



wwPDB EM Validation Summary Report ⓘ

Mar 20, 2026 – 02:44 PM UTC

PDB ID : 8D5C / pdb_00008d5c
EMDB ID : EMD-27208
Title : anti-HIV-1 gp120-sCD4 complex antibody CG10 Fab in complex with B41-sCD4
Authors : Yang, Z.; Bjorkman, P.J.; Gershoni, J.M.
Deposited on : 2022-06-04
Resolution : 3.90 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : **NOT EXECUTED**
MapQ : **FAILED**
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

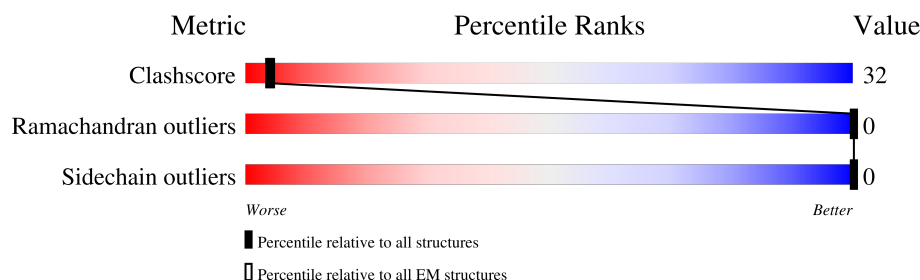
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.90 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



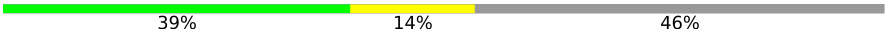
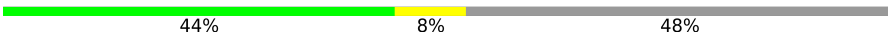
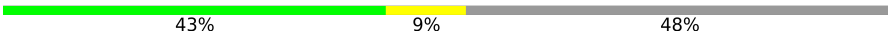
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	229148	23984
Ramachandran outliers	224038	23583
Sidechain outliers	223484	23102

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	X	153	49% 35% 16%
1	Y	153	47% 37% 16%
1	Z	153	42% 42% 16%
2	A	516	37% 36% 27%
2	B	516	40% 33% 27%
2	C	516	26% 47% 27%
3	D	183	30% 67% .
3	E	183	47% 49% .
3	F	183	38% 58% .

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Mol	Chain	Length	Quality of chain
4	H	228	
4	I	228	
4	P	228	
5	J	218	
5	L	218	
5	Q	218	

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 26109 atoms, of which 4739 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 Envelope glycoprotein gp41.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	X	129	Total	C	N	O	S	0	0
			1042	661	177	196	8		
1	Y	129	Total	C	N	O	S	0	0
			1042	661	177	196	8		
1	Z	129	Total	C	N	O	S	0	0
			1042	661	177	196	8		

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
X	559	PRO	ILE	engineered mutation	UNP B3UEZ6
X	605	CYS	THR	engineered mutation	UNP B3UEZ6
Y	559	PRO	ILE	engineered mutation	UNP B3UEZ6
Y	605	CYS	THR	engineered mutation	UNP B3UEZ6
Z	559	PRO	ILE	engineered mutation	UNP B3UEZ6
Z	605	CYS	THR	engineered mutation	UNP B3UEZ6

- Molecule 2 is a protein called Envelope glycoprotein gp160.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A	377	Total	C	N	O	S	0	0
			2952	1855	519	554	24		
2	B	377	Total	C	N	O	S	0	0
			2952	1855	519	554	24		
2	C	377	Total	C	N	O	S	0	0
			2952	1855	519	554	24		

There are 108 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-4	MET	-	expression tag	UNP B3UES2
A	-3	ASP	-	expression tag	UNP B3UES2
A	-2	ALA	-	expression tag	UNP B3UES2

