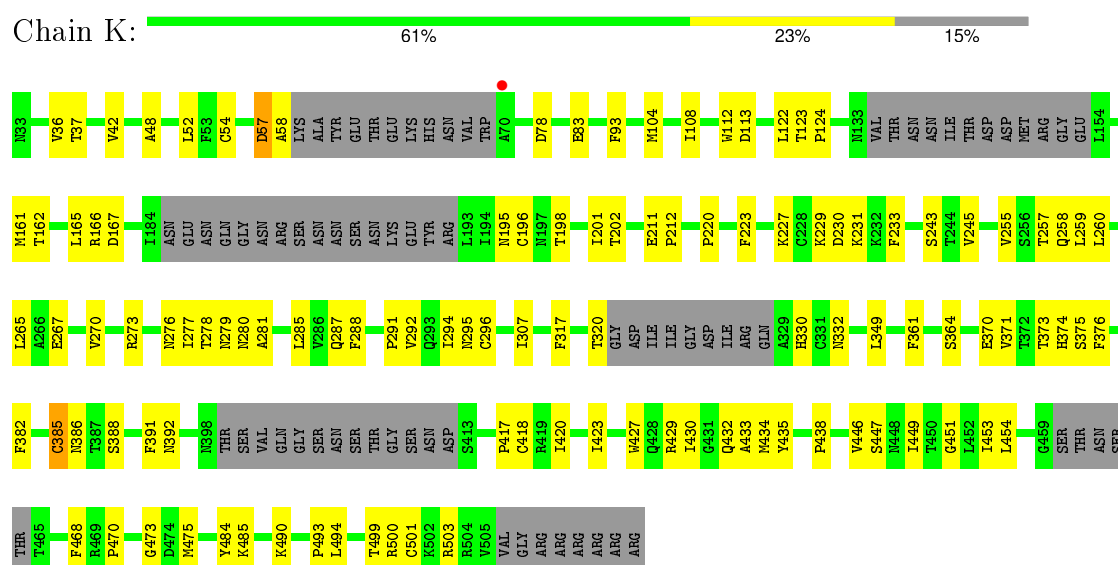
• Molecule 4: BG505 Env gp120

Chain G:



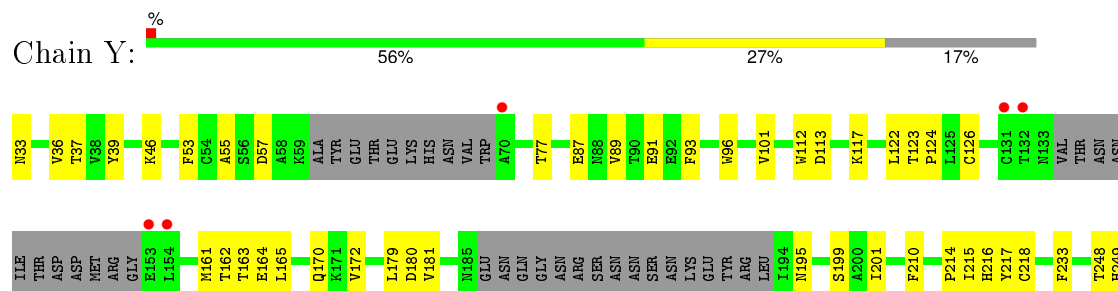
• Molecule 4: BG505 Env gp120

Chain K:



• Molecule 4: BG505 Env gp120

Chain Y:





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	117.74Å 195.22Å 119.09Å 90.00° 101.60° 90.00°	Depositor
Resolution (Å)	29.73 – 3.58 29.73 – 3.58	Depositor EDS
% Data completeness (in resolution range)	99.0 (29.73-3.58) 99.1 (29.73-3.58)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.43 (at 3.55Å)	Xtriage
Refinement program	PHENIX (1.10pre_2100: ???)	Depositor
R, R_{free}	0.239 , 0.286 0.236 , 0.287	Depositor DCC
R_{free} test set	2011 reflections (3.29%)	DCC
Wilson B-factor (Å ²)	130.2	Xtriage
Anisotropy	0.027	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.23 , 77.0	EDS
Estimated twinning fraction	0.029 for l,-k,h	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Outliers	0 of 61166 reflections	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	22299	wwPDB-VP
Average B, all atoms (Å ²)	149.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.40% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: BMA, NAG, 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	0.30	1/1700 (0.1%)	0.50	1/2334 (0.0%)
1	D	0.31	1/1656 (0.1%)	0.50	1/2280 (0.0%)
1	H	0.32	1/1720 (0.1%)	0.50	1/2359 (0.0%)
2	B	0.29	0/973	0.52	0/1327
2	J	0.28	0/974	0.51	0/1325
2	X	0.29	0/962	0.47	0/1309
3	C	0.26	0/1628	0.47	0/2221
3	E	0.26	0/1594	0.46	0/2181
3	L	0.26	0/1574	0.46	0/2159
4	G	0.33	1/2916 (0.0%)	0.49	0/4002
4	K	0.33	1/3047 (0.0%)	0.52	0/4172
4	Y	0.30	1/3009 (0.0%)	0.49	1/4119 (0.0%)
All	All	0.30	6/21753 (0.0%)	0.49	4/29788 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
4	G	0	1