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	MET	-	expression tag	UNP B3UES2
A	0	LYS	-	expression tag	UNP B3UES2
A	1	ARG	-	expression tag	UNP B3UES2
A	2	GLY	-	expression tag	UNP B3UES2
A	3	LEU	-	expression tag	UNP B3UES2
A	4	CYS	-	expression tag	UNP B3UES2
A	5	CYS	-	expression tag	UNP B3UES2
A	6	VAL	-	expression tag	UNP B3UES2
A	7	LEU	-	expression tag	UNP B3UES2
A	8	LEU	-	expression tag	UNP B3UES2
A	9	LEU	-	expression tag	UNP B3UES2
A	10	CYS	-	expression tag	UNP B3UES2
A	11	GLY	-	expression tag	UNP B3UES2
A	12	ALA	-	expression tag	UNP B3UES2
A	13	VAL	-	expression tag	UNP B3UES2
A	14	PHE	-	expression tag	UNP B3UES2
A	15	VAL	-	expression tag	UNP B3UES2
A	16	SER	-	expression tag	UNP B3UES2
A	17	PRO	-	expression tag	UNP B3UES2
A	18	SER	-	expression tag	UNP B3UES2
A	19	GLN	-	expression tag	UNP B3UES2
A	20	GLU	-	expression tag	UNP B3UES2
A	21	ILE	-	expression tag	UNP B3UES2
A	22	HIS	-	expression tag	UNP B3UES2
A	23	ALA	-	expression tag	UNP B3UES2
A	24	ARG	-	expression tag	UNP B3UES2
A	25	PHE	-	expression tag	UNP B3UES2
A	26	ARG	-	expression tag	UNP B3UES2
A	27	ARG	-	expression tag	UNP B3UES2
A	28	GLY	-	expression tag	UNP B3UES2
A	29	ALA	-	expression tag	UNP B3UES2
A	30	ARG	-	expression tag	UNP B3UES2
A	501	CYS	ALA	conflict	UNP B3UES2
B	-4	MET	-	expression tag	UNP B3UES2
B	-3	ASP	-	expression tag	UNP B3UES2
B	-2	ALA	-	expression tag	UNP B3UES2
B	-1	MET	-	expression tag	UNP B3UES2
B	0	LYS	-	expression tag	UNP B3UES2
B	1	ARG	-	expression tag	UNP B3UES2
B	2	GLY	-	expression tag	UNP B3UES2
B	3	LEU	-	expression tag	UNP B3UES2
B	4	CYS	-	expression tag	UNP B3UES2

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Chain	Residue	Modelled	Actual	Comment	Reference
B	5	CYS	-	expression tag	UNP B3UES2
B	6	VAL	-	expression tag	UNP B3UES2
B	7	LEU	-	expression tag	UNP B3UES2
B	8	LEU	-	expression tag	UNP B3UES2
B	9	LEU	-	expression tag	UNP B3UES2
B	10	CYS	-	expression tag	UNP B3UES2
B	11	GLY	-	expression tag	UNP B3UES2
B	12	ALA	-	expression tag	UNP B3UES2
B	13	VAL	-	expression tag	UNP B3UES2
B	14	PHE	-	expression tag	UNP B3UES2
B	15	VAL	-	expression tag	UNP B3UES2
B	16	SER	-	expression tag	UNP B3UES2
B	17	PRO	-	expression tag	UNP B3UES2
B	18	SER	-	expression tag	UNP B3UES2
B	19	GLN	-	expression tag	UNP B3UES2
B	20	GLU	-	expression tag	UNP B3UES2
B	21	ILE	-	expression tag	UNP B3UES2
B	22	HIS	-	expression tag	UNP B3UES2
B	23	ALA	-	expression tag	UNP B3UES2
B	24	ARG	-	expression tag	UNP B3UES2
B	25	PHE	-	expression tag	UNP B3UES2
B	26	ARG	-	expression tag	UNP B3UES2
B	27	ARG	-	expression tag	UNP B3UES2
B	28	GLY	-	expression tag	UNP B3UES2
B	29	ALA	-	expression tag	UNP B3UES2
B	30	ARG	-	expression tag	UNP B3UES2
B	501	CYS	ALA	conflict	UNP B3UES2
C	-4	MET	-	expression tag	UNP B3UES2
C	-3	ASP	-	expression tag	UNP B3UES2
C	-2	ALA	-	expression tag	UNP B3UES2
C	-1	MET	-	expression tag	UNP B3UES2
C	0	LYS	-	expression tag	UNP B3UES2
C	1	ARG	-	expression tag	UNP B3UES2
C	2	GLY	-	expression tag	UNP B3UES2
C	3	LEU	-	expression tag	UNP B3UES2
C	4	CYS	-	expression tag	UNP B3UES2
C	5	CYS	-	expression tag	UNP B3UES2
C	6	VAL	-	expression tag	UNP B3UES2
C	7	LEU	-	expression tag	UNP B3UES2
C	8	LEU	-	expression tag	UNP B3UES2
C	9	LEU	-	expression tag	UNP B3UES2
C	10	CYS	-	expression tag	UNP B3UES2

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Chain	Residue	Modelled	Actual	Comment	Reference
C	11	GLY	-	expression tag	UNP B3UES2
C	12	ALA	-	expression tag	UNP B3UES2
C	13	VAL	-	expression tag	UNP B3UES2
C	14	PHE	-	expression tag	UNP B3UES2
C	15	VAL	-	expression tag	UNP B3UES2
C	16	SER	-	expression tag	UNP B3UES2
C	17	PRO	-	expression tag	UNP B3UES2
C	18	SER	-	expression tag	UNP B3UES2
C	19	GLN	-	expression tag	UNP B3UES2
C	20	GLU	-	expression tag	UNP B3UES2
C	21	ILE	-	expression tag	UNP B3UES2
C	22	HIS	-	expression tag	UNP B3UES2
C	23	ALA	-	expression tag	UNP B3UES2
C	24	ARG	-	expression tag	UNP B3UES2
C	25	PHE	-	expression tag	UNP B3UES2
C	26	ARG	-	expression tag	UNP B3UES2
C	27	ARG	-	expression tag	UNP B3UES2
C	28	GLY	-	expression tag	UNP B3UES2
C	29	ALA	-	expression tag	UNP B3UES2
C	30	ARG	-	expression tag	UNP B3UES2
C	501	CYS	ALA	conflict	UNP B3UES2

- Molecule 3 is a protein called T-cell surface glycoprotein CD4.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	D	176	Total	C	N	O	S	0	0
			1370	856	240	270	4		
3	E	176	Total	C	N	O	S	0	0
			1370	856	240	270	4		
3	F	176	Total	C	N	O	S	0	0
			1370	856	240	270	4		

- Molecule 4 is a protein called CG10 Fab heavy chain.

Mol	Chain	Residues	Atoms					AltConf	Trace	
4	H	122	Total	C	H	N	O	S	0	0
			1790	617	832	150	186	5		
4	I	119	Total	C	H	N	O	S	0	0
			1766	608	825	150	178	5		
4	P	104	Total	C	H	N	O	S	0	0
			1523	512	721	132	153	5		

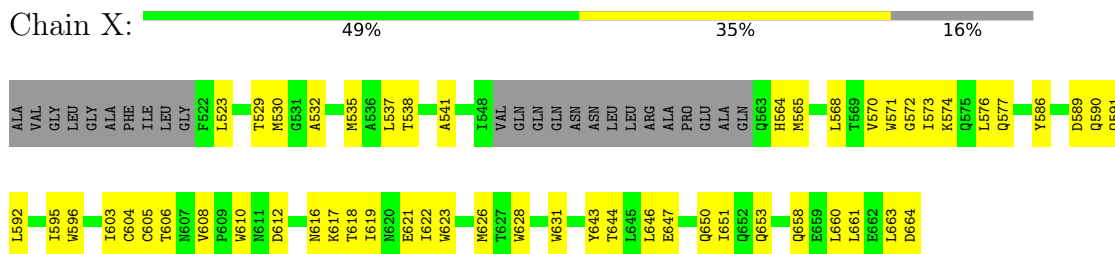
- Molecule 5 is a protein called CG10 Fab light chain.