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	G	309	ILE	C-N	9.34	1.49	1.33
4	K	385	CYS	CB-SG	-8.54	1.67	1.82
4	Y	378	CYS	CB-SG	-5.71	1.72	1.81
1	H	213	PRO	N-CD	5.22	1.55	1.47
1	D	213	PRO	N-CD	5.21	1.55	1.47

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	212	GLU	C-N-CD	5.82	140.62	128.40
4	Y	273	ARG	NE-CZ-NH1	-5.77	117.42	120.30
1	H	212	GLU	C-N-CD	5.71	140.38	128.40
1	D	212	GLU	C-N-CD	5.68	140.33	128.40

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	G	309	ILE	Mainchain

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1655	0	1577	36	0
1	D	1614	0	1511	47	0
1	H	1675	0	1600	52	0
2	B	956	0	898	70	0
2	J	957	0	915	38	0
2	X	945	0	905	36	0
3	C	1593	0	1489	19	0
3	E	1560	0	1438	22	0
3	L	1540	0	1382	24	0
4	G	2857	0	2565	79	0
4	K	2984	0	2763	105	0
4	Y	2947	0	2734	124	0
5	A	14	0	13	0	0
5	B	42	0	37	3	0
5	G	112	0	98	14	0
5	H	28	0	25	0	0
5	J	70	0	62	2	0
5	K	98	0	85	7	0
5	X	56	0	49	3	0
5	Y	112	0	98	4	0
6	B	11	0	8	1	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	G	22	0	16	0	0
6	J	11	0	9	0	0
6	K	33	0	26	2	0
6	X	11	0	9	0	0
6	Y	33	0	26	0	0
7	B	22	0	20	0	0
7	G	110	0	94	4	0
7	J	11	0	10	0	0
7	K	110	0	93	6	0
7	X	11	0	10	0	0
7	Y	99	0	84	13	0
All	All	22299	0	20649	599	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 14.

The worst 5 of 599 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:645:LEU:O	2:B:649:SER:HB2	1.16	1.32
4:K:231:LYS:HD2	4:K:267:GLU:CD	1.61	1.21
2:B:645:LEU:O	2:B:649:SER:CB	1.88	1.19
4:G:278:THR:HG22	5:G:1020:NAG:O6	1.40	1.15
2:B:650:GLN:O	2:B:654:GLU:N	1.77	1.15

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	220/244 (90%)	212 (96%)	8 (4%)	0	100 100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	D	220/244 (90%)	210 (96%)	10 (4%)	0	100	100
1	H	223/244 (91%)	214 (96%)	9 (4%)	0	100	100
2	B	120/153 (78%)	107 (89%)	13 (11%)	0	100	100
2	J	120/153 (78%)	112 (93%)	8 (7%)	0	100	100
2	X	117/153 (76%)	108 (92%)	9 (8%)	0	100	100
3	C	212/215 (99%)	210 (99%)	2 (1%)	0	100	100
3	E	212/215 (99%)	209 (99%)	3 (1%)	0	100	100
3	L	212/215 (99%)	208 (98%)	4 (2%)	0	100	100
4	G	382/479 (80%)	358 (94%)	23 (6%)	1 (0%)	46	83
4	K	391/479 (82%)	372 (95%)	19 (5%)	0	100	100
4	Y	383/479 (80%)	367 (96%)	16 (4%)	0	100	100
All	All	2812/3273 (86%)	2687 (96%)	124 (4%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	G	312	GLY