Mol	Chain	Residues	Atoms						AltConf	Trace
5	L	113	Total	C	H	N	O	S	0	0
			1646	537	787	143	175	4		
5	J	113	Total	C	H	N	O	S	0	0
			1646	537	787	143	175	4		
5	Q	113	Total	C	H	N	O	S	0	0
			1646	537	787	143	175	4		

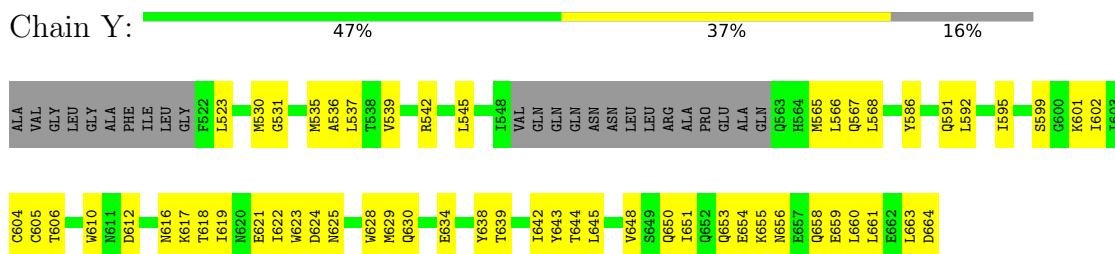
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. 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: Envelope glycoprotein gp41



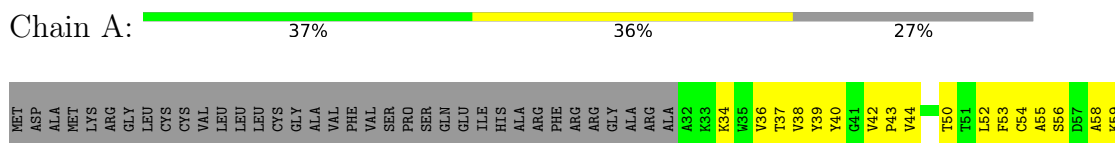
- Molecule 1: Envelope glycoprotein gp41



- Molecule 1: Envelope glycoprotein gp41



- Molecule 2: Envelope glycoprotein gp160



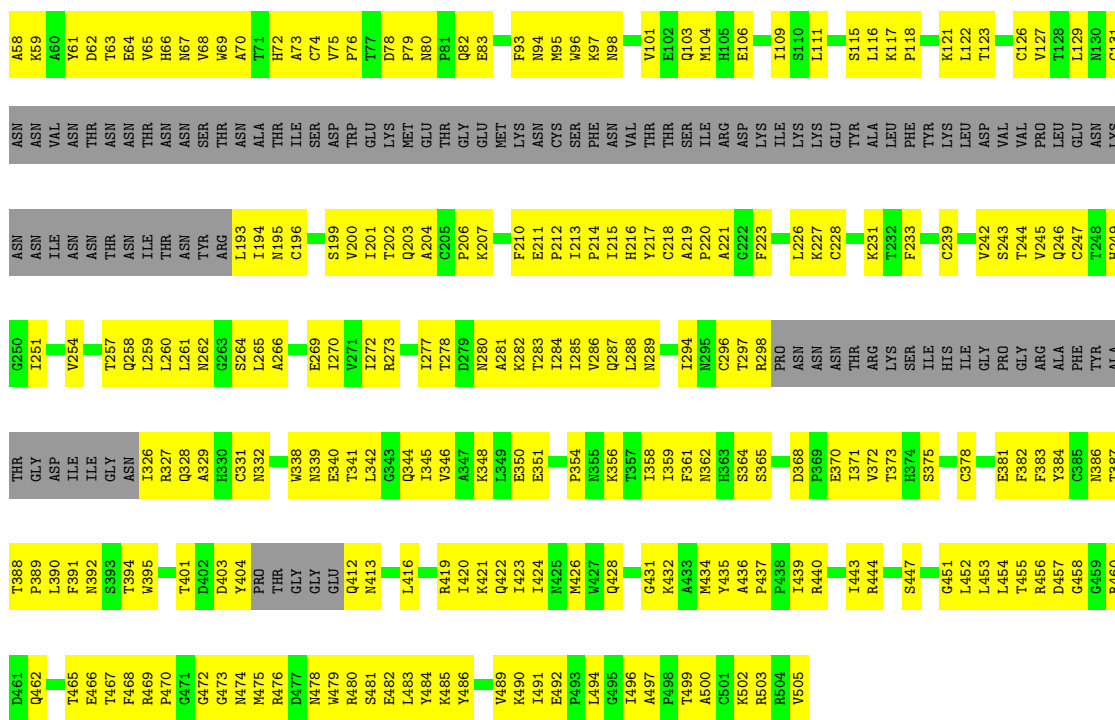


Category	Percentage
Used	40%
Used a little	33%
Not used	27%

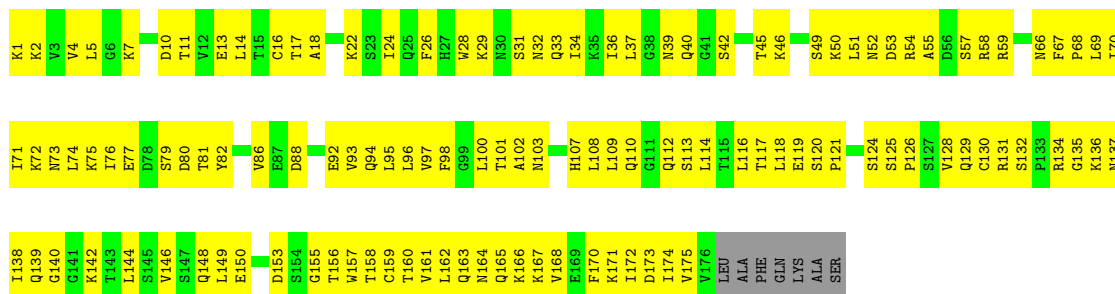


Digital Tool Type	Percentage
Used	26%
Not used	47%
Don't know	27%

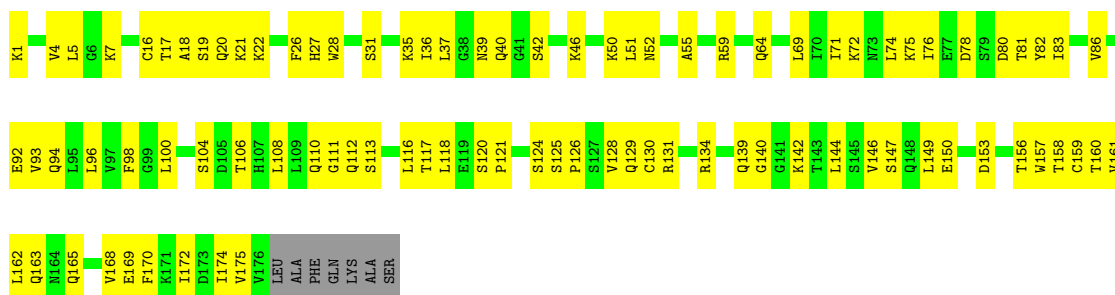




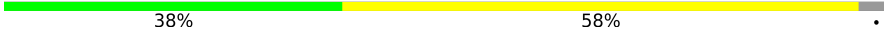
- Molecule 3: T-cell surface glycoprotein CD4