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	184/210 (88%)	182 (99%)	2 (1%)	80	92
1	D	175/210 (83%)	175 (100%)	0	100	100
1	H	185/210 (88%)	184 (100%)	1 (0%)	92	97
2	B	99/129 (77%)	99 (100%)	0	100	100
2	J	100/129 (78%)	98 (98%)	2 (2%)	63	87
2	X	99/129 (77%)	98 (99%)	1 (1%)	82	93
3	C	170/182 (93%)	170 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	E	163/182 (90%)	163 (100%)	0	100	100
3	L	157/182 (86%)	157 (100%)	0	100	100
4	G	289/427 (68%)	285 (99%)	4 (1%)	74	91
4	K	315/427 (74%)	311 (99%)	4 (1%)	76	92
4	Y	312/427 (73%)	310 (99%)	2 (1%)	90	97
All	All	2248/2844 (79%)	2232 (99%)	16 (1%)	88	96

5 of 16 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	J	604	CYS
2	J	614	TRP
4	K	418	CYS
1	H	210	ARG
2	X	650	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	651	ASN
4	K	374	HIS
4	Y	33	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry

82 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	NAG	A	1000	-	14,14,15	0.50	0	15,19,21	0.44	0
5	NAG	B	1030	2,5	14,14,15	0.58	0	15,19,21	0.51	0
5	NAG	B	1031	5,6	14,14,15	0.37	0	15,19,21	0.56	0
6	BMA	B	1032	5,7	11,11,12	0.94	0	15,15,17	0.79	0
7	MAN	B	1033	6	11,11,12	0.67	0	15,15,17	1.23	2 (13%)
7	MAN	B	1034	6	11,11,12	0.72	0	15,15,17	1.05	2 (13%)
5	NAG	B	1040	2	14,14,15	0.28	0	15,19,21	0.48	0
5	NAG	G	1000	5,4	14,14,15	0.37	0	15,19,21	0.47	0
5	NAG	G	1001	5,6	14,14,15	0.66	1 (7%)	15,19,21	0.48	0
6	BMA	G	1002	5,7	11,11,12	0.72	0	15,15,17	0.81	0
7	MAN	G	1003	7,6	11,11,12	0.37	0	15,15,17	1.11	1 (6%)
7	MAN	G	1004	7	11,11,12	0.59	0	15,15,17	1.17	2 (13%)
7	MAN	G	1005	7	11,11,12	0.82	0	15,15,17	1.00	2 (13%)
7	MAN	G	1006	7,6	11,11,12	0.55	0	15,15,17	1.12	2 (13%)
7	MAN	G	1007	7	11,11,12	0.44	0	15,15,17	1.26	2 (13%)
7	MAN	G	1008	7	11,11,12	0.73	0	15,15,17	0.89	1 (6%)
7	MAN	G	1009	7	11,11,12	0.66	0	15,15,17	0.99	2 (13%)
5	NAG	G	1020	5,4	14,14,15	0.32	0	15,19,21	0.40	0
5	NAG	G	1021	5,6	14,14,15	0.23	0	15,19,21	0.43	0
6	BMA	G	1022	5,7	11,11,12	0.95	0	15,15,17	1.08	1 (6%)
7	MAN	G	1023	7,6	11,11,12	0.79	1 (9%)	15,15,17	1.09	2 (13%)
7	MAN	G	1024	6	11,11,12	0.76	0	15,15,17	1.01	2 (13%)
7	MAN	G	1025	7	11,11,12	0.63	0	15,15,17	1.01	2 (13%)
5	NAG	G	1040	5,4	14,14,15	0.62	1 (7%)	15,19,21	0.48	0
5	NAG	G	1041	5	14,14,15	0.16	0	15,19,21	0.29	0
5	NAG	G	1042	5,4	14,14,15	0.46	0	15,19,21	0.34	0
5	NAG	G	1043	5	14,14,15	0.14	0	15,19,21	0.28	0
5	NAG	H	1000	1,5	14,14,15	0.70	1 (7%)	15,19,21	0.46	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	NAG	H	1001	5	14,14,15	0.17	0	15,19,21	0.44	0
5	NAG	J	1030	2,5	14,14,15	0.45	0	15,19,21	0.26	0
5	NAG	J	1031	5,6	14,14,15	0.21	0	15,19,21	0.50	0
6	BMA	J	1032	5,7	11,11,12	0.75	0	15,15,17	0.67	0
7	MAN	J	1033	6	11,11,12	0.53	0	15,15,17	0.97	2 (13%)
5	NAG	J	1040	2,5	14,14,15	0.40	0	15,19,21	0.64	0
5	NAG	J	1041	5	14,14,15	0.19	0	15,19,21	0.48	0
5	NAG	J	1042	2	14,14,15	0.58	0	15,19,21	0.70	1 (6%)
5	NAG	K	1000	5,4	14,14,15	1.09	1 (7%)	15,19,21	0.94	2 (13%)
5	NAG	K	1001	5,6	14,14,15	0.82	1 (7%)	15,19,21	0.45	0
6	BMA	K	1002	5,7	11,11,12	0.80	0	15,15,17	0.96	0
7	MAN	K	1003	7,6	11,11,12	0.51	0	15,15,17	0.95	2 (13%)
7	MAN	K	1004	7	11,11,12	0.71	0	15,15,17	0.91	1 (6%)
7	MAN	K	1005	7	11,11,12	0.55	0	15,15,17	1.09	2 (13%)
7	MAN	K	1006	7,6	11,11,12	0.99	1 (9%)	15,15,17	0.89	1 (6%)
7	MAN	K	1007	7	11,11,12	0.60	0	15,15,17	1.08	2 (13%)
7	MAN	K	1008	7	11,11,12	0.85	1 (9%)	15,15,17	0.84	1 (6%)
7	MAN	K	1009	7	11,11,12	0.77	0	15,15,17	0.88	0
5	NAG	K	1020	5,4	14,14,15	0.43	0	15,19,21	0.70	1 (6%)
5	NAG	K	1021	5,6	14,14,15	0.39	0	15,19,21	0.39	0
6	BMA	K	1022	5,7	11,11,12	0.95	1 (9%)	15,15,17	0.86	0
7	MAN	K	1023	7,6	11,11,12	0.83	1 (9%)	15,15,17	1.12	2 (13%)
7	MAN	K	1024	6	11,11,12	0.71	0	15,15,17	1.04	2 (13%)
7	MAN	K	1025	7	11,11,12	0.91	0	15,15,17	0.95	1 (6%)
5	NAG	K	1040	4	14,14,15	0.58	0	15,19,21	0.40	0
5	NAG	K	1041	5,4	14,14,15	0.62	1 (7%)	15,19,21	0.45	0
5	NAG	K	1042	5,6	14,14,15	0.18	0	15,19,21	0.25	0
6	BMA	K	1043	5	11,11,12	0.55	0	15,15,17	0.68	0
5	NAG	X	1030	2,5	14,14,15	0.76	1 (7%)	15,19,21	0.68	1 (6%)
5	NAG	X	1031	5,6	14,14,15	0.23	0	15,19,21	0.50	0
6	BMA	X	1032	5,7	11,11,12	0.81	0	15,15,17	0.82	0
7	MAN	X	1033	6	11,11,12	0.73	0	15,15,17	1.15	2 (13%)
5	NAG	X	1040	2,5	14,14,15	0.57	1 (7%)	15,19,21	0.63	0
5	NAG	X	1041	5	14,14,15	0.23	0	15,19,21	0.23	0
5	NAG	Y	1000	5,4	14,14,15	0.37	0	15,19,21	0.47	0
5	NAG	Y	1001	5,6	14,14,15	0.66	1 (7%)	15,19,21	0.47	0
6	BMA	Y	1002	5,7	11,11,12	0.72	0	15,15,17	0.81	0
7	MAN	Y	1003	7,6	11,11,12	0.38	0	15,15,17	1.11	1 (6%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
7	MAN	Y	1004	7	11,11,12	0.59	0	15,15,17	1.17	2 (13%)
7	MAN	Y	1005	7	11,11,12	0.81	0	15,15,17	1.01	2 (13%)
7	MAN	Y	1006	7,6	11,11,12	0.55	0	15,15,17	1.12	2 (13%)
7	MAN	Y	1007	7	11,11,12	0.44	0	15,15,17	1.26	2 (13%)
7	MAN	Y	1008	7	11,11,12	0.73	0	15,15,17	0.88	1 (6%)
7	MAN	Y	1009	7	11,11,12	0.67	0	15,15,17	0.99	2 (13%)
5	NAG	Y	1020	5,4	14,14,15	0.40	0	15,19,21	0.88	1 (6%)
5	NAG	Y	1021	5,6	14,14,15	0.21	0	15,19,21	0.48	0
6	BMA	Y	1022	5,7	11,11,12	0.86	0	15,15,17	0.98	1 (6%)
7	MAN	Y	1023	6	11,11,12	0.74	0	15,15,17	1.21	2 (13%)
7	MAN	Y	1024	6	11,11,12	0.75	0	15,15,17	0.98	2 (13%)
5	NAG	Y	1040	4	14,14,15	0.50	0	15,19,21	0.57	0
5	NAG	Y	1041	4	14,14,15	0.96	1 (7%)	15,19,21	0.77	1 (6%)
5	NAG	Y	1042	5,4	14,14,15	0.35	0	15,19,21	0.61	1 (6%)
5	NAG	Y	1043	5,6	14,14,15	0.28	0	15,19,21	0.28	0
6	BMA	Y	1044	5	11,11,12	0.54	0	15,15,17	0.68	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	NAG	A	1000	-	-	0/6/23/26	0/1/1/1
5	NAG	B	1030	2,5	-	0/6/23/26	0/1/1/1
5	NAG	B	1031	5,6	-	0/6/23/26	0/1/1/1
6	BMA	B	1032	5,7	-	0/2/19/22	0/1/1/1
7	MAN	B	1033	6	-	0/2/19/22	0/1/1/1
7	MAN	B	1034	6	-	0/2/19/22	0/1/1/1
5	NAG	B	1040	2	-	0/6/23/26	0/1/1/1
5	NAG	G	1000	5,4	-	0/6/23/26	0/1/1/1
5	NAG	G	1001	5,6	-	0/6/23/26	0/1/1/1
6	BMA	G	1002	5,7	-	0/2/19/22	0/1/1/1
7	MAN	G	1003	7,6	-	0/2/19/22	0/1/1/1
7	MAN	G	1004	7	-	0/2/19/22	0/1/1/1
7	MAN	G	1005	7	-	0/2/19/22	0/1/1/1
7	MAN	G	1006	7,6	-	0/2/19/22	0/1/1/1
7	MAN	G	1007	7	-	0/2/19/22	0/1/1/1
7	MAN	G	1008	7	-	0/2/19/22	0/1/1/1
7	MAN	G	1009	7	-	0/2/19/22	0/1/1/1