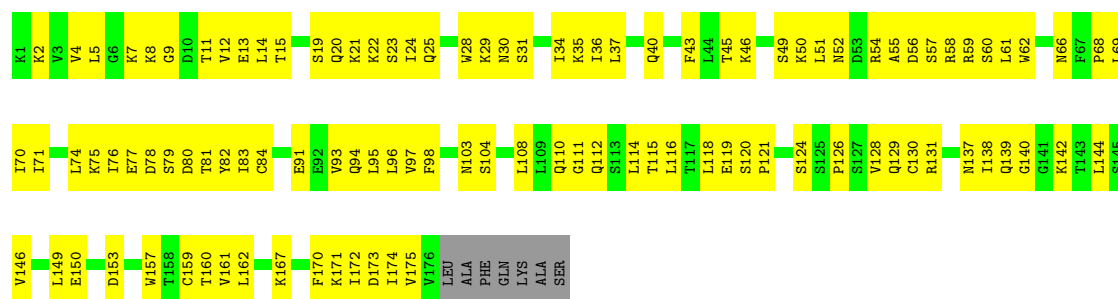


- Molecule 3: T-cell surface glycoprotein CD4

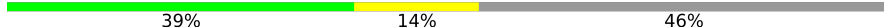


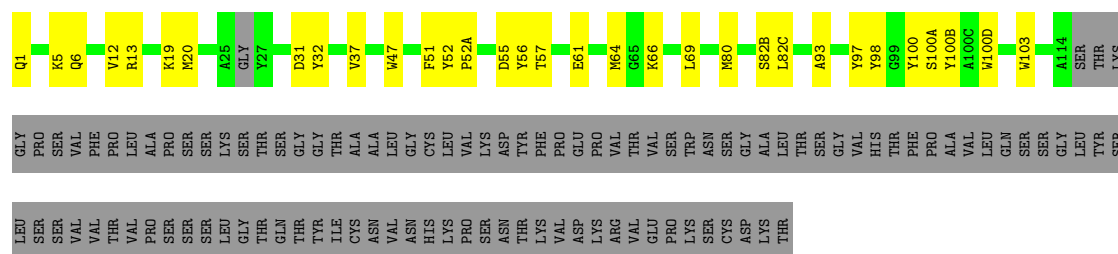
- Molecule 3: T-cell surface glycoprotein CD4