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	NAG	G	1020	5,4	-	0/6/23/26	0/1/1/1
5	NAG	G	1021	5,6	-	0/6/23/26	0/1/1/1
6	BMA	G	1022	5,7	-	0/2/19/22	0/1/1/1
7	MAN	G	1023	7,6	-	0/2/19/22	0/1/1/1
7	MAN	G	1024	6	-	0/2/19/22	0/1/1/1
7	MAN	G	1025	7	-	0/2/19/22	0/1/1/1
5	NAG	G	1040	5,4	-	0/6/23/26	0/1/1/1
5	NAG	G	1041	5	-	0/6/23/26	0/1/1/1
5	NAG	G	1042	5,4	-	0/6/23/26	0/1/1/1
5	NAG	G	1043	5	-	0/6/23/26	0/1/1/1
5	NAG	H	1000	1,5	-	0/6/23/26	0/1/1/1
5	NAG	H	1001	5	-	0/6/23/26	0/1/1/1
5	NAG	J	1030	2,5	-	0/6/23/26	0/1/1/1
5	NAG	J	1031	5,6	-	0/6/23/26	0/1/1/1
6	BMA	J	1032	5,7	-	0/2/19/22	0/1/1/1
7	MAN	J	1033	6	-	0/2/19/22	0/1/1/1
5	NAG	J	1040	2,5	-	0/6/23/26	0/1/1/1
5	NAG	J	1041	5	-	0/6/23/26	0/1/1/1
5	NAG	J	1042	2	-	0/6/23/26	0/1/1/1
5	NAG	K	1000	5,4	-	0/6/23/26	0/1/1/1
5	NAG	K	1001	5,6	-	0/6/23/26	0/1/1/1
6	BMA	K	1002	5,7	-	0/2/19/22	0/1/1/1
7	MAN	K	1003	7,6	-	0/2/19/22	0/1/1/1
7	MAN	K	1004	7	-	0/2/19/22	0/1/1/1
7	MAN	K	1005	7	-	0/2/19/22	0/1/1/1
7	MAN	K	1006	7,6	-	0/2/19/22	0/1/1/1
7	MAN	K	1007	7	-	0/2/19/22	0/1/1/1
7	MAN	K	1008	7	-	0/2/19/22	0/1/1/1
7	MAN	K	1009	7	-	0/2/19/22	0/1/1/1
5	NAG	K	1020	5,4	-	0/6/23/26	0/1/1/1
5	NAG	K	1021	5,6	-	0/6/23/26	0/1/1/1
6	BMA	K	1022	5,7	-	0/2/19/22	0/1/1/1
7	MAN	K	1023	7,6	-	0/2/19/22	0/1/1/1
7	MAN	K	1024	6	-	0/2/19/22	0/1/1/1
7	MAN	K	1025	7	-	0/2/19/22	0/1/1/1
5	NAG	K	1040	4	-	0/6/23/26	0/1/1/1
5	NAG	K	1041	5,4	-	0/6/23/26	0/1/1/1
5	NAG	K	1042	5,6	-	0/6/23/26	0/1/1/1
6	BMA	K	1043	5	-	0/2/19/22	0/1/1/1
5	NAG	X	1030	2,5	-	0/6/23/26	0/1/1/1
5	NAG	X	1031	5,6	-	0/6/23/26	0/1/1/1
6	BMA	X	1032	5,7	-	0/2/19/22	0/1/1/1

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	MAN	X	1033	6	-	0/2/19/22	0/1/1/1
5	NAG	X	1040	2,5	-	0/6/23/26	0/1/1/1
5	NAG	X	1041	5	-	0/6/23/26	0/1/1/1
5	NAG	Y	1000	5,4	-	0/6/23/26	0/1/1/1
5	NAG	Y	1001	5,6	-	0/6/23/26	0/1/1/1
6	BMA	Y	1002	5,7	-	0/2/19/22	0/1/1/1
7	MAN	Y	1003	7,6	-	0/2/19/22	0/1/1/1
7	MAN	Y	1004	7	-	0/2/19/22	0/1/1/1
7	MAN	Y	1005	7	-	0/2/19/22	0/1/1/1
7	MAN	Y	1006	7,6	-	0/2/19/22	0/1/1/1
7	MAN	Y	1007	7	-	0/2/19/22	0/1/1/1
7	MAN	Y	1008	7	-	0/2/19/22	0/1/1/1
7	MAN	Y	1009	7	-	0/2/19/22	0/1/1/1
5	NAG	Y	1020	5,4	-	0/6/23/26	0/1/1/1
5	NAG	Y	1021	5,6	-	0/6/23/26	0/1/1/1
6	BMA	Y	1022	5,7	-	0/2/19/22	0/1/1/1
7	MAN	Y	1023	6	-	0/2/19/22	0/1/1/1
7	MAN	Y	1024	6	-	0/2/19/22	0/1/1/1
5	NAG	Y	1040	4	-	0/6/23/26	0/1/1/1
5	NAG	Y	1041	4	-	0/6/23/26	0/1/1/1
5	NAG	Y	1042	5,4	-	0/6/23/26	0/1/1/1
5	NAG	Y	1043	5,6	-	0/6/23/26	0/1/1/1
6	BMA	Y	1044	5	-	0/2/19/22	0/1/1/1

The worst 5 of 15 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	K	1000	NAG	O5-C1	-4.00	1.37	1.43
5	K	1001	NAG	O5-C1	-3.02	1.38	1.43
5	X	1030	NAG	O5-C1	-2.72	1.39	1.43
5	Y	1001	NAG	O5-C1	-2.43	1.39	1.43
5	H	1000	NAG	O5-C1	-2.40	1.39	1.43

The worst 5 of 66 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	K	1023	MAN	O2-C2-C3	-2.54	105.07	110.19
7	Y	1023	MAN	O2-C2-C3	-2.52	105.11	110.19
7	K	1007	MAN	O2-C2-C3	-2.46	105.24	110.19
7	G	1009	MAN	O2-C2-C3	-2.43	105.29	110.19
7	Y	1009	MAN	O2-C2-C3	-2.42	105.32	110.19

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

33 monomers are involved in 58 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	1030	NAG	1	0
5	B	1031	NAG	3	0
6	B	1032	BMA	1	0
5	G	1000	NAG	2	0
5	G	1001	NAG	1	0
7	G	1005	MAN	1	0
7	G	1009	MAN	3	0
5	G	1020	NAG	7	0
5	G	1021	NAG	2	0
5	G	1042	NAG	1	0
5	G	1043	NAG	1	0
5	J	1030	NAG	1	0
5	J	1031	NAG	1	0
5	J	1040	NAG	1	0
5	J	1041	NAG	1	0
5	K	1000	NAG	1	0
5	K	1001	NAG	1	0
6	K	1002	BMA	1	0
7	K	1009	MAN	5	0
5	K	1020	NAG	2	0
5	K	1021	NAG	2	0
6	K	1022	BMA	1	0
7	K	1025	MAN	1	0
5	K	1041	NAG	1	0
5	X	1030	NAG	2	0
5	X	1031	NAG	3	0
7	Y	1004	MAN	1	0
7	Y	1005	MAN	5	0
7	Y	1007	MAN	1	0
7	Y	1009	MAN	6	0
5	Y	1021	NAG	2	0
5	Y	1041	NAG	2	0
5	Y	1042	NAG	1	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 [i](#)