Chain F:  38% 58%



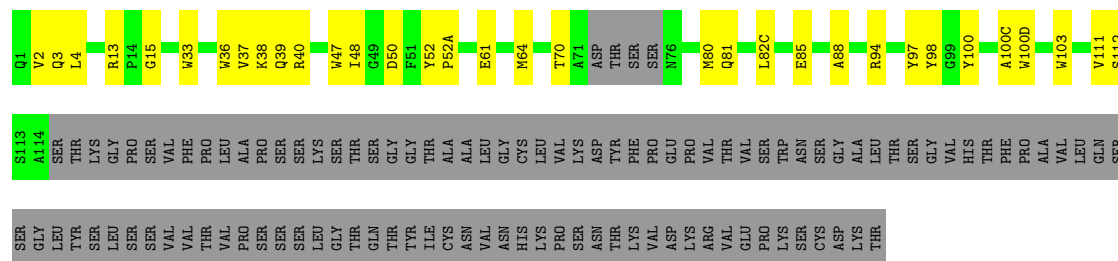
• Molecule 4: CG10 Fab heavy chain

Chain H:  39% 14% 46%



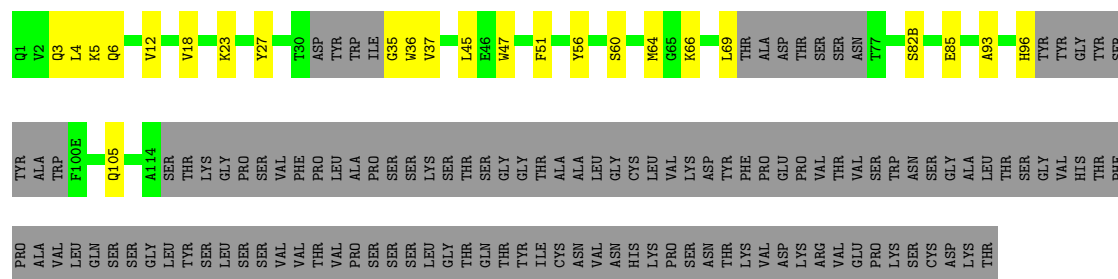
• Molecule 4: CG10 Fab heavy chain

Chain I:  38% 14% 48%

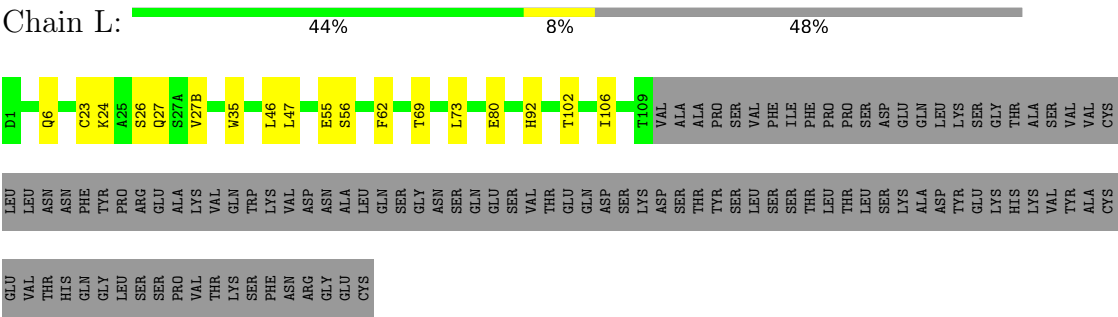


• Molecule 4: CG10 Fab heavy chain

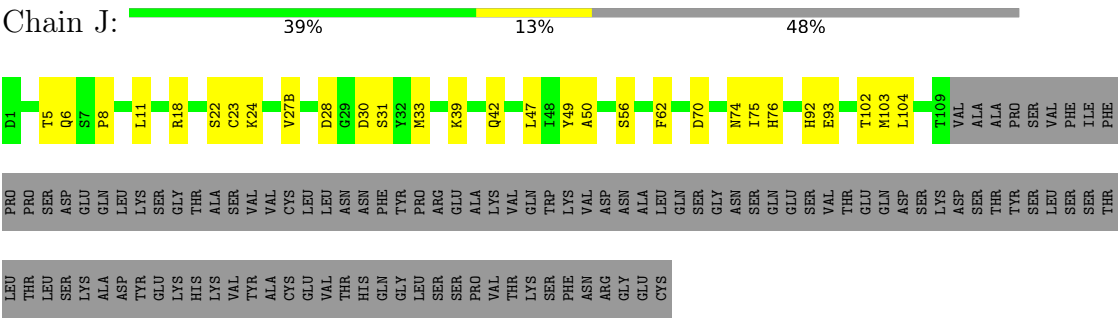
Chain P:  35% 11% 54%



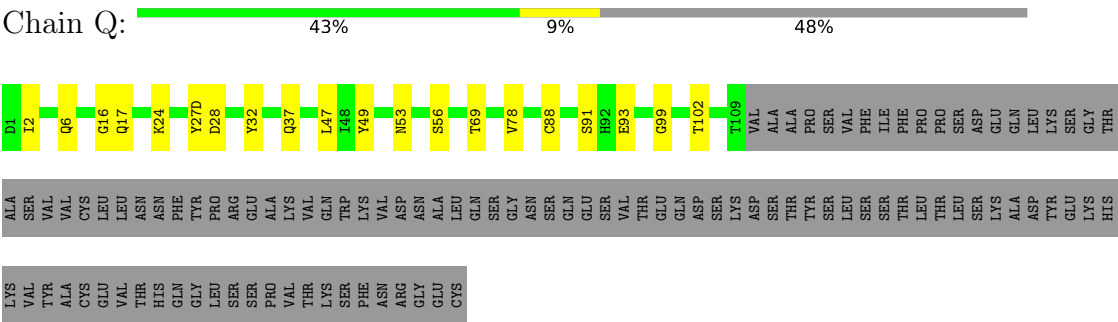
• Molecule 5: CG10 Fab light chain



● Molecule 5: CG10 Fab light chain



● Molecule 5: CG10 Fab light chain



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	134746	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	1800	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	X	0.08	0/1061	0.22	0/1437
1	Y	0.08	0/1061	0.20	0/1437
1	Z	0.10	0/1061	0.26	0/1437
2	A	0.10	0/3015	0.29	0/4100
2	B	0.09	0/3015	0.26	0/4100
2	C	0.10	0/3015	0.29	0/4100
3	D	0.08	0/1389	0.27	0/1873
3	E	0.09	0/1389	0.24	0/1873
3	F	0.07	0/1389	0.25	0/1873
4	H	0.12	0/988	0.37	0/1344
4	I	0.15	0/971	0.37	0/1319
4	P	0.10	0/821	0.24	0/1107
5	J	0.14	0/880	0.32	0/1197
5	L	0.11	0/880	0.29	0/1197
5	Q	0.11	0/880	0.25	0/1197
All	All	0.10	0/21815	0.28	0/29591