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

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	224/244 (91%)	-0.54	1 (0%) 93 90	94, 133, 173, 216	0
1	D	224/244 (91%)	-0.41	1 (0%) 93 90	102, 155, 201, 272	0
1	H	227/244 (93%)	-0.60	0 100 100	71, 121, 164, 195	0
2	B	124/153 (81%)	-0.60	1 (0%) 87 81	76, 115, 180, 236	0
2	J	124/153 (81%)	-0.63	1 (0%) 87 81	67, 113, 178, 255	0
2	X	121/153 (79%)	-0.56	1 (0%) 87 81	74, 119, 177, 325	0
3	C	214/215 (99%)	-0.41	3 (1%) 78 69	91, 144, 203, 230	0
3	E	214/215 (99%)	-0.37	0 100 100	99, 167, 215, 277	0
3	L	214/215 (99%)	-0.61	0 100 100	80, 122, 209, 246	0
4	G	398/479 (83%)	-0.41	1 (0%) 94 92	71, 167, 231, 277	0
4	K	405/479 (84%)	-0.42	1 (0%) 95 93	63, 167, 248, 316	0
4	Y	397/479 (82%)	-0.35	6 (1%) 76 68	66, 176, 239, 315	0
All	All	2886/3273 (88%)	-0.46	16 (0%) 90 85	63, 147, 222, 325	0

The worst 5 of 16 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	104	GLY	4.6
4	Y	153	GLU	3.3
3	C	12	SER	3.1
4	Y	132	THR	3.1
2	X	649	SER	3.0

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 ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

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
5	NAG	Y	1042	14/15	0.72	0.39	2.92	104,118,150,154	14
5	NAG	B	1040	14/15	0.88	0.24	2.65	112,132,141,143	0
5	NAG	G	1021	14/15	0.93	0.22	2.13	118,136,148,155	0
5	NAG	X	1030	14/15	0.92	0.26	1.34	70,86,110,126	14
5	NAG	X	1031	14/15	0.93	0.23	1.09	80,98,116,132	14
5	NAG	J	1030	14/15	0.93	0.23	1.04	56,77,98,109	14
5	NAG	J	1031	14/15	0.91	0.28	0.88	93,103,111,125	14
5	NAG	G	1020	14/15	0.86	0.22	0.69	117,135,150,161	14
5	NAG	K	1021	14/15	0.85	0.26	0.36	134,146,162,176	14
7	MAN	K	1004	11/12	0.97	0.20	0.19	75,91,95,104	11
5	NAG	B	1031	14/15	0.91	0.21	-0.10	106,124,138,153	0
5	NAG	Y	1000	14/15	0.91	0.23	-0.13	94,113,131,135	14
5	NAG	K	1041	14/15	0.85	0.25	-0.13	113,135,148,161	0
5	NAG	Y	1021	14/15	0.90	0.18	-0.14	155,168,187,195	0
5	NAG	K	1020	14/15	0.85	0.20	-0.17	115,132,139,142	14
7	MAN	K	1009	11/12	0.95	0.16	-0.25	103,124,132,145	0
5	NAG	G	1000	14/15	0.95	0.17	-0.44	49,72,100,112	14
5	NAG	K	1042	14/15	0.85	0.23	-0.44	114,128,145,149	14
5	NAG	Y	1020	14/15	0.86	0.14	-0.55	153,171,178,184	0
7	MAN	Y	1004	11/12	0.91	0.17	-0.60	117,125,141,149	11
6	BMA	Y	1002	11/12	0.93	0.17	-0.73	95,106,115,125	11
7	MAN	Y	1009	11/12	0.93	0.12	-0.82	122,126,136,150	0
7	MAN	G	1009	11/12	0.97	0.16	-0.90	104,106,118,121	11
5	NAG	K	1000	14/15	0.95	0.18	-0.92	46,63,97,107	14
7	MAN	G	1004	11/12	0.95	0.16	-1.08	116,122,139,143	0
5	NAG	G	1042	14/15	0.88	0.20	-1.15	132,145,171,173	0
5	NAG	B	1030	14/15	0.97	0.14	-1.25	69,88,120,138	0
5	NAG	H	1001	14/15	0.62	0.80	-	165,177,184,185	14
5	NAG	H	1000	14/15	0.83	0.36	-	96,125,147,148	14
7	MAN	K	1006	11/12	0.96	0.11	-	117,130,153,157	0

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
5	NAG	G	1001	14/15	0.95	0.15	-	82,95,126,133	0
5	NAG	A	1000	14/15	0.50	0.42	-	157,166,174,175	14
5	NAG	Y	1001	14/15	0.87	0.35	-	73,88,99,102	14
7	MAN	G	1003	11/12	0.94	0.16	-	124,128,138,144	0
7	MAN	K	1005	11/12	0.94	0.23	-	80,85,98,107	11
7	MAN	Y	1024	11/12	0.74	0.20	-	168,173,179,183	0
7	MAN	Y	1003	11/12	0.90	0.21	-	117,120,124,131	11
7	MAN	Y	1023	11/12	0.84	0.20	-	170,174,183,187	0
5	NAG	J	1040	14/15	0.78	0.22	-	155,164,174,179	0
5	NAG	G	1040	14/15	0.90	0.30	-	125,137,150,154	14
7	MAN	G	1008	11/12	0.74	0.31	-	157,162,178,181	0
5	NAG	G	1041	14/15	0.87	0.29	-	157,164,178,178	14
6	BMA	K	1022	11/12	0.67	0.28	-	152,163,172,186	0
5	NAG	X	1040	14/15	0.93	0.13	-	124,140,154,155	0
7	MAN	Y	1007	11/12	0.87	0.34	-	110,123,137,141	11
7	MAN	G	1005	11/12	0.91	0.18	-	126,127,144,162	0
7	MAN	K	1007	11/12	0.91	0.15	-	123,128,153,162	0
7	MAN	B	1033	11/12	0.75	0.51	-	119,131,141,143	11
5	NAG	J	1041	14/15	0.56	0.55	-	133,170,179,180	14
7	MAN	J	1033	11/12	0.79	0.20	-	184,196,201,202	0
7	MAN	Y	1005	11/12	0.89	0.22	-	115,121,131,133	11
5	NAG	Y	1040	14/15	0.76	0.31	-	167,180,199,208	0
5	NAG	K	1001	14/15	0.94	0.21	-	58,63,79,90	14
5	NAG	X	1041	14/15	0.90	0.25	-	158,170,180,183	0
7	MAN	X	1033	11/12	0.63	0.40	-	205,211,221,222	0
7	MAN	B	1034	11/12	0.67	0.54	-	126,135,143,153	11
5	NAG	Y	1043	14/15	0.64	0.40	-	145,169,180,182	14
5	NAG	G	1043	14/15	0.87	0.18	-	155,163,180,181	0
7	MAN	K	1025	11/12	0.46	0.40	-	172,209,213,214	0
6	BMA	Y	1022	11/12	0.89	0.26	-	152,158,170,178	0
5	NAG	Y	1041	14/15	0.76	0.26	-	106,127,145,151	14
7	MAN	G	1006	11/12	0.95	0.15	-	115,129,156,157	0
7	MAN	G	1025	11/12	0.84	0.15	-	182,193,197,198	0
6	BMA	X	1032	11/12	0.75	0.27	-	147,166,181,198	0
5	NAG	J	1042	14/15	0.81	0.31	-	115,125,139,145	14
7	MAN	G	1007	11/12	0.91	0.18	-	114,133,145,153	0
7	MAN	K	1023	11/12	0.67	0.32	-	175,177,194,206	0
7	MAN	K	1008	11/12	0.83	0.23	-	148,156,162,166	0
7	MAN	Y	1006	11/12	0.89	0.33	-	109,115,125,126	11
5	NAG	K	1040	14/15	0.71	0.67	-	135,156,179,185	14
6	BMA	K	1002	11/12	0.93	0.12	-	93,110,127,142	0
7	MAN	K	1003	11/12	0.96	0.16	-	101,105,114,129	11

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
6	BMA	G	1022	11/12	0.93	0.18	-	132,136,155,163	0
6	BMA	K	1043	11/12	0.81	0.29	-	147,151,156,158	11
6	BMA	B	1032	11/12	0.78	0.23	-	135,148,156,157	11
7	MAN	G	1024	11/12	0.78	0.25	-	164,169,181,185	0
7	MAN	G	1023	11/12	0.92	0.25	-	171,189,201,208	0
6	BMA	J	1032	11/12	0.81	0.25	-	139,150,171,186	11
7	MAN	K	1024	11/12	0.79	0.33	-	168,174,187,187	0
6	BMA	G	1002	11/12	0.96	0.11	-	103,116,128,142	0
6	BMA	Y	1044	11/12	0.70	0.27	-	184,194,202,210	0
7	MAN	Y	1008	11/12	0.67	0.55	-	121,125,133,138	11

6.5 Other polymers [i](#)

There are no such residues in this entry.