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	X	1042	0	1026	81	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	Y	1042	0	1026	61	0
1	Z	1042	0	1025	89	0
2	A	2952	0	2895	202	0
2	B	2952	0	2895	179	0
2	C	2952	0	2894	307	0
3	D	1370	0	1398	170	0
3	E	1370	0	1398	103	0
3	F	1370	0	1398	178	0
4	H	958	832	882	31	0
4	I	941	825	875	25	0
4	P	802	721	762	21	0
5	J	859	787	812	26	0
5	L	859	787	812	12	0
5	Q	859	787	812	22	0
All	All	21370	4739	20910	1369	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 1369 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:C:131:CYS:HG	2:C:193:LEU:N	1.44	1.12
3:E:140:GLY:HA3	3:E:144:LEU:HD21	1.30	1.10
2:A:260:LEU:HD12	2:A:451:GLY:HA3	1.38	1.05
3:E:130:CYS:HA	3:E:159:CYS:HA	1.40	1.04
3:D:129:GLN:HG2	3:D:139:GLN:HE22	1.23	1.03

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	X	125/153 (82%)	120 (96%)	5 (4%)	0	100	100
1	Y	125/153 (82%)	120 (96%)	5 (4%)	0	100	100
1	Z	125/153 (82%)	119 (95%)	6 (5%)	0	100	100
2	A	369/516 (72%)	344 (93%)	25 (7%)	0	100	100
2	B	369/516 (72%)	340 (92%)	29 (8%)	0	100	100
2	C	369/516 (72%)	340 (92%)	29 (8%)	0	100	100
3	D	174/183 (95%)	162 (93%)	12 (7%)	0	100	100
3	E	174/183 (95%)	157 (90%)	17 (10%)	0	100	100
3	F	174/183 (95%)	165 (95%)	9 (5%)	0	100	100
4	H	118/228 (52%)	107 (91%)	11 (9%)	0	100	100
4	I	115/228 (50%)	102 (89%)	13 (11%)	0	100	100
4	P	96/228 (42%)	93 (97%)	3 (3%)	0	100	100
5	J	111/218 (51%)	101 (91%)	10 (9%)	0	100	100
5	L	111/218 (51%)	102 (92%)	9 (8%)	0	100	100
5	Q	111/218 (51%)	107 (96%)	4 (4%)	0	100	100
All	All	2666/3894 (68%)	2479 (93%)	187 (7%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all 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	X	113/130 (87%)	113 (100%)	0	100	100
1	Y	113/130 (87%)	113 (100%)	0	100	100
1	Z	113/130 (87%)	113 (100%)	0	100	100
2	A	332/453 (73%)	332 (100%)	0	100	100
2	B	332/453 (73%)	332 (100%)	0	100	100
2	C	332/453 (73%)	332 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	D	160/165 (97%)	160 (100%)	0	100	100
3	E	160/165 (97%)	160 (100%)	0	100	100
3	F	160/165 (97%)	160 (100%)	0	100	100
4	H	98/191 (51%)	98 (100%)	0	100	100
4	I	95/191 (50%)	95 (100%)	0	100	100
4	P	83/191 (44%)	83 (100%)	0	100	100
5	J	93/187 (50%)	93 (100%)	0	100	100
5	L	93/187 (50%)	93 (100%)	0	100	100
5	Q	93/187 (50%)	93 (100%)	0	100	100
All	All	2370/3378 (70%)	2370 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 26 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	374	HIS
2	C	262	ASN
4	I	96	HIS
2	C	67	ASN
2	C	374	HIS

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Map visualisation

This section contains visualisations of the EMDB entry EMD-27208. These allow visual inspection of the internal detail of the map and identification of artifacts.

Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

This section was not generated.

6.2 Central slices

This section was not generated.

6.3 Largest variance slices

This section was not generated.

6.4 Orthogonal standard-deviation projections (False-color)

This section was not generated.

6.5 Orthogonal surface views

This section was not generated.

6.6 Mask visualisation

This section was not generated. No masks/segmentation were deposited.

7 Map analysis ⓘ

This section contains the results of statistical analysis of the map.

7.1 Map-value distribution ⓘ

This section was not generated.

7.2 Volume estimate versus contour level ⓘ

This section was not generated.

7.3 Rotationally averaged power spectrum ⓘ

This section was not generated. The rotationally averaged power spectrum had issues being displayed.

8 Fourier-Shell correlation ⓘ

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit ⓘ

This section was not generated